

**YIELD LINKAGE DRAG IN QUALITY PROTEIN MAIZE INBRED LINES AND
HYBRIDS**

By

ISAAC KODZO AMEGBOR

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Promoter: Prof. Maryke T. Labuschagne

Co-promoters: Dr. Angeline van Biljon

Dr. Nemera Shargie

Dr. Amsal T. Tarekegne

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SUMMARY

The development of high yielding and stable quality protein maize (QPM) hybrids is important for increasing grain yield output per unit area, to support the fight against hunger and malnutrition in sub-Saharan Africa (SSA), as well as for feed supplement formulation for the animal and poultry industries. Despite the development of QPM genotypes with increased lysine and tryptophan content, important information is lacking on the yield potential of QPM genotypes compared to non-QPM (normal) genotypes. The main objective of this study was to quantify grain yield reduction (if any) due to the QPM trait. The specific objectives were to: (i) compare QPM and non-QPM inbred lines for yield and yield related traits, as well as quality traits, and determine stability for grain yield, (ii) compare QPM and non-QPM hybrids for yield and yield stability, (iii) estimate the combining ability for grain yield and quality traits of QPM and non-QPM inbred lines (iv) estimate the heritability, variance components, principal components, correlation coefficients, and do path analysis of grain yield, and agronomic and quality traits. In this study, 130 single cross hybrids were developed from 33 QPM and non-QPM inbred lines and four testers (two QPM and two non-QPM). Five hybrid checks (two QPM and three non-QPM, all single cross hybrids) were included, obtained from the International Maize and Wheat Improvement Center, Zimbabwe. The 135 hybrids together with the 40 inbred lines were evaluated in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons. The inbred lines were evaluated at seven locations using a 5 x 16 alpha lattice design, while the hybrids were evaluated at 13 locations using a 5 x 27 alpha lattice design with two replications. In the field experiments, two plants per plot were self-pollinated for the determination of zein, tryptophan, amylose and starch, protein, oil, moisture and fibre contents. In the inbred line trials, the top six performing lines out-yielded the best yielding check by 15%. Although the top two inbred lines were non-QPM, three of the six top yielding inbred lines were QPM. The QPM inbred line average yield was 0.29 ton ha⁻¹ higher than for non-QPM inbreds. Inbred lines 39, 27 and 10 had protein content above 9%, while lines 2, 5 and 16 had tryptophan concentrations above 0.09%. The best performing hybrids were a QPM cross of line 11 x CZL15049 (entry 41) followed by a non-QPM hybrid involving line 28 x CZL15049 (entry 108). The best QPM hybrid outperformed the best non-QPM hybrid by 8.81%. In addition, the best QPM hybrid, genotype 41, outperformed the best non-QPM check (Pioneer) and best QPM check (CBI) by 50.45 and 52.24%, respectively. Despite this, QPM hybrids yielded 13.90% lower than

non-QPM genotypes on average. The additive main effects and multiplicative interaction (AMMI) and genotype main effect plus genotype by environment interaction (GGE) biplots identified genotypes 108 and 12 as the most stable and high yielding hybrids. QPM hybrid 41 and non-QPM hybrids 108 and 12 were the highest yielding genotypes. Both additive and non-additive genetic effects were important in the expression of measured traits, with non-additive gene action controlling the inheritance of grain yield. Inbred lines 11, 14 and 28 and non-QPM tester CML444 showed desirable general combining ability effects for grain yield. Based on the specific combining ability values, crosses 41, 85, 99, 105, 105 and 121 were identified as the best hybrids across the 13 locations for grain yield. Hybrids 45, 69 and 6 had a high quality index, while hybrids 45 and 57 had high tryptophan content. Hybrids 51 and 37 had high values for starch and oil contents, respectively. Additive genetic effects were predominant in the control of the quality traits. Broad sense heritability estimates were higher than 80% for the traits measured. Most of the hybrids displayed heterosis for grain yield, with some having very high values. In conclusion, QPM inbred lines yielded higher than non-QPM lines, but QPM hybrids yielded 13.9% less than non-QPM hybrids. So it would seem that there is yield drag associated with increased protein quality in hybrids in this specific set of material. There were, however, specific QPM hybrids that had excellent and stable yield, which can be considered for commercial release.

Keywords: combining ability, grain yield, heterosis, maize, tryptophan, protein

DECLARATION

I, Isaac Kodzo Amegbor declare that the thesis hereby submitted for Doctoral Degree in Plant Breeding in the Department of Plant Sciences (Plant Breeding), Faculty of Natural and Agricultural Sciences, University of the Free State, Bloemfontein, South Africa is my personal, original and independent work which has not previously been submitted by me at any other University, Faculty or Institution of higher education. I declare that, the source of genetic materials, reference materials and financial sources leading to the acquisition of this qualification have been duly acknowledged. I furthermore cede copyright of this dissertation in favour of the University of the Free State and all content of this write-up can only be published after the approval of my Promoter in any journal of media.

DEDICATION

This piece of work is dedicated to my lovely wife Philipine Aseye Amegbor and all well wishers

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After years of intensive research and reading, I am glad that this thesis is finally completed through hard work, dedication and the contribution of many people. I see this aspect as one of the most difficult and challenging aspect of thesis writing due to the possibility of unintended omissions that might made by not capturing all the people who have in one way or the other assisted in the successful completion of this work.

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LIST OF ABBREVIATIONS

AMMI	Additive Main Effects and Multiplicative Interaction
ANOVA	Analysis of variance
ASI	Anthesis-silking interval
BPH	Better-parent heterosis
BLUPs	Best linear unbiased predictors
CIMMYT	International Maize and Wheat Improvement Center
CV	Coefficient of variation
DA	Days to 50% anthesis
DF	Degree of freedom
DS	Days to silking
EA	Ear aspect
EH	Ear height
EPP	Ears per plant
ER	Ear rot
GCA	General combining ability
GDP	Gross domestic product
GEI	Genotype x environment interaction
GGE	Genotype main effect plus genotype by environment interaction
GY	Grain yield
G x E	Genotype by environment
H ²	Broad sense heritability
h ²	Narrow sense heritability
HC	Husk cover
HSGCA	Specific and general combining ability of heterotic groups
IITA	International Institute of Tropical Agriculture
MET	Multi-environment trials
Moist	Moisture
MPH	Mid-parent heterosis
NARES	National Agricultural Research and Extension Systems
NaOH	Sodium hydroxide
NIR	Near-infrared transmission spectroscopy
PCA	Principal component analysis

PH	Plant height
Prot	Protein
QI	Quality index
QPM	Quality protein maize
r_G	Genetic correlation coefficient
RL	Root lodging
r_P	Phenotypic correlation coefficient
RP-HPLC	Reverse phase high-performance liquid chromatography
Rpm	Revolution per minute
RV	Relative value
SAS	Statistical analysis software
SCA	Specific combining ability
SE	Standard error
SL	Stalk lodging
SSA	Sub-Saharan Africa
TFA	Trifluoroacetic acid
Trypt	Tryptophan
UNICEF	United Nations Children's Fund
USDA	United States Department of Agriculture

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CHAPTER ONE

INTRODUCTION

Maize (*Zea mays* L.) is ranked among the top three cultivated crops in the world. It is the most widely cultivated cereal crop in the world and serves as a primary food source for nearly a billion people, predominantly in the developing world (Babu and Prasanna 2014; Bekele and Rao 2014). Based on the demand for the crop and stress factors affecting its production, it has been estimated that maize yields need to increase by 60% by 2050 to address increasing population demand (Ray et al. 2013; Epule et al. 2017). In 2019, global maize production was 1 123.65 million ton, however, the United States Department of Agriculture (USDA) projected that there would be a decrease in the 2020 global maize production by 0.95%, which will amount to about 10.63 million ton (USDA 2020). The top world maize producer is the United States with 361 million metric ton in 2017 and 347.80 million metric ton in 2019, while South Africa is the leading producer in Africa with 14.90 million ton in 2015 and 16 million ton in 2019 (Outreach 2017; USDA 2020).

Even though normal maize contains about 10% protein, it has major nutritional constraints as human food. This is because the endosperm is deficient in two essential amino acids, namely lysine and tryptophan (Babu and Prasanna 2014; Njeri et al. 2017; Liu et al. 2019). Malnutrition as a result of nutrient deficiency affects nearly half of the world's population, particularly in the developing countries, due to over-reliance on major staple crops such as maize, rice and cassava with little or no available micronutrients (UNICEF 2003; De Groote et al. 2014). Nutrient deficiency results from prolonged lack of nutrients in the diet and malnutrition occurs when the body does not obtain the necessary nutrients to perform its functions (UNICEF 2003). Consequently, infants constantly fed on normal maize with little or without any balanced protein supplements from animal sources, suffer from malnutrition and develop diseases such as kwashiorkor (Badu-Apraku and Lum 2010; Manjeru et al. 2019). Residual effects of malnutrition could also result in night blindness in adults, a higher risk of child and maternal mortality as well as susceptibility to several infectious diseases (Badejo 2018; Manjeru et al. 2019; Prasanna et al. 2020).

Plant based products are a vital source of nutrients and minerals for millions of people in tropical Africa and other developing areas of the world (Tawanda et al. 2011). To address

problems posed by malnutrition, efforts were made to develop maize cultivars with enhanced levels of these essential amino acids, which was started in 1963 by Mertz et al. (1964). These scientists identified a mutant gene *opaque-2* (*o2*) in maize that lead to the same amount of protein as normal maize but with elevated levels of the essential amino acids lysine and tryptophan, which improves the protein quality. Over the past three decades, researchers from the International Maize and Wheat Improvement Center (CIMMYT) and other international and national agricultural institutes/stations continued the work of Mertz and others, which focused on enhancing the nutritional composition of normal maize (Manjeru et al. 2019; Setimela et al. 2017; Kaur et al. 2019). Their efforts led to the development of improved products from the soft *o2* maize with good agronomic traits as well as high lysine and tryptophan contents, and this was termed quality protein maize (QPM) (Vasal et al. 1993; CIMMYT 2000; Vivek et al. 2008; Eshetie 2017; O’Kennedy and Fox 2017; Mansilla et al. 2019). QPM may supply about 70 to 73% of human protein requirements compared to 46% from normal maize and constitute biological value of 80% protein compared to 40 to 57% for normal maize and 86% for eggs. In addition, QPM has been reported to have 90% relative value (RV) of milk compared to 40% RV for normal maize (Bressani 1992; Masindeni 2013; Eshetie 2017; Mebratu et al. 2019).

Consumption of higher carbohydrate food products among poorer sections of the population in the under-developed and developing countries leads to other health related diseases such diabetes, obesity, heart diseases as well as other metabolic syndromes. This has intensified research to breed new crop varieties with enhanced amino acid content, which can be consumed through maize-based food ingredients (Ai and Jane 2016). Because of the multi-purpose use of maize for humans and animals, it serves as an important source of micronutrients (Sinha et al. 2011). Maize kernels consist of 61 to 78% starch, 6 to 12% protein, and 3 to 6% fat (Sinha et al. 2011; Ai and Jane 2016; Singh et al. 2019). Protein exists largely in the form of zein proteins (β , γ and α), and kernels also contain fibre and unsaturated oil (Sabagh et al. 2017; Salleh et al. 2019; Singh et al. 2019).

Because of the high yield potential of hybrids, they are used in the developed countries for increased maize production even though open pollinated varieties are still being cultivated in the developing countries. For hybrids to be developed, it is crucial to know the combining ability of inbred lines that are used as parents for hybrid production in breeding

programmes. Maize production can be enhanced by gathering useful information on the heterotic pattern and genetic variability of the inbred lines, which is important in breeding programmes. Combining ability studies provide information on the genetic mechanisms controlling the inheritance of quantitative traits and enable breeders to select suitable parents for further improvement or use in hybrid breeding for commercial purposes (Ali et al. 2012; Njeri et al. 2017; Kanwar and Nag 2019; Mansilla et al. 2019). Combining ability enhances crossbreeding by facilitating the preliminary selection of inbred lines, which perform well in crosses. Eventually, an entire population of high performing hybrids can be generated (Nduwumuremyi et al. 2013). The general combining ability (GCA) and specific combining ability (SCA) of inbred lines are important aspects to consider when selecting materials for hybrid development and population improvement in maize breeding. While GCA measure average contribution a parental line to hybrid performance in a series of hybrid combinations in comparison to other parental lines in the same series of hybrid combinations and this is due to additive gene action. On the other hand, SCA is the contribution of an inbred to hybrid performance in a cross with a specific other inbred in relation to its contributions in crosses with an array of other parental lines (Haydar and Paul 2014). Therefore, combining ability is used extensively in the breeding of several economic crop species (Mengesha 2013; Mebratu et al. 2019).

In spite of the nutritional benefits of QPM genotypes, one of the drawbacks reported for QPM is reduced grain yield compared to non-QPM (normal) genotypes (Derera et al. 2014; Tandzi et al. 2017; Oloyede-Kamiyo and Adetumbi 2017). Contrary to this, Mebratu et al. (2019) reported relatively increased yield in QPM genotypes. To the farmer, the most important aspect of cultivated crops, most especially maize hybrids, is grain yield. Several researchers reported on the superiority of non-QPM to QPM varieties in terms of grain yield (Pixley 2003; Bhatnagar et al. 2004; Krivanek et al. 2007). Another major drawback is that the gene(s) responsible for QPM are recessive. Nuss et al. (2011) noted that, the *o2* gene responsible for suppressing the synthesis of maize amino acids such as zein, tryptophan and lysine thereby simultaneously increases the synthesis non-zein proteins that are richer sources of tryptophan and lysine. Since endosperm modification is a quantitatively inherited trait and has complex genetic control and lacks reliable molecular markers linked to the endosperm modifier loci, a light table is presently used to physically select for endosperm hardness (Hossain et al. 2008). This means that QPM maize must be

segregated from normal maize in the farmers' field or the normal pollen will pollinate some of the QPM plants and hide the expression of the trait.

There are several studies on biochemical analyses on QPM to determine the lysine and tryptophan content of the grains (Mbuya et al. 2011; Wegary et al. 2011). Wessel-Beaver et al. (1985) and Tandzi et al. (2017) observed that it is difficult to combine high grain yield with high-quality protein content in elite maize varieties because these two characteristics are often negatively correlated, hence, improving yield may adversely affect protein quality and vice versa. Because either the grain yield is directly involved in the process of seed modification or the modifier gene(s) could be tightly linked to those responsible for protein synthesis (Prasanna et al. 2001). Therefore, if maize genotypes are nutritionally enhanced but are low yielding, it would not be economically viable to the farmer, and this may lead to rejection even after release.

The present study was done to assess possible yield reduction or “linkage drag” due to increased protein quality in selected QPM inbred lines and hybrids, with the aim of generating information on possible yield linkage drag, and to determine combining ability effects, heritability and yield stability of crosses between QPM lines and QPM and non-QPM lines. The nature of trait associations between grain yield, quality traits as well as its associated characters, was determined in order to select superior genotypes from the genetic material studied. Therefore, this study explored QPM and non-QPM lines recently developed by CYMMIT to substantiate if indeed there is a yield reduction of QPM compared to non-QPM genotypes.

The specific aims of this study were to:

- To compare QPM and non-QPM inbred lines for yield and quality traits
- To compare hybrids from these QPM and non-QPM inbred lines for yield and quality traits
- To estimate the combining ability for yield and yield related traits as well as quality traits of QPM and non-QPM inbred lines
- Estimate the heritability, variance components, principal components, path analysis and correlation coefficients of grain yield and quality traits of the hybrids

References

- Ai Y and Jane JL (2016) Macronutrients in corn and human nutrition. *Comprehensive Reviews in Food Science and Food Safety* 15: 581-598.
- Ali F, Irfan AS, Rahman H, Mohammad N, Durrishahwar, Muhammad YK, Ihteram U and Jianbing Y (2012) Heterosis for yield and agronomic attributes in diverse maize germplasm. *Australian Journal of Crop Science* 6: 455-462.
- Babu R and Prasanna BM (2014) Molecular breeding for quality protein maize (QPM). In: Tuberosa R, Graner A and Frison E (eds), *Genomics of Plant Genetic Resources*. Springer, pp. 490-505.
- Badejo AA (2018) Elevated carotenoids in staple crops: The biosynthesis, challenges and measures for target delivery. *Journal of Genetic Engineering and Biotechnology* 16: 553-562.
- Badu-Apraku B and Lum AF (2010) The pattern of grain yield response of normal and quality protein maize cultivars in stressed and non-stressed environments. *Agronomy Journal* 102: 381-394.
- Bekele A and Rao TN (2014) Estimates of heritability, genetic advance and correlation study for yield and it's attributes in maize (*Zea mays* L.). *Journal of Plant Sciences* 2: 1-4.
- Bhatnagar S, Betran FJ and Rooney LW (2004) Combining abilities of quality protein maize inbreds. *Crop Science* 44: 1997-2005.
- Bressani R (1992) Nutritional value of high-lysine maize in humans. In ET Mertz (ed.), *Quality Protein Maize*. American Association of Cereal Chemists. St. Paul, MN, pp. 205-225.
- CIMMYT (2000) CIMMYT in 1999-2000. Science and Sustenance. Mexico, D.F.: CIMMYT.
- De Groote H, Chege CK, Tomlins K and Gunaratna NS (2014) Combining experimental auctions with a modified home-use test to assess rural consumers' acceptance of quality protein maize, a biofortified crop. *Food Quality and Preference Journal* 38: 1-13.
- Derera J, Pixley KV, Giga DP and Makanda I (2014) Resistance of maize to the maize weevil:III. Grain weight loss assessment and implications for breeding. *Journal of Stored Products Research* 59: 25-35.
- Epule TE, Ford JD and Lwasa S (2017) Projections of maize yield vulnerability to droughts and adaptation options in Uganda. *Land Use Policy* 65: 154-163.

- Eshetie T (2017) Review of quality protein maize as food and feed: In alleviating protein deficiency in developing countries. *American Journal of Food and Nutrition* 5: 99-105.
- Haydar FMA and Paul NK (2014) Combininbg ability analysis for different yield trails in maize. *Bangladesh Journal of Plant Breeding and Genetics* 27: 1-5.
- Hossain F, Prassana BM, Kumar R and Singh BB (2008) Genetic analysis of kernel modification in Quality Protein Maize genotypes. *Indian Journal of Genetics* 68: 1-9.
- Kanwar SS and Nag YK (2019) To study correlation and path analysis in rice breeding lines. *International Journal of Current Microbiology and Applied Sciences* 8: 2481-2487.
- Kaur N, Singh B and Sharma S (2019) Comparison of quality protein maize (QPM) and normal maize with respect to properties of instant porridge. *LWT - Food Science and Technology* 99: 291-298.
- Krivanek AF, De Groote H, Gunaratna NS, Diallo A and Friesen D (2007) Breeding and disseminating quality protein maize (QPM) for Africa. *African Journal of Biotechnology* 6: 312-324.
- Liu Z, Cao X, Ren S, Wang J and Zhang H (2019) Physicochemical characterization of a zein prepared using a novel aqueous extraction technology and tensile properties of the zein film. *Industrial Crops and Products* 130: 57-62.
- Manjeru P, van Biljon A and Labuschagne M (2019) The development and release of maize fortified with provitamin A carotenoids in developing countries. *Critical Reviews in Food Science and Nutrition* 59: 1284-1293.
- Mansilla PS, Nazar MC and Pérez GT (2019) Evaluation and comparison of protein composition and quality in half-sib families of *opaque-2* maize (*Zea mays* L.) from Argentina. *Agriscientia* 36: 39-53.
- Masindeni DR (2013) Evaluation of South African high quality protein maize (*Zea mays* L.) inbred lines under optimum and low nitrogen conditions and the identification of suitable donor parents. PhD thesis in Plant Breeding, University of the Free State, Soth Africa.
- Mbuya K, Nkongolo KK and Kalonji-Mbuyi A (2011) Nutritional analysis of quality protein maize varieties selected for agronomic characteristics in a breeding program. *International Journal of Plant Breeding and Genetics* 5: 317-327.

- Mebratu A, Wegary D, Mohammed W, Teklewold A and Tarekegne A (2019) Genotype × environment interaction of quality protein maize hybrids under contrasting management conditions in Eastern and Southern Africa. *Crop Science* 59: 1576-1589.
- Mengesha WA (2013) Genetic diversity, stability, and combining ability of maize genotypes for grain yield and resistance to NCLB in the mid-altitude sub-humid agro-ecologies of Ethiopia. MSc thesis in Plant Breeding, University of the Free State, South Africa.
- Mertz ET, Bates ET and Nelson OE (1964) Mutant genes that change protein composition and increase lysine content of maize endosperm. *Science* 145: 279-280.
- Nduwumuremyi A, Pangirayi T and Slyvestre H (2013) Mating designs: Helpful tool for quantitative plant breeding analysis. *Journal of Plant Breeding and Genetics* 1: 117-129.
- Njeri SG, Makumbi D, Warburton ML, Diallo A, Jumbo MB and Chemining'wa G (2017) Genetic analysis of tropical quality protein maize (*Zea mays* L.) germplasm. *Euphytica* 213: 1-19.
- Nuss ET and Tanumihardjo S (2011) Quality Protein Maize for Africa: Closing the protein inadequacy gap in vulnerable populations. American Society for Nutrition. *Advances in Nutrition* 2: 217-214.
- O'Kennedy KO and Fox G (2017) Zein characterisation of South African maize hybrids and their respective parental lines using MALDI-TOF MS. *Food Analytical Methods* 10: 1661-1668.
- Oloyede-Kamiyo QO and Adetumbi JA (2017) Relationship between seed physical traits and maize weevil (*Sitophilus zeamais*) damage parameters in selected quality protein maize (QPM) varieties. *Journal of Stored Products Research* 73: 42-46.
- Outreach IPB (2017) Maize in Africa. International Plant Biotechnology Outreach. http://ipbo.vib-ugent.be/wp-content/uploads/2015/02/vib_fact_MaizeForAfrica_EN_2017_LR.pdf
- Pixley KV (2003) The development and promotion of quality protein maize in Sub-Saharan Africa; Progress Report; CIMMYT: Harare, Zimbabwe.
- Prasanna BM, Vasal SK, Kassahun B and Singh NN (2001) Quality Protein Maize. *Current Science* 81: 1308-1319.
- Prasanna BM, Palacios-Rojas N, Hossain F, Muthusamy V, Menkir A, Dhliwayo T, Ndhlela T, Vicente FS, Nair SK, Vivek BS, Zhang X, Olsen M and Fan X (2020) Molecular breeding for nutritionally enriched maize : Status and prospects. *Frontiers in Genetics* 10: 1-16.

- Ray DK, Mueller ND, West PC and Foley JA (2013) Yield trends are insufficient to double global crop production by 2050. PLoS ONE 8: 1-8. e66428. doi:10.1371/journal.pone.0066428
- Sabagh AEl, Hossain A, Barutçular C, Anjorin FB, Islam MS, Ratnasekera D, Kizilgeçi F, Yadav GS, Yıldırım M and Saneoka H (2017) A review on various factors which affecting sustainable maize (*Zea mays* L.) production under drought stress. Journal of Experimental Biology and Agricultural Sciences 5: 1-9.
- Salleh SN, Fairus AAH, Mohd Nizam Zahary MN, Raj NB and Jalil AMM (2019) Unravelling the effects of soluble dietary fibre supplementation on energy intake and perceived satiety in healthy adults: evidence from systematic review and meta-analysis of randomised-controlled trials. Foods 8: 1-22. doi:10.3390/foods8010015
- Setimela PS, Gasura E and Tarekegne AT (2017) Evaluation of grain yield and related agronomic traits of quality protein maize hybrids in Southern Africa. Euphytica 213:1-14.
- Singh N, Singh S and Shevkani K (2019) Maize: Composition, bioactive constituents, and unleavened bread. In: Preedy VR and Watson RR (eds), Flour and Breads and Their Fortification in Health and Disease Prevention. Second edition. Academic Press, pp. 111-121. doi:10.1016/b978-0-12-814639-2.00009-5
- Sinha AK, Kumar V, Makkar HPS, De Boeck G and Becker K (2011) Non-starch polysaccharides and their role in fish nutrition - A review. Food Chemistry 127: 1409-1426.
- Tandzi LN, Mutengwa CS, Ngonkew ELM, Woïn N and Gracen V (2017) Breeding for quality protein maize (QPM) varieties: A review. Agronomy 80: 1-16.
- Tawanda M, Tendekayi HG, Andrew HS, Michael AG, Robert MR and Guangwen T (2011) Yellow maize with high β -carotene is an effective source of vitamin A in healthy Zimbabwean men. American Journal of Clinical Nutrition 94: 510-519.
- UNICEF (2003). http://www.unicef.org/nutrition/index_iodine.html UNICEF
- USDA (2020) United States Department of Agriculture. [http://www. Worldagricultural production.com/crops/corn.aspx](http://www.Worl dagricultural production.com/crops/corn.aspx).
- Vasal SK, Srinivasan G, Pandey S, Gonzalez FC, Crossa J and Beck DL (1993) Heterosis and combining ability of CIMMYT's quality protein maize germplasm: I. Lowland tropical. Crop Science 33: 46-51.

- Vivek BS, Krivanek AF, Palacios-Rojas N, Twumasi-Afriyie S and Diallo AO (2008) Breeding quality protein maize (QPM): Protocols for developing QPM cultivars. CIMMYT, Mexico, D.F.
- Wegary D, Labuschagne MT and Vivek BS (2011) Protein quality and endosperm modification of quality protein maize (*Zea mays* L.) under two contrasting soil nitrogen environments. Field Crops Research 121: 408-415.
- Wessel-Beaver L, Lambert RJ and Dudley JW (1985) Genetic variability and correlations in a modified endosperm texture *opaque-2* maize population. Crop Science 25: 129-132.

CHAPTER TWO

LITERATURE REVIEW

2.1 Maize: economic importance and production

Maize (*Zea mays* L. 2x = 20) is ranked as the third most important cereal crop after wheat and rice, in the world. Maize is the most globally cultivated cereal across diverse agro-ecologies and geographical locations ranging from low to high altitudes. Over the past few decades, the crop has gained wider acceptability among rural farmers in Africa and has replaced other traditionally cultivated cereals such as pearl millet (*Pennisetum glaucum*) and sorghum (*Sorghum bicolor*) in many of the African countries.

The importance of maize for uses such as food for humans, feed for animals and as an industrial crop, is incomparable to any other food crop cultivated in sub-Saharan Africa (SSA). Civilization revolves more around maize than any other crop (Amudalat 2015). In Africa, maize is grown primarily for its carbohydrate-rich kernel, serving as staple food for more than 300 million people, both in the rural and urban areas (Bänziger and Diallo 2001). Maize is cultivated as food and feed crop in SSA, where it provides energy and protein for both humans and livestock (Ngaboyisonga 2008) and accounts for about 70% of the total caloric intake for people living in SSA and other developing countries (Martin et al. 2000; Edmonds et al. 2009).

Furthermore, maize serves as source of revenue through export within the African continent (Asea 2005). In South Africa and most of the countries in SSA, maize is grown mainly as food and feed crop. In 2014 for example, maize was the most-produced cereal crop worldwide with more than 1 022 million ton from 170 countries with a cultivated area of approximately 181 million hectare (Outreach 2017). In 2019, global maize production was 1 123.65 million ton however, the USDA projected that there would be a decrease in 2020 global maize production by 0.95% which will amount to about 10.63 million ton (USDA 2020). The top world maize producer is the United States of America with 361 metric ton in 2017 and 406.3 metric ton in 2019 while South Africa is the leading producer in Africa with 14.9 million ton in 2015 and 16 million ton in 2019 (Outreach 2017; USDA 2020). The maize crop is widely adapted to diverse agro-ecologies and has an estimated average grain yield of 4.8 t ha⁻¹ in South Africa and 1.8 t ha⁻¹ in Nigeria (Amudalat 2015;

Outreach 2017). Because of increasing population and higher demand for the crop by millions of households in West Africa, Eastern and Southern Africa, it is expected that the production area will double by 2050 to meet the increasing demand (Ray et al. 2013). Hence, increased maize production and productivity will play a crucial role in ensuring food security in SSA, where maize is grown largely by smallholder, resource-poor farmers, who rely mainly on rainfall (SARI 1996).

2.2 Importance and nutritional quality of QPM and non-QPM in SSA

Undernourishment is a chronic problem worldwide, especially in rural communities of SSA, where people rely chiefly on staple foods which are carbohydrate sources and have restricted access to a varied diet. Breeding for biofortified crops with enriched nutritional quality can help improve nutritional deficiencies in SSA and other developing regions. This could be achieved if nutritionally enhanced crops are accepted, produced and are made available in large quantities for consumption by both humans and animals (De Groote et al. 2014).

Non-QPM, which is generally cultivated, provides little or no nutritional benefits as food and feed for humans and other monogastric animals. Maize provides micronutrients like vitamin B complex, β -carotene and essential minerals, i.e. magnesium, zinc, phosphorus, copper, etc. However the endosperm of non-QPM is deficient in two essential proteins, lysine and tryptophan, even though the endosperm contains about 10% protein and about 73% starch and 4% oil (Annor and Badu-Apraku 2016). The deficiency of these essential amino acids can negatively affect human and animal growth (Prasanna et al. 2001). As a result, infants who are constantly fed with normal endosperm maize with little or no protein supplements from animal products suffer from malnutrition, and this often leads to the development of pellagra and other health related diseases (Babu and Prasanna 2014). The development, adoption and cultivation of QPM with higher concentrations of tryptophan and lysine contents can significantly reduce malnutrition and its related diseases, as well as death, in low-income countries in the developing world (Mbuya et al. 2011).

Lysine and tryptophan have to be supplied through the diet for adequate availability for synthesis of proteins. Therefore, lysine and tryptophan are often considered as the most essential amino acids for the body, while the remaining amino acids are considered non-

essential, since they can be synthesized through metabolism (Giwa and Ikujenlola 2009). QPM can supply about 70 to 80% of human protein requirements, depending on the variety, while non-QPM genotypes can only supply a maximum of 46%. The biological value of protein, which measures how effectively the body absorbs and utilises amino acids, is 80% for QPM, which is comparable to 86% found in egg, while for normal endosperm maize it is 40 to 57% (Babu and Prasanna 2014; Teklewold et al. 2015). The available protein content of QPM is 90% of the RV of milk, while RV of normal endosperm maize is 40% (Bressani 1992; Badu-Apraku and Lum 2010; Dang 2010; Badu-Apraku and Fakorede 2017; Eshetie 2017). QPM genotypes can therefore be an effective approach for health restoration in malnourished populations.

QPM genotypes were reported to exhibit consistently increased levels of tryptophan concentration, about twice the biological value of normal endosperm maize protein (Bressani 1992; Tandzi et al. 2017). For maize grain to be classified as QPM, it must have a quality index (QI) equal or above 0.8, where QI is the proportion of tryptophan to protein present in a particular sample or genotype (Wegary et al. 2011; 2014; Masindeni 2013; Twumasi-Afriye et al. 2016; Tandzi et al. 2017). Ignjatovic-Micic et al. (2013) and Tandzi et al. (2017) observed that the QI of hybrid maize resulting from hybridizing QPM and ordinary maize lines was in the range of 0.71 to 0.74, which was superior to the standard hybrids with 0.57 to 0.62, however it was less than the QPM threshold which is 0.80.

Consumption of maize products with enhanced lysine and tryptophan could help alleviate the growing challenge posed by malnutrition in several parts of the world (Menkir et al. 2008; Mpofu et al. 2012). Several authors have reported on the nutritional values of QPM over non-QPM through feeding experiments involving livestock, especially monogastric animals, as well as children (Akuamoah-Boateng 2002; Mpofu et al. 2012). Children who were fed with meals made from QPM were observed to have less sick days compared to those fed with food products from normal maize. Consequently, consumption of food products from QPM genotypes rather than normal maize resulted in 12% increase in the body mass and 9% increase in the rate of growth (height) among infants and children of school going age suffering from slight to moderate under nutrition (Gunaratna et al. 2010; Tandzi et al. 2017).

Studies have shown that within some African countries in Southern Africa, for example Lesotho, Malawi and Zambia, consumption of about 100 g of a QPM food product is essential for children of school going age to sustain the adequacy of lysine, and this accounts for about a 40% reduction in maize intake requirements relative to normal maize (Nuss and Tanumihardjo 2011; Tandzi et al. 2017). As with normal maize, QPM germplasm also has varying maturity groups, as well as varied grains both in colour and texture (Vasal 1999).

2.3 Development of QPM genotypes

Genetic enhancement for nutritional value in maize commenced in 1963 by Mertz et al. (1964) who identified mutant *opaque-2* (*o2*) maize that contains an amount of protein equal to that in normal endosperm maize (Premalatha and Kalamani 2010). However, *o2* maize contains about twice the normal levels of lysine and tryptophan, which increases the protein quality in normal maize (Badu-Apraku and Lum 2010).

In spite of this advancement, the *o2* maize produced undesirable traits such as soft, opaque kernels instead of having hard and translucent endosperm. Other undesirable traits included the chalky nature of the *o2* kernels, the plants also produced smaller ears and grain yields were 8 to 15% lower than those of normal endosperm maize genotypes (Badu-Apraku and Lum 2010; Wegary et al. 2011). Similarly, *o2* maize was found to be more vulnerable to several factors such as fungi and insects attacks and often produced lower grain weight than ordinary maize, because air spaces surround its loosely packed starch granules with a corresponding decrease in grain yield (Singh and Venkatesh 2006; Ram 2014). These conditions resulted in farmer's refusal to adopt *o2* maize.

The effort of researchers at CIMMYT made it possible to integrate the gene of *o2* maize with genetic modifiers from ordinary maize to harden the *o2* maize kernels and made the endosperm translucent with increased grain yields. The modification in the endosperm has resulted in the new type of maize designated as QPM that contains the high nutritional value of *o2* maize as well as modified kernel structure of traditional maize cultivars (Werle et al. 2014). CIMMYT has made substantial advancement in developing QPM germplasm with the *o2* gene integrated with other gene modifiers. Also, over the past two decades, the International Institute of Tropical Agriculture (IITA) together with the National Agricultural Research and Extension Systems (NARES) have intensified work on

developing and promoting the adoption of QPM genotypes with varying maturity periods with tolerance to biotic and abiotic stresses. QPM materials have been usually used to develop QPM cultivars that are now widely exploited in several countries in West, East, Southern and Central Africa (Krivanek et al. 2007).

In addition to the *o2* identified by breeders, other lysine mutant genes discovered were *o1*, *o5*, *o9-11*, *o13*, *o17*, *fl2*, *fl3*, Mucronate and Defective endosperm B30 however, these mutant genes could not be used successfully in other breeding programmes due to the significant loss in grain yield by genotypes resulting from these mutant genes (Gibbon and Larkins 2005; Sarika et al. 2018). Yang et al. (2005) indicated that, a search for improved mutant gene with increased lysine and tryptophan led to the discovery of another recessive mutant gene from Robertson's Mutator stocks, and this was named *opaque16* (*o16*) Tripathy et al. (2017). Sarika et al. (2017) reported that, *o16* gene located on chromosome 8 has more lysine and tryptophan concentrations than *o2* mutant genes and the *o16* genes does not create higher degree of opaqueness as noted for *o2*. One of the disadvantages of *o2* is the low lysine content which does not meet standards for food and fodder production (Zhang et al. 2013). To ameliorate this defects, molecular breeding approach was used to pyramid *o2* and *o16* mutant genes into a single genetic material using single-sequence repeats (SSRs) markers which led to the development of *o2o2* and *o16o16* genotypes with lysine content increased by 30 to 60% (Yang et al. 2005; Pukalenthly et al. 2020). Even though *o16* mutants were found to have high lysine, the effect of *o16* on increased accumulation of lysine was also reported by Yang et al. (2005) and Zhang et al. (2013).

2.4 Importance of heterosis, heterotic groups and patterns in breeding

The term heterosis or hybrid vigour was first used by Shull in 1908 to express the unexpected performance of the F_1 individuals obtained from crossing two genetically diverse breeding lines (Duvick and Brown 1981). Similarly, Mather and Jinks (1971) and de Franca (1983) coined heterosis as the extent to which the average of any F_1 generation performs better than its better parent, or an average of its parents.

The two main theories used to elucidate the manifestation of heterosis are: (i) the dominance theory proposed by Bruce (1910) and Keeble and Pellow (1910) who stated that, the recessive and deleterious alleles present in the parental lines are transferred to the F_1 progeny and subsequent generations. In this model, additive genetic effects of

favourable genes increase the superior phenotype of the F_1 over each parent and (ii) the overdominance theory by Shull (1911) and East and Hayes (1912) proposed the overdominance hypothesis, which states that heterosis is a result of heterozygosity or the fitness of heterozygotes over their homozygous parents. According to this model, novel alleles are interchanged between contrasting parents with differing alleles and this results in expression of superiority of the F_1 's to the homozygous parents. Shull (1948), Sprague et al. (1962), de Franca (1983), Premalatha and Kalamani (2010) and Fu et al. (2014) subsequently affirmed that dominance is the main cause of heterosis in crop breeding. Even though the importance of heterosis in maize production has been reported, the inherent mechanisms and most importantly, the physiological and biochemical mechanisms of these phenomena are yet to be fully elucidated (Blum 2013). In addition, epistasis which is the essential component of the genetic architecture of polygenic traits that occurs when the genes controlling a trait interact such that the phenotypic effect of a gene is nonlinearly dependent on the allelic state of at least one other gene in the genome plays an important role in heterosis among F_1 hybrids (Kaeppeler 2012; Kerwin et al. 2017). Even though epistasis influences heterosis, this is often not estimated statistically due to the interactive nature of genes at different loci (Kaeppeler 2012).

The expression of superiority of hybrids over their parents is based on how diverse the two parents are. Hence, two parental lines which manifest relatively large magnitudes of heterosis from their crosses can be said to be genetically unrelated compared to two parental lines that exhibit little or no heterosis in their F_1 hybrids. In maize breeding or production, it is estimated that heterosis could range from 15 to 50% to increase yield potential and improves adaptation to various stresses (Saleh et al. 2002; Lippman and Zamir 2006; Chairi et al. 2016). In a study by Saleh et al. (2002), high levels of heterosis for grain yield, grain weight per ear, cob weight were seen, while adequate values were obtained in normal endosperm maize for plant and ear heights, number of kernel rows per ear and number of kernels per ear row. Nigussie and Zelleke (2001) noted that hybridizing of maize genotypes obtained from dissimilar genetic backgrounds often resulted in better utilization of hybrid vigour.

Grouping of inbred lines into defined heterotic groups could significantly enhance breeding efficiency (Hallauer and Miranda 1988; Fan et al. 2014, 2016). There are several heterotic grouping methods and patterns available, which are being exploited by researchers to

classify maize parental lines into heterotic groups depending on the breeding objectives. In order to maximize the utilization of heterosis, parental lines are assigned into distinct groups before crosses are made in breeding programmes. Crossing of inbred lines from two different heterotic groups result in hybrids with superior genetic manifestations of the traits of interest (Tollenaar et al. 2004; Aguiar et al. 2008; Fu et al. 2014).

A heterotic group, according to Fischer et al. (2010) and Melchinger and Gumber (1998), is considered as a set of similar or dissimilar parents having the same or different genetic backgrounds which exhibit similar combining ability effects and heterotic response when hybridised with parental lines from genetically distinct germplasm groups. On the other hand, heterotic pattern could be referred to as two heterotically distinct groups, which express high heterosis and hybrid performance. Grouping of parents into well-defined heterotic groups helps to prevent the development and evaluation of hybrids or genotypes that should have been eliminated, in order to allow maximum heterosis to be fully exploited by crossing parents resulting from a different genetic base (Terron et al. 1997). A number of methods of classifying inbred lines into heterotic group are used widely across the world in several breeding programmes. The traditional method of estimating combining ability exploits the SCA approach with given information on line-pedigree of the parental lines and/or information gathered on hybrid yield through field evaluations to apportion the lines into a heterotic group (Fan et al. 2004; Musila et al. 2010; Wegary et al. 2014; Adebayo and Menkir 2015; Bari et al. 2016). The SCA method of grouping inbred parents based on grain yield into heterotic groups have been utilised by several researchers (Melani and Carena 2005; Legesse et al. 2009; Kanyamasoro et al. 2012; Woyengo et al. 2015). In spite of the importance of the SCA method of grouping, the effects of grain yield of parental lines have often been reported to be under the influence of the interaction between the parents as well as their interaction with the environment (Munaro et al. 2011). Due to environmental effects, this often results in assigning the same parental lines into different heterotic groups when used in different studies (Legesse et al. 2009; Dragicevic et al. 2016). Also, in some studies, molecular markers were used to estimate genetic resemblance or distance to assign maize parental lines into dissimilar heterotic groups (Barata and Carena 2006; Munaro et al. 2011; Reid et al. 2011). Because of the limitations and unreliability of the SCA method of grouping inbred lines, Fan et al. (2008) suggested the use of SCA and GCA of heterotic groups (HSGCA). This method combines both SCA and GCA effects as a more suitable approach for classifying parental lines into heterotic groups.

This methodology has been found to be superior to the use of the SCA method (Fan et al. 2009; Badu-Apraku et al. 2013) as well as using only genetic markers for assigning inbred lines into heterotic groups (Badu-Apraku et al. 2013). Mostly, assigning inbred lines into a heterotic group either by SCA, molecular markers or HSGCA is generally dependent on only one trait, mostly grain yield. This has several limitations, since grain yield is a polygenic character controlled by several genes influenced by other traits, which is characterised by low heritability, especially when the study is carried out under stress conditions. In spite of the above grouping methods, the best way to assign inbreds to heterotic groups is to cross the inbreds onto specific tester inbreds. Any inbred that produces superior hybrids when crossed onto a tester inbred is in the opposite heterotic group from the tester (Gracen, unpublished data). Hence, inbreds are said to belong to different groups if for example those in group A combine well with those in group B. Similarly, if inbreds in group A does not combine well with inbreds from group B, then A and B are in the same (or closely related) heterotic group(s) (Gracen, unpublished data). Also, newly developed inbreds that exhibit greater heterosis with a specific tester are said to be complementary in heterotic pattern to the tester and can be classed as being anti to that tester (Gracen, unpublished data).

2.5 Significance of combining ability studies in breeding

As a result of increased yield potential of hybrid varieties, they are used worldwide to attain increased maize yield. In plant breeding programmes, it is essential to understand how inbred lines or parents combine for the development of hybrids. Therefore, grain yield can be improved by gathering useful and essential facts about the heterotic pattern and genetic variability of the parents, which is important in breeding for field crops (Amegbor et al., 2017; Bhandari et al. 2017).

The term “combining ability” was first used by Sprague and Tatum (1942). Vacaro et al. (2002) noted that the performance of any genetic material is dependent on its potential per se performance as well as the combining ability of the line in crosses. Combining ability studies generate useful information on the genetic mechanisms governing how quantitative traits are inherited and this assists plant breeders to select superior parental lines for further crop improvement or use in hybrid production for commercial purposes (Abuali et al. 2012; Ali et al. 2012).

There are two types of combining ability commonly used in biometrical genetics and these are GCA and SCA (Abuali et al. 2012; Haydar and Paul 2014). The GCA is average contribution an inbred makes to hybrid performance in a series of hybrid combinations in comparison to other inbreds in the same series of hybrid combinations and this is due to additive gene action, while the SCA, on the other hand, the contribution of an inbred to hybrid performance in a cross with a specific other inbred in relation to its contributions in crosses with an array of other inbreds (Abuali et al. 2012; Sharief et al. 2009; Haydar and Paul 2014).

Sprague and Tatum (1942), Griffing (1956) and Muraya et al. (2006) indicated that, with respect to genetic variance, GCA signifies additive gene action while SCA on the other hand represents non-additive gene action involving dominance and epistasis. Researchers can make good use of information generated from combining ability studies for developing high yielding inbred lines primarily breeders develop high yield in hybrids, inbred line performance *per se* is of lesser importance as well as hybrids. Hence, relevant information of combining ability is vital in the choice of appropriate parents for hybridization and identification of promising hybrids in breeding programmes (Machikowa and Laosuwan 2011). Selection and progress in breeding is easier for characters with high additive genetic variance rather than those with higher dominance genetic variance. This is because dominance is mainly composed of intra-locus gene interactions among the individuals (Muraya et al. 2006; Gissa 2008). This suggests that, in subsequent generations characterised by random mating, the association between the individuals will be interrupted and consequently results in restructuring as well as recombination of genes in the next generation from parents to offspring (Muraya et al. 2006).

Genes that are additive in nature have a good chance of improving that trait by increasing the desirable genes for efficient selection. GCA and SCA effects can be assessed by using biometrical approaches. The diallel cross technique is one of the most commonly used methods because of its combinations with all other lines in a particular study. Detailed methodology for the estimation of gene effects and variances in diallel cross analysis has been provided by Griffing (1956). Also, several studies reported that non-additive genetic variances are of great importance in the inheritance of grain yield and other quantitative traits that are of economic importance (Darrah and Hallauer 1972; Gangashetty et al. 2016; Bhusal and Lal 2017). However, for unselected materials, the additive genetic variance

assumes a greater role than non-additive variance (Badu-Apraku et al. 2013; Menkir et al. 2017; Mastrodomenico et al. 2018; Manjeru et al. 2019). It is important to note that, for hybrid development, non-additive variance is far more important in providing heterosis and superior performance.

2.6 Line x tester mating design

Even though there are several mating designs used in plant breeding, they all come with advantages and disadvantages. Several researchers reported on the use of diallel and North Carolina mating designs. However, it becomes more expensive to handle when there are many lines that are used in generating the hybrids. Therefore, in a study with a relatively high number of inbred lines, it is essential to use line x tester analysis to obtain genetic information on all the inbred lines.

The line x tester mating design is an extension of the topcross design, where more than one tester is used instead of one tester as used in a topcross (Nduwumuremyi et al. 2013). Line x tester mating design for estimating GCA and SCA for hybrid development was first proposed by Kempthorne (1957) and was extensively used by several researchers such as Sharma (2006) and Nduwumuremyi et al. (2013). In this design, the hybridization is conducted between lines, which are used as females and broad based testers as males, where each tester is crossed to a line in a one to one fashion, to generate a number of female x male crosses (Muruya et al. 2006; Sharma 2006).

Line x tester is one of the simplest mating designs that estimates genetic information for both full-sibs and half-sibs concurrently, unlike in the case of the topcross that provides information only on half-sibs. This design estimates SCA of every cross and it does not only provide GCA of parents but of the testers as well, as lines and testers are different sets of genotypes (Sharma 2006). Furthermore, it is also used in estimating various types of gene actions that are important in the expression of quantitative traits (Rashid et al. 2007).

2.7 Genotype by environment interactions and stability studies

Multi-environment trials (MET) are conducted by plant breeders to evaluate new or improved genotypes developed across several environments or locations replicated in years before they are recommended and released for production on commercial basis. From

MET, the average performance(s) or ranking of the genotypes are generally inconsistent from one environment to another as a result of influence of environment on the genotypes (Martin 2000; Sorensen 2010; Mebratu et al. 2019).

The interference that exist between the genotype and environment is known as genotype x environment interaction (GEI). This interaction may confound the selection process and thereby recommendation of a superior genotype for a target environment will be affected (Ebdon and Gauch 2002; Gauch 2006; Xu et al. 2014). Analysis of variance (ANOVA) is performed on the genetic materials studied across environments to identify superior genotypes in the presence of GEI in MET. After the analysis, when significant GEI variance was identified, one of the various methods for determining the stability of genetic materials can be deployed to select the most stable and consistent genotype(s). GEI has been reported in many breeding programmes in several cultivated crops, especially maize (Alwala et al. 2010; Zali et al. 2011; Xu et al. 2014; Zhang et al. 2016).

GEI in major maize production environments is a result of climatic and environmental factors such as drought, low soil nitrogen, temperature, rainfall, duration of the cropping period, soil chemical properties (such as soil pH) and socio-economic issues that compel farmers to engage in sub-optimal application of agro inputs such as fertilizer (Bänziger et al. 2006). GEI decreases the relationship between the phenotypic and genotypic values and as a result, it leads to improper assessment of gene and combining ability effects among the traits that are highly influenced by environmental factors, making selection difficult (Farshadfar et al. 2000, 2011).

Analysis of GEI is important to gather relevant data on the performance of the genetic materials in terms of adaptability and stability. Maize hybrids, which are high yielding with enhanced nutritional composition and comparatively stable when grown in different environments, is of prime significance to commercial maize production in SSA (Edmeades et al. 1997; Beck et al. 2003). Živanović et al. (2004) and Mastrodomenico et al. (2018) stated that grain yield stability in maize is partly under genetic control and thus appropriate for selection.

Two of the most powerful statistical tools used for the analysis of METs data on maize trials are the Additive Main Effects and Multiplicative Interaction (AMMI) model reported

by Zobel et al. (1988), Gauch and Zobel (1997) and de Abreu et al. (2019). The other tool is the genotype main effect plus genotype by environment interaction (GGE) biplot method recommended by Yan et al. (2000). One of the advantages of the AMMI model is that it is able to integrate the ANOVA for not only the cultivar but also effects from the environment as well as the principal components analysis (PCA) of the interaction between genotype and environment. In addition, it provides better estimates and serves as a useful method for understanding GEI and attaining better yield estimates provided by the AMMI analysis. The interaction between genotype and environment is displayed in a biplot where PCA scores are provided with double-centred PCA (Mitrović et al. 2012; Abakemal et al. 2016).

The PCA values are plotted against each other and the interpretation of GEI components is primarily based on the graph provided. The GGE allows grouping of genotypes based on similarity in their performances across varied environments or locations because the biplot enables and integrates genotypic stability statistics of the genotypes. Furthermore, the GGE biplot methodology provides visual (graphical) performance of interaction estimates. GGE biplots integrate ANOVA and PCA by apportioning sums of squares of genotypes and GEI. This is significant in genotype assessment by deploying a PCA based method. The biplot method is used for the determination and assessment of genotypes evaluated under diverse environments based on environment-centred PCA (Mitrović et al. 2012; Erdemc 2018). The GGE biplot provides the first principal component (PC1) and second principal component (PC2) which are attained by decomposition of singular values of multi-location trials yield data (Yan et al. 2007; Mitrović et al. 2012). In addition, the GGE analysis allows the highest yielding genotypes across different environments to be identified, to compare their consistency in performance from varied environmental conditions, and identification of superior and ideal genotypes as well as mega-environments (model of regional distribution or target environment) (Yan et al. 2007; Alwala et al. 2010; Badu-Apraku et al. 2011).

As a result of the broad information provided by AMMI and GGE biplots, several researchers have assessed the usefulness and efficiency of AMMI and GGE biplot analyses for analysing data obtained from GEI. Alwala et al. (2010) reported that, one of the major disadvantages of the AMMI model in examining stability is that it is not sensitive to crossover effects, which is the main part of GEI. Additionally, the AMMI methodology does not provide any significance to the plant scientist for genotypic and site evaluation

when analysing MET data, because there is no obvious biological differentiation between the two terms, that is genotype and GEI. The GGE biplot has been identified as a powerful statistical model that overcomes the limitations associated with AMMI. The GGE biplot is an efficient statistical tool used for identifying not only the best performing cultivar or genotype in a specific environment, but it is also capable of identifying an ideal environment for a particular genotype (Yan et al. 2007; Masindeni 2013; Zhang et al. 2016). Furthermore, this method is capable of comparing a given set of genotypes in separate environments. Also it can identify the best genotype for each environment and can differentiate mega-environments, determine average yield and stability of the genotypes, and has the ability to discriminate between environments (Zerihun 2011; Yan et al. 2007; Farshadfar 2012; Krisnawati and Adie 2018).

Contrary to the reports from other researchers about the usefulness of GGE biplots, several researchers found the AMMI to be highly effective for the analysis of MET and also the best to describe the GEI in maize research trial across several locations and environments (Gruneberg et al. 2005; Kandus et al. 2010). On the other hand, Stojaković et al. (2010) and Mitrović et al. (2012) documented that both AMMI and GGE biplot models provided similar results when used in their study. On the other hand, Yan et al. (2007), Farshadfar (2012) and Koundinya et al. (2019) in independent studies, concluded that the GGE biplot model was superior to the AMMI biplot in mega-environment analysis and genotype evaluations.

2.8 The importance of heritability in plant breeding

Information on the mode of inheritance of grain yield, essential secondary traits and quality traits in maize production will be beneficial for development of appropriate breeding approaches for improving these traits. This is because varying environmental conditions adversely affect heritability of grain yield and quality traits, thereby implicate selection of superior individuals (Songsri et al. 2008; Visscher et al. 2008; Hemmatabadi et al. 2016). The genetic improvement of grain yield and its related traits as well as quality traits relies on the nature and the degree of variability in available germplasm. Most of the traits that are of interest to the breeder, in this case yield and quality, are complex traits and hence are polygenically controlled. In order to carry out successful selection in a breeding programme, it is important not to consider only heritability of desired traits but also the evidence of association among various yield related and quality traits and their relationship

with grain yield (Bekele and Rao 2014). Heritability is considered essential in breeding programmes because parents used in developing hybrids transfer only one copy of their genes each to the formed individual through descent (Visscher et al. 2008; Ogunniyan and Olakojo 2014). Visscher et al. (2008) suggested that in addition to combining ability, selection should be based on heritability of traits, both broad sense (H^2) and narrow sense (h^2), and correlation between yield and secondary traits even though this might not be efficient as combining ability estimates.

2.9 Correlation among traits in plant breeding

In most breeding programmes, increase of yield is the primary objective. However, as a result of interactions between genotype and the environment, the full expression of grain yield and other traits that are quantitatively inherited are variable under varying environmental conditions (Qi et al. 2010; Gangashetty et al. 2016). As a result, for selection of grain yield and quality traits to be efficient, it is important to consider traits that contribute to yield. The polygenic nature of grain yield often leads to variability across varied environmental conditions (Machikowa and Laosuwan 2011). Subsequently, grain yield and quality traits enhancement in maize can be realised through exploitation of the association between grain yield, quality traits and their related characters. Correlations have been exploited in several studies for indirect selection of yield and quality traits. (Machikowa and Laosuwan 2011; Amini et al. 2013; Adesoji et al. 2015).

Correlation measures the association that exist between traits in a given gene pool. Genotypic and phenotypic correlations are found where characters have a cause and effect association, whereby one trait is dependent on the other trait such that variation in the independent variable causes a change in the dependent variable (du Toit et al. 1997; Adesoji et al. 2015). Phenotypic correlation (r_P) is controlled by genetic make-up of the genotypes and environmental effects while genetic correlation (r_G) is only due to the additive genetic variance. The association between two traits may be attributed to pleiotropism and/or linkage disequilibrium (Hallauer and Miranda 1988; Falconer 1989). Information on correlations is crucial in maize breeding to aid in the identification of superior genotypes with higher grain yield through indirect selection achieved via selection of secondary traits (Bello and Olaoye 2009). However, it is important to note that correlations among traits are not adequate to describe the significance of each trait in contributing to final grain yield (Sreckov et al. 2011). Bizeti et al. (2004) further noted that,

these inadequacies often lead to observed dissimilarities that are due to more than one indirect cause. As a result, it is important to conduct in-depth studies on trait associations to fully understand the contribution of each character and then rank their importance for targeting in selection. One of the ways of achieving this is to use the path coefficient analysis to assess the relationship among these traits (Udensi and Ikpeme 2012; Adesoji et al. 2015).

In relation to breeding for QPM hybrids with enhanced quality traits, it is important that protein quality has a positive relationship with other kernel quality characteristics, which is essential to success of breeding for quality traits. The study of the correlations between quality traits of maize, such as endosperm hardness, protein quality, starch and other traits related to endosperm hardness, is important for kernel modification in breeding programmes by crossing genotypes with hard kernels with the genotypes with higher amounts of amino acids but having soft kernels (Wessel-Beaver et al. 1985; Gissa 2008). Several reports indicated that, as the amount of protein and tryptophan increased, there is also a decrease in the endosperm modification (Vasal et al. 1980; Wegary et al. 2011; Tulu 2014; Aman et al., 2016). In addition, Sharma et al. (2017) noted that traits such as number of kernels per cob, tryptophan and lysine contents and grain yield per plant showed high values for heritability, genetic advance and genetic correlations. Gissa (2008) reported a negative relationship between grain yield and protein quality, and grain yield and kernel modification, hence there is a need to conduct chemical analysis on the maize endosperm for tryptophan and lysine before classifying a genotypes as QPM (Idikut et al. 2009; Aliu et al. 2012). Pixley and Bjarnason (2002), Aliu et al. (2012) and Mural et al. (2012) reported insignificant genotypic correlation between endosperm texture, protein content and grain yield.

2.10 Evaluation and chemical analysis of inbred lines

Several studies have reported on the evaluation of QPM inbred lines for combining ability under varying environmental conditions to identify QPM donors and testers using several mating designs (Živanović et al. 2006; Mbuya et al. 2012; Amin et al. 2014; Sarika et al. 2018). Amin et al. (2014) and Sarika et al. (2018) reported differing data on the yield performance of inbred lines and their progenies. As a result of inconsistencies in performance of inbred lines under different field conditions, there is a need to evaluate the

newly developed QPM lines for agronomic characters and also conduct chemical analysis on the selected lines.

2.11 Success in breeding for quality and yield drag

In the developed countries, maize is primarily used as feed for animals because of its rich energy value, which is due to the high starch content present in the endosperm. However, in SSA and other developing countries across the globe, maize forms a major part of the human diet, where it supplies daily calories and to some extent protein and other essential amino acids (de Oliveira et al. 2004). Kernel protein content is polygenically controlled (Mittelman et al. 2003; Aliu et al. 2012; Tripathy et al. 2017).

QPM has much higher levels of lysine and tryptophan than normal maize. It has been reported that the yield gap between QPM and non-QPM materials ranges between 10 to 15% for grain yield, which is predominantly characterised by a slower drying rate, greater part of the cob which is affected by kernel rots and consequently, lower kernel weight in the QPM material (Vasal 2002; Li and Vasal 2016; Tandzi et al. 2017).

To overcome the problems associated with the *o2* mutation, breeders over the past four decades have introgressed gene modifiers from normal maize to harden the endosperm of QPM genotypes without reduction in lysine and tryptophan contents (Mertz et al. 1964; Kumar et al. 2011; Gupta et al. 2013; Pandey et al. 2016; Krishna et al. 2017). This was done not only by conventional breeding but also through molecular approaches to broaden the genetic variability of QPM varieties with increased yield comparable to normal maize (Tandzi et al. 2017). In spite of the unprecedented progress made to harden the endosperm of QPM varieties with enhanced yield, there has been several contradictory reports about the yield of QPM against that of non-QPM genotypes. There are available reports of normal maize being superior in terms of grain yield compared to QPM varieties (Bhatnagar et al. 2004; Krivanek et al. 2007) while Pixley and Bjarnason (1993) reported that QPM hybrids yielded better than non-QPM hybrids. Interaction between genes, which control major traits can cause yield reduction ('yield drag' and 'event lag' effects) (Shi et al. 2013). The yield gap between non-QPM and QPM genotypes is termed as yield drag. Until now, there is no available information on yield drag (reduction in grain yield as a result of the QPM trait) to truly quantify if indeed QPM yields are lower than non-QPM or if their yields are

comparable. Therefore, this study seeks to examine the yield gap between QPM and their non-QPM counterparts. The other drawback of QPM hybrids is that they must be grown in isolation from normal hybrids or cross pollinations across fields will cover the recessive QPM character.

References

- Abakemal D, Shimelis H and Derera J (2016) Genotype-by-environment interaction and yield stability of quality protein maize hybrids developed from tropical-highland adapted inbred lines. *Euphytica* 209: 757-769.
- Abuali AI, Abdelmulla AA, Khalafalla MM, Atif Elsadig Idris AE and Osman AM (2012) Combining ability and heterosis for yield and yield components in maize. *Australian Journal of Basic and Applied Sciences* 6: 36-41.
- Adebayo MA and Menkir A (2015) Combining ability of adapted and exotic drought-tolerant maize inbred lines under full irrigation and rainfed conditions in Nigeria. *Journal of Crop Improvement* 29: 117-130.
- Adesoji AG, Abubakar IU and Labe DA (2015) Character association and path coefficient analysis of maize (*Zea mays* L.) grown under incorporated legumes and nitrogen. *Journal of Agronomy* 14: 158-163.
- Aguiar CG, Schuster I, Amaral AT, Scapim CA and Vieira ESN (2008) Heterotic groups in tropical maize germplasm by test crosses and simple sequence repeat markers. *Genetics and Molecular Research* 7: 1233-1244.
- Akuamoa-Boateng A (2002) Quality protein maize: infant feeding trials in Ghana. Ghana Health Service, Ashanti, Ghana. Cochran WG and Cox GM. 1957. *Experimental Design*. 2nd ed. John Wiley & Sons, Inc. New York, NY.
- Ali F, Irfan AS, Rahman H, Mohammad N, Durrishahwar, Muhammad YK, Ihteram U and Jianbing Y (2012) Heterosis for yield and agronomic attributes in diverse maize germplasm. *Australian Journal of Crop Science* 6: 455-462.
- Aliu S, Rusinovci I, Fetahu S and Simeonovska E (2012) Genetic diversity and correlation estimates for grain yield and quality traits in Kosovo local maize (*Zea mays* L.) populations. *Notulae Scientia Biologicae* 4: 121-128.

- Alwala S, Kwolek T, McPherson M, Pellowc MJ and Meyer D (2010) A comprehensive comparison between Eberhart and Russell joint regression and GGE biplot analyses to identify stable and high yielding maize hybrids. *Field Crops Research* 119: 225–230.
- Aman J, Bantte K, Alamerew S and Tolera B (2016) Evaluation of quality protein maize (*Zea mays* L) hybrids at Jimma, Western Ethiopia. *Journal Forensic Anthropology* 1: 1-6.
- Amegbor IK, Badu-Apraku B and Annor B (2017) Combining ability and heterotic patterns of extra-early maturing white maize inbreds with genes from *Zea diploperennis* under multiple environments. *Euphytica* 213: 1-16.
- Amin MN, Amiruzzaman M, Ahmed A and Ali MR (2014) Evaluation of inbred lines of maize (*Zea mays* L.) through line $\times$ tester method. *Bangladesh Journal Agricultural Research* 39: 675-683.
- Amini Z, Khodambashi M and Houshmand S (2013) Correlation and path coefficient analysis of seed yield related traits in maize. *International Journal of Agriculture and Crop Sciences* 5: 2217-2220.
- Amudalat BO (2015) Maize: Panacea for hunger in Nigeria. *African Journal of Plant Science* 9: 155-174.
- Annor B and Badu-Apraku B (2016) Gene action controlling grain yield and other agronomic traits of extra-early quality protein maize under stress and non-stress conditions. *Euphytica* 212: 213-228.
- Asea A (2005) Stress proteins and initiation of immune response: Chaperokine activity of *hsp72*. *Exercise Immunology Review* 11: 34-45.
- Babu R and Prasanna B.M (2014). Molecular breeding for quality protein maize (QPM). In: Tuberosa R, Graner A and Frison E (eds), *Genomics of Plant Genetic Resources*. Springer, pp. 490-505.
- Badu-Apraku B and Fakorede MAB (2017) Breeding of quality protein and provitamin A maize: In: *Advances in genetic enhancement of early and extra-early maize for sub-Saharan Africa*. Springer Int Publ., pp. 217-244. doi:10.1007/978-3-319-64852-1.
- Badu-Apraku B and Lum AF (2010) The pattern of grain yield response of normal and quality protein maize cultivars in stressed and non-stressed environments. *Agronomy Journal* 102: 381-394.

- Badu-Apraku B, Akinwale RO, Menkir A, Obeng-Antwi K, Osuman AS, Coulibaly N, Onyibe JE, Yallou GC, Abdullai MS and Didjara A (2011) Use of GGE biplot for targeting early maturing maize cultivars to mega-environments in west Africa. *African Crop Science Journal* 19: 79-96.
- Badu-Apraku B, Oyekunle M, Fakorede MAB, Vroh I, Akinwale RI and Aderounmu M (2013) Combining ability, heterotic patterns and genetic diversity of extra-early yellow inbreds under contrasting environments. *Euphytica* 192: 413-433.
- Bänziger M and Diallo A (2001) Progress in developing drought and N stress tolerant maize cultivars for Eastern and Southern Africa. Seventh Eastern and Southern Africa Maize Conference, 11-15 February, pp. 189-194.
- Bänziger M, Setimela PS, Hodson D and Vivek V (2006). Breeding for improved abiotic stress tolerance in maize adapted to southern Africa. *Agricultural Water Management* 80: 212-224.
- Barata C and Carena MJ (2006) Classification of North Dakota maize inbred lines into heterotic groups based on molecular and testcross data. *Euphytica* 151: 339-349.
- Bari MAA, Carena MJ and Pereira MG (2016) Identification of heterotic patterns between expired proprietary, NDSU, and industry short-season maize inbred lines. *Crop Breeding and Applied Biotechnology* 16: 274-281.
- Beck D, Ba M and Edmeades GO (2003) Genetic analysis of inbred and hybrid grain yield under stress and nonstress environments in tropical maize. *Crop Science* 43: 807-817.
- Bekele A and Rao TN (2014) Estimates of heritability, genetic advance and correlation study for yield and it's attributes in maize (*Zea mays* L.). *Journal of Plant Science* 2: 1-4.
- Bello OB and Olaoye G (2009) Combining ability for maize grain yield and other agronomic characters in a typical southern Guinea Savannah ecology of Nigeria. *African Journal of Biotechnology* 8: 2518-2522.
- Bhandari HR, Bhanu AN, Srivastava K, Singh MN, Shreya and Hemantaranjan A (2017) Assessment of genetic diversity in crop plants - An overview. *Advances in Plants and Agriculture Research* 7: 1-8.
- Bhatnagar S, Betran FJ and Rooney LW (2004) Combining abilities of quality protein maize inbreds. *Crop Science* 44: 1997-2005.
- Bhusal TN and Lal GM (2017) Relationship among heterosis, combining ability and SSR based genetic distance in single cross hybrids of maize (*Zea Mays* L). *Vegetos* 30: 1-10.

- Bizeti HS, Carvalho CGP, Souza JRP and Destro D (2004) Path analysis under multicollinearity in soybean. *Brazilian Archives of Biology and Technology* 47: 669-676.
- Blum A (2013) Heterosis, stress, and the environment: a possible road map towards the general improvement of crop yield. *Journal Experimental Botany* 64: 4829-4837.
- Bressani R (1992) Nutritional value of high-lysine maize in humans. In: Mertz ET (ed), *Quality Protein Maize*. American Association of Cereal Chemists. St. Paul, MN, pp. 205-225.
- Bruce AB (1910) The Mendelian theory of heredity and the augmentation of vigor. *Science* 32: 627-628.
- Chairi F, Elazab A, Sanchez-Bragado R, Aras JL and Serret MD (2016) Heterosis for water status in maize seedlings. *Agricultural Water Management* 164:100-109.
- Dang NC (2010) Improvement of protein quality in waxy maize (*Zea mays* L.) by doubled haploid and marker assisted selection techniques. PhD thesis: University of Thai Nguyen.
- Darrah LL and Hallauer AR (1972) Genetic effects estimated from generation means in four diallel sets of maize inbred. *Crop Science* 12: 615-621.
- De Abreu VM, Von Pinho EVR, Mendes-Resende MP, Balestre M, Lima AC, Santos HO and Von Pinho RG (2019) Combining ability and heterosis of maize genotypes under water stress during seed germination and seedling emergence. *Crop Science* 58: 1-11
- De Franca JGE (1983) Genetic and combining ability analysis of some agronomic and grain quality characters in sorghum (*Sorghum bicolor* (L.) Moench). MSc Thesis, Andhra Pradesh Agricultural University.
- De Groote H, Gunaratna N, Okuro J, Wondimu A, Chege C and Tomlins K (2014) Consumer acceptance of quality protein maize (QPM) in East Africa. *Journal of the Science of Food and Agriculture* 94: 3201-3212.
- De Oliveira JP, Chaves LJ, Duarte JB, Brasil EM, Ferreira Júnior LT and Ribeiro KO (2004) Teor de proteína no grão em populações de milho de alta qualidade protéica e seus cruzamentos. *Pesquisa Agropecuária Tropical* 34: 45-51.
- Dragicevic V, Mladenovic-Drinic S, Stojiljkovic M, Filipovic M, Nikolic B, Babic V, and Kravic N (2016) Maize inbreds from different heterotic groups as favorable sources for increased potential bioavailability of magnesium, iron, manganese and zinc. *Chilean Journal of Agricultural Research* 76: 213-219.

- du Toit AS, Booysen J and Human JJ (1997) Use of linear regression and correlation matrix in the evaluation of CERES3 (Maize) 14: 177-181. South African Journal of Plant and Soil 14: 177-182.
- Duvick DN and Brown WL (1981) Current breeding methods in maize. In: Snee J and Hendricksen T (eds), Plant Breeding Perspectives. Wageningen, Holand: Pudoc, pp. 190-203.
- East EM and Hayes HK (1912) Heterozygosis in evolution and in plant breeding. U.S. Department of Agriculture Bulletin.
- Ebdon JS and Gauch HG (2002) Additive main effect and multiplicative interaction analysis of national Turfgrass performance trials: I. Interpretation of genotype environment $\times$ interaction. Crop Science 42: 489-496.
- Edmeades GO, Bänziger M, Mickelson HR and Peña-Valdivia CB (1997) Developing drought- and low N-tolerant maize. Proceedings of Symposium, March 25-29, 1996, CIMMYT, El Batán, Mexico D.F., pp. 1-543.
- Edmonds DE, Abreu SL, West A, Caasi DR, Conley TO, Daft MC, Desta B, England BB, Farris CD, Nobles TJ, Patel NK, Rounds EW, Sanders BH, Shawaqfeh SS, Lakmini, Lokuralalage, Manandhar R and Raun WR (2009) Cereal nitrogen use efficiency in Sub Saharan Africa. Journal of Plant Nutrition 32: 2107-2122.
- Erdemc I (2018) Investigation of genotype $\times$ environment interaction in chickpea genotypes using AMMI and GGE biplot analysis. Turkish Journal of Field Crops 23: 20-26.
- Eshetie T (2017) Review of quality protein maize as food and feed: In alleviating protein deficiency in developing countries. American Journal of Food Nutrition 5: 99-105.
- Falconer DS (1989) Introduction to quantitative genetics. Longman Scientific and Technical Group Ltd, 3rd ed. John Wiley and Sons, New York
- Fan XM, Chen HM, Tan J, Xu CX, Zhang YD, Luo LM, Huang YX and Kang MS (2008) Combining abilities for yield and yield components in maize. Maydica 53: 39-46.
- Fan XM, Tan J, Yang JY and Chen HM (2004) Combining ability and heterotic grouping of ten temperate, subtropical and tropical quality protein maize inbreds. Maydica 49: 267-272.
- Fan XM, Yin XF, Zhang YD, Bi YQ, Liu L, Chen HM and Kang MS (2016) Combining ability estimation for grain yield of maize exotic germplasm using testers from three heterotic groups. Crop Science 56: 2527-2535.

- Fan XM, Zhang YD, Yao WH, Bi YQ, Liu L, Chen HM and Kang MS (2014) Reciprocal diallel crosses impact combining ability, variance estimation, and heterotic group classification. *Crop Science* 54: 89-97.
- Fan XM, Zhang YM, Yao WH, Chen HM, Tan J, Xu CX, Han XL, Luo LM and Kang MS (2009) Classifying maize inbred lines into heterotic groups using a factorial mating design. *Agronomy Journal* 101: 106-112.
- Farshadfar E (2012) GGE Biplot analysis of genotype $\times$ environment interaction in chickpea genotypes. *Australian Journal of Crop Science* 6:1074-1079.
- Farshadfar E, Farshadfar M and Kiani M (2011) Involvement of chromosome 5R carrying the genes controlling yield and yield stability in rye (*Secale cereale* cv. Imperial). *European Journal of Scientific Research* 59: 352-360.
- Farshadfar E, Farshadfar M and Sutka J (2000) Combining ability analysis of drought tolerance in wheat over different water regimes. *Acta Agronomica Hungarica* 48: 353-361.
- Fischer S, Maurer HP, Würschum T, Möhring J, Piepho HP, Schön CC, Thiemt EM, Dhillon BS, Weissmann EA, Melchinger AE and Reif JC (2010) Development of heterotic groups in triticale. *Crop Science* 50: 584.
- Fu D, Xiao M, Hayward A, Fu Y, Jiang G and Zhang H (2014) Utilization of crop heterosis: A review. *Euphytica* 197: 161-173.
- Gangashetty PI, Motagi BN, Pavan R and Roodagi MB (2016) Breeding crop plants for improved human nutrition through biofortification: Progress and Prospects. In: Al-Khayri J, Jain S and Johnson D (eds), *Advances in Plant Breeding Strategies: Agronomic, Abiotic and Biotic Stress Traits*, 2nd ed. Springer Netherlands, pp 35-68. doi 10.1007/978-3-319-22518-0_2
- Gauch HG (2006) Statistical analysis of yield trials by AMMI and GGE. *Crop Science* 46: 1488-1500.
- Gauch HG and Zobel RW (1997) Identifying mega-environments and targeting genotypes. *Crop Science* 37: 311-326.
- Gracen VE (2020) Grouping of inbred lines into heterotic groups. Chapter 6. *Breeding F1 Hybrid Crops* (unpublished).
- Gibbon BC and Larkins BA (2005) Molecular genetic approaches to developing quality protein maize. *Trends in Genetics* 21: 227-233.

- Gissa DW (2008) Genotypic variability and combining ability of quality protein maize inbred lines under stress and optimal conditions. PhD Thesis in Plant Breeding, University of the Free State, South Africa.
- Giwa EO and Ikujenlola AV (2009) Application of quality protein maize in the formulation of broiler's finisher feed. *Journal of Science, Food and Hospitality* 1: 47-50.
- Griffing BA (1956) Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal Biology Science* 9: 463-493.
- Gruneberg WJ, Manrique K, Zhang D and Hermann M (2005) Genotype x environment interactions for a diverse set of sweetpotato clones evaluated across varying ecographic conditions in Peru. *Crop Science* 45: 2160-2171.
- Gunaratna NS, De Groote H, Nestel P, Pixley KV and McCabe G (2010) Evaluating the impact of biofortification: A meta-analysis of community-based studies on quality protein maize (QPM). *Food Policy* 35: 202-210.
- Gupta HS, Babu R, Agarwal PK, Mahajan V, Hossain F and Nepolean T (2013) Accelerated development of quality protein maize hybrid through marker-assisted introgression of *opaque-2* allele. *Plant Breeding* 132: 77-82.
- Hallauer AR and Miranda JB (1988) Quantitative genetics in maize breeding. 2nd ed. Iowa State University Press, Ames.
- Haydar FMA and Paul NK (2014) Combininbg ability analysis for different yield trails in maize. *Bangladesh Journal of Plant Breeding and Genetics* 27: 1-5.
- Hemmatabadi RN, Seidavi A and Gharahveysi S (2016) A review on correlation, heritability and selection in silkworm breeding. *Journal of Applied Animal Research* 44: 9-23.
- Idikut L, Atalay AI, Kara SN and Kamalak A (2009) Effect of hybrid on starch, protein and yields of maize grain. *Journal of Animal and Veterinary Advances* 8: 1945-1947.
- Ignjatovic-Micic D, Kostadinovic M, Stankovic G, Markovic K, Vancetovic J, Bozinovic S and Andjelkovic V (2013) Biochemical and agronomic performance of quality protein maize hybrids adapted to temperate regions. *Maydica* 58: 311-317.
- Kaeppler S (2012) Heterosis: Many genes, many mechanisms-end the search for an undiscovered unifying theory. *ISRN Botany* 2012: 1-12.
- Kandus M, Almorza D, Boggio R and Salerno JC (2010) Statistical models for evaluating the genotype-environment interaction in maize (*Zea mays* L.). *International Journal of Experimental Botany* 79: 39-46.

- Kanyamasoro MG, Karungi J, Asea G and Gibson P (2012) Determination of the heterotic groups of maize inbred lines and the inheritance of their resistance to the maize weevil. *African Crop Science Journal* 20: 99-104.
- Keeble F and Pellow E (1910) The mode of inheritance of stature and time of flowering in peas. *Genetics* 1: 47-56.
- Kempthorne O (1957) An introduction to genetic statistics. John Wiley and Sons, New York.
- Kerwin RE, Feusier J, Muok A, Lin C, Larson B, Copeland D, Corwin JA, Rubin MJ, Francisco M, Li B, Joseph B, Weinig C and Kliebenstein DJ (2017) Epistasis $\times$ environment interactions among *Arabidopsis thaliana* glucosinolate genes impact complex traits and fitness in the field. *New Phytologist* 215:1249-1263.
- Koundinya AVV, Pandit MK, Ramesh D and Mishra P (2019) Phenotypic stability of eggplant for yield and quality through AMMI, GGE and cluster analyses. *Scientia Horticulturae* 247: 216-223.
- Krishna MSR, Surender M and Sokka Reddy S (2017) Marker assisted breeding for introgression of *opaque-2* allele into elite maize inbred line BML-6. *Acta Ecologica Sinica* 37: 340-345.
- Krisnawati A and Adie MM (2018) Genotype by environment interaction and yield stability of soybean genotypes. *Indonesian Journal of Agricultural Science* 19: 25-32.
- Krivanek AF, De Groote H, Gunaratna N, Diallo A and Friesen D (2007) Breeding and disseminating quality protein maize (QPM) for Africa. *African Journal of Biotechnology* 6: 312-324.
- Kumar J, Jaiswal V, Kumar A, Kumar N, Mir RR, Kumar S, Dhariwal R, Tyagi S, Khandelwal M, Prabhu KV, Prasad R, Balyan HS and Gupta PK (2011) Introgression of a major gene for high grain protein content in some Indian bread wheat cultivars. *Field Crops Research* 123: 226-233.
- Legesse BW, Pixley KV and Botha AM (2009) Combining ability and heterotic grouping of highland transition maize inbred lines. *Maydica* 54:1-9.
- Li JS and Vasal SK (2016) Maize: quality protein maize. In: Wrigley C, Corke H, Seetharaman K and Faubion J (eds), *Encyclopedia of Food Grains*. 2nd. Ed. Elsevier, pp. 212-216.
- Lippman ZB and Zamir D (2006) Heterosis: Revisiting the magic. *Trends in Genetics* 23: 60-65.

- Machikowa T and Laosuwan P (2011) Path coefficient analysis for yield of early maturing soybean. *Sonklanakarin Journal of Science and Technology* 33: 365-368.
- Manjeru P, van Biljon A and Labuschagne M (2019) The development and release of maize fortified with provitamin A carotenoids in developing countries. *Critical Reviews in Food Science and Nutrition* 59: 1284-1293.
- Martin N (2000) Gene-environment interaction and twin studies. In: Spector T, Snieder H, and MacGregor A (eds), *Advances in twin and sib-pair analysis*. Greenwich Medical Media, London, pp. 143-150.
- Martin RV, Washington R and Downing TE (2000) Seasonal maize forecasting for South Africa and Zimbabwe derived from an agroclimatological model. *Journal of Applied Meteorology* 39: 473-479.
- Masindeni DR (2013) Evaluation of South African high quality protein maize (*Zea mays* L.) inbred lines under optimum and low nitrogen conditions and the identification of suitable donor parents. PhD Thesis in Plant Breeding, University of the Free State, South Africa.
- Mastrodomenico AT, Haegele JW, Seebauer JR and Below FE (2018) Yield stability differs in commercial maize hybrids in response to changes in plant density, nitrogen fertility, and environment. *Crop Science* 58: 230-241.
- Mather K and Jinks JL (1971) *Biometrical genetics. The study of continuous variation*. Cornell University Press, New York.
- Mbuya K, Nkongolo KK and Narendrula R (2012) Development of quality protein maize (QPM) inbred lines and genetic diversity assessed with ISSR markers in a maize breeding program. *American Journal of Experimental Agriculture* 2: 626-640.
- Mbuya K, Nkongolo KK and Kalonji-Mbuyi A (2011) Nutritional analysis of quality protein maize varieties selected for agronomic characteristics in a breeding programme. *International Journal of Plant Breeding and Genetics* 5: 317-327.
- Mebratu A, Wegary D, Mohammed W, Teklewold A and Tarekegne A (2019) Genotype × environment interaction of quality protein maize hybrids under contrasting management conditions in Eastern and Southern Africa. *Crop Science* 59: 1576-1589.
- Melani MD, Carena MJ (2005) Alternative maize heterotic patterns for the Northern Corn Belt. *Crop Science* 45: 2186.
- Melchinger AE and Gumber RK (1998) Overview of heterosis and heterotic groups in agronomic crops. In: Lamkey KR and Staub JE (ed), *Concepts and breeding of heterosis in crop plants*. CSSA, Madison, WI, pp. 29-44.

- Menkir A, Maziya-Dixon B, Mengesha W, Rocheford T and Alamu EO (2017) Accruing genetic gain in pro-vitamin A enrichment from harnessing diverse maize germplasm. *Euphytica* 213: 1-12.
- Menkir A, White WS, Maziya-Dixon B, Rocheford T and Weiping L (2008) Carotenoid diversity in tropical adapted yellow maize inbred lines. *Food Chemistry* 109: 521-529.
- Mertz ET, Bates ET and Nelson OE (1964) Mutant genes that change protein composition and increase lysine content of maize endosperm. *Science* 145: 279-280.
- Mitrović B, Stanisavljevi D, Treski S, Stojaković M, Ivanović M, Bekavac G and Rajković M (2012) Evaluation of experimental maize hybrids tested in multi-location trials using ammi and GGE biplot analyses. *Turkish Journal of Field Crops* 17: 35-40.
- Mittelman A, Filho J, Lima G, Klain C and Tanaka R (2003) Potential of the ESA23B maize population for protein and oil content improvement. *Scientia Agricola* 60: 319-327.
- Mpofu IDT, Sibanda S, Shonihwa A and Pixley K (2012) The nutritional value of quality protein maize for weaner pigs. *Journal of Petroleum and Environmental Biotechnology* 3: 129.
- Munaro EM, Eyherabide GH, D'Andrea KE, Cirilobmm AG and Otegui, ME (2011) Heterosis x environment interaction in maize: What drives heterosis for grain yield? *Field Crops Research* 124: 441-449.
- Mural RV Chikkalingaiah and Hittalmani S (2012) Correlation study for protein content, grain yield and yield contributing traits in quality protein maize (QPM) (*Zea mays* L.) *Electronic Journal of Plant Breeding* 3: 747-752.
- Muraya MM, Ndirangu CM and Omolo EO (2006) Heterosis and combining ability in diallel crosses involving maize (*Zea mays* L.) S1 lines. *Australian Journal of Experimental Agriculture* 46: 387-393.
- Musila RN, Diallo OA, Makumbi D and Njoroge K (2010) Combining ability of early-maturing quality protein maize inbred lines adapted to Eastern Africa. *Field Crops Research* 119: 231-237.
- Nduwumuremyi A, Tongoona P, Habimana S and Husbandry A (2013) Mating designs: helpful tool for quantitative plant breeding analysis. *Journal of Plant Breeding and Genetics* 1: 117-129.
- Ngaboyisonga C (2008) Quality protein maize under stress environments: gene action and genotype $\times$ environment effects. PhD Thesis, University of Nairobi, Kenya.

- Nigussie M and Zelleke H (2001) Heterosis and combining ability in a diallel among eight elite maize populations. *African Crop Science Journal* 9: 471- 479.
- Nuss ET and Tanumihardjo SA (2011) Quality protein maize for Africa: Closing the protein inadequacy gap in vulnerable populations. *Advances in Nutrition* 2: 217-224.
- Ogunniyan DJ and Olakojo SA (2014) Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). *Nigerian Journal of Genetics* 28 24-28.
- Outreach IPB (2017) Maize in Africa. International Plant Biotechnology Outreach 1–55. http://ipbo.vib-ugent.be/wp-content/uploads/2015/02/vib_fact_MaizeForAfrica_EN_2017_LR.pdf
- Pandey N, Hossain F, Kumar K, Vishwakarma AK, Muthusamy V, Saha S, Agrawal PK, Guleria SK, Reddy SS, Thirunavukkarasu N and Gupta HS (2016) Molecular characterization of endosperm and amino acids modifications among quality protein maize inbreds. *Plant Breeding* 135: 47-54.
- Pixley KV and Bjarnason MS (1993) Combining ability for yield and protein quality among modified-endosperm *opaque-2* tropical maize inbreds. *Crop Science* 33: 1229-1234.
- Pixley KV and Bjarnason MS (2002) Stability of grain yield, endosperm modification, and protein quality of hybrid and open-pollinated quality protein maize cultivars. *Crop Science* 42: 1882-1890.
- Prasanna BM, Vasal SK, Kassahun B and Singh NN (2001) Quality protein maize. *Current Science* 81: 1308-1319.
- Premlatha M and Kalamani A (2010) Heterosis and combining ability studies for grain yield and growth characters in maize (*Zea Mays* L.). *Indian Journal of Agricultural Research* 44: 62-65.
- Pukalenty, B., Manickam, D., Adhimoolam, K., Mahesh, S. G., Ramanathan, N., Chandran, S. Sampathrajan V, Rajasekaran R, ArunachalamK, Senthil K, Muthusamy V, Hossain F and Natesan, S. (2020) Marker aided introgression of *opaque-2* (o2) allele improving lysine and tryptophan in maize (*Zea mays* L.). *Physiology and Molecular Biology of Plants* 26:1925-1930.
- Qi X, Li ZH, Jiang LL, Yu XM, Ngezahayo F and Liu B (2010) Grain yield heterosis in *Zea mays* L. shows positive correlation with parental difference in CHG methylation. *Crop Science* 50: 2338-2346.

- Ram L (2014) Improvement of non-QPM lines through introgression of QPM genes. PhD Thesis, Banaras Hindu University.
- Rashid M, Cheema AA and Ashraf M (2007). Line x tester analysis in Basmati rice. Pakistan Journal of Botany 39: 2035-2042.
- Ray DK, Mueller ND, West PC and Foley JA (2013) Yield Trends Are Insufficient to Double Global Crop Production by 2050. PLoS ONE 8: e66428.
- Reid LM, Xiang K, Zhu X, Baum BR and Molnar SJ (2011) Genetic diversity analysis of 119 Canadian maize inbred lines based on pedigree and simple sequence repeat markers. Canadian Journal Plant Sciences 91: 651-661.
- Saleh G, Abdullah D and Anuar AR (2002) Performance, heterosis and heritability in selected tropical maize single, double and three-way cross hybrids. Journal of Agricultural Sciences 138: 21-28.
- Sarika K, Hossain F, Muthusamy V, Baveja A, Zunjare R, Goswami R, Thirunavukkarasu N, Saha S and Gupta HS (2017) Exploration of novel *opaque16* mutation as a source for high lysine and tryptophan in maize endosperm. Indian Journal of Genetic and Plant Breeding 77: 59-64.
- Sarika K, Hossain F, Muthusamy V, Zunjare RU, Baveja A, Goswami R, Bhat JS, Saha S and Gupta HS (2018) Marker-assisted pyramiding of *opaque2* and novel *opaque16* genes for further enrichment of lysine and tryptophan in sub-tropical maize. Plant Science 272: 142-152.
- SARI (Savanna Agricultural Research Institute) (1996) Annual Report. SARI, Ghana.
- Sharief AE, El-Kalla SE, Gado HE and Abo-Yousef HAE (2009) Heterosis in yellow maize. Australian Journal of Crop Science 3: 146-154.
- Sharma JR (2006) Statistical and biometrical techniques in plant breeding. First ed. New Age International, Mohan lal Printers, Delhi.
- Sharma P, Punia MS, Kamboj MC, Singh N and Chand M (2017) Evaluation of quality protein maize crosses through line x tester analysis for grain yield and quality traits. Agricultural Science Digest 37: 42-45.
- Shi G, Chavas JP and Lauer J (2013) Commercialized transgenic traits, maize productivity and yield risk. Nature Biotechnology 31: 111-114.
- Shull GH (1911) The genotypes of maize. American Naturalist 45: 234-252.
- Shull GH (1948) What is heterosis? Genetics 33: 439-446.

- Singh NN and Venkatesh S (2006) Development of quality protein maize inbred lines. In: Kaloo G, Rai M, Singh M and Kumar S (eds), *Heterosis in Crop Plants*. Res. Book Center, New Delhi, pp. 102-113.
- Songsri P, Jogloy S, Kesmala T, Vorasoot N, Akkasaeng C, Patanothai and Holbrook CC (2008) Heritability of drought resistance traits and correlation of drought resistance and agronomic traits in peanut. *Crop Science* 48: 2245-2253.
- Sorensen D (2010) The genetics of environmental variation. In: *Proceedings of the 9th World Congress on Genetics Applied to Livestock*. Leipzig, Germany.
- Sprague GF and Tatum LA (1942) General versus specific combining ability in single crosses of corn. *Journal of the American Society of Agronomy* 34: 923-928.
- Sprague GF, Russell WA, Pennyr H, Horneran W and Hanson DWD (1962) Effect of epistasis on grain yield in maize. *Crop Science* 2: 205-208.
- Sreckov Z, Nastasic A, Bocanski J, Djalovic I, Vukosavljev M and Jockovic B (2011) Correlation and path analysis of grain yield and morphological traits in test-cross populations of maize. *Pakistan Journal of Botany* 43: 1729-1731.
- Stojaković M, Ivanović M, Jocković D, Bekavac G, Purar B, Nastasić A, Stanisavljević D, Mitrović B, Treskić S and Laišić R (2010) NS maize hybrids in production regions of Serbia. *Field and Vegetable Crops Research* 47: 93-102.
- Tandzi LN, Mutengwa CS, Ngonkew ELM, Woïin N and Gracen V (2017) Breeding for quality protein maize (QPM) varieties: A review. *Agronomy* 80: 1-16.
- Teklewold A, Wegary D, Tadesse A, Tadesse B, Bantte K, Friesen D and Prasanna BM (2015) Quality protein (QPM) maize. A guide to the technology and its promotion in Ethiopia. CIMMYT.
- Terron A, Preciado E, Cordova H, Mickelson H and Lopez R (1997) Determinacion del patron heterotico de 30 lineas de maiz derivadas del la poblacion 43 SR del CIMMYT. *Agronomy Mesoam* 8: 26-34.
- Tollenaar M, Ahmadzadeh A and Lee EA (2004) Physiological basis of heterosis for grain yield in maize. *Crop Science* 44: 2086-2094.
- Tripathy SK, Ithape DM, Maharana M and Prusty AM (2017) Quality Protein Maize (QPM): Genetic basis and breeding perspective. *Tropical Plant Research* 4: 145-152.
- Tulu BN (2014) Correlation and path coefficients analysis studies among yield and yield related traits of quality protein maize (QPM) inbred lines. *International Journal of Plant Breeding and Crop Science* 1: 6-17.

- Twumasi-Afriye S, Rojas PN, Friesen D, Teklewold A, Gissa DW, De Groote H and Prasanna BM (2016) Guidelines for the quality control of Quality Protein Maize (QPM) seed and grain: Technical bulletin. Addis Ababa, Ethiopia. CGIAR. CIMMYT.
- Udensi O and Ikpeme EV (2012) Correlation and path coefficient analyses of seed yield and its contributing traits in *Cajanus cajan* (L.) Millsp. American Journal of Experimental Agriculture 2: 351-358.
- USDA (2020) United States Department of Agriculture
<http://www.worldagriculturalproduction.com/crops/corn.aspx>.
- Vacaro E, Fernandes J, Neto B, Pegoraro DG, Nuss CN and Conccicao LH (2002) Combining ability of twellaw maize population. Pesquisa Agropecuária Brasileira 37: 67-72.
- Vasal SK (1999) Quality Protein Maize Story. In: Improving Human Nutrition Through Agriculture: The Role of International Agricultural Research: International Food Policy Research Institute Workshop held at the International Rice Research Institute, October 5-7, Los Banos, Philippines. <http://www.ifpri.cgiar.org/sites/default/files/publications/vasal.pdf>.
- Vasal SK (2002) Quality protein maize: Overcoming the hurdles. Journal of Crop Production 6: 193-227.
- Vasal SK Villegas E, Bjarnason M, Gelaw B and Goertz P (1980) Genetic modifiers and breeding strategies in developing hard endosperm *opaque-2* materials. In: Pollmer WG and Phipps RH (eds), Improvement of quality traits of maize for grain and silage use. Nijhoff, The Hague, Netherlands, pp. 37-71.
- Visscher PM, Hill WG and Wray NR (2008) Heritability in the genomics era - Concepts and misconceptions. Nature Reviews Genetics 9: 255-266.
- Wegary D, Labuschagne MT and Vivek BS (2011) Protein quality and endosperm modification of quality protein maize (*Zea mays* L.) under two contrasting soil nitrogen environments. Field Crop Research 121: 408-415.
- Wegary D, Vivek BS and Labuschagne MT (2014) Combining ability of certain agronomic traits in quality protein maize under stress and nonstress environments in Eastern and Southern Africa. Crop Science 54: 1004-1014.
- Werle AJK, Ferreira FRA, Pinto RJB, Mangolin CA, Scapim CA and Gonçalves LSA (2014) Diallel analysis of maize inbred lines for grain yield, oil and protein. Crop Breeding and Applied Biotechnology 14: 23-28.

- Wessel-Beaver L, Lambert RJ and Dudley JW (1985) Genetic variability and correlations in a modified endosperm texture *opaque-2* maize population. *Crop Science* 25: 129-132.
- Xu N, Fok M, Zhang G, Li J and Zhou Z (2014) The application of GGE biplot analysis for evaluating test locations and mega-environment investigation of cotton regional trials. *Journal of Integrative Agriculture* 13: 1921-1933.
- Yan W K, Kang M S, Ma B, Woods S and Cornelius PL (2007). GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Science* 47: 643-655.
- Yan W, Hunt LA, Sheng Q and Szlavnics Z (2000) Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science* 40: 597-605.
- Yang W, Zheng Y, Zheng W and Feng R (2005) Molecular genetic mapping of a high-lysine mutant gene (*opaque-16*) and the double recessive effect with *opaque-2* in maize. *Molecular Breeding* 15: 257–269.
- Zali H, Farshadfar E and Sabaghpour SH (2011) Non-parametric analysis of phenotypic stability in chickpea (*Cicer arietinum* L.) genotypes in Iran. *Crop Breeding Journal* 1: 89-100.
- Zerihun J (2011) GGE – biplot analysis of multi–environment yield trials of barley (*Hordeum vulgare* L.) genotypes in southeastern Ethiopian highlands. *International Journal of Plant Breeding and Genetics* 5: 59-75.
- Zhang W, Yang W, Wang M, Wang W, Zeng G, Chen Z and Cai Y (2013) Increasing lysine content of waxy maize through introgression of *opaque-2* and *opaque-16* genes using molecular assisted and biochemical development. *PLoS ONE* 8(2): e56227. doi:10.1371/journal.pone.0056227
- Zhang PP, Song H, Ke XW, Jin XJ , Yin LH , Liu Y, Qu Y , Su W, Feng NJ, Zheng DF and Feng BL (2016) GGE biplot analysis of yield stability and test location representativeness in proso millet (*Panicum miliaceum* L.) genotypes. *Journal of Integrative Agriculture* 15: 1218-1227.
- Živanović T, Maja Vračarević M, Krstanović S and Šurlan-Momirović G (2004) Selection on uniformity and yield stability in maize. *Journal of Agricultural Science* 49: 117-130.
- Živanović T, Vuckovic S, Prodanovic S and Todorovic G (2006) Evaluation of inbred lines as sources of new alleles for improving elite maize hybrid. *Cereal Research Communications* 34: 941-948.

Zobel RW, Wright MJ and Gauch HG (1988) Statistical analysis of a yield trial. *Agronomy Journal* 80: 388-393.

CHAPTER THREE

QUALITY AND NON-QUALITY PROTEIN MAIZE INBRED LINES: STABILITY AND PERFORMANCE IN SOUTHERN AFRICA

3.1 Abstract

Malnutrition as a result of deficiency of essential nutrients in cereal food products and consumption of a poorly balanced diet is a major challenge facing millions of people in developing countries. However, developing maize inbred lines which are high yielding with enhanced nutritional traits for hybrid development, still remains a challenge. This study evaluated 40 inbred lines: 26 quality protein maize (QPM) based lines, nine non-QPM lines and five checks (three QPM and two non-QPM) at seven optimum environments in Zimbabwe and South Africa during the 2017/2018 cropping season. The objective of the study was to identify high yielding and stable QPM inbred lines and to determine the level of association between measured traits, and assess the performance of the lines for quality traits and zein proteins. The experimental design used at all locations was a 5 x 8 alpha lattice design with two replications. Observations were made on grain yield and yield components, agronomic characteristics as well as quality traits. The results showed that genotypes varied significantly for all the measured traits. The top six performing lines out-yielded the best yielding check by more than 15%. The top two performers (also the most stable performers) were non-QPM, but three of the six top performers were non-QPM. The average yield of QPM lines was higher than that of non-QPM lines, and several high yielding and stable QPM lines were identified. Inbred lines 39, 27 and 10 had protein content above 9.0% while lines 16, 5 and 2 had tryptophan concentrations above 0.09%. The predominant zein proteins were 21.87% β -zein, 64.87% γ -zein and 65.17% α -zein. The first four principal components (PC's) from PCA accounted for 98% of the total variation among the traits with PC1 explaining 82% of the variation. The GGE biplot captured 71.18% of the total variation due to the interaction between genotype and environment. The high yielding and stable lines identified in this study could be exploited by breeding programmes for the development of high yielding QPM hybrid(s) in sub-Saharan Africa.

Keywords: Inbred line development, grain yield, stability, quality protein maize, trait association, principal component analysis, “Which won where”.

3.2 Introduction

Malnutrition, due to a lack of a balanced diet, has become a chronic disease in under-developed and developing countries, affecting about two billion people (Sarika et al. 2018), leading to about 45% child mortality among infants under five years (Black et al. 2013). Consequently, malnutrition has become an international problem and has caused an 11% loss of annual gross domestic product (GDP) in Africa and other developing countries (Sarika et al. 2018). Maize is the third most important staple cereal food crop in the world after wheat and rice, and contributes about 30% of food-calorie intake and is a source of protein for more than 4 billion people in 94 developing countries (Shiferaw et al. 2011).

In addition to being a source of carbohydrate and proteins for humans, maize serves as source of feed to animals and industrial purposes in developed countries. Even though maize plays a crucial food role for billions of people, its endosperm contains inadequate lysine and tryptophan, which are essential amino acids for human and other monogastric animals. These essential, but limited, amino acids have, in some cases, been supplemented in food products at the point of milling through food biofortification to raise nutrient levels to those of meat, egg, fish and milk, which are the best sources of protein. Hence, to make quality protein available to the poorer section of people in society, there is a need to develop plant-based food products with enhanced nutritional content (Eshetie 2017). This has led to the development of QPM in the 1960's through conventional breeding, to ameliorate nutritional content of the traditionally cultivated varieties to combat malnutrition. Scientists from both national and international maize research programmes work on enhancing the levels of essential amino acids. Development of biofortified crop varieties with improved nutritional value through conventional breeding approaches provides a sustainable and cost-effective solution to combat malnutrition (Gupta et al. 2015). Maize parental lines are the fundamental genetic materials essential for understanding the mechanism and principles of breeding. Inbred lines have been utilized effectively in several studies in the areas of applied plant genetics and molecular breeding (Liu et al. 2003; Semagn et al. 2012; Wegary et al. 2018).

Over the past years, a large number of QPM inbred lines have been developed and successfully used as parents in generating hybrids and synthetic varieties (Njeri et al. 2017; Sood et al. 2017; Wegary et al. 2018). Inbred lines also serve as source of favourable genes for crop improvement (Menkir et al. 2003). Inbred lines or hybrids are better sources of genetic materials for maize production than open pollinated varieties. Parental materials form the basis on which the development of stable and high yielding maize hybrids revolve (Chandel et al. 2014). As such, inbred lines should be extensively evaluated at different locations for consistency in performance of grain yield and other traits of interest. Examining GEI is very important in crop development because several factors contribute to the performance of a genotype as the production environment is variable. GEI studies enable superior cultivars and environments to be identified (de Oliveira et al. 2019). Even though there are several methods available for identifying the stability of maize genotypes, the GGE biplot analysis has been reported to be more efficient than other methods, because it makes use of first and second component axes and predicts mean performance of each genotype in each environment (Yan and Holland 2010; Santos et al. 2017; de Oliveira et al. 2019). There is currently limited information on yield performance and stability of new QPM inbred lines developed by CIMMYT, even though studies have been conducted to group QPM inbred lines into heterotic groups. Therefore, the objective of this study was to identify high yielding and stable QPM inbred lines and to determine associations among yield and yield components as well as agronomic characteristics.

3.3 Materials and methods

3.3.1 Genetic material and field evaluation

The genetic material used consisted of 26 QPM based inbred lines and nine non-QPM lines as well as five commercial checks (three QPM and two non-QPM) (Table 3.1) developed by CIMMYT, Zimbabwe. The experiment was carried out under optimum conditions at Cedara (latitude -29.54°, longitude 30.26°, with elevation of 1066 m above sea level, with reddish brown clay soils) and Potchefstroom (latitude -26.73°, longitude 27.08°, with elevation of 1349 m above sea level, with brown sandy loam soils) in South Africa. Trials were grown under normal and misting conditions (which is used to induce diseases) in Harare (latitude 17°46', longitude 31°02', with elevation of 1406 m above sea level), Glendale (latitude 17°31', longitude 31°3', with elevation 1147 above sea level) and Glendale (late planting thus two months after main planting season) and Gwebi (latitude

17°13', longitude 31°E, altitude of 1406 above sea level) in Zimbabwe during the 2017/2018 cropping season.

The experimental design used was a 5 x 8 alpha lattice design with two replications at all locations. The experimental unit was one-row plots, each 4 m long with inter-row spacing of 0.75 m and spacing within rows of 0.25 m. Two seeds were planted per hill and seedlings later thinned to one plant per hill at four weeks after emergence to give a final plant population density of about 53 333 plants ha⁻¹. At Potchefstroom, the fertilizer regime consisted of compound fertilizer 3:2:1 (25) + Zn, applied as a basal application at planting, at a rate of 200 kg NPK ha⁻¹. LAN with 28% N was used for top-dressing in two equal splits at 28 and 56 days after emergence at a rate of 100 kg ha⁻¹ each. At Cedara, MAP at 250 kg ha⁻¹ was applied at planting, and LAN given at 150 kg ha⁻¹ in two equal splits of 75 kg ha⁻¹ at 28 and 56 days after emergence. For the Zimbabwe trials, fertilizers were applied at the recommended rate of 250 kg ha⁻¹ N, 83 kg ha⁻¹ P and 111 kg ha⁻¹ K. Basal fertilizer application was done in the form of NPK, and additional N application was done four weeks after seed emergence. Pre-emergence herbicides; Gramoxone, Basagram and 2, 4-D were applied to control weeds and after that hand weeding was done to make sure that the fields were relatively free of weeds. Insecticides; Carbaryl and Karate were applied to control stalk borer and cutworms, respectively. Carbaryl was applied at planting stage while Karate was applied at planting and seedling emergence stages.

3.3.2 Data collection

Data was recorded on days to 50% anthesis (DA) and silking (DS). Anthesis-silking interval (ASI) was calculated as the difference between DS and DA. Plant height (PH; cm) was measured as the length from the base of the plant to the last leaf (flag leaf) while ear height (EH; cm) was measured from the base to the node bearing the top ear. Root lodging (RL; %) was measured as the percentage of plants leaning more than 30° from the vertical, while stalk lodging (SL; %) was also recorded on plants with broken stalks below the ear. Number of ears per plant (EPP) was calculated by dividing the total number of ears per plot by the number of plants at harvest. Ear aspect (EA) was rated on a scale of 1 to 5 where 1 = clean, uniform, large, and well-filled ears; while 5 = ears with undesirable features such as diseased and rotten ears, small ears and ears that are not well filled with grains. Number of rotten ears was counted and converted to percentage. At harvest, field weight

(kg plot⁻¹) of the harvested ears was measured, followed by determination of moisture content. Grain yield (t ha⁻¹) was computed based on 80% shelling percentage.

3.3.3 Obtaining seed samples for quality traits analyses

The seed samples used were obtained by selfing two cobs from each entry in the two replications from four sites out of the seven used for the inbred trials. The self-pollinated seeds were harvested and the two cobs per entry were shelled and bulked for determination of tryptophan, starch, fibre, moisture, protein and oil. Amylose/amylopectin and zein proteins were also analysed.

3.3.4 Zein extraction and determination of zein fractions using reverse phase high-performance liquid chromatography

For the extraction of zein proteins, an aqueous solution containing 70% ethanol (Sigma; 96% v/v); 24.5% filtered double distilled water, 5% beta-mercaptoethanol (Sigma; ≥ 99% v/v) and 0.5% sodium acetate (Saarchem AR; w/v) was prepared as a stock solution (Gupta et al. 2016; O’Kennedy and Fox 2017). One ml of the prepared solution was added to 200 mg maize in a 2 ml reaction tube to digest the protein. The samples were vortexed for 30 min and later centrifuged for 30 min at 6 000 revolution per min (rpm). After which the supernatant was transferred to a new 2 ml reaction tube and again centrifuged for another 30 min at 6 000 rpm. After centrifugation, the remaining supernatant was transferred into a glass vial for reverse phase high-performance liquid chromatography (RP-HPLC) analysis. In the case where the supernatant could not be injected into the HPLC system, they were stored in a refrigerator at 4°C.

The RP-HPLC was done on a Shimadzu Prominence LC System using a Jupiter C18 column of 250 x 4.6 mm, with a 5 µm particle size and 300 Å pore size. Samples of 50 µl were injected and eluted with the solvent at 1 ml per minute flow rate with a column temperature of 55°C. The two solvents used were labelled A and B. Solvent A was made up of LiChrosolv Acetonitrile (Merck) containing 0.1% HiPersolv trifluoroacetic acid (TFA) (VWR chemicals) and Solvent B was filtered deionised water comprising of 0.1% (v/v) TFA and was set to run for 75 min per sample. Zein fractions were determined in a chromatograph using a Shimadzu Class-VP 6.14 SP1. Based on the distinct peak retention time, β-, γ- and α-zeins were determined.

Table 3.1 Description of the QPM and non-QPM inbred lines and checks used in the study

Code	Name	Donor	Description
L1	CZL1330	QPM progeny	Conversion of early maturing elite drought and low N stress tolerant inbred line
L2	CZL15041	QPM progeny	Conversion of Medium maturing elite MSV tolerant inbred line
L3	CZL15055	QPM progeny	Conversion of early maturing elite drought and low N stress tolerant inbred line
L4	CZL15073	QPM progeny	Conversion of early maturing elite drought and low N stress tolerant inbred line
L5	CZL1471	QPM progeny	Conversion of medium maturing elite Southern Africa adapted mid-altitude inbred line with high GCA
L6	TL135470	QPM progeny	Conversion of medium maturing elite Southern Africa adapted mid-altitude inbred line with high GCA
L7	VL06378	QPM progeny	Conversion of late maturing elite mid-altitude adapted inbred line with high GCA
L8	TL155805	QPM progeny	Conversion of late maturing elite mid-altitude adapted inbred line with high GCA
L9	TL147078	QPM progeny	Conversion of late maturing elite mid-altitude adapted inbred line with high GCA
L10	TL147070	QPM progeny	Conversion of late maturing elite mid-altitude adapted inbred line with high GCA
L11	TL13609	QPM progeny	Conversion of medium maturing elite drought tolerant mid-altitude adapted inbred line
L12	TL145743	QPM progeny	Introgressed with temperate germplasm
L13	TL156614	QPM progeny	Conversion of early maturing elite drought and low N stress tolerant inbred line
L14	CZL1477	QPM progeny	Conversion of medium maturing elite mid-altitude adapted inbred line with high GCA
L15	CZL15074	QPM donor	Conversion of elite inbred lines with mid-altitude to highland adaptation
L16	CZL0616	QPM progeny	Conversion of elite inbred lines with mid-altitude to highland adaptation
L17	CZL083	QPM progeny	Conversion of elite MSV tolerant inbred line
L18	CML572	Non-QPM parent	Elite early maturing drought and low N stress tolerant inbred line with high GCA
L19	EBL167787	Non-QPM check	Elite medium maturing MSV tolerant inbred line
L 20	CZL0520	Non-QPM parent	Elite medium maturing MSV tolerant inbred line
L 21	CZL99005	Non-QPM parent	Elite medium maturing Southern Africa adapted inbred line
L 22	CML502	QPM donor	Sub-tropical adapted
L 23	CZL0920	QPM donor	Sub-tropical adapted
L 24	CML144	QPM donor	Sub-tropical adapted
L 25	CML159	QPM donor	Mid-altitude adapted
L 26	CML181	QPM donor	Sub-tropical adapted
L 27	CML197	Non-QPM parent	Mid-altitude adapted
L 28	CML312SR	Non-QPM parent	Mid-altitude adapted, MSV tolerant
L 29	CML488	Non-QPM parent	Mid-altitude adapted, drought tolerant
L 30	CML491	QPM donor	Sub-tropical adapted
L 31	LH51	Non-QPM parent	Temperate adapted inbred line
L 32	CZL00025	Non-QPM parent	Mid-attitude to highland adapted
L33	CZL15049	QPM tester	Mid-altitude adapted
L34	CZL059	QPM tester	Mid-altitude adapted
L35	CML444	Non-QPM tester	Mid-altitude adapted
L36	CML395	Non-QPM tester	Mid-altitude adapted
L37	CZL01005	QPM check	Southern Africa adapted
L38	CML511	QPM check	Mid-altitude adapted
L39	CML 312	Non-QPM check	Mid-altitude adapted
L40	CZL1470	QPM check	Mid-altitude adapted

3.3.5 Determination of amylose using iodine

Amylose content was determined following the protocol developed by Deja Cruz and Khush (2000). Absolute ethanol was diluted with distilled water to 95% concentration. Forty g sodium hydroxide (NaOH) was dissolved in double distilled water and made to 1 L. Acetic acid was prepared from 57.2 ml of glacial acetic acid ($M_r = 60.05$; density = 1.05 g per ml) added to 1 L distilled water and the iodine solution was prepared by dissolving 0.2 g iodine and 2.0 g potassium iodide in 100 ml distilled water. Maize kernels were milled using a Fritsch (Fritsch Industries, Idar-Oberstein, Germany) analysis grinder fitted with a 0.5 mm sieve. A $0.1\text{g} \pm 0.0001\text{ g}$ sample was weighed into 15 ml tubes for analysis. A tube containing no flour was included as a reagent blank. In addition, a positive sample of known amylose percentage (64% maize amylose) was included. One ml of 95% ethanol (v/v) was added to each tube. A 9 ml NaOH solution was added followed by mixing thoroughly through vortexing with the tubes tightly closed. The samples were placed in boiling water to gelatinise the starch for 30 min. After removing the samples from the boiling water, they were allowed to cool for 1 hour at room temperature and then centrifuge for 5 min at 3 000 rpm. Of this starch solution, 100 μl was transferred into a clean 15 ml test tube and 20 μl 1M acetic acid was added, followed by adding 200 μl iodine solution. The final volume was made up to 10 ml using double distilled water. It was thoroughly mixed and left to stand for 20 min for colour development to take place, before reading the absorbance at 620 nm on a UV vis spectrophotometer (JENWAY Spectrophotometer Model 7315, Designed and Manufactured by Bibby Scientific LTD Stone, Staffs, UK, ST15 OSA).

3.3.6 Preparation of amylose standard curve

One hundred mg potato amylose (Sigma A0512) was weighed into a 15 ml test tube. A tube containing no amylose was used as reagent blank. One ml of 95% ethanol was added to each tube. Tubes were vortexed thoroughly, after which 9 ml of 1M NaOH solution was added to each tube. Tubes were heated in a boiling water bath for 10 min to gelatinise the starch. Tubes were then cooled to room temperature (1 hour) and made up to 10 ml with distilled water, followed by thorough vortexing. This stock solution was used to prepare a dilution series in 15 ml test tubes as indicated in Table 3.2 below.

Table 3.2 Description of samples used for the amylose standard curve

Tube No.	Volume of amylose stock solution taken	Volume of 1M acetic acid added	Volume of iodine solution (μL)	Volume of distilled water added to	Amylose
Blank	0.00 mL = 0 μL	0.02 mL = 20 μL	200	9.78 mL	0.0
1	0.02 mL = 20 μL	0.02mL = 20μL	200	9.76 mL	0.2
2	0.04 mL = 40 μL	0.04 mL = 40μL	200	9.72 mL	0.4
3	0.06 mL = 60 μL	0.06mL = 60μL	200	9.68 mL	0.6
4	0.08 mL = 80 μL	0.08mL = 80μL	200	9.64 mL	0.8
5	0.10 mL = 100 μL	0.10mL = 100μL	200	9.60 mL	1.0
6	0.15 mL = 150 μL	0.15mL = 150μL	200	9.50 mL	1.5
7	0.20 mL = 200 μL	0.20mL = 200μL	200	9.40 mL	2.0
8	0.25 mL = 250 μL	0.25mL = 250μL	200	9.30 mL	2.5
9	0.30 mL = 300 μL	0.30mL = 300μL	200	9.20 mL	3.0
10	0.35 mL = 350 μL	0.35mL = 350μL	200	9.10 mL	3.5
11	0.40 mL = 400 μL	0.40mL = 400 μL	200	9.00 mL	4.0

1M acetic acid was added as described in the table above followed by 200 μl iodine solution to each tube. Double distilled water was added to bring the total volume to 10 ml. It was mixed well and was allowed to stand for 20 min at room temperature. Samples were read at 620 nm absorbance using the blank to zero the spectrophotometer.

Figure 3.1 shows the standard curve developed and was used in the calculation of the amylose content in each sample. The amylose percentage was calculated as follows:

$$\text{Amylose \%} = \frac{\text{Total amylose in sample (mg)}}{\text{Sample mass (mg)}} \times 100$$

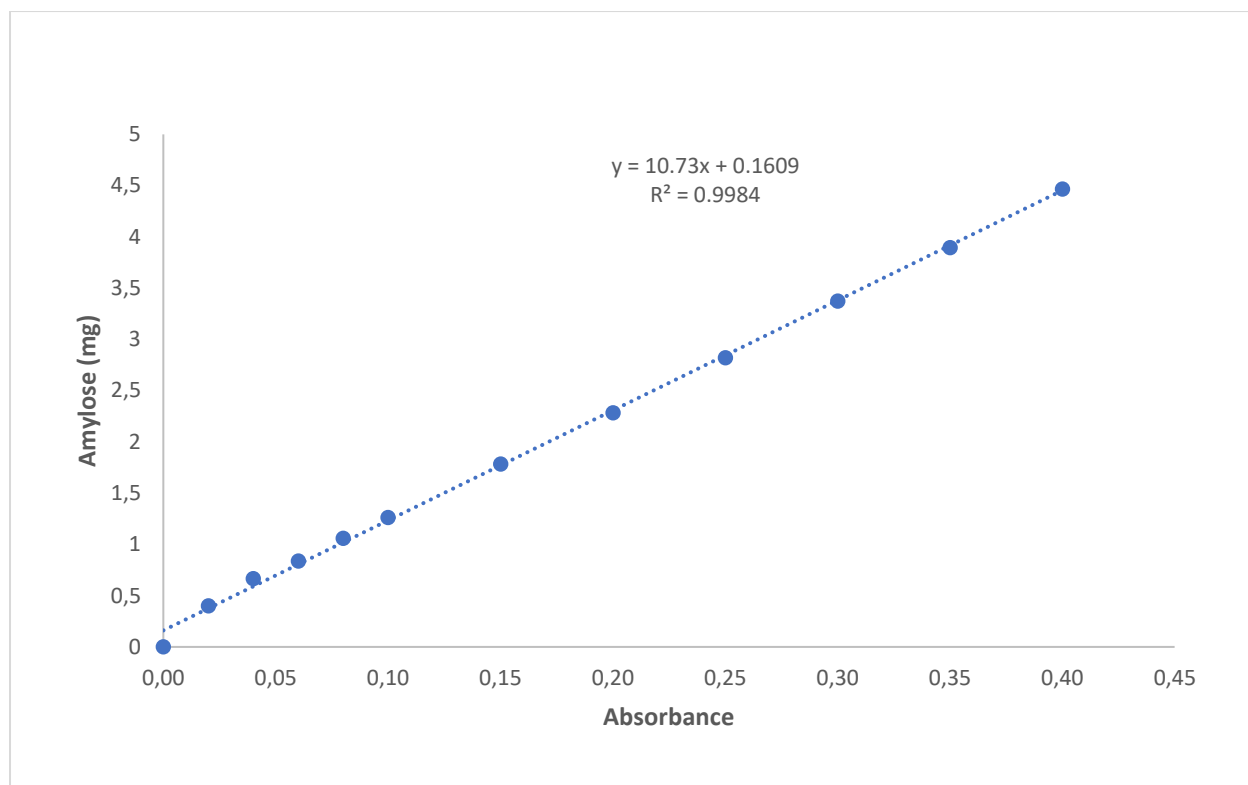


Figure 3.1 Standard curve developed for amylose determination

3.3.7 Determination of tryptophan

3.3.7.1 Seed sample selection, milling and defatting

Fifty kernels of uniform size were selected from the bulked seed samples. The selected kernels were clean and had no rotten kernels. The kernels were milled into a fine flour using a Fritsch analysis grinder. The ground samples were passed through a built-in 0.5 mm sieve. Two g of the sieved samples were placed into 50 ml Falcon tubes for defatting. A mixture of 10 ml chloroform and methanol in a 2:1 ratio (v/v) was added to each sample and was kept at 4°C for 12 hours. After standing to reach room temperature, the samples were washed three times using the same amount of above mixture using commercial filter paper (Grade: 3 hw Art.no.: 3.303.185). The samples, which were trapped in the filter paper, were left in open air to dry. The dried samples were stored at 4°C for tryptophan determination.

3.3.7.2 Determination of tryptophan content

A standard curve was first developed (Figure 3.2) using glyoxylic acid reaction, DL-tryptophan, ferric chloride and sulphuric acid (H₂SO₄) according to the protocol of Nurit et al. (2009). Concentrations of 0, 10, 15, 20, 25 and 30 µg ml⁻¹ were prepared from the DL-tryptophan stock solution in 0.1 M sodium acetate (pH 7). A 1 ml aliquot was transferred from each sample into a 15 ml glass tube and 3 ml of colorimetric reagent was added into each test tube. The samples were vortexed for 8-10 sec and then incubated in a water bath at 64°C for 30 min to enable colour development. After 30 min, the samples were taken from the water bath and then cooled at room temperature for optical density readings using a spectrophotometer (Jenway Spectrophotometer Model 7315, Designed and Manufactured by Bibby Scientific LTD Stone, Staffs, UK, ST15 OSA). The readings obtained were used in drawing a calibration curve with the slope having a unit of OD_{560nm} x ml µg⁻¹.

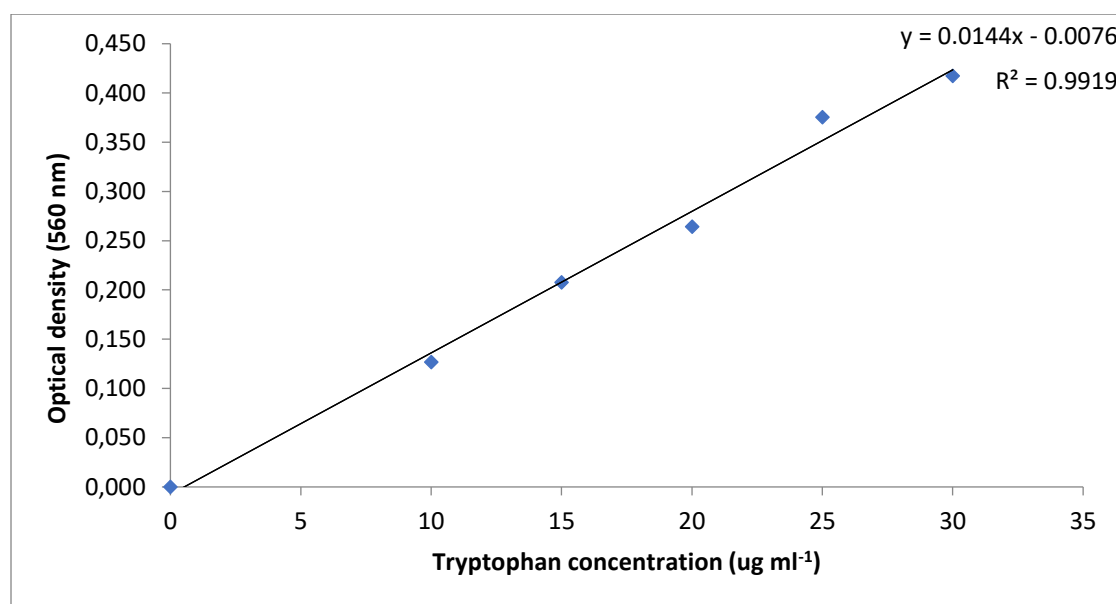


Figure 3.2 Standard curve developed and used in the calculation of tryptophan contents of the samples analysed

Tryptophan percentage was then calculated following Nurit et al. (2009) as:

$$\text{Tryptophan (\%)} = \frac{\text{OD}_{560\text{nm}}}{\text{slope}} \times \frac{\text{hydrolysis volume}}{\text{sample weight}} \times 100$$

Papain and sodium acetate solutions were prepared on a daily basis as required. Chemicals and reagents were prepared as follows:

One mg ml⁻¹ papain was dissolved in 0.165 M sodium acetate solution. Sodium acetate solution was prepared by dissolving 13.6 g of sodium acetate in 1 000 ml of double distilled water and stored in the refrigerator at 4°C. A 30 N of H₂SO₄ stock solution was prepared by adding 833.30 ml of H₂SO₄ (96%) concentration slowly into a glass beaker with 166.70 ml of double distilled water making a volume of 1000 ml while placed on ice, it was allowed to cool down to room temperature. A 7 N of H₂SO₄ stock solution was prepared by mixing 35 ml 30 N of H₂SO₄ and 115 ml of double distilled water to prepare 150 ml 7 N of H₂SO₄. Required reagents were prepared daily. Reagent A was made up of 0.1 M glyoxilic acid by weighing 0.736 g of glyoxilic acid into a 100 ml glass beaker. Thereafter, 80 ml of 7 N H₂SO₄ was added, which was shaken gently until all the granules of the glyoxilic acid was dissolved completely. Reagent B, consisted of 1.8 mM ferric chloride, where 0.0389 g was added to reagent A. This mixture was called reagent C. Reagent D, which could also be referred to as the colorimetric reagent, was formed by adding 80 ml of 30 N H₂SO₄ to reagent C. Aluminium foil was used to wrap the glass beaker containing the colorimetric reagent to prevent light and oxygen interactions.

For tryptophan analysis, 0.08 g of each defatted sample was placed in a 15 ml Falcon tube and 3 ml of the papain and sodium acetate solution was added to digest the samples. For daily analysis, two blank controls with papain and sodium acetate solution were added to calibrate the spectrophotometer to zero before reading the actual samples. The tubes containing the samples were vortexed for 10 sec. The vortexed samples were incubated in the water bath at a temperature of 64°C for 16 hours. During incubation, the samples were vortexed twice, an hour after putting the samples into the water bath and one hour before the end of the incubation period. The samples were taken out of the water bath after the incubation period and allowed to cool down to an ambient temperature, then vortexed and centrifuged at 3 600 rpm for 5 min. One ml of the hydrolysate from each sample was transferred into glass tubes and 3 ml of the colorimetric reagent was added. The samples were vortexed for 10 sec then placed into the water bath at 64°C for 30 min. The samples were taken out of the water bath and were cooled down to room temperature after which optical density or absorbance was read at 560 nm with a spectrophotometer (Jenway Spectrophotometer Model 7315).

3.3.8 Starch determination

A polarimetric method was used to determine total starch following Caprita et al. (2011). Ground maize samples (2.5 g) were weighed into 100 ml Erlenmeyer flasks. Fifty ml of a 32% GR HCL (Merck) solution was added and the flasks placed in the water bath at 95°C for 15 min. After this, the samples were removed and allowed to cool down to 20°C after which the samples were transferred into 100 ml volumetric flasks. A 10 ml 4% GR tungstonphosphoric acid (Sigma) solution was added followed by adding double distilled water to make up the volume to 100 ml. The mixture was gently shaken and inverted for several times to allow the water to mix thoroughly with the tungstonphosphoric acid. The mixture was then double filtered using Whatman no. 4 filter paper until a volume of about 70 ml was achieved. The filtrate was then read on an automatic polarimeter (ATAGO® AP-300) at 589 nm.

The percentage of starch in the sample was computed as follows:

$$\text{Starch (\%)} = \frac{100000 \times P}{L \times [\alpha]_D^{20^\circ} \times S}$$

Where P = the measured angle of the optical rotation in degree;

L = Length (dm) of the sample tube

$[\alpha]_D^{20^\circ}$ = specific rotation of the pure starch

S = Exact mass of the sample weight out

3.3.9 Determination of protein, oil, moisture and fibre

A total of 500 g of the self-pollinated seeds for each sample was used for protein, oil, moisture and fibre content determination using near-infrared transmission spectroscopy (NIR) using a Perten Grain Analyzer (Model DA 7250, Perten, Instruments AB, Sweden), with three subsamples for each sample. Agri-Envrion Solutions (www.aelab.co.za) calibrated the NIR instrument before use. Results from the wet chemistry for 50 samples was used in the calibration for all parameters determined using the NIR. The correlation between the wet chemistry and the NIR values was more than 90%, making the NIR values reliable (data not shown). The percentage of oil, protein, moisture and fibre contents were expressed on a dry matter percentage weight basis (%wt).

3.3.10 Data analysis

ANOVA was done on plot means for grain yield and all measured traits from the field and laboratory experiments with PROC GLM in SAS (SAS Institute, 2011 version 9.4). Prior to the ANOVA, best linear unbiased predictors (BLUPs) of plot means for all traits across the seven environments were calculated. In the combined ANOVA, location, replications and blocks of each experiment were regarded as random factors while entries were considered as fixed effects. The PCA was performed on the phenotypic variables and correlation matrix was obtained from the BLUPs for all the measured traits using the PRINCOMP in SAS. The PCA was used to identify quantitative phenotypic characters that represent independent systems of trait variation.

The grain yield data was subjected to GGE biplot analysis to determine inbred line stability according to Yan (2001) and Yan et al (2001) using GenStat edition 16 (GenStat 2012). Genetic correlation coefficient (r_G) estimates were determined to show the level of association between grain yield and its components and among other yield components and agronomic traits using SAS.

3.4 Results

3.4.1 Analysis of variance for individual and combined locations

At Harare and Gwebi, the inbred lines varied significantly for grain yield and most of the other characteristics examined, except anthesis-silking interval, root and stalk lodgings, husk cover and ear rot (Table 3.3). Harare, under misting conditions, showed significant variation between the inbreds for grain yield, days to anthesis, anthesis-silking interval, plant and ear heights, root lodging, ears per plant and ear rot, while the rest of the traits were not statistically different ($P > 0.05$). Apart from root lodging, ears per plant, husk cover and ear aspect did not differ significantly at Glendale. The rest of the traits differed significantly. At the Glendale late planting there were significant differences for most of the traits measured, except root lodging, ears per plant and husk cover. The trials established at Cedara and Potchefstroom showed significant variations for the inbred lines for almost all the traits except anthesis-silking interval, root and stalk lodging at both locations, and ear rot at Cedara. Across the seven locations, genotypes varied significantly for all the traits examined, except stalk lodging. GEI was significant for all traits except for anthesis-silking interval, stalk lodging and husk cover (Table 3.3).

3.4.2 Performance of inbred lines across locations

The grain yield ranged from 0.75 t ha⁻¹ for QPM inbred line 27 to 3.73 t ha⁻¹ for non-QPM inbred line 29 with an average of 2.45 t ha⁻¹ (Table 3.4). Days to anthesis and ASI varied among the lines, ranging from 71.28 to 85.02 days and -1.49 to 3.75, respectively. Inbred line 2 was the most prolific genotype producing nearly two cobs per plant (Table 3.4). Ear rot ranged from 1.05 for line 27 to 7.71 for line 26. Ear aspect varied among the lines.

3.4.3 Analysis for variance for quality traits and zein proteins in 40 inbred lines

The biochemical analysis for the seed samples grown at Cedara showed significant variations among the inbred lines for the traits analysed except for protein and β -zein, while the seed samples from Potchefstroom produced significant differences for all quality traits analysed. Harare seed samples also showed significant variation among the inbred lines for all the traits except amylose and γ -zein; while moisture, oil, fibre and tryptophan contents were the only traits showing significant variation for seed samples obtained from Gwebi (Table 3.5). The combined ANOVA for the seed samples across the four locations for all traits revealed significant variations, while GEI also influenced the majority of the traits analysed except protein, starch, γ -zein and α -zein.

3.4.4 Performance of the lines for quality traits across four locations

Moisture content varied from 11.87% for line 38 to 14.02% for line 19. Protein ranged from 5.80 to 10.19% for inbred lines 40 (QPM) and 39 (non-QPM check), respectively. Oil content ranged from 3.05 to 6.22% for lines 30 (QPM) and 20 (non-QPM), respectively. Starch content ranged from 57.49 to 67.49% for inbred lines 14 (QPM) and 28 (non-QPM), respectively. Amylose ranged from 31.32% for line 32 (non-QPM) to 83.57% for line 6 (QPM). Fibre content varied from 2.46 to 2.98% for genotypes 9 and 6, respectively (both QPM). Tryptophan contents ranged from 0.034% for line 36 (non-QPM) to 0.094% for line 16 (QPM). Beta-zein ranged from 2.26 to 21.87% for lines 21 and 6, respectively; γ -zein ranged from 18.49% for 39 to 64.69% for 24 and values of 19.93 to 65.17% for α -zein was recorded for lines 25 and 35, respectively (Table 3.6). Quality index (QI) of the inbred lines ranged from 0.37 to 1.38 for line 39 and line 25, respectively. All the QPM lines have higher QI than non-QPM lines.

Table 3.3 Analysis of variance for grain yield and other agronomic traits of 40 inbred lines evaluated in seven environments in Zimbabwe and South Africa during the 2017/2018 cropping season

Source	DF	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	ER	EA
Harare												
Rep	1	0.04	59.51**	42.05*	720.00**	551.25*	2.74	0.01	0.01	0.38	1.74	0.11
Block(rep)	14	0.43*	4.05	5.45	219.48**	101.29	0.78	0.07	0.03	17.15	0.73	0.10
Entry	39	1.74**	30.20**	6.78	315.33**	268.57**	0.47	0.09	0.08**	15.13	5.40**	0.39**
Error	25	0.19	8.25	9.42	83.29	90.23	0.77	0.13	0.02	13.68	1.65	0.13
Gwebi												
Rep	1	0.11	39.20*	1.80	475.31*	52.81	1.27	0.01	0.01	8.68	2.39	0.45
Block(rep)	14	0.15	4.43	1.42	75.65	81.51	4.06	0.59	0.05	5.56	1.15	0.11
Entry	39	1.17**	24.15**	1.55	369.02**	207.60**	7.49	0.46	0.25**	3.74	6.18**	0.43**
Error	25	0.24	6.27	1.61	75.12	67.74	4.05	0.49	0.05	3.47	1.85	0.17
Harare-misting												
Rep	1	2.01*	22.05*	5.51	61.25	86.11	0.19	0.01	0.07	0.99	0.99	0.16
Block(rep)	14	0.23	3.07	3.24	93.59	65.28*	0.58	0.35	0.04	3.26	3.26	0.09
Entry	39	0.47*	19.43**	7.16**	352.60**	240.99**	0.43ns	0.28	0.07**	6.77	6.77	0.26*
Error	25	0.23	3.44	2.47	83.14	29.78	0.34	0.29	0.02	4.58	4.58	0.12
Glendale												
Rep	1	2.08	0.31	4.05	11.25	1.25	24.52*	1.88	0.01	4.22	1.06	0.01
Block(rep)	14	1.91	1.87	0.90	453.39*	258.13*	12.14**	0.97	0.24	1.89	4.70	0.15
Entry	39	6.11**	8.89**	2.28*	457.40**	244.62**	7.31*	1.24	0.33	2.25	8.61**	0.62
Error	25	1.76	2.76	1.05	165.65	92.40	3.21	0.89	0.18	2.59	3.37	0.22
Glendale –late												
Rep	1	2.08	0.31	4.05	11.25	1.25	24.52*	1.88	0.01	4.22	1.06	0.01
Block(rep)	14	1.91	1.87	0.90	453.39*	258.13*	12.14**	0.98	0.24	1.89	4.70	0.15
Entry	39	6.11*	8.89**	2.28*	457.40**	244.62**	7.31*	1.23	0.33	2.25	8.61**	0.61**
Error	25	1.76	2.76	1.05	165.65	92.40	3.20	0.89	0.18	2.59	3.37	0.22
Cedara												
Rep	1	0.01	9.80	1.01	361.25	106.95	0.04	0.12	0.08	0.20	2.43	0.80*
Block(rep)	14	0.11	5.33	2.32	244.25	185.41*	3.70	1.54	0.04	0.16	2.028	0.16
Entry	39	1.87**	18.21**	2.93	419.76**	317.74**	2.39	1.54	0.16**	0.33**	3.77	0.63**
Error	25	0.16	2.54	3.08	164.27	81.52	1.88	1.11	0.06	0.10	2.13	0.19
Potchefstroom												
Rep	1	0.05	5.00	0.11	74.11	11.25	0.11	0.20	0.24*	0.013	0.31	0.15
Block(rep)	14	0.21	2.95	1.74	274.53**	70.57	0.39	0.17	0.05	0.20	4.70	0.45
Entry	39	5.39**	40.25**	4.89	535.59**	368.68**	0.31	0.44	0.08*	1.02**	8.66**	1.47**
Error	25	0.33	6.38	3.84	68.68	36.87	0.19	0.30	0.04	0.21	2.91	0.31
Across locations												
Environment(E)	6	83.25**	5073.51**	64.60**	19851.21**	11885.76**	239.94**	7.23**	3.09**	96.94**	196.56**	9.16**
Rep (E)	7	0.65	21.02**	8.42*	312.84**	162.55*	4.13*	0.45	0.08	2.43	3.33	0.26
Block(E*Rep)	98	0.50	3.80	3.03	211.86**	115.99**	3.21**	0.56	0.07	4.36	2.50	0.20
Genotype (G)	39	5.56**	93.42**	8.40**	1863.13**	1131.66**	4.97**	0.66	0.42**	3.76	15.71**	1.10**
G x E	232	1.12**	6.67**	3.54	154.00*	95.30*	2.64**	0.58	0.11**	3.87	5.70**	0.51**
Error	172	0.49	4.93	3.86	116.11	74.01	1.70	0.51	0.06	3.55	2.83	0.19
R-Square		0.94	0.98	0.76	0.94	0.93	0.90	0.78	0.87	0.764226	0.88	0.89

DF = degree of freedom; GY = grain yield; DA = Days to anthesis; ASI = anthesis silking interval; PH = plant height; EH = ear height; RL = root lodging; SL = stalk lodging; EPP = ear per plant; HC = husk cover. ER = ear rot; EA = ear aspect *P<0.05, **P<0.01

Table 3.4 Mean grain yield and other agronomic traits of 40 inbred lines evaluated at seven locations in Southern Africa during the 2017/2018 cropping season

Line code	Line status	GY	DA	ASI	PH	EH	EPP	RL	SL	ER	EA
		t ha ⁻¹			cm			%			1-5
L1	QPM	3.15	77.27	1.43	172.76	85.32	1.25	2.41	1.58	3.16	2.98
L2	QPM	2.79	76.72	1.19	189.28	93.00	1.58	3.39	1.08	4.31	3.29
L3	QPM	3.57	71.28	1.47	158.18	61.68	1.00	1.74	1.42	5.01	3.00
L4	QPM	2.95	72.45	1.82	160.25	63.21	1.16	2.82	1.33	5.81	3.49
L5	QPM	2.22	72.44	1.60	133.17	58.51	1.20	4.08	1.60	3.77	3.22
L6	QPM	3.23	72.33	3.75	148.55	63.35	1.50	4.24	1.28	3.29	3.23
L7	QPM	1.18	77.06	0.66	173.87	77.45	1.05	2.62	1.15	3.52	3.97
L8	QPM	1.89	76.28	2.03	159.33	75.36	0.94	1.96	1.48	4.57	3.50
L9	QPM	1.71	80.74	1.63	180.75	92.94	1.13	2.01	1.14	4.24	3.52
L10	QPM	2.76	81.99	1.66	191.38	99.28	1.26	3.23	1.07	3.21	2.99
L11	QPM	1.76	74.94	3.15	161.34	68.68	0.79	1.66	1.30	3.25	3.33
L12	QPM	2.96	78.74	0.82	155.77	70.53	1.20	1.90	1.60	3.77	3.01
L13	QPM	2.86	76.52	1.57	170.48	76.18	1.27	1.61	1.05	4.82	3.20
L14	QPM	1.34	75.54	1.24	185.98	85.85	1.07	3.53	0.84	3.14	3.78
L15	QPM	2.67	78.49	-0.15	151.55	77.95	1.08	2.07	1.25	3.65	3.19
L16	QPM	2.59	79.62	2.81	158.54	75.21	1.12	2.24	1.15	2.95	2.82
L17	QPM	3.16	80.76	0.19	184.36	95.07	1.29	3.49	2.11	2.29	2.69
L18	non-QPM	1.69	72.91	2.93	149.48	60.30	0.98	2.27	1.48	5.44	3.13
L19	non-QPM	1.22	77.77	2.11	159.02	67.56	1.00	2.11	1.19	6.25	3.69
L 20	non-QPM	2.39	73.94	1.43	165.81	83.56	1.15	2.66	1.18	4.65	3.67
L 21	QPM	2.31	80.40	-1.49	147.57	81.81	0.83	2.55	1.58	3.80	3.11
L 22	QPM	1.23	81.13	1.58	166.19	64.97	0.93	2.59	1.09	4.27	3.82
L 23	QPM	2.88	78.94	0.80	159.53	65.84	1.16	1.47	1.17	5.00	2.99
L 24	QPM	3.25	78.24	0.22	162.94	76.38	1.40	2.86	1.24	3.32	3.08
L 25	QPM	1.70	77.01	1.56	159.08	67.92	1.11	2.49	1.24	5.77	3.79
L 26	QPM	2.80	72.75	0.17	145.71	65.88	1.18	1.56	0.98	7.71	3.85
L 27	non-QPM	0.75	85.02	-1.05	203.66	126.29	0.88	1.00	1.04	1.05	1.82
L 28	non-QPM	3.71	72.27	1.29	146.27	65.77	1.38	2.26	0.97	3.51	2.84
L 29	non-QPM	3.73	78.44	0.94	152.97	70.49	1.39	2.30	1.18	2.43	2.86
L 30	QPM	3.20	79.97	2.08	170.37	82.47	1.35	1.23	1.16	3.49	3.01
L 31	non-QPM	1.35	71.44	2.37	146.27	67.16	0.82	2.44	1.13	5.06	3.58
L 32	non-QPM	1.87	75.35	1.13	181.83	91.28	0.92	2.04	1.60	3.97	3.44
L33	QPM	2.84	74.41	2.07	143.64	60.05	1.01	1.64	1.12	4.46	3.11
L34	QPM	2.58	80.24	1.69	180.21	92.14	1.33	2.56	1.95	2.74	2.87
L35	non-QPM	3.27	76.70	-0.59	158.92	80.94	1.11	2.63	1.39	2.74	2.83
L36	non-QPM	2.91	77.53	1.21	170.30	81.91	1.03	1.83	0.90	3.38	2.77
L37	QPM	3.18	73.94	1.67	155.45	82.58	0.98	2.45	1.20	7.02	3.16
L38	QPM	1.15	72.87	2.54	150.13	56.41	1.25	1.01	1.41	3.35	3.54
L39	non-QPM	1.39	77.49	1.68	156.01	69.71	0.76	1.84	1.05	4.76	3.53
L40	QPM	2.51	75.59	1.42	168.56	76.34	1.56	3.33	1.17	5.71	3.29
QPM mean		2.50	76.85	1.42	163.62	75.60	1.17	2.44	1.30	4.19	3.27
Non-QPM mean		2.21	76.26	1.22	162.78	78.63	1.04	2.13	1.19	3.93	3.11
Total mean		2.45	76.70	1.40	162.80	75.91	1.13	2.39	1.27	4.21	3.26
SE		0.70	2.22	1.96	10.78	8.60	0.25	1.30	0.71	1.68	0.43

† GY= grain yield; DA = days to anthesis; ASI = anthesis silking interval; PH = plant height; EH = ear height; EPP = ear per plant; RL = root lodging; SL = stalk lodging; ER = ear rot; EA = ear aspect; SE = standard error

Table 3.5 Analysis of variance of quality traits analysed for 40 inbred lines at four environments in Zimbabwe and South Africa during the 2017/2018 cropping season

Source	DF	Moisture %	Protein %	Oil %	Fibre %	Starch %	Tryptophan %	Amylose %	β-Zein	γ-Zein	α-Zein	QI
Cedara												
Rep	1	0.16	0.61	0.03	0.01	23.62*	0.000003	15.77	54.90	14.30	110.80	0.03
Block(rep)	14	0.18	0.34	0.37	0.01	2.36	0.000026	13.24*	31.38	284.91	357.91	0.01
Entry	39	0.61*	0.86	1.44*	0.04*	9.59*	0.000700**	224.68**	29.47	814.77**	596.97*	0.11**
Error	20	0.30	0.59	0.47	0.02	4.81	0.000026	3.99	43.81	185.02	277.94	0.01
Potchefstroom												
Rep	1	0.56	0.01	0.82	0.03	5.61	0.00012*	3.43	2.89	506.42	184.40	0.01
Block(rep)	14	0.14	0.26	0.61	0.02	1.93	0.00001	13.95*	1.05	113.45	123.29	0.01
Entry	39	0.42*	1.77**	1.77**	0.08**	11.59**	0.00007**	127.90**	2.56*	626.25**	749.91**	0.11**
Error	20	0.17	0.41	0.44	0.01	3.38	0.00001	5.62	1.09	173.98	102.07	0.01
Harare												
Rep	1	0.15	0.01	0.01	0.02	0.44	0.00005	25.97	51.47	265.39	1124.40*	0.05
Block(rep)	14	0.30	0.11	0.07	0.03	0.40	0.00003	2355.03	39.93	316.37	98.22	0.03
Entry	39	0.42	2.12*	1.05*	0.04*	3.16**	0.00048**	2459.23ns	159.55**	455.05	491.71**	0.16**
Error	20	0.28	0.45	0.08	0.01	0.13	0.00004	1861.53	31.43	279.22	132.02	0.01
Gwebi												
Rep	1	0.06	0.23	0.30	0.00	0.04	0.00005	23.99	34.95	8228.20*	52.26	0.01
Block(rep)	14	0.04	0.51	0.11	0.00	0.89	0.00003	4.93	13.56	491.27	758.97	0.01
Entry	39	0.22*	2.33	0.97*	0.010*	4.70	0.00050**	166.79	11.12	390.22	591.20	0.11**
Error	20	0.07	1.00	0.13	0.00	1.41	0.00002	7.54	23.68	454.75	806.43	0.01
Across locations												
Environment (E)	3	29.43**	199.54*	7.50*	1.50**	719.28**	0.00654**	2294.19*	55.91	4084.39**	381.51	251.05
Rep(E)	4	0.23	0.21	0.29	0.03*	7.43	0.00005	17.29	35.85	2253.57**	367.96	12673.33
Block(E*rep)	55	0.16	0.31	0.30	0.02	1.42	0.00004	596.79*	21.48	301.50	334.60	16640.09**
Entry	39	0.45*	3.51**	2.24**	0.10**	11.95**	0.00182**	944.42*	67.04**	1194.45**	1131.98**	10912.92**
E*Entry	107	0.37*	0.70	0.68*	0.03**	3.21	0.00026**	769.36*	39.66*	361.73	409.82	5065.21
Error	56	0.21	0.56	0.37	0.01	3.27	0.00003	43.57	24.76	273.24	329.62	251.05

*P<0.05, **P<0.01; QI = quality index

Table 3.6 Means of quality traits for 40 inbred lines analysed across four environments in Zimbabwe and South Africa during the 2017/2018 cropping season

Line code	Line status	Moisture %	Protein %	Fat %	Starch %	Fibre %	Tryptophan %	QI	Amylose %	β -Zein %	γ -Zein %	α -Zein %
L1	QPM	12.10	7.21	4.27	65.69	2.88	0.081	1.12	41.23	17.47	49.47	33.06
L2	QPM	12.56	8.43	4.00	65.30	2.48	0.090	1.07	44.24	4.22	43.24	40.56
L3	QPM	12.43	7.36	5.17	63.72	2.72	0.080	1.09	42.04	4.95	43.22	28.08
L4	QPM	12.67	8.09	3.81	66.53	2.62	0.066	0.82	45.92	5.99	29.77	52.49
L5	QPM	12.37	8.35	5.57	62.55	2.61	0.091	1.09	38.94	4.78	61.46	21.86
L6	QPM	12.31	6.38	3.83	66.72	2.98	0.076	1.19	83.57	21.87	39.94	38.19
L7	QPM	12.32	8.87	3.44	59.18	2.93	0.089	1.00	77.12	5.11	57.99	25.03
L8	QPM	12.36	8.94	5.14	62.66	2.66	0.079	0.88	46.10	5.65	35.73	46.96
L9	QPM	12.87	9.01	4.92	62.74	2.46	0.089	0.99	49.46	5.18	54.66	28.31
L10	QPM	12.56	9.15	6.22	60.45	2.71	0.075	0.82	37.30	5.81	37.52	56.67
L11	QPM	12.22	6.89	5.34	63.24	2.66	0.076	1.10	35.38	4.35	41.21	42.48
L12	QPM	12.81	7.26	3.64	66.05	2.54	0.077	1.06	36.07	6.16	55.58	26.54
L13	QPM	12.39	6.75	4.26	66.56	2.84	0.082	1.21	34.67	5.36	56.16	38.51
L14	QPM	12.34	8.18	4.02	57.49	2.83	0.083	1.01	33.75	5.02	56.04	27.07
L15	QPM	13.05	6.96	4.33	66.32	2.60	0.079	1.14	44.08	6.60	56.04	25.69
L16	QPM	12.42	8.98	5.06	63.61	2.53	0.094	1.05	44.12	4.71	49.60	45.69
L17	QPM	12.27	6.69	5.30	65.11	2.68	0.086	1.29	48.00	4.81	60.26	34.93
L18	non-QPM	12.29	8.43	3.54	65.94	2.73	0.035	0.42	39.82	6.04	36.07	46.14
L19	non-QPM	14.02	8.83	3.63	63.46	2.59	0.036	0.41	48.10	6.05	24.97	57.01
L 20	non-QPM	12.42	8.17	4.50	65.06	2.81	0.040	0.49	49.42	4.52	21.67	61.87
L 21	QPM	12.54	9.13	3.80	64.74	2.69	0.042	0.46	44.46	2.26	32.64	52.88
L 22	QPM	12.77	7.62	4.46	62.51	2.78	0.081	1.06	37.23	5.38	51.73	42.90
L 23	QPM	12.01	8.60	3.74	63.97	2.71	0.074	0.86	39.01	4.83	36.06	47.22
L 24	QPM	12.43	7.87	4.05	64.71	2.50	0.085	1.08	43.61	5.71	64.69	29.60
L 25	QPM	12.20	6.10	4.95	64.48	2.78	0.084	1.38	53.18	6.81	61.62	19.93
L 26	QPM	12.39	8.53	3.86	65.64	2.72	0.078	0.91	39.37	3.06	43.13	53.81
L 27	non-QPM	12.59	9.52	5.92	63.84	2.83	0.038	0.40	33.60	3.92	23.83	36.22
L 28	non-QPM	12.34	7.09	4.07	67.49	2.57	0.035	0.49	36.04	5.64	32.26	62.10
L 29	non-QPM	12.73	7.79	5.34	66.32	2.63	0.042	0.54	39.48	3.55	30.58	53.81
L 30	QPM	12.37	6.98	3.05	64.52	2.64	0.042	0.60	44.73	6.63	50.15	31.55
L 31	non-QPM	12.26	8.34	3.88	64.94	2.65	0.050	0.60	39.40	2.35	26.42	59.02
L 32	non-QPM	11.92	8.57	4.12	63.63	2.82	0.042	0.49	31.32	3.76	26.95	57.26
L33	QPM	12.15	6.63	5.65	65.38	2.88	0.085	1.28	50.20	4.27	57.41	38.32
L34	QPM	12.29	6.54	5.44	65.39	2.71	0.076	1.16	46.65	4.63	55.58	27.87
L35	non-QPM	12.18	8.17	4.70	64.68	2.70	0.041	0.50	46.37	3.43	31.41	65.17
L36	non-QPM	12.24	7.16	4.77	66.42	2.76	0.034	0.47	31.88	6.85	29.98	63.16
L37	QPM	12.31	6.67	4.13	66.14	2.84	0.066	0.99	37.68	4.19	59.29	24.53
L38	QPM	11.87	7.50	5.14	66.40	2.72	0.080	1.07	39.50	5.27	31.79	27.41
L39	non-QPM	12.70	10.19	5.20	62.63	2.62	0.038	0.37	45.71	5.30	18.49	40.70
L40	QPM	12.00	5.80	4.72	64.48	2.97	0.074	1.28	44.49	4.93	55.98	39.08
	QPM mean	12.39	7.64	4.53	64.22	2.71	0.078		44.90	6.07	49.24	36.11
	Non-QPM mean	12.51	8.39	4.52	64.95	2.70	0.039		40.10	4.67	27.51	54.77
	Total mean	12.42	7.79	4.53	3.27	2.71	0.068		43.57	5.77	43.26	41.24
	SE	0.46	0.75	0.61	1.81	0.11	0.005		22.34	4.98	16.53	18.16

SE = Standard error; QPM = quality protein maize; non-QPM = non quality protein maize; QI = quality index

3.4.5 Correlation among grain yield and agronomic traits

Grain yield was significantly and positively correlated with plant height, ear height and ears per plant while it was negatively correlated with anthesis-silking interval, ear rot and ear aspect (Table 3.7). However, no significant correlation was observed between days to anthesis and grain yield; grain yield and husk cover; grain yield and stalk lodging; and days to anthesis and plant height. Ears per plant had significant negative correlation with husk cover, ear rot and ear aspect. Also, weak significant genotypic correlation ($r_G = 0.23$) was obtained between husk cover and ear rot.

Table 3.7 Genotypic correlation coefficients (r_G) between grain yield and agronomic traits of 40 QPM inbred lines evaluated at seven locations during the 2017/2018 growing season

	DA	ASI	PH	EH	RL	SL	EPP	HC	ER	EA
GY	-0.07	-0.14**	0.16**	0.25**	-0.03	-0.04	0.38**	0.11	-0.15**	-0.48**
DA		-0.18**	-0.10	0.11*	-0.20**	0.21**	-0.26**	0.33**	0.33**	-0.20**
ASI			0.09*	0.02	0.03	-0.05	-0.11**	-0.14**	0.01	0.11**
PH				0.83**	-0.08	-0.17**	0.07	-0.16**	-0.20**	-0.11**
EH					-0.16**	-0.10*	0.01	-0.07	-0.09	-0.18**
RL						-0.02	0.31**	-0.20**	-0.23**	-0.01
SL							-0.05	0.10*	0.04	-0.05
EPP								-0.17**	-0.23**	-0.15**
HC									0.23**	-0.06
ER										0.18**

† GY= grain yield; DA = days to anthesis; ASI = anthesis-silking interval; PH= plant height; EH= ear height; RL = root lodging; SL = stalk lodging; EPP = ear per plant; HC = husk cover; ER = ear rot; EA = ear aspect; *P<0.05, **P<0.01

3.4.6 Principal component analysis for agronomic traits of 35 QPM inbred lines and five checks evaluated in seven environments

The first four principal components (PCs) explained 98% of the variation (Table 3.8). The first three PCs were significant, however, PC1 alone accounted for 82% of the variation. The most important traits in this PC were plant and ear height. The second and third PC's explained 10.5 and 4.8% of the variation, respectively. The most important trait in these PC's were days to anthesis and stalk lodging for PC2 while the most important trait in PC3 were days to anthesis and plant height. Ear rot was the most important trait in PC4 and this PC contributed only 0.72% to the total variation

Table 3.8 Eigen values, proportion of the total variance represented by first four principal components, cumulative percent variance and component loading of different traits in 35 QPM inbred lines and five checks

Traits	PC1	PC2	PC3	PC4
Grain yield	0.0157	0.0143	-0.0317	0.0052
Days to anthesis	-0.0333	0.6928	0.7044	-0.1178
Anthesis-silking interval	0.0008	-0.0405	-0.0535	-0.0241
Plant height	0.7951	-0.4086	0.4461	0.0396
Ear height	0.6049	0.5788	-0.5445	-0.0344
Root lodging	-0.0055	-0.0543	-0.0080	-0.6275
Stalk lodging	-0.0046	0.0170	0.0119	-0.0158
Ears per plant	0.0022	-0.0077	-0.0046	-0.0310
Huck cover	-0.0100	0.0627	0.0518	0.2564
Ear rot	-0.0212	0.0933	0.0384	0.7211
Ear aspect	-0.0048	-0.0164	-0.0120	0.0454
Eigenvalue	856.61	109.21	49.53	7.44
Proportion (%)	0.82	0.11	0.05	0.01
Cumulative	0.82	0.93	0.98	0.98

3.4.7 Yield performance and stability of 35 QPM inbred lines and five checks under seven growing conditions

The GGE biplots for grain yield of 40 QPM and non-QPM inbred lines and checks are presented in Figures 3.3 and 3.4. From Figure 3.3, the polygon view of the GGE biplot, it is clear which inbred line performed best in each environment. At the vertices of the polygon are the lines located away from the origin of the biplot in varied directions, such that all cultivars fall within the polygons. This suggested that the vertex entry in each sector of the polygon represented the highest yielding inbred in the location that fell within that particular sector. From the 35 inbred lines and five checks, entries 3 (QPM), 7 (QPM), 19 (non-QPM check), 24 (QPM), 29 (non-QPM), 35 (non-QPM) and 39 (non-QPM check) were identified as the highest yielding genotypes. Lines 3 and 35 performed best at Potch-18, line 29 performed best at Cedara-18, Harare, Harare misting and Glendale late, while entry 24 was also performed well at Glendale. On the other hand, lines 7, 19 and 39 were not adapted specifically to any of the environments in the present study. The GGE biplot identified three mega environments. Potch-18 and Glendale were identified as separate environments while Cedara, Harare, Harare misting and Glendale late were grouped into one mega environment.

PC1 and PC2 respectively explained 57.28% and 20.70% of the variance, which, together is 77.98% of the total variance (Figure 3.4). The figure represents the means vs. the stability of the 40 lines evaluated. A set of lines parallel to the double-arrow line passes the whole range of the entries, dividing them based on their mean performances. The inbred lines were ranked along the average-tester axis, with the arrow pointing to a higher value based on their mean performances across the seven environments. The vertical green line separates the entries into below and above average means (Figure 3.4). The single-arrow line that passes through the biplot origin and the average environment is referred to as the average-tester axis; this line points to the average environment from the biplot origin.

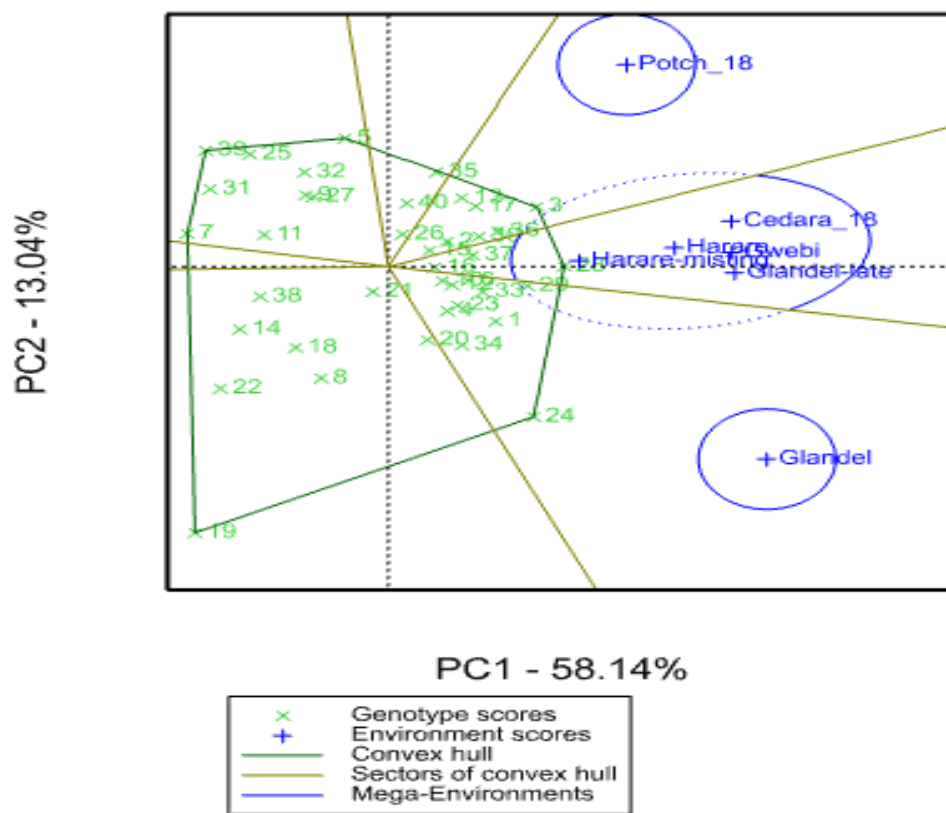


Figure 3.3 “Which won where” genotype plus genotype x environment interaction biplot of grain yield of 35 QPM inbred lines and five checks evaluated under seven environments (Cedara, Glendale, Glendale late plating, Harare, Harare misting, Gwebi and Potchefstroom)

Principal component (PC1 and PC2) accounted for 71.18% of yield variation. The average yield of the inbred line was estimated based on the distance from the markers on the average-tester axis. The stability of the inbred lines was also estimated by their projection onto the average-tester coordinate y-axis single-arrow line. The further a genotype is from the average tester axis, the less stable it is, and those closer to the average tester axis are stable. Hence, the most stable and high yielding lines identified were inbred lines 23 (QPM), 28 (non-QPM) and 29 (non-QPM) while inbred line 24 (QPM) was a very unstable, but high yielding line. From Figure 3.4, a long environmental vector axis discriminated the inbred lines. With the longest vectors from the origin, Potch was the most discriminating of the genotypes, followed by Glendale, while the rest of the environments were moderately discriminating.

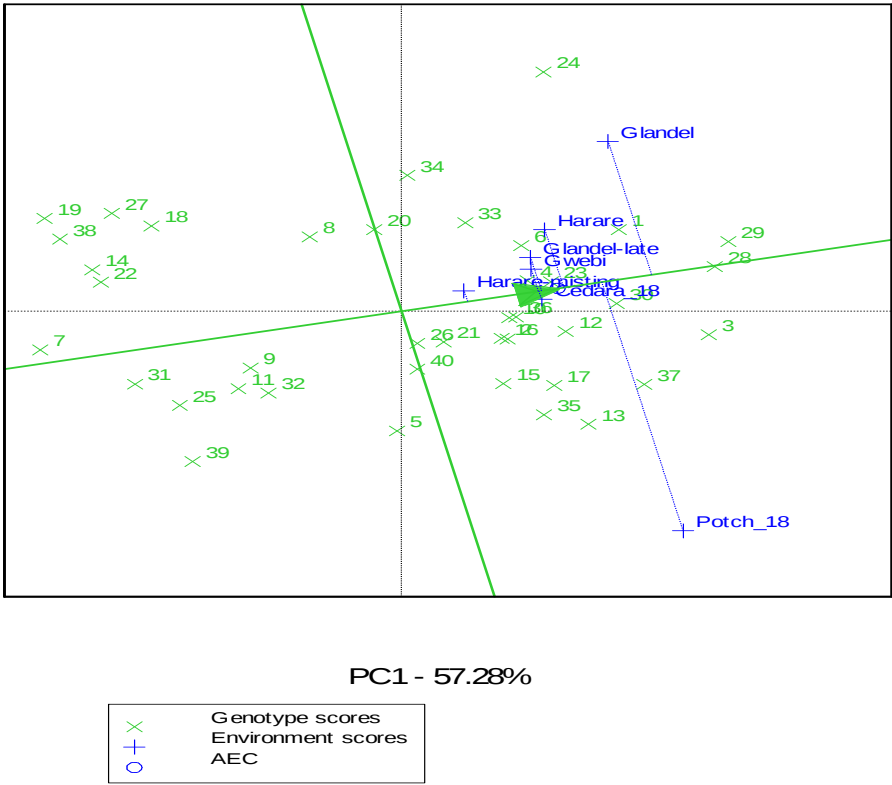


Figure 3.4 The entry/tester genotype plus genotype x environment biplot based on grain yield of 35 QPM inbred lines and five checks evaluated in seven environments (Cedara, Glendale, Glendale late plating, Harare, Harare misting, Gwebi and Potchefstroom)

3.5 Discussion

The differences recorded among the inbred lines evaluated for grain yield and other agronomic characters across the test environments showed that there is a prospect of choosing ideal inbred lines, which could be used in hybrid development if they have superior SCA with other lines. The QPM lines had a higher average yield than the non-QPM lines, indicating no yield penalty due to improved protein quality. Although the two top performers were non-QPM, three of the six top performers were QPM lines. Substantial differences were evident between the seven test environments. The significant inbred x environment interactions in combination with stability estimates from GGE biplot results indicate the presence of a crossover association (Mebratu et al. 2019), which may complicate selecting high yielding and superior lines across a wide range of environments. Several QPM lines were identified which were high yielding and stable.

Significant site mean squares for grain yield and most traits across environments showed that the test environments were distinctive in discriminating among the inbred lines. The highly significant site variance indicated that the environments used for the study were variable and this will aid in the selection of inbred lines for the development of superior QPM hybrids across a wide range of environments in Southern Africa.

The significant negative correlation between grain yield and anthesis-silking interval, grain yield and ear rot as well as grain yield and ear aspect indicated that these traits are inversely related, hence could be considered as essential traits in breeding for QPM genotypes. These results confirm the earlier work conducted by Betrán et al. (2003) and Akhtar et al. (2011) who detected negative phenotypic correlation between grain yield and days to anthesis. The presence of positive and significant correlation of grain yield with number of ears per plant, with plant height, and with ear height indicates that these traits can be used for selecting high yielding QPM genotypes corroborating the findings of Pixley and Bjarnason (2002), and Babu and Prasanna (2014) as well as Tulu (2014). However, the husk cover has significant implications for ear rot, suggesting that it could be considered as a secondary trait since ear rot affects grain yield and quality, as exposed tips could serve as entry point for water and pathogens, thereby reducing grain yield.

PCA simplifies the complexity in high-dimensional data while retaining trends and patterns. This converts the data into fewer dimensions, which summarize the traits of

interest (Lever et al. 2017). From this study, the most discriminatory traits were days to anthesis, plant and ear heights, root lodging and ear rot. PCA has been used by several researchers in combination with correlation for identifying and classifying genetic materials. The PCA method becomes useful when screening germplasm with several descriptor variables (Kamara et al. 2003; Salihu et al. 2006). The results corroborate the studies conducted by Upadyayula et al. (2006) and Suryanarayana et al. (2017) who reported that when traits are correlated, PCA derived from the components of the eigenvectors of the phenotypic covariance or correlation matrix could be used to identify linear combinations of traits.

Substantial differences were recorded for the quality traits analysed among the 40 inbred lines, indicating significant genetic variation, therefore superior inbred lines could be selected to serve as parents for development of QPM hybrids with improved quality traits. The significant GEI observed for all the quality traits analysed, except for protein and α -zein, indicated that the environment played an important role in the performance of these lines. Therefore, even though lines with good quality traits were developed, these traits are influenced by environmental factors. Zimmer et al. (2016) and Siracusa et al. (2017) found differences in amino acids contents as a result of variation in soil nitrogen contents on cowpea and different planting dates of buckwheat. This is also consistent with the results of Singh et al. (2019) who reported on the influence of the environment on oil content suggesting both genetic and environmental factors contribute to the performance of quality traits as evident in the present study.

Generally, the range of the starch content values in the present study for the inbred lines is comparable to the values by Sharma and Carena (2016) and Lu et al. (2019). Similarly, amylose, which is a major constituent of starch, varied for the lines evaluated. The amylose contents for inbred lines studied is consistent with the values obtained by Weiwei et al. (2016) and Li et al. (2018, 2020). The existence of variation for protein content at each and combined locations indicated the presence of genetic variability for protein synthesis among the lines developed. Even though protein content of 10.19% has been recorded in this study, it is lower than the 11.60% reported by Mansilla et al. (2019). There was a large difference between QPM and non-QPM for zein composition, with QPM inbreds having significantly more β - and γ -zein than non-QPM, while non-QPM inbreds had far more α -zein than QPM inbreds. Mansilla et al. (2019) observed that maize kernels with hard

endosperm produced more α -zein (22 and 19 kDa). O’Kennedy and Fox (2017) and Mansilla et al. (2019) reported on a decline of 22 and 19 kDa zein band intensity of QPM genotypes, corroborating the results of the present study. Also, the QPM lines were found to be superior to the non-QPM lines for QI. This is usually expected since the tryptophan content of QPM genotypes are higher than the non-QPM genotypes. The values recoded for the QI by the QPM lines studied far exceeded the values reported by Musila et al. (2010). The lines with high QI values can be selected and hybridised for the development of QPM hybrids and populations.

3.6 Conclusions

The present study identified promising QPM inbred lines based on the wide genetic variation among the 40 inbred lines evaluated for grain yield and agronomic characters. The best inbred lines for grain yield and agronomic characters included inbred lines 29 (non-QPM), 28 (non-QPM), 3 (QPM), 35 (non-QPM), 24 (QPM), 6 (QPM) and 30 (QPM). Based on GGE biplot, the most promising and desirable inbreds in this study were lines 28 (non-QPM), 9 (QPM) and 30 (QPM) across all seven environments. Inbred lines 39, 27 and 10 had protein content above 9.0%, while lines 2, 5 and 16 contained tryptophan concentrations of 0.09% or above. The study further showed that the correlation between grain yield and some secondary traits such as ear aspect and ear rot should be considered when breeding for QPM genotypes. The potential QPM inbred lines identified in this study could be exploited by the breeding programmes in sub-Saharan Africa for development of suitable QPM hybrids to reduce malnutrition.

References

- Akhtar N, Mehmood T, Ahsan M, Aziz A, Ashraf M, Ahmad S, Asif M and Safdar E (2011) Estimation of correlation coefficients among seed yield and some quantitative traits in wheat (*Triticum aestivum* L.). African Journal of Agricultural Research 6: 152-157.
- Babu R, and Prasanna BM (2014) Molecular Breeding for Quality Protein Maize (QPM). In: Tuberosa R, Graner A and Frison E (eds), Genomics of Plant Genetic Resources. Springer, pp. 490-505. doi: 10.1007/978-94-007-7575-6

- Betrán FJ, Beck D, Bänziger M and Edmeades GO (2003) Genetic analysis of inbred and hybrid grain yield under stress and non-stress environments in tropical maize. *Crop Science* 43: 807-817.
- Black RE, Victora CG, Walker SP, Bhutta ZA, Christian P, De Onis M, Ezzati M, Grantham-Mcgregor S, Katz J, Martorell R and Uauy R (2013) Maternal and child undernutrition and overweight in low-income and middle-income countries. *Lancet* 382: 427-451.
- Caprita R, Caprita A and Cretescu I (2011) Effective extraction of soluble non-starch polysaccharides and viscosity determination of aqueous extracts from wheat and barley. *Proceedings of the World Congress on Engineering and Computer Science* 2: 1-3.
- Chandel U, Mankotia SB and Thakur K (2014) Evaluation of CIMMYT maize (*Zea Mays* L.) germplasm by tropical inbred testers. *Bangladesh Journal of Botany* 43: 131-139.
- de Oliveira TRA, de Carvalho HWL, de Oliveira GHF, Costa EFN, Gravina GA, dos Santos RD and Filho JLSC (2019). Hybrid maize selection through GGE biplot analysis. *Bragantia* 78: 166-174.
- Deja Cruz N and Khush GS (2000). Rice grain quality evaluation procedures. In: Aromatic rice. Singh RK, Singh US and Khush GS (eds), Oxford and IBA publishing Co pvt Ltd, New Dheli, Calcuta.
- Eshetie T (2017). Review of quality protein maize as food and feed: In alleviating protein deficiency in developing countries. *American Journal of Food and Nutrition* 5: 99-105.
- GenStat (2012). Introduction to GenStat for Windows. 16th ed. VSN International, Hemel Hemstead, Hertfordshire HPI. IES, UK
- Gupta HS, Hossain F and Muthusamy V (2015) Biofortification of maize: an Indian perspective. *Indian Journal of Genetics* 75: 1-22.
- Gupta J, Wilson BW and Vadlan PV (2016) Evaluation of green solvents for a sustainable zein extraction from ethanol industry DDGS. *Biomass and Bioenergy* 85: 313-319.
- Kamara AY, Menkir A, Badu-Apraku B and Ibikunle O (2003) The influence of drought stress on growth, yield and yield components of selected maize genotypes. *Journal of Agricultural Science* 141: 43-50.
- Lever J, Krzywinski M and Altman N (2017) Principal component analysis. *Nature Publishing Group* 14: 641-642.

- Li C, Huang Y, Huang R, Wu Y and Wang W (2018) The genetic architecture of amylose biosynthesis in maize kernel. *Plant Biotechnology Journal* 16: 688-695.
- Li H, Dhital S, Flanagan BM, Mata J, Gilbert EP and Gidley (2020) Food hydrocolloids High-amylose wheat and maize starches have distinctly different granule organization and annealing behaviour : A key role for chain mobility. *Food Hydrocoll* 105: 105820.
- Liu K, Goodman M, Buckler E, Muse S, Smith JS and Doebley J (2003) Genetic structure and diversity among maize inbred lines as inferred from DNA microsatellites. *Genetics* 165: 2117-2128.
- Lu X, Chen J, Zheng M, Guo J, Qi J, Chen Y, Miao S and Zheng B (2019) Effect of high-intensity ultrasound irradiation on the stability and structural features of coconut-grain milk composite systems utilizing maize kernels and starch with different amylose contents. *Ultrason-Sonochemistry* 55: 135-148.
- Mansilla PS, Nazar MC and Pérez GT (2019) Evaluation and comparison of protein composition and quality in half-sib families of *opaque-2* maize (*Zea mays* L.) from. *Agriscientia* 36: 39-53.
- Mebratu A, Wegary D, Mohammed W, Teklewold A and Tarekegne A (2019) Genotype $\times$ environment interaction of quality protein maize hybrids under contrasting management Conditions in Eastern and Southern Africa. *Crop Science* 59: 1576-1589.
- Menkir A, Badu-Apraku B and Adepoju A (2003) Evaluation of heterotic patterns of IITA lowland white maize inbred lines. *Maydica* 48: 161-170.
- Musila RN, Diallo AO, Makumbi D and Njoroge K (2010) Combining ability of early-maturing quality protein maize inbred lines adapted to Eastern Africa. *Field Crops Research* 119: 231-237.
- Njeri SG, Makumbi D, Warburton ML, Diallo A, Jumbo MB and Chemining'wa G (2017) Genetic analysis of tropical quality protein maize (*Zea mays* L.) germplasm. *Euphytica* 213: 1-19.
- Nurit E, Tiessen A, Pixley K and Palacios-Rojas N (2009) Reliable and inexpensive colorimetric method for determining protein-bound tryptophan in maize kernels. *Journal of Agricultural and Food Chemistry* 57: 7233-7238.
- O'Kennedy K and Fox G (2017) Zein characterisation of South African maize hybrids and their respective parental lines using MALDI-TOF MS. *Food Analytical Methods* 10: 1661-1668.

- Pixley KV and Bjarnason MS (2002) Stability of grain yield, endosperm modification and protein quality of hybrid and open-pollinated quality protein maize cultivars. *Crop Science* 42: 1882-1890.
- Salihu S, Grausgruber H and Ruckenbauer P (2006) Agronomic and quality performance of international winter wheat genotypes grown in Kosovo. *Cereal Research Communications* 34: 957-964.
- Santos A, do Amaral Júnior AT, Kurosawa RNF, Gerhardt IFS and Neto RF (2017) GGE biplot projection in discriminating the efficiency of popcorn lines to use nitrogen. *Ciência e Agrotecnologia* 41: 22-31.
- Sarika K, Hossain F, Muthusamy F, Zunjare RU, Baveja A, Goswami R, Bhat JS, Saha S and Gupta HS (2018) Marker-assisted pyramiding of *opaque2* and novel *opaque16* genes for further enrichment of lysine and tryptophan in sub-tropical maize. *Plant Science* 272: 142-152.
- SAS Institute (2011) Statistical Analysis Software (SAS) user's guide.
- Semagn K, Magorokosho C, Vivek BS, Makumbi D, Beyene Y, Mugo S, Prasanna BM and Warburton ML (2012) Molecular characterization of diverse CIMMYT maize inbred lines from eastern and southern Africa using single nucleotide polymorphic markers. *BMC Genomics* 13: 113.
- Sharma S and Carena MJ (2016) Grain quality in maize (*Zea mays* L.): breeding implications for short-season drought environments. *Euphytica* 212: 247-260.
- Shiferaw B, Prasanna BM, Hellin J and Bänziger M (2011) Crops that feed the world 6. Past successes and future challenges to the role played by maize in global food security. *Food Security* 3: 307-327.
- Singh AA, Agrawal SB, Shahi JP and Agrawal M (2019) Yield and kernel nutritional quality in normal maize and quality protein maize cultivars exposed to ozone. *Journal of the Science of Food and Agriculture* 99: 2205-2214.
- Siracusa L, Gresta F, Sperlinga E and Ruberto G (2017) Effect of sowing time and soil water content on grain yield and phenolic profile of four buckwheat (*Fagopyrum esculentum* Moench.) varieties in a Mediterranean environment *Journal of Food Composition and Analysis* 62: 1-7.
- Sood A, Thakur K, Sharma PN, Gupta D, Singode A, Rana R and Lata S (2017) A comprehensive study of variation in selected QPM and Non-QPM maize inbred lines. *Agricultural Research* 6: 103-113.

- Suryanarayana L, Sekhar MR, Babu DR, Ramana AV and Rao VS (2017) Cluster and principal component analysis in maize. *International Journal of Current Microbiology and Applied Sciences* 6: 360-365.
- Tulu BN (2014) Correlation and path coefficients analysis studies among yield and yield related traits of quality protein maize (QPM) inbred lines. *International Journal of Plant Breeding and Crop Science* 1: 6-17.
- Upadyayula N, Wassom J, Bohn MO and Rocheford TR (2006) Quantitative trait loci analysis of phenotypic traits and principal components of maize tassel inflorescence architecture. *Theoretical and Applied Genetics* 113: 1395-1407.
- Wegary D, Vivek BS and Labuschagne MT (2018) Genetic relationships and heterotic structure of quality protein maize (*Zea mays* L.) inbred lines adapted to eastern and southern Africa. *Euphytica* 214: 1-11.
- Weiwei L, Juan X, Beijiu C, Suwen Z, Qing M and Huan M (2016) Anaerobic biodegradation, physical and structural properties of normal and high-amylose maize starch films. *International Journal of Agricultural and Biological Engineering* 9: 184-193.
- Yan W (2001) GGE biplot - a Windows application for graphical analysis of multi environment trial data and other types of two-way data. *Agronomy Journal* 93: 1111-1118.
- Yan W and Holland JB (2010) A heritability-adjusted GGE biplot for test environment evaluation. *Euphytica* 171: 355-369.
- Yan W, Cornelius PL, Crossa J and Hunt LA (2001) Two types of GGE biplots for analyzing multi-environment trial data. *Crop Science* 41: 656-663.
- Zimmer S, Messmer M, Haase T, Piephoe HP, Mindermann A, Schulz H, Habekuß A, Ordon F, Wilboisg KP and Heß J (2016) Effects of soybean variety and Bradyrhizobium strains on yield, protein content and biological nitrogen fixation under cool growing conditions in Germany. *European Journal of Agronomy* 72: 38-46.

CHAPTER FOUR

COMPARISON OF GRAIN YIELD AND YIELD STABILITY OF QUALITY PROTEIN AND NON-QUALITY PROTEIN MAIZE HYBRIDS

4.1 Abstract

Development of high yielding and stable QPM hybrids is important for increasing grain yield output per unit area as well supporting the fight against malnutrition in SSA. Maize, in general, serves as an income generator and staple food crop for millions of people in SSA. Despite the development of QPM genotypes with increased lysine and tryptophan, information is lacking on yield potential of QPM genotypes compared to non-QPM genotypes. Therefore, the objectives of this study were to compare the yield of QPM and their non-QPM counterparts as well as examine the yield stability of these genotypes using GGE and AMMI biplot models. A total of 130 hybrids were developed by crossing 33 QPM and non-QPM inbred lines to four elite testers (two QPM and two non-QPM) using a line x tester mating design. Hybrids were evaluated together with five commercial hybrid checks (three QPM and two non-QPM) for two years at 13 locations in Zimbabwe and South Africa. The trial was arranged in a 5 x 27 alpha lattice with two replications. The results showed significant genotype, environment and GEI effects. The best performing hybrids identified in this study were a QPM hybrid of line 11 x CZL15049 (entry 41), followed by a non-QPM hybrid of line 28 x CZL15049 (entry 108). The best QPM hybrid outperformed the best non-QPM hybrid by 8.81%. In addition, the best QPM hybrid (genotype 41) outperformed the best non-QPM check (Pioneer) and best QPM check (CBI) by 50.45 and 52.24%, respectively. In spite of this, the QPM hybrids yielded 13.9% less on average than non-QPM hybrids. The AMMI analyses indicated that the grain yield performance of QPM and non-QPM hybrids were highly affected by environment coupled with large GEI. The AMMI and GGE biplot analysis permitted estimation of interaction effect of a genotype in each environment and helped to identify genotypes best suited for specific environments. The discriminating power vs. representativeness view of the GGE biplot was an effective tool for test environments evaluation. The AMMI and GGE biplots identified genotypes 108 and 12 as the most stable and high yielding hybrids. QPM hybrids 41 and 120 and non-QPM hybrids 108 and 12 were the highest yielding genotypes in this study. Hence, the promotion of these superior hybrids for adoption and release will not

only enhance grain yield output but also help improve nutritional status of people who depend on maize products as their staple meal.

Keywords: Yield reduction, quality protein maize, non-quality protein maize, yield stability, mega environments.

4.2 Introduction

In SSA and other developing regions across the globe, maize forms a major part of the human diet as it supplies daily calories and, to some extent, protein and other essential amino acids (Nuss and Tanumihardjo 2011; Chaudhary et al. 2014; De Groote et al. 2014). Grain yield and kernel protein content are polygenically controlled which makes it difficult for the two traits to be improved simultaneously (Mittelman et al. 2003; Aliu et al. 2012; Tripathy et al. 2017). QPM has much higher levels of the essential amino acids lysine and tryptophan than normal maize. It has been reported that the gap between QPM and non-QPM grain yield ranges between 10 to 15%, which is predominantly characterized by slower drying rate, higher susceptibility to kernel rot and lower kernel weight (Mukanga et al. 2011; Tandzi et al. 2017; Darrah et al. 2019). To overcome the problems associated with the *o2* mutation, breeders, over the past five decades, have introgressed gene modifiers from normal maize to harden the endosperm of QPM genotypes without reduction in lysine and tryptophan content (Mertz et al. 1964; Kumar et al. 2011; Gupta et al. 2013; Pandey et al. 2016; Krishna et al. 2017). This was done not only through conventional breeding but also through molecular approaches to enhance the genetic variability of QPM genotypes with increased yield comparable to normal maize (Tandzi et al. 2017). In spite of the unprecedented progress made to harden the endosperm of QPM varieties with enhanced yield, there have been several contradictory reports about the yield of QPM compared to non-QPM genotypes. There are reports of normal maize being superior for grain yields compared to QPM varieties (Bhatnagar et al. 2004; Krivanek et al. 2007) while Pixley and Bjarnason (1993) reported that QPM hybrids yielded better than non-QPM hybrids. Interaction between genes which control major traits can cause yield reduction or “yield drag” and “event lag effects” (Shi et al. 2013). Yield drag usually refers to reduction in yield after major genes are added to a genotype compared to the genotype without the added gene. There is almost no information on yield drag (reduction in grain yield as a result of adding the QPM trait to a non-QPM inbred or hybrid) to truly quantify if addition

of the QPM trait results in lower yield than non-QPM genotypes. Analysis of GEI is important to determine performance of genetic materials in terms of adaptability and stability. Maize hybrids which are high yielding with enhanced nutritional composition and comparatively stable for grain yield when grown in different environments are important to commercial maize production in SSA (Edmeades et al. 1997; Beck et al. 2003). Živanović et al. (2004) and Mastrodomenico et al. (2018) stated that grain yield stability in maize is partly under genetic control and thus appropriate for selection of superior and high yielding genotypes. Therefore, this study was conducted to examine the yield gap, if present, between hybrid QPM and their non-QPM counterparts as well as to examine the stability of these genotypes.

4.3 Materials and methods

4.3.1 Genetic material

This study was carried out during the 2017/2018 and 2018/2019 cropping seasons at 13 locations in South Africa and Zimbabwe. The genetic materials used in the study were developed from germplasm from various genetic backgrounds. Some were obtained from conversion of normal endosperm maize to QPM lines with genes from early maturing elite drought and low N stress tolerant inbred lines, conversion of medium maturing elite MSV tolerant inbred lines, Southern Africa adapted mid-altitude inbred lines with high GCA, conversion of medium maturing elite Southern Africa adapted mid-altitude inbred lines with high GCA and introgressing of temperate germplasm (See Table 3.1 in Chapter 3). Consequently, the lines were selected based on their yield potential and quality traits. A total of 33 QPM and non-QPM inbred lines obtained from CIMMYT Zimbabwe were crossed with four elite testers, two QPM and two non-QPM (Table 4.1) to generate 132 single cross hybrids (Table 4.2). However, because of unavailability of seed, two crosses were discarded, bringing the total number of hybrids to 130. Five commercial hybrids (two QPM and three non-QPM) were used as checks. Hence, 135 hybrids were included in this study (Table 4.2).

Table 4.1 Description of the inbred lines and testers used to create hybrids

Line	Name	Donor
L1	CZL0920	QPM
L2	CZL1330	QPM progeny
L3	CZL15041	QPM progeny
L4	CZL15055	QPM progeny
L5	CZL15073	QPM progeny
L6	CZL1471	QPM progeny
L7	TL135470	QPM progeny
L8	VL06378	QPM progeny
L9	TL155805	QPM progeny
L10	TL147078	QPM progeny
L11	TL147070	QPM progeny
L12	TL13609	QPM progeny
L13	TL145743	QPM progeny
L14	TL156614	QPM progeny
L15	CZL1477	QPM progeny
L16	CZL15074	QPM progeny
L17	CZL0616	QPM progeny
L18	CZL083	QPM progeny
L19	CML572	Non-QPM parent
L20	EBL167787	Non-QPM parent
L21	CZL0520	Non-QPM parent
L22	CZL99005	Non-QPM parent
L23	CML502	QPM donor
L24	CML144	QPM donor
L25	CML159	QPM donor
L26	CML181	QPM donor
L27	CML197	QPM donor
L28	CML312SR	Non-QPM parent
L29	CML488	Non-QPM parent
L30	CML491	Non-QPM parent
L31	LH51	QPM donor
L32	CZL00025	Non-QPM parent
L35	CML444	Non-QPM parent
Tester		
T1	CZL15049	QPM tester
T2	CZL059	QPM tester
T3	CML444	Non-QPM tester
T4	CML395	Non-QPM tester

Table 4.2 Description of the 130 QPM and non-QPM hybrids and the five commercial checks used in the study

Entry	Cross	Entry	Cross	Entry	Cross	Entry	Cross	Entry	Cross
1	L1 x CZL15049 (QPM)	28	L7 x CML395 (non-QPM)	55	L14 x CML444 (non-QPM)	82	L21 x CML444 (non-QPM)	109	L28 x CZL059 (non-QPM)
2	L1 x CZL059 (QPM)	29	L8 x CZL15049 (QPM)	56	L14 x CML395 (non-QPM)	83	L21 x CML395 (non-QPM)	110	L28 x CML444 (non-QPM)
3	L1 x CML444 (non-QPM)	30	L8 x CZL059 (QPM)	57	L15 x CZL15049 (QPM)	84	L22 x CZL15049 (non-QPM)	111	L28 x CML395 (non-QPM)
4	L1 x CML395 (non-QPM)	31	L8 x CML444 (non-QPM)	58	L15 x CZL059 (QPM)	85	L22 x CZL059 (non-QPM)	112	L29 x CZL15049 (non-QPM)
5	L2 x CZL15049 (QPM)	32	L8 x CML395 (non-QPM)	59	L15 x CML444 (non-QPM)	86	L22 x CML444 (non-QPM)	113	L29 x CZL059 (non-QPM)
6	L2 x CZL059 (QPM)	33	L9 x CZL15049 (QPM)	60	L15 x CML395 (non-QPM)	87	L22 x CML395 (non-QPM)	114	L29 x CML444 (non-QPM)
7	L2 x CML444 (non-QPM)	34	L9 x CZL059 (QPM)	61	L16 x CZL15049 (QPM)	88	L23 x CZL15049 (QPM)	115	L29 x CML395 (non-QPM)
8	L2 x CML395 (non-QPM)	35	L9 x CML444 (non-QPM)	62	L16 x CZL059 (QPM)	89	L23 x CZL059 (QPM)	116	L30 x CZL15049 (non-QPM)
9	L3 x CZL15049 (QPM)	36	L9 x CML395 (non-QPM)	63	L16 x CML444 (non-QPM)	90	L23 x CML444 (non-QPM)	117	L30 x CZL059 (non-QPM)
10	L3 x CZL059 (QPM)	37	L10 x CZL15049 (QPM)	64	L16 x CML395 (non-QPM)	91	L23 x CML395 (non-QPM)	118	L30 x CML444 (non-QPM)
11	L3 x CML444 (non-QPM)	38	L10 x CZL059 (QPM)	65	L17 x CZL15049 (QPM)	92	L24 x CZL15049 (QPM)	119	L30 x CML395 (non-QPM)
12	L3 x CML395 (non-QPM)	39	L10 x CML444 (non-QPM)	66	L17 x CZL059 (QPM)	93	L24 x CZL059 (QPM)	120	L31 x CZL15049 (QPM)
13	L4 x CZL15049 (QPM)	40	L10 x CML395 (non-QPM)	67	L17 x CML444 (non-QPM)	94	L24 x CML444 (non-QPM)	121	L31 x CZL059 (QPM)
14	L4 x CZL059 (QPM)	41	L11 x CZL15049 (QPM)	68	L17 x CML395 (non-QPM)	95	L24 x CML395 (non-QPM)	122	L31 x CML444 (non-QPM)
15	L4 x CML444 (non-QPM)	42	L11 x CZL059 (QPM)	69	L18 x CZL15049 (QPM)	96	L25 x CZL15049 (QPM)	123	L31 x CML395 (non-QPM)
16	L4 x CML395 (non-QPM)	43	L11 x CML444 (non-QPM)	70	L18 x CZL059 (QPM)	97	L25 x CZL059 (QPM)	124	L32 x CZL15049 (non-QPM)
17	L5 x CZL15049 (QPM)	44	L11 x CML395 (non-QPM)	71	L18 x CML444 (non-QPM)	98	L25 x CML444 (non-QPM)	125	L32 x CML444 (non-QPM)
18	L5 x CZL059 (QPM)	45	L12 x CZL15049 (QPM)	72	L18 x CML395 (non-QPM)	99	L25 x CML395 (non-QPM)	126	L32 x CML395 (non-QPM)
19	L5 x CML444 (non-QPM)	46	L12 x CZL059 (QPM)	73	L19 x CZL15049 (non-QPM)	100	L26 x CZL15049 (QPM)	127	L35 x CZL15049 (non-QPM)
20	L5 x CML395 (non-QPM)	47	L12 x CML444 (non-QPM)	74	L19 x CZL059 (non-QPM)	101	L26 x CZL059 (QPM)	128	L35 x CZL059 (non-QPM)
21	L6 x CZL15049 (QPM)	48	L12 x CML395 (non-QPM)	75	L19 x CML444 (non-QPM)	102	L26 x CML444 (non-QPM)	129	L35 x CML444 (non-QPM)
22	L6 x CZL059 (QPM)	49	L13 x CZL15049 (QPM)	76	L19 x CML395 (non-QPM)	103	L26 x CML395 (non-QPM)	130	L35 x CML395 (non-QPM)
23	L6 x CML444 (non-QPM)	50	L13 x CZL059 (QPM)	77	L20 x CZL15049 (non-QPM)	104	L27 x CZL15049 (QPM)	131	ZS261 (Check QPM1)
24	L6 x CML395 (non-QPM)	51	L13 x CML444 (non-QPM)	78	L20 x CML444 (non-QPM)	105	L27 x CZL059 (QPM)	132	Mama MQ623 (Check QPM2)
25	L7 x CZL15049 (QPM)	52	L13 x CML395 (non-QPM)	79	L20 x CML395 (non-QPM)	106	L27 x CML444 (non-QPM)	133	PHB30G19 (Check Non-QPM1)
26	L7 x CZL059 (QPM)	53	L14 x CZL15049 (QPM)	80	L21 x CZL15049 (non-QPM)	107	L27 x CML395 (non-QPM)	134	SC627 (Check Non-QPM2)
27	L7 x CML444 (non-QPM)	54	L14 x CZL059 (QPM)	81	L21 x CZL059 (non-QPM)	108	L28 x CZL15049 (non-QPM)	135	SC513 (Check Non-QPM3)

4.3.2 Experimental sites, design and agronomic practices

The study was conducted at 13 locations in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons (Table 4.3).

Table 4.3 Site description for the test locations in South Africa and Zimbabwe

Site	Location name	Country	Latitude	Longitude	Elevation above sea level (m)
S1	Harare	Zimbabwe	17°46'S	31°02'E	1406
S2	Gwebi	Zimbabwe	17°13'S	31°E'	1406
S3	Bindura	Zimbabwe	17 °18'S	31° 02'E	1480
S4	Harare-misting	Zimbabwe	17°46'S	31°02'E	1406
S5	Rattrey-Arnold	Zimbabwe	17° 67'S	31° 17'E	1462
S6	Glendale	Zimbabwe	17°31'S	31°3'E	1147
S7	Lionsdel	Zimbabwe	17°25'S	30° 02'E	1232
S8	Cedara 2018	South Africa	-29°54'S	30°26'E	1066
S9	PotchTB8-18	South Africa	-26°73'S	27°08'E	1349
S10	PotchR8-18	South Africa	-26°73'S	27°06'E	1349
S11	Potch 2019	South Africa	-26°74'S	27°08'E	1349
S12	Cedara 2019	South Africa	-29°71'S	30°26'E	1066
S13	Glendale	Zimbabwe	17°31'S	31°3'E	1147

PotchTB8-18=Potchefstroom TB8 2018; PotchR8-18= Potchefstroom R8 2018

The experiments were established using a 5 x 27 alpha lattice experimental design (Patterson and Williams 1976) with two replications at 13 locations. At each location, the experimental unit used was single row plots of 5.2 m long with inter-row spacing of 0.75 m and within rows spacing of 0.25 m. Two seeds were planted per hill and seedlings later thinned to one plant per hill, four weeks after emergence, to give a final plant population density of about 53 333 plants ha⁻¹. In Potchefstroom the fertilizer regime consisted of compound fertilizer 3:2:1 (25) + Zn, applied as a basal application at planting, at a rate of 200 kg NPK ha⁻¹. LAN with 28% N was used for top-dressing in two equal splits at 28 and 56 days after emergence at a rate of 100 kg ha⁻¹ each. At Cedara, MAP at 250 kg ha⁻¹ was applied at planting, and LAN given at 150 kg ha⁻¹ in two equal splits of 75 kg ha⁻¹ at 28 and 56 days after emergence. For the Zimbabwe trials, fertilizers were applied at the recommended rate of 250 kg ha⁻¹ N, 83 kg ha⁻¹ P, and 111 kg ha⁻¹ K. Basal fertilizer application was done in the form of NPK, and additional N application was done four weeks after seedling emergence. Pre-emergence herbicides Gramoxone, Basagram and 2, 4-D were applied to control weeds and after that hand weeding was done to make sure that the fields were relatively free of weeds. Insecticides Carbaryl and Karate were applied to control stalk borer and cutworms, respectively. Carbaryl was applied at planting stage

while Karate was applied at planting and seedling emergence stages.

4.3.3 Data collection

This was done as described in Chapter 3.

4.3.4 Statistical analyses

Grain yield data and other measured parameters were subjected to ANOVA for each location and combined locations using PROC GLM procedure in SAS (SAS Institute, 2011 version 9.4) to test the significance of genotype, environment/location and GEI. In the model, the hybrids or genotypes were regarded as fixed while environments, replications nested in environment and blocks within replications across environments were treated as random factors. Before the ANOVA, BLUPs of plot means for all traits across the seven environments were calculated.

4.3.5 GGE biplot analysis

The GGE biplot graphical method was deployed to study the relationship and the interaction between genotype and the environment and also to examine stability of grain yield (Yan et al. 2000). The grain yield obtained from the multi-location trials was expressed by the formula:

$$Y_{ij} - \bar{Y}_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij},$$

where, Y_{ij} is the average yield of genotype i in environment j ; $\bar{Y}_j$ is the average grain yield for all the genotypes in environment j ; λ_1 and λ_2 are the singular values decompositions for the first and second principal components, PC1 and PC2, respectively; ξ_{i1} and ξ_{i2} are vector scores of genotype i on PC1 and PC2, respectively; η_{j1} and η_{j2} are vector scores of environment j on PC1 and PC2, respectively; and ε_{ij} is the residual of the model associated with the genotype i in environment j .

4.3.6 AMMI analysis

In addition to the GGE biplot analysis, the grain yield data of 30 selected genotypes (top 15, middle 5, bottom 5 and the 5 checks) from the 135 genotypes were subjected to AMMI analysis to determine the relationships among genotypes, environments and GEI. The

AMMI model was used in several studies (Zobel et al. 1988; Gauch and Zobel 1988; Crossa 1990). The AMMI model uses PCA to determine the multiplicative effects. The AMMI analysis was conducted using the GGE biplot software Windows application that fully automates biplot analysis (Yan 2001) following the GGE model:

$$Y_{ijr} = \mu + e_j + \sum_{k=1}^x \lambda_k \alpha_{ik} \gamma_{jk} \varepsilon_{ijr}$$

Y_{ijr} = observation of the r th replicate of the i th genotype in the j th environment, μ = the overall means, e_j = main effect of the j th environment, x = matrix rank {gge}_{ij} when {gge}_{ij} = $g_i + g_{ej}$, λ_k = the singular value for principal component k , α_{ik} = the eigenvector score for genotype i and component k , γ_{jk} = the eigenvector score for environment j and component k , and ε_{ijr} = the error for genotype i and environment j and replicate r .

4.3.7 Estimation of yield reduction of QPM vs non-QPM hybrids

From the ANOVA, means for each hybrid were obtained. They were then separated according to the crosses made, thus lines that were crossed with QPM testers and lines crossed with non-QPM testers. It is important to note that each line was crossed with two QPM and two non-QPM testers, except for two lines, 20 and 32, which were crossed with only one QPM tester. The averages for means for each line as obtained in crosses for both QPM and non-QPM were obtained and consequently, yield reduction was calculated using the formula below:

$$\text{Yield drag} = \frac{(\text{Yield of QPM hybrid} - \text{Yield of non-QPM hybrid})}{\text{Yield of non-QPM hybrid}} \times 100$$

4.4 Results

4.4.1 Analysis of variance for grain yield measured at Potchefstroom, Cedara and Zimbabwe during the 2018 and 2019 cropping seasons

The ANOVA at separate locations and across locations for grain yield and other measured traits of the 135 hybrids evaluated in 13 locations is presented in Table 4.4. At Cedara, there were variations among the tested hybrids for grain yield and all the other traits except for anthesis-silking interval, ears per plant, husk cover and ear rot.

Table 4.4 Mean squares from analysis of variance for grain yield and other agronomic traits of 135 hybrids evaluated under optimal growing conditions at Cedara (2017/2018 and 2018/2019), Potchefstroom (2017/2018 and 2018/2019) and Zimbabwe (2017/2018)

Source	DF	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	ER	EA
Cedara												
Year	1	114.57**	2352.09**	0.31	191064.46**	104931.96**	21630.66**	13639.12**	0.01	19.08**	30964.80**	0.73*
Rep(Year)	2	7.09*	85.56**	1.63	3153.57**	2300.26**	471.98*	272.57	0.09*	4.91**	1363.54*	0.65*
Block(Year*Rep)	104	1.89*	10.10**	1.44	574.53**	343.90**	186.29*	297.78**	0.02	0.52**	515.17	0.23*
Entry	134	5.69**	28.52**	1.11	508.85**	577.21**	234.68**	325.55**	0.01	0.23	458.55	0.31*
Year*Entry	134	5.30**	7.07*	0.89	281.00*	223.97*	213.40*	252.72**	0.02	0.26	436.55	0.40*
Error	164	1.21	4.94	1.34	212.94	150.91	118.14	146.91	0.02	0.20	21.45	0.19
Potchefstroom												
Site	2	1996.14**	710.72**	0.87	29307.18**	14019.62**	1630.01**	12549.02**	5.15**	19.56**	11772.21**	0.30
Rep(Site)	3	5.75*	19.93**	0.42	2220.08**	5259.83**	93.03	1383.80**	0.46**	0.39	187.19	0.25
Block(Site*Rep)	156	1.86	5.09**	0.85*	244.98**	166.54**	81.77	218.29**	0.04	0.30**	124.85	0.17
Entry	134	9.34**	41.38**	1.42**	618.22**	805.50**	116.05**	243.18**	0.06**	0.27**	241.83**	0.28**
Site*Entry	268	4.15**	3.77**	0.79	113.62	97.97*	117.65**	226.99**	0.04	0.31**	158.58*	0.30**
Error	246	1.60	2.66	0.65	106.19	68.32	69.31	124.32	0.03	0.17	107.52	0.17
Zimbabwe												
Site	7	1184.02**	8224.87**	118.33**	210736.67**	96209.59**	68121.40**	933.93**	1.78**	57.65**	7643.70**	11.07**
Rep(Site)	8	4.75**	21.78**	7.02**	3737.23**	3874.83**	925.38**	46.54	0.07*	3.97	295.57**	0.79**
Block(Site*Rep)	416	1.24*	4.65	1.27	367.43**	215.95**	252.48**	25.93	0.03	11.39	86.62*	0.13**
Entry	134	8.87**	67.90**	1.98**	2116.63**	1565.90**	236.97**	40.75**	0.12**	13.90*	228.58**	0.76**
Site*Entry	936	1.71**	5.10**	1.33*	240.90	159.88*	185.16**	34.10**	0.04*	11.49	105.27**	0.16**
Error	654	0.99	4.06	1.15	226.52	134.08	134.07	26.15	0.02	11.26	69.59	0.09

†DF= degree of freedom; GY (t ha⁻¹) = Grain yield; DA = Days to anthesis; ASI = anthesis silking interval; PH = plant height; EH = ear height; RL = root lodging; SL = stalk lodging; EPP= ear per plant; HC = husk cover; ER = ear rot; EA = ear aspect. *P<0.05, **P<0.01

Table 4.5 Mean squares from combined analysis of variance for grain yield and other agronomic traits of 135 hybrids evaluated at 13 locations in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons

Source	DF	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	ER	EA
Rep(site)	13	1413.63**	13808.47**	134.41**	209318.02**	73936.40**	43115.36**	14959.39**	3.16**	191.33**	37224.83**	8.33**
Block(rep*site)	624	5.34**	31.17**	4.67**	3297.32**	3952.20**	663.55**	389.91**	0.16**	3.29	434.86**	0.64**
Site	12	14.30**	115.08**	2.10**	2671.50**	2410.75**	224.03**	171.01**	0.12**	8.29	357.78**	0.75**
Entry	134	1.48**	5.59**	1.20*	371.04**	224.23**	202.91**	112.14**	0.03*	7.16	161.37*	0.16**
Entry*site	1474	3.03**	5.57**	1.19*	224.22**	164.88**	175.37**	112.85**	0.04**	7.35	169.98**	0.23**
Error	1242	1.17	3.88	1.07	196.66	121.49	116.66	67.42	0.03	6.99	132.59	0.12

†DF= degree of freedom; GY (t ha⁻¹) = Grain yield; DA = Days to anthesis; ASI = anthesis silking interval; PH = plant height; EH = ear height; RL = root lodging; SL = stalk lodging; EPP = ear per plant; HC = husk cover; ER = ear rot; EA = ear aspect. *P<0.05, **P<0.01

There was significant year x genotype interaction for grain yield. For the trials conducted at Potchefstroom, significant differences were observed for all the traits and also significant year x genotype interaction for grain and all measured traits, except for anthesis-silking interval, plant height and ears per plant. At Zimbabwe, there were significant genotypes as well as genotype x location interaction effects for all characteristics except for plant height and husk cover

4.4.2 Combined analysis of variance for measured traits across 13 locations for the trials conducted in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons

There were significant variations ($P < 0.05$) for grain yield and most of the traits measured across the 13 locations (Table 4.6). Furthermore, the effect of environment as well as GEI was significant ($P < 0.01$) for grain yield.

4.4.3 Mean of grain yield and agronomic traits of QPM and non-QPM hybrids as well the five commercial checks

The mean grain yield of the hybrids ranged from 2.31 to 8.61 t ha⁻¹ across the 13 environments for genotypes 70 and 41, respectively (Table 4.5). The least days to 50% pollen shed were 67 for genotype 124, while genotype 70 shed pollen at 80 days after planting. Also, anthesis-silking interval ranged between 0.42 and 2.29. Ears per plant ranged from 0.71 to 1.33. On the other hand, husk cover ranged from 0.18 to 4.69 while ear rot ranged from 2.26 to 30% (Table 4.7).

4.4.4 Yield performance and stability of 135 QPM and non-QPM hybrids across 13 locations

4.4.4.1 “Which-won-where” biplots

The GGE biplots for grain yield of 135 QPM and non-QPM hybrids including the five hybrid checks are shown in Figure 4.1. From the polygon view of the GGE biplots, it is clear which hybrid performed best in each environment. At the vertices of the polygon are the hybrids located away from the origin of the biplot in varied directions, such that all hybrids fall within the polygons. This suggested that the vertex entry in each sector of the polygon represented the highest yielding hybrid at the location that fell within that

particular sector. Of the 135 hybrids evaluated, entries 23, 41, 56, 70, 87 and 108 were identified as the highest yielding genotypes.

Table 4.6 Mean grain yield of 30 selected hybrids from the individual locations used for the GGE and AMMI biplot analyses

Hybrid	Research sites												
	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
8	9.49	6.73	1.40	3.49	7.63	9.16	4.52	8.27	11.69	11.70	4.16	8.60	7.26
12	9.36	6.90	1.78	4.42	8.63	11.06	5.51	8.10	11.64	10.19	3.07	5.73	7.00
13	7.24	4.64	2.50	2.56	5.55	7.42	3.72	4.47	7.12	8.48	4.22	6.24	6.00
16	7.76	7.10	3.42	3.51	6.94	9.10	5.13	10.16	11.21	10.74	4.46	7.70	7.95
23	8.53	4.02	1.80	2.82	5.11	9.91	6.00	7.09	18.08	11.00	4.91	7.18	7.28
26	7.07	5.55	1.05	2.26	4.11	5.01	5.00	7.36	11.17	5.95	3.85	7.06	5.29
28	8.78	5.20	2.35	3.54	8.27	9.43	5.05	6.85	16.43	12.05	5.20	10.62	5.47
34	8.83	5.73	1.46	2.77	5.38	6.58	4.56	6.15	5.94	7.81	2.64	6.58	5.87
41	11.08	5.99	2.05	4.16	6.40	11.19	5.29	7.91	15.55	13.96	3.89	8.31	8.31
46	7.17	5.63	2.44	3.57	5.72	5.90	3.76	6.49	6.79	6.75	2.20	6.41	6.19
52	10.42	6.46	2.81	4.28	6.83	9.29	5.79	6.43	10.90	12.26	5.72	11.16	6.13
56	8.06	5.64	1.33	3.24	7.92	11.23	5.02	5.32	16.56	10.69	3.91	10.75	7.80
62	6.11	3.84	1.37	2.38	3.26	7.03	3.64	6.58	3.82	9.32	0.98	4.43	4.87
63	5.68	4.18	1.41	2.63	5.12	9.89	4.02	3.47	7.34	5.73	3.03	3.57	5.27
66	4.91	3.50	1.55	2.01	3.30	4.26	3.55	8.84	7.74	7.13	0.88	4.56	3.99
70	11.18	1.36	1.12	0.48	1.50	2.83	1.06	1.59	2.24	5.99	0.49	0.43	1.75
78	4.99	5.04	1.75	3.30	4.35	4.22	3.78	3.82	5.86	6.86	4.13	9.05	4.14
79	10.17	7.03	2.20	3.74	7.33	8.64	5.03	6.98	11.19	9.40	4.77	9.49	7.54
87	3.50	2.77	1.14	1.23	3.05	3.45	3.22	2.08	7.92	5.09	2.43	4.01	3.73
97	5.86	3.68	0.72	2.24	3.44	2.48	4.30	7.59	5.18	6.10	0.88	3.15	4.28
99	8.65	6.45	1.48	3.65	8.55	11.86	5.64	9.15	12.75	8.88	4.28	6.51	7.17
101	8.57	5.66	1.25	3.69	4.35	8.26	4.78	5.76	6.26	7.02	3.30	7.26	4.21
108	11.79	5.79	2.47	4.83	8.10	11.47	6.12	7.44	9.86	14.77	4.49	6.91	7.03
120	10.27	5.58	1.56	3.94	6.63	11.40	4.69	6.49	11.78	12.94	4.57	7.79	7.80
121	5.66	4.26	1.70	2.60	3.63	7.79	3.50	3.22	4.53	7.69	1.85	4.33	5.78
131	5.68	4.92	2.08	2.70	3.19	6.97	4.71	8.28	10.81	11.42	4.09	3.54	5.62
132	5.74	4.10	2.89	2.85	6.35	8.78	3.96	3.78	5.94	9.34	4.33	7.68	5.38
133	8.03	5.25	1.05	4.23	5.83	6.21	4.78	7.13	7.57	11.35	5.31	6.92	4.11
134	5.86	4.66	1.27	3.27	4.04	6.65	4.42	5.01	11.97	8.90	2.25	7.73	5.13
135	5.08	4.31	2.67	2.17	3.84	4.90	3.56	5.63	9.80	9.74	2.53	4.94	4.71

NB: Description of the sites are presented in Table 4.3

Table 4.7 Means of grain yield and agronomic traits measured for 40 (top 20, middle 10, poorest 5) selected hybrids including the five checks, evaluated across 13 locations during the 2018 and 2019 cropping seasons in South Africa and Zimbabwe

Entry	GY	ASI	DA	PH	EH	ER	RL	SL	EPP	HC	EA
	t ha ⁻¹			cm			%			1-5	
41	8.61	1.27	73.02	239.55	124.66	14.08	8.98	7.06	1.09	1.03	2.63
108	7.95	0.99	73.99	233.50	132.83	18.13	7.69	1.72	1.06	0.71	2.68
12	7.51	1.00	73.82	247.59	141.11	5.26	4.64	3.56	1.12	0.55	2.65
52	7.49	1.49	73.87	222.65	124.43	10.86	4.81	7.37	1.20	0.52	2.84
28	7.45	1.25	69.97	217.71	122.60	14.23	5.75	0.89	1.11	2.52	2.85
56	7.45	1.11	72.47	230.56	124.20	27.19	5.13	3.11	0.99	3.19	2.83
99	7.42	1.68	72.90	222.14	120.96	10.99	5.96	7.15	1.14	0.65	2.93
120	7.37	1.71	74.36	225.18	114.38	9.87	9.25	4.89	1.01	0.01	2.88
16	7.36	1.15	70.07	226.45	120.73	12.92	5.56	5.12	1.01	0.83	2.66
23	7.27	1.62	71.39	221.18	119.56	16.34	7.72	11.86	1.07	1.55	2.81
8	7.24	0.88	70.80	220.55	116.11	13.54	6.66	9.49	1.25	2.04	2.90
79	7.18	1.21	70.72	231.13	125.67	18.62	8.83	2.13	1.12	0.33	2.72
130	7.05	0.42	70.26	226.83	122.46	18.46	4.96	5.14	1.07	1.56	2.65
95	6.70	1.06	76.85	228.58	122.29	18.58	3.22	3.31	1.15	0.85	2.96
91	6.69	1.26	75.47	231.57	119.42	16.23	8.70	-0.11	1.04	0.58	2.98
96	6.64	1.46	73.80	222.64	117.85	10.05	8.11	8.06	1.05	1.02	2.89
109	6.17	1.86	77.62	255.13	151.23	8.39	11.89	10.99	1.21	0.42	2.49
98	6.15	1.24	74.52	231.98	129.12	4.28	5.27	6.04	1.06	1.04	2.67
90	6.09	1.75	76.78	237.41	128.66	9.41	4.79	8.24	1.02	1.71	2.85
100	6.07	1.96	70.82	208.56	99.94	13.48	9.04	9.21	0.93	0.00	2.70
131	5.65	1.09	69.47	226.53	112.45	29.79	9.05	6.63	1.07	0.93	3.17
132	5.56	1.57	69.81	208.40	105.10	14.19	6.71	1.26	1.09	2.77	3.02
133	5.83	2.29	71.73	243.16	121.16	10.26	5.60	2.67	1.06	0.99	2.42
134	5.29	1.08	70.22	222.51	114.79	18.81	10.90	0.25	0.97	0.98	2.97
135	4.71	1.63	68.65	226.09	112.78	22.07	12.38	0.63	0.95	1.40	3.35
2	5.93	1.11	73.77	241.15	129.07	11.78	5.45	4.42	1.13	1.18	2.87
107	5.93	1.15	68.81	211.90	111.93	19.98	10.34	1.07	1.09	1.66	2.91
1	5.64	0.83	69.42	221.96	105.60	10.99	7.70	5.87	1.10	1.20	2.88
34	5.40	1.60	75.52	234.22	130.99	8.73	9.69	4.12	1.14	0.90	2.86
26	5.27	2.01	71.40	221.68	118.44	15.32	8.74	9.89	1.06	2.29	2.87
46	5.23	1.32	76.22	243.59	130.30	8.42	6.87	7.85	1.06	0.82	2.87
13	5.08	1.58	68.82	208.48	100.89	14.78	7.55	11.69	1.01	2.30	2.92
63	4.63	1.80	74.84	218.13	117.29	17.62	9.47	6.91	0.99	1.03	3.16
78	4.48	0.97	72.61	240.40	134.82	15.85	6.94	3.62	1.00	0.76	2.67
121	4.45	1.01	76.85	219.72	121.13	9.94	7.85	9.17	1.16	1.30	3.03
62	4.28	1.29	76.73	215.17	118.95	12.06	9.14	6.77	1.03	1.02	3.39
66	4.21	1.96	77.20	217.14	121.10	7.46	6.16	8.86	0.94	1.14	3.39
97	3.90	1.11	77.98	210.58	121.78	8.08	7.01	14.18	1.01	0.45	3.21
87	2.94	0.91	77.51	186.37	107.17	15.73	3.50	3.06	0.94	1.59	3.45
70	2.31	2.25	79.68	201.79	111.21	5.00	12.00	9.24	0.71	3.01	3.78
R-Square	0.95	0.81	0.98	0.95	0.94	0.87	0.89	0.87	0.83	0.73	0.85
SE	1.08	1.03	1.97	14.02	11.02	11.51	10.80	8.21	0.17	2.65	0.35
Mean	6.08	1.34	72.86	227.26	121.24	12.90	7.75	6.08	1.06	1.20	2.83

GY (t ha⁻¹) = Grain yield; PH = plant height; EH = ear height; ASI = anthesis silking interval; DA = Days to anthesis; RL = root lodging; SL = stalk lodging; HC = huck cover; EPP = ear per plant; ER = ear rot; EA = ear aspect

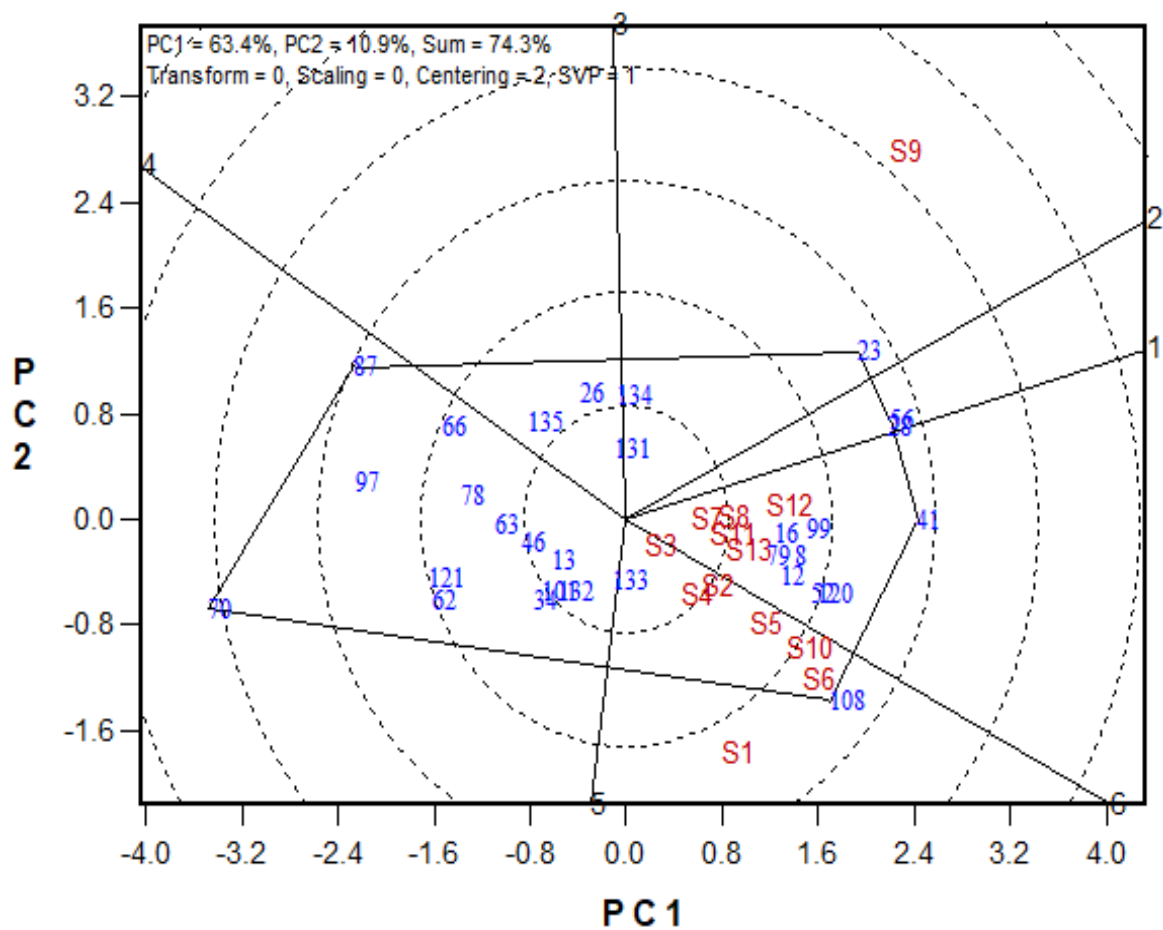


Figure 4.1 “Which-won-where” genotype plus genotype x environment interaction biplot of grain yield of 30 QPM and non-QPM maize hybrids evaluated at 13 locations during 2017/2018 and 2018/2019 cropping seasons

Only genotypes 23, 131 and 134 were adapted to S9 while genotype 108 was adapted to S2, S3, S4, S5, S6 and S10. Hybrids 12, 16, 41, 56, 98 and 99 were adapted to sites S1, S7, S8, S12 and S13. The remaining genotypes, for example 70, 78, 87 and 97, were not adapted to any of the 13 environments used in this study. The GGE biplot identified three mega environments. Sites S7, S8, S11, S12 and S13 grouped into one environment while S9 stood alone. The third group involves S1, S2, S3, S4, S5, S6 and S10. PC1 explained 63.4% for the total variation while PC2 on the other hand accounted for 10.9% of the variation. Together, PC1 and PC2 accounted for 74.3% of the variation in grain yield (Figure 4.1).

4.4.4.2 Stability analysis of the 135 hybrids

Presented in Figure 4.2 is the “means vs. the stability” of the 30 hybrids selected from 135 hybrids evaluated. The set of lines parallel to the double-arrow line passes the whole range of the entries, dividing them based on their mean performances. Thereby, the hybrids were ranked along the average-tester axis, with the arrow pointing to a higher value based on their mean performances across the 13 environments. The vertical blue line separates the entries into below and above average means. Principal component (PC 1 and PC 2) contribute 74.3% to yield variation. The information on genotypes and sites for the GGE biplot are presented in Tables 4.2 and 4.3, respectively.

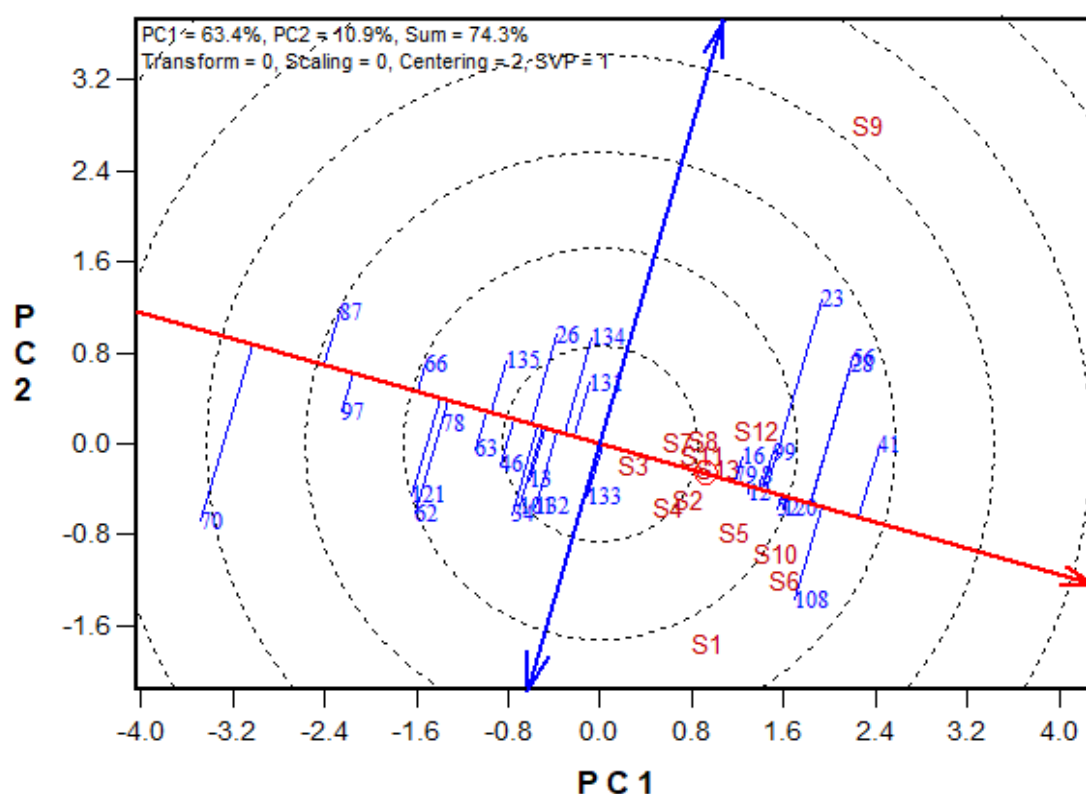


Figure 4.2 Entry/tester genotype plus genotype x environment biplot based on grain yield of 30 QPM and non-QPM maize hybrids evaluated at 13 locations during 2017/2018 and 2018/2019 cropping seasons.

The red and single-arrowed line, which passes through the biplot origin and the average environment, is referred to as the average-tester axis. This line points to the average environment from the biplot origin (Figure 4.2). The average yield of the hybrid is estimated by the distance from the markers on the average-tester axis. The stability of the

hybrids is therefore estimated by their projection onto the average-tester coordinate y-axis single-arrow line. The further a genotype is from the average tester axis, the less stable it is, and those closer to the average tester axis are stable. Hence, the most stable and high yielding hybrids identified were 12, 16, 19 and 20. Even though hybrids 41 and 108 are identified as the highest yielding genotypes, they were fairly unstable. The most unstable hybrids were 23 and 56.

4.4.4.3 AMMI analysis for grain yield

Grain yield performance of 30 selected hybrids is shown in Figure 4.3. From the graph, the vertical dotted line represents the average performance for grain yield and divides the graph into below and above yielding environments. The horizontal dotted line on the other hand (y-ordinate) is the interaction principal component 1 (IPC1) value of zero. Thus, genotypes that are positioned at the right side of the vertical dotted line performed better than the grand mean and vice versa for the cultivars at the left side of vertical line. Genotypes close to the horizontal dotted line have little interaction with the environment, and are considered to be more stable than those far away from the horizontal line. The site (E), genotype (G) and the IPC1 accounted for 86.1% of the entire variation for grain yield across the 13 locations. Genotypes 108, 16, 52 and 79 were identified as the stable and high yielding genotypes by the AMMI model. The information on genotypes and sites for the AMMI biplot are presented in Tables 4.2 and 4.3, respectively.

4.4.5 Quantifying grain yield reduction or yield increase due to the QPM trait

Cumulatively, QPM genotypes yielded 13.90% lower than non-QPM genotypes. Lines that were crossed with two QPM testers yielded less than those that were crossed with two non-QPM testers) (Table 4.8). However, the best performing genotype among the 135 genotypes evaluated was a QPM genotype. The best performing QPM hybrid genotype, 41, out-yielded the best performing non-QPM hybrid genotype 108 by 8.51%. Also, the best QPM hybrid had 52.40 and 33.60% higher grain yield than the best QPM and non-QPM hybrid checks, respectively. For the checks used in the present study, two of the four were non-QPM, which performed relatively better than the QPM checks.

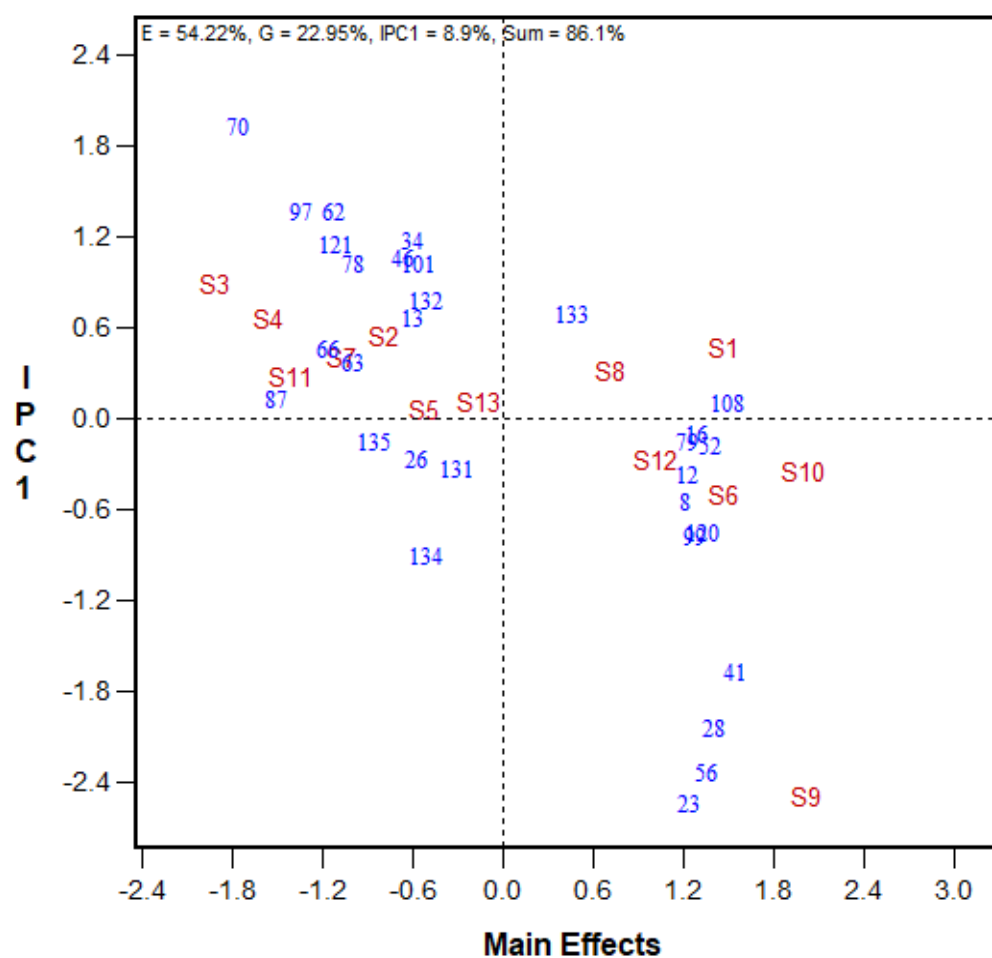


Figure 4.3 AMMI biplot of grain yield data and the first interaction principal component axis (IPCA 1) of 30 QPM, non-QPM and check hybrids evaluated at 13 locations in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons

Table 4.8 Comparison of grain yield and quantification of yield differences of QPM vs. non-QPM hybrids and checks

QPM hybrids					Non-QPM hybrids					Yield reduction (YR) %			
Entry	Line	Tester	GY (t ha ⁻¹)	Av. GY (t ha ⁻¹)	Entry	Line	Tester	GY (t ha ⁻¹)	Av. GY (t ha ⁻¹)	QPM vs. non-QPM	QPM vs. best non-QPM hybrid	QPM vs. best QPM check	QPM vs. best non-QPM check
1	1	1	5.79	6.01	3	1	3	5.63	6.09	-1.37	-29.3	-1.95	-0.78
2	1	2	6.23		4	1	4	6.56			-24.1	5.36	6.62
5	2	1	6.08	6.03	7	2	3	5.91	6.71	-10.1	-25.8	2.89	4.13
6	2	2	5.98		8	2	4	7.51			-27.1	1.19	2.41
9	3	1	5.97	5.72	11	3	3	6.18	6.97	-17.9	-27.2	1.06	2.27
10	3	2	5.46		12	3	4	7.76			-33.4	-7.55	-6.44
13	4	1	5.1	5.73	15	4	3	6.77	7.2	-20.5	-37.8	-13.7	-12.6
14	4	2	6.35		16	4	4	7.63			-22.5	7.49	8.78
17	5	1	5.65	6.08	19	5	3	6.26	6.74	-9.71	-31.1	-4.39	-3.24
18	5	2	6.51		20	5	4	7.21			-20.6	10.22	11.54
21	6	1	6.22	6	23	6	3	7.46	7.19	-16.6	-24.1	5.33	6.59
22	6	2	5.77		24	6	4	6.92			-29.6	-2.38	-1.21
25	7	1	5.45	5.46	27	7	3	6.44	7.01	-22.2	-33.5	-7.75	-6.64
26	7	2	5.46		28	7	4	7.58			-33.4	-7.57	-6.46
29	8	1	6.48	6.18	31	8	3	7.17	7.02	-11.9	-21	9.58	10.89
30	8	2	5.89		32	8	4	6.87			-28.2	-0.32	0.88
33	9	1	6.74	6.16	35	9	3	6.89	7.03	-12.3	-17.8	14.1	15.47
34	9	2	5.59		36	9	4	7.18			-31.9	-5.48	-4.34
37	10	1	7.53	6.86	39	10	3	6.91	7.09	-3.32	-8.23	27.33	28.85
38	10	2	6.19		40	10	4	7.27			-24.5	4.76	6.02
41	11	1	8.9	7.56	43	11	3	7.56	7.21	4.89	8.48	50.51	52.32
42	11	2	6.23		44	11	4	6.86			-24	5.44	6.71
45	12	1	5.25	5.36	47	12	3	5.83	6.27	-14.6	-36	-11.2	-10.2
46	12	2	5.47		48	12	4	6.72			-33.3	-7.49	-6.38
49	13	1	7.21	6.22	51	13	3	7.45	7.56	-17.7	-12.1	22.03	23.49
50	13	2	5.23		52	13	4	7.67			-36.2	-11.5	-10.5

† GY= grain yield of individual QPM hybrids; Av. GY QPM = average grain yield of lines crossed with the two QPM testers; Non-QPM GY = grain yield of individual non-QPM hybrids; Av. GY for non-QPM = average grain yield of lines crossed with the two non-QPM testers; YR = yield reduction

Table 4.8 Comparison of grain yield and quantification of yield differences of QPM vs. non-QPM hybrids and checks (continued)

QPM hybrids					Non-QPM hybrids					Yield reduction (YR) %			
Entry	Line	Tester	GY (t ha ⁻¹)	Av. GY (t ha ⁻¹)	Entry	Line	Tester	GY (t ha ⁻¹)	Av. GY (t ha ⁻¹)	QPM vs. non-QPM	QPM vs. best non-QPM hybrid	QPM vs. best QPM check	QPM vs. best non-QPM check
53	14	1	6.73	6.8	55	14	3	6.27	7.01	-3.1	-17.9	13.95	15.32
54	14	2	6.86		56	14	4	7.75			-16.4	16	17.39
57	15	1	5.82	5.98	59	15	3	7.25	6.88	-13.1	-29.1	-1.6	-0.42
58	15	2	6.14		60	15	4	6.51			-25.1	3.97	5.21
61	16	1	5.93	5.21	63	16	3	4.78	5.49	-5.15	-27.7	0.3	1.51
62	16	2	4.49		64	16	4	6.2			-45.2	-24	-23.1
65	17	1	6.89	5.7	67	17	3	6.56	6.81	-16.3	-16	16.61	18.01
66	17	2	4.51		68	17	4	7.05			-45.1	-23.8	-22.9
69	18	1	6.34	4.36	71	18	3	6.34	6.65	-34.4	-22.6	7.36	8.65
70	18	2	2.38		72	18	4	6.96			-71	-59.8	-59.3
-	-	-	-	-	73	19	1	5.83	-	-	-	-	-
-	-	-	-	-	74	19	2	6.11	-	-	-	-	-
-	-	-	-	-	75	19	3	6.21	-	-	-	-	-
-	-	-	-	-	76	19	4	5.9	-	-	-	-	-
-	-	-	-	-	77	20	1	5.71	-	-	-	-	-
-	-	-	-	-	78	20	3	4.52	-	-	-	-	-
-	-	-	-	-	79	20	4	7.35	-	-	-	-	-
-	-	-	-	-	80	21	1	6.02	-	-	-	-	-
-	-	-	-	-	81	21	2	6.04	-	-	-	-	-
-	-	-	-	-	82	21	3	5.73	-	-	-	-	-
-	-	-	-	-	83	21	4	6.51	-	-	-	-	-
-	-	-	-	-	84	22	1	7.29	-	-	-	-	-
-	-	-	-	-	85	22	2	6.82	-	-	-	-	-
-	-	-	-	-	86	22	3	6.62	-	-	-	-	-
-	-	-	-	-	87	22	4	3.08	-	-	-	-	-
88	23	1	5.47	5.62	90	23	3	6.41	6.65	-15.5	-33.2	-7.37	-6.26
89	23	2	5.77		91	23	4	6.89			-29.7	-2.42	-1.25

† GY= grain yield of individual QPM hybrids; Av. GY QPM = average grain yield of lines crossed with the two QPM testers; Non-QPM GY = grain yield of individual non-QPM hybrids; Av. GY for non-QPM = average grain yield of lines crossed with the two non-QPM testers; YR = yield reduction

Table 4.8 Comparison of grain yield and quantification of yield differences of QPM vs. non-QPM hybrids and checks (continued)

QPM hybrids					Non-QPM hybrids					Yield reduction (YR) %			
Entry	Line	Tester	GY (t ha ⁻¹)	Av. GY (t ha ⁻¹)	Entry	Line	Tester	GY (t ha ⁻¹)	Av. GY (t ha ⁻¹)	QPM vs. non-QPM	QPM vs. best non-QPM hybrid	QPM vs. best QPM check	QPM vs. best non-QPM check
92	24	1	5.58	5.8	94	24	3	6.91	6.96	-16.6	-31.9	-5.53	-4.4
93	24	2	6.02		95	24	4	7.01			-26.5	1.92	3.15
96	25	1	6.96	5.56	98	25	3	6.36	7.02	-20.7	-15.1	17.81	19.22
97	25	2	4.16		99	25	4	7.68			-49.2	-29.5	-28.7
100	26	1	6.36	5.88	102	26	3	6.9	6.83	-13.9	-22.4	7.63	8.92
101	26	2	5.39		103	26	4	6.75			-34.2	-8.75	-7.65
104	27	1	5.49	5.6	106	27	3	5.89	6.01	-6.82	-33	-7.04	-5.93
105	27	2	5.7		107	27	4	6.12			-30.5	-3.59	-2.43
-	-	-	-	-	108	28	1	8.2		-	-	-	-
-	-	-	-	-	109	28	2	6.35		-	-	-	-
-	-	-	-	-	110	28	3	6.85		-	-	-	-
-	-	-	-	-	111	28	4	6.75		-	-	-	-
-	-	-	-	-	112	29	1	5.73		-	-	-	-
-	-	-	-	-	113	29	2	6.63		-	-	-	-
-	-	-	-	-	114	29	3	5.93		-	-	-	-
-	-	-	-	-	115	29	4	6.54		-	-	-	-
-	-	-	-	-	116	30	1	6.63		-	-	-	-
-	-	-	-	-	117	30	2	5.89		-	-	-	-
-	-	-	-	-	118	30	3	5.91		-	-	-	-
-	-	-	-	-	119	30	4	6.52		-	-	-	-
120	31	1	7.56	6.11	122	31	3	6.81	7.03	-13.2	-7.82	27.9	29.44
121	31	2	4.65		123	31	4	7.25			-43.2	-21.2	-20.3
-	-	-	-	-	124	32	1	4.71	-	-	-	-	-
-	-	-	-	-	125	32	3	5.18	-	-	-	-	-
-	-	-	-	-	126	32	4	5.27	-	-	-	-	-
-	-	-	-	-	127	35	1	5.83	-	-	-	-	-
-	-	-	-	-	128	35	2	6.18	-	-	-	-	-
-	-	-	-	-	129	35	3	6.32	-	-	-	-	-
-	-	-	-	-	130	35	4	7.13	-	-	-	-	-
-	-	-	-	-	133	-	-	5.91	-	-	-	-	-
131	-	-	5.84	-	134	-	-	5.61	-	-	-28.7	-1.13	0
132	-	-	5.66	-	135	-	-	4.77	-	-	-31	-4.31	-3.17

† GY= grain yield of individual QPM hybrids; Av. GY QPM = average grain yield of lines crossed with the two QPM testers; Non-QPM GY = grain yield of individual non-QPM hybrids; Av. GY for non-QPM = average grain yield of lines crossed with the two non-QPM testers; YR = yield reduction

4.5 Discussion

The results suggest that there is a prospect of identifying improved QPM hybrids, which could be used for commercialisation in SSA. Substantial differences were evident between the 13 test environments indicating that hybrids could be identified to suit target locations. The environment had a very large influence on grain yield as has been reported in other studies (Maazou et al. 2016; Priyadarshan 2019). The significant GEI together with stability estimates from the GGE biplot analyses indicated the presence of crossover association (Mebratu et al. 2019), which may complicate selecting high yielding and superior hybrids across a wide range of environments. Significant site mean squares for grain yield and most measured traits across environments showed that the test environments were distinctive in discriminating among the 135 hybrids. The highly significant site variance indicated that the environments used for the study were variable and this will aid in the selection of superior QPM hybrids across a wide range of environments in Southern Africa for commercialization.

When average yields of QPM and non-QPM hybrids were compared across all environments, the non-QPM genotypes were found to have superior yield compared to the QPM genotypes. This is consistent with the results of studies conducted previously (Wegary et al. 2013; Ababulgu et al. 2018; Tilahun et al. 2018) even though those studies might not have considered the volume of the genetic materials used in this study. In addition, the conditions and the environments under which the studies were performed could have played a role in the outcome of the studies. This study showed that QPM lines crossed with QPM testers produced some excellent hybrids compared to some non-QPM hybrids. The average yield for line 11 crossed with QPM testers 1 and 2, genotypes 41 and 42, produced grain yield of 4.85% higher than when line 11 was crossed with non-QPM testers 3 and 4 (genotypes 43 and 44). Hybrids 84 and 85 obtained from non-QPM line 28 crossed with QPM testers 1 and 2 recorded 0.07% increased grain yield over line 28 crossed with non-QPM testers 3 and 4 thus genotypes 86 and 87. Therefore, in the current study, the best performing hybrid was a QPM hybrid, although QPM hybrids in general produced 13.9% less yield than non-QPM hybrids. Previous reports stated that QPM genotypes are inferior in terms of grain against non-QPM hybrids (Singh et al. 2014). This suggested that some QPM hybrids have the potential to produce comparable grain yield to non-QPM hybrids. The increased grain yield of the best QPM over the best non-QPM hybrids

confirmed results from an earlier study (Setimela et al. 2017) that also found QPM genotypes yielding 12 to 25% above the non-QPM genotypes used as checks.

From this study across the 13 locations under optimum conditions, it is possible that outstanding QPM genotypes could be selected for commercial production in SSA. The AMMI biplot is very useful because of its discriminatory ability in the identification and selection of superior genotypes (Wang et al. 2016). Hybrids 108, 16, 52 and 79, which were identified by the AMMI biplot analysis as high-yielding and stable across the test locations, indicated that these genotypes can be grown under optimal conditions in SSA without a grain yield penalty.

QPM hybrids 41 and non-QPM hybrids 108, 12 and 20 had the highest yield and stability across locations. Hybrids 108 and 41 were identified as the best performing hybrids. Among these four superior genotypes, hybrids 20 and 12 were the most consistent across all the locations, however, their yield potential was not comparable to that of hybrids 108 and 41. Superior and outstanding QPM hybrid 41 was adapted to five locations while the best non-QPM hybrid 108 on the other hand, was well adapted to seven of the 13 locations used, indicating that these hybrids have the potential to be produce high and stable yield in wider maize growing environments in Southern Africa under rainfed conditions.

The AMMI analysis was effective in discriminating among the various environments. The GGE biplot identified all 13 locations used as superior environments for maize production. However, with the use of the AMMI biplot, only six locations were considered ideal environments. While the AMMI biplot accounted for 86.1% of the total yield variation, the GGE biplot accounted for 74.3% of variation. There was also variation for stability of the genotypes between the two models. The GGE biplot identified genotype 108 as high yielding but relatively unstable. The AMMI model on the other hand identified the same genotype as high yielding and highly stable. The two models are superior tools in identifying superior genotypes but they could classify genotypes and environments differently, confirming the earlier studies of Yan et al. (2007), Hadasch et al. (2017) and Erdemci (2018).

This study is of great interest for maize breeding programmes and seed companies to tackle the issues surrounding the cultivation of QPM genotypes in terms of the low yield reported

in several studies (Ababulgu et al. 2018; Kaur et al. 2019). The excellent yield performance of some of the QPM hybrids across the test locations will be of importance to countries that rely heavily on maize as their major staple food. The outcome of this study suggests that further evaluation should be carried out to identify superior and stable QPM genotypes. These results suggest that the outstanding hybrids should be extensively tested in on-farm trials in SSA and vigorously promoted for adoption and commercialization to contribute to food and nutritional security in the sub-region.

4.6 Conclusions

The best performing hybrid identified in this study was a QPM hybrid involving the cross between line 11 x tester 1 (CZL15049), followed by a non-QPM hybrid involving line 28 x tester 1 (CZL15049), hybrids 41 and 108, respectively. The best QPM hybrid outperformed the best non-QPM hybrid by 8.81% but overall, non-QPM hybrids yielded better than QPM hybrids. In addition, the best QPM hybrid genotype 41 outperformed best non-QPM check (Pioneer PHB30G19) and best QPM check (CBI) by 50.45 and 52.24%, respectively. The AMMI analyses indicated that the grain yield performance of QPM and non-QPM hybrids were highly affected by environmental effects. The AMMI and GGE biplot analysis permitted estimation of interaction effect of a genotype in each environment and it helped to identify genotypes best suited for specific environments. The GGE biplot identified three mega environments. In addition, the discriminating power vs. representativeness view of the GGE biplot was an effective tool for test environments evaluation. The AMMI and GGE biplots identified genotypes 108 and 12 as the most stable and high yielding hybrids. QPM hybrids 41 and 120 (L30 x CZL15049) and non-QPM hybrid 12 and 108 were found to be the high yielding genotypes. Hence, the promotion of these superior hybrids for adoption and release will not only enhance grain yield output but also help improve nutritional status of people who depend on maize products for their livelihood.

References

Ababulgu D, Shimelis H, Laing M and Beyene A (2018) Phenotypic characterization of elite quality protein maize (QPM) inbred lines adapted to tropical-highlands and the association studies using SSR markers. *Australia Journal of Crop Science* 12: 22-31.

- Aliu S, Rusinovci I, Fetahu S and Simeonovska E (2012) Genetic diversity and correlation estimates for grain yield and quality traits in Kosovo local maize (*Zea mays* L.) populations. *Notulae Scientia Biologicae* 4: 121-128.
- Beck D, Ba M and Edmeades GO (2003) Genetic analysis of inbred and hybrid grain yield under stress and nonstress environments in tropical maize. *Crop Science* 43: 807-817.
- Bhatnagar S, Betran FJ and Rooney LW (2004) Combining abilities of quality protein maize inbreds. *Crop Science* 44: 1997-2005.
- Chaudhary DP, Kumar D, Verma R, Langyan S and Sangwan S (2014) Nutritional Quality of Maize. In: Chaudhary DP, Kumar, S and Singh S (eds), *Maize: Nutrition Dynamics and Novel Uses*. Springer, pp. 135-140.
- Crossa J (1990) Statistical analyses of multilocation trials. *Advances in Agronomy* 44: 55-85.
- Darrah LL, McMullen MD and Zuber MS (2019) Breeding, Genetics and Seed Corn Production. In: Serna-Saldivar SO (ed), *Corn Chemistry and Technology*. Elsevier, pp. 19-41. doi:10.1016/b978-0-12-811971-6.00002-4
- De Groote H, Chege CK, Tomlins K and Gunaratna NS (2014) Combining experimental auctions with a modified home-use test to assess rural consumers' acceptance of quality protein maize, a biofortified crop. *Food Quality and Preference* 38: 1-13.
- Edmeades GO, Bänziger M, Mickelson HR and Peña-Valdivia CB (eds) (1997) Developing drought- and low N-tolerant maize. *Proceedings of a Symposium*, March 25-29, 1996. CIMMYT, El Batán, Mexico, D.F., pp. 1-543.
- Erdemci I (2018) Investigation of genotype $\times$ environment interaction in chickpea genotypes using AMMI and GGE biplot analysis. *Turkish Journal of Field Crops* 23: 20-26.
- Gauch HG and Zobel RW (1988) Predictive and postdictive success of statistical analyses of yield trials. *Theoretical and Applied Genetics* 76: 1-10.
- Gupta HS, Babu R, Agarwal PK, Mahajan V, Hossain F and Thirunavukkarasu N (2013) Accelerated development of quality protein maize hybrid through marker-assisted introgression of *opaque-2* allele. *Plant Breeding* 132: 77-82.
- Hadasch S, Forkman J and Piepho HP (2017) Cross-validation in AMMI and GGE models: A comparison of methods. *Crop Science* 57: 264-274.
- Kaur N, Singh B and Sharma S (2019) Comparison of quality protein maize (QPM) and normal maize with respect to properties of instant porridge. *LWT-Food Science and Technology* 99: 291-298.

- Krishna MSR, Surender M and Reddy S (2017) Marker assisted breeding for introgression of *opaque-2* allele into elite maize inbred line BML-6. *Acta Ecologica Sinica* 37: 340-345.
- Krivanek AF, De Groote H, Gunaratna N, Diallo A and Friesen D (2007) Breeding and disseminating quality protein maize (QPM) for Africa. *African Journal of Biotechnology* 6: 312-324.
- Kumar J, Jaiswal V, Kumar A, Kumar N, Mir RR, Kumar S, Dhariwal R, Tyagi S, Khandelwal M, Prabhu KV, Prasad R, Balyan HS and Gupta PK (2011) Introgression of a major gene for high grain protein content in some Indian bread wheat cultivars *Field Crops Research* 123: 226-233.
- Maazou A-RS, Tu J, Qiu J and Liu Z (2016) Breeding for drought tolerance in Maize (*Zea mays* L.). *American Journal of Plant Sciences* 7: 1858-1870.
- Mastrodomenico AT, Haegele JW, Seebauer JR and Below FE (2018) Yield stability differs in commercial maize hybrids in response to changes in plant density, nitrogen fertility, and environment. *Crop Science* 58: 230-241.
- Mebratu A, Wegary D, Mohammed W, Teklewold A and Tarekegne A (2019) Genotype $\times$ environment interaction of quality protein maize hybrids under contrasting management conditions in eastern and southern Africa. *Crop Science* 59: 1576-1589.
- Mertz ET, Bates ET and Nelson OE (1964) Mutant genes that change protein composition and increase lysine content of maize endosperm. *Science* 145: 279-280.
- Mittelman A, Filho J, Lima G, Klain C and Tanaka R (2003) Potential of the ESA23B maize population for protein and oil content improvement. *Scientia Agricola* 60: 319-327.
- Mukanga M, Derera J, Tongoona P and Laing MD (2011) Farmers perceptions and management of maize ear rots and their implications for breeding for resistance. *African Journal for Agricultural Research* 6: 45544-4554.
- Nuss ET and Tanumihardjo SA (2011) Quality Protein maize for Africa: Closing the protein inadequacy gap in vulnerable populations. *Advances in Nutrition* 2: 217-224.
- Pandey N, Hossain F, Kumar K, Vishwakarma AK, Muthusamy V, Saha S, Agrawal PK, Guleria SK, Reddy SS, Thirunavukkarasu N and Gupta HS (2016) Molecular characterization of endosperm and amino acids modifications among quality protein maize inbreds. *Plant Breeding* 135: 47-54.
- Patterson H and Williams E (1976) A new class of resolvable incomplete block designs. *Biometrika* 63: 83-92.

- Pixley KV and Bjarnason MS (1993) Combining ability for yield and protein quality among modified-endosperm *opaque-2* tropical maize inbreds. *Crop Science* 33: 1229-1234.
- Priyadarshan PM (2019) Genotype-by-Environment Interactions. In: Priyadarshan PM (ed), *Plant Breeding: Classical to Modern*. Springer, Singapore, pp. 457-472.
- SAS Institute. 2011. *Statistical Analysis Software (SAS) user's guide*.
- Setimela PS, Gasura E and Tarekegne AT (2017) Evaluation of grain yield and related agronomic traits of quality protein maize hybrids in Southern Africa. *Euphytica* 213: 289.
- Shi G, Chavas JP and Lauer J (2013) Commercialized transgenic traits, maize productivity and yield risk. *Nature Biotechnology* 31: 111-114.
- Singh AA, Agrawal SB, Shahi JP and Agrawal M (2014) Assessment of growth and yield losses in two *Zea mays* L. cultivars (quality protein maize and nonquality protein maize) under projected levels of ozone. *Environmental Science and Pollution Research* 21: 2628-2641.
- Tandzi LN, Mutengwa CS, Ngonkew ELM, Woïñ N and Gracen V (2017) Breeding for quality protein maize (QPM) varieties: A Review. *Agronomy* 7: 1-16.
- Tilahun B, Azimach G, Keno T, Chibsa T, Garoma B, Abebe B, Tulu D, Tafa Z and Chalchisa D (2018) Test cross performance and combining ability of newly introduced quality protein maize (*Zea mays*) inbred lines for grain yield and agronomic traits evaluated in mid-altitude agro-ecological zones of Ethiopia. *South African Journal of Plant and Soil* 36: 173-180.
- Tripathy SK, Ithape DM, Maharana M and Prusty AM (2017) Quality protein maize (QPM): Genetic basis and breeding perspective. *Tropical Plant Research* 4: 145-152.
- Wang R, HuD, Huiquan Zheng H, Yan S and Wei R (2016) Genotype x environmental interaction by AMMI and GGE biplot analysis for the provenances of *Michelia chapensis* in South China. *Journal of Forestry Research* 27: 659-664.
- Wegary D, Vivek B and Labuschagne M (2013) Association of parental genetic distance with heterosis and specific combining ability in quality protein maize. *Euphytica* 191: 205-216.
- Yan W, Hunt LA, Sheng Q and Szlavnic Z (2000) Cultivar evaluation and mega environment investigation based on the GGE biplot. *Crop Science* 40: 597-605.
- Yan W, Kang MS, Ma B, Woods S and Cornelius PL (2007) GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Science* 47: 643-655.

- Yan W (2001) GGE biplot- a windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agronomy Journal* 93: 1111-1118.
- Živanović T, Vračarević M, Krstanović S and Šurlan-Momirović G (2004) Selection on uniformity and yield stability in maize. *Journal of Agricultural Sciences* 49: 117-130.
- Zobel RW, Wright MJ and Gauch HG (1988) Statistical analysis of a yield trial. *Agronomy Journal* 80: 388-393.

CHAPTER FIVE

COMBINING ABILITY ANALYSIS AND ASSOCIATION AMONG AGRONOMIC TRAITS OF QUALITY AND NON-QUALITY PROTEIN MAIZE INBRED LINES

5.1 Abstract

Development of high yielding QPM hybrids would fight hunger and malnutrition of the increasing human population and help meet the high demand of maize for human consumption, industrial use and feed for animal and poultry. However, most maize genotypes being cultivated and consumed, particularly in SSA, are normal endosperm maize. It is therefore important to explore and understand the genetic mechanisms conditioning the inheritance of grain yield and other essential traits used in the development of superior maize genotypes. Exploitation of GCA and SCA for maize improvement has been documented in several studies on temperate and tropical genotypes of various maturity groups. In spite of this, only limited information is available on genetic studies involving QPM genotypes for hybrid development. The main objective of this study was to determine the combining ability for grain yield and other agronomic traits of QPM and non-QPM inbred lines with two QPM and two non-QPM testers. Nine non-QPM and 24 QPM lines were crossed with four elite testers having QPM and non-QPM backgrounds to generate 130 hybrids. The 130 single cross hybrids were evaluated at 13 locations in South Africa and Zimbabwe during the 2018 and 2019 cropping seasons. The results showed significant GCA for lines and testers as well significant SCA for hybrids between lines and testers for most of the measured traits. Both additive and non-additive genetic effects were important in the expression of traits, with non-additive gene action controlling the inheritance of grain yield. Inbred lines 11 (QPM), 14 (QPM) and 28 (non-QPM) and non-QPM tester CML444 showed desirable GCA effects for grain yield, indicating that these lines in combination with tester CML444 should be considered when targeting development of superior maize genotypes with QPM traits. Lines 1 (QPM), 2 (QPM), 8 (QPM), 13 (QPM) and 30 (non-QPM) were prolific, while QPM tester CZL059 was the only tester to display positive significant GCA for ears per plant, which is a major contributor to grain yield. The SCA grouping method showed that QPM testers were superior to non-QPM testers in discriminating the lines for grain yield. Based on the SCA values, crosses 120, 108, 105, 99, 85 and 41 were identified as the best hybrids across the

locations. It is recommended that maize breeding programmes targeting the development of high yielding QPM hybrids should exploit lines with high GCA values if they produce hybrids with high SCA. In addition, the identified superior hybrids may be further evaluated and consequently promoted for release which could increase incomes of farmers and help to alleviate poverty, hunger and malnutrition in southern Africa and SSA at large.

Keywords: Combining ability, quality traits, grain yield, yield reduction

5.2 Introduction

Maize (*Zea mays* L) ranks among the top three most important cereal crops worldwide based on its yield potential and adaptability to several agro-ecological environments. In maize breeding programmes, inbred lines are used to generate hybrids for commercial production. Because of their increased yield potential, hybrid maize varieties are used worldwide to attain higher grain yield. In breeding, it is essential to understand how inbred lines or parents combine for the development of superior hybrids (Amegbor et al. 2017; de Abreu et al. 2019). The term “combining ability” was first used by Sprague and Tatum (1942). Vacaro et al. (2002) and Wegary et al. (2013) noted that the performance of any genetic material is dependent on its potential *per se* performance as well as the combining ability of the lines in crosses, however since heterosis for superior performance is controlled primarily by SCA, lines should be selected based on their SCA with testers. Combining ability studies generate useful information on the genetic mechanisms governing how quantitative traits are inherited and this assists plant breeders in selecting superior parental lines for further crop improvement or use in hybrid production for commercial purposes (Abuali et al. 2012; Ali et al. 2012; Saif-ul-Malook et al. 2016).

Two types of combining ability are commonly used in breeding and biometrical genetics, and these are general combining ability (GCA) and specific combining ability (SCA) (Abuali et al. 2012; Haydar and Paul 2014). The GCA is the average contribution an inbred makes to hybrid performance in a series of hybrid combinations in comparison to other inbreds in the same series of hybrid combinations and this is due to additive gene action while SCA the contribution of an inbred to hybrid performance in a cross with a specific other inbred in relation to its contributions in crosses with an array of other inbreds (Sprague and Tatum 1942; Haydar and Paul 2014). In developing hybrids, one must choose

an appropriate mating design to generate the hybrids. Even though there are several mating designs used in plant breeding, they all come with advantages and disadvantages. Several researchers use the diallel and North Carolina mating designs. However, it is very expensive to use a diallel when there is a high number of lines used in generating the hybrids. Therefore, in a study with a relatively high number of inbred lines, it is better to use the line x tester mating design. This mating design for estimating GCA and SCA for hybrid development was first proposed by Kempthorne (1957) and has been extensively used by several researchers such as Sharma (2006), Nduwumuremyi et al. (2013), Wegary et al. (2014) and Tilahun et al. (2019). In this design, hybrids are made between lines which are used as females and testers as males. Each tester is crossed to each line to generate hybrids (Maruya et al. 2006; Sharma 2006; Sharief et al. 2009; Abuali et al. 2012; Haydar and Paul 2014).

The genetic improvement of grain yield and its related traits relies on the nature and the degree of genetic variation in available germplasm. Grain yield is the most important trait of interest to the breeder and farmer and grain yield is a complex trait controlled by several genes. However, it is important to consider associations of yield related traits with grain yield (Bekele and Rao 2014). It is useful to understand the relationship between grain yield and its related traits (Qi et al. 2010; Gangashetty et al. 2016). The objective of this study was to determine the combining ability for grain yield and related traits for QPM and non-QPM inbred lines crossed with two QPM and two non-QPM testers, and the relationship between the measured traits.

5.3 Materials and methods

5.3.1 Germplasm, field evaluation and data collection

The materials and methodology for the field evaluations used in this study are the same as described in Chapters 3 and 4. Observations were made on traits reported in Chapter 3. Tables 4.1 and 4.2 in Chapter 4 contain the names of the inbred lines and testers (Table 4.1) used in generating the hybrids (Table 4.2).

5.3.2 Data analysis

The data obtained from 13 locations (Table 4.3) were combined to estimate GCA, SCA, heritability and correlation. Line x tester analysis was done according to Singh and Chaudhary (1985). The GCA and SCA and their standard errors were computed for grain yield and other measured traits using the PROC Mixed Procedure in SAS version 9.4 (SAS 2011). The variation among hybrids was partitioned into sources due to lines, testers and line x testers. GCA of testers (male) was obtained based on their performance in the F₁ hybrid combinations with all possible lines (females). Similarly, GCA of each line was also determined based on the performance of F₁ hybrids with all possible testers. GCA and SCA effects were determined for each agronomic trait for each location and across locations following the procedure described by He et al. (2018).

The general linear model for line x tester mating design is:

$$Y_{ijkl} = \mu + a_1 + b_{kl} + v_{ij} + (av)_{ijl} + \varepsilon_{ijkl}$$

where Y_{ijkl} = observed value from each experimental unit;

μ = population mean; a_1 = location effect;

b_{kl} = block or replication effect within each location;

v_{ij} = F₁ hybrid effect = $g_i + g_j + s_{ij}$. i.e. $v_{ij} = g_i + g_j + s_{ij}$,

where g_i = GCA for the i th parental line;

g_j = GCA effects of j^{th} tester;

s_{ij} = SCA for the ij^{th} F₁ hybrid

$(av)_{ijl}$ = interaction effect between i^{th} F₁ hybrid and l^{th} location

ε_{ijkl} = residual effect (Table 5.1).

Heterotic groupings were made based on SCA of grain yield as described by Agbaje et al. (2008). Classification of an inbred line into a heterotic group was based on the significant ($P < 0.05$) positive SCA effects with one of the testers or significant ($P < 0.05$) negative SCA effects with the other with a mean yield of the tester hybrid being equal to or greater than one standard error (SE) above the grand mean of all testcrosses (Agbaje et al. 2008).

Table 5.1 General form of analysis of variance for line x tester design repeated over locations

Source	Df	MS	Expected mean square	
			Model I	Model II
Replication (r)	r-1			
Lines (f)	f-1	M ₁	$\sigma^2 + rf \frac{1}{m-1} + \sum_t g_t^2$	$\sigma^2 + v_{sca} + rf_{gca(m)}$
Tester (m)	m-1	M ₂	$\sigma^2 + rm(\frac{1}{f-1}) + \sum_j g_j^2$	$\sigma^2 + rv_{sca} + rm_{gca(f)}$
Line x Tester	(f-1)(m-1)	M ₃	$\sigma^2 + r[\frac{1}{(m-1)(f-1)} + \sum_i \sum_j s_{ij}]$	$\sigma^2 + rv_{sca}$
Error	(r-1)(fm-1)	M ₄	σ^2	σ^2

Nduwumuremyi et al. (2013)

5.3.3 Estimation of grain yield reduction

The grain yield of the hybrids, days to anthesis, plant height and tryptophan content of the inbred lines were used to estimate yield reduction. The hybrids and lines were grouped into QPM, non-QPM and resulting QPM, thus each group consisted of three genotypes (QPM, non-QPM and resulting QPM). The resulting lines were developed from a cross between QPM genotypes and non-QPM genotypes. For each group, resulting QPM genotypes were used as the standard and consequently, increase in grain yield for QPM or non-QPM was calculated based on the grain yield of the resulting QPM genotypes using the formula:

$$\text{Yield reduction of QPM} = \frac{(\text{yield of resulting QPM} - \text{yield of QPM})}{\text{yield of QPM}} \times 100$$

$$\text{Yield reduction of non-QPM} = \frac{(\text{yield of resulting QPM} - \text{yield of non-QPM})}{\text{yield of non-QPM}} \times 100$$

5.4 Results

5.4.1 Analysis of variance for general and specific combining ability of 130 hybrids evaluated at Potchefstroom, Cedara and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons

The ANOVA for combining ability for trials conducted at Potchefstroom during 2018 and 2019 cropping seasons showed significant effects of line and tester and for line x tester for all the traits measured excepted for stalk lodging and husk cover (Table 5.2). At Cedara, line x tester SCA effect was also significant for most of the traits except stalk lodging and husk cover. Apart from grain yield, ear aspects and root lodging, other traits measured were not significant for site x line x tester.

At Cedara, ANOVA for the two seasons revealed significant ($P < 0.01$) line GCA for grain yield, days to pollen shed, plant and ear heights, ear aspect, root and stalk lodging. GCA for tester was not significant for anthesis-silking interval, ear aspect, ears per plant, husk cover and number ear rots (Table 5.2). Site had significant interaction with line for grain yield, days to pollen shed, ear aspect, root lodging and ear rot, while site x tester was significant for grain yield, days to pollen shed, plant height, ear aspect and root lodging.

The ANOVA of the trials conducted at eight sites in Zimbabwe showed significant line GCA for all the traits measured (Table 5.2). Similarly, tester GCA was also significant for all the measured traits, except for husk cover. Site x line was also significant for the traits measured, except husk cover, while, apart from plant height and husk cover, site x tester effect was significant for all measured traits. The SCA for line x tester was not significant for root lodging, stalk lodging and husk cover. Site x line x tester effect in Zimbabwe trials was significant for grain yield, ear aspect, ears per plant, stalk lodging and ear rot.

Table 5.2 Mean squares from analysis of variance for general and specific combining ability for grain yield and other agronomic traits of 130 QPM hybrids at Potchefstroom, Cedara and Zimbabwe during the 2018 and 2019 cropping seasons

Source	DF	GY	DA	ASI	PH	EH	EA	EPP	RL	SL	HC	ER
Potchefstroom 2018 and 2019												
Rep	1	1.84	0.16	0.93	3969.03**	88.68	0.25	0.11	78.85	987.71	0.02	215.12
Year	2	2845.99**	979.25**	1.84	42125.48**	19741.85**	0.64*	7.57**	2226.26**	18372.80**	29.23**	17594.95**
Line	32	9.23**	128.13**	1.87**	1662.64**	2019.68**	0.41**	0.09**	185.09**	547.55**	0.49**	750.64**
Tester	3	172.26**	729.93**	9.04**	9143.28**	16352.36**	0.97**	0.28**	539.30**	2178.98**	0.94**	674.00**
Year*Line	64	5.65**	5.99**	1.15**	260.16**	123.79	0.55**	0.05*	143.32**	468.26**	0.48**	258.04**
Year*Tester	6	18.03**	17.85**	0.49	800.75**	231.26	2.49**	0.21**	1114.46**	1699.07**	0.08	184.42
Line*Tester	94	8.17**	7.42**	1.13**	614.15**	327.58**	0.25*	0.06**	100.84*	152.33	0.26	149.15*
Year*Line*Tester	188	4.38**	3.32	0.59	183.07	141.04	0.24	0.04	96.61*	210.01*	0.30*	191.11**
Error	389	1.69	3.68	0.73	163.35	145.07	0.17	0.04	75.92	171.04	0.23	113.65
Cedara 2018 and 2019												
Rep	1	3.73	14.89	2.22	1246.21	1467.31*	0.042	0.005	1005.94**	40.35	5.10**	3.82
Year	1	114.08**	2324.27**	0.18	186831.04**	104032.73**	0.56	0.001	19476.29**	13144.50**	18.19**	29362.80**
Line	32	7.92**	95.59**	1.71	726.71**	1068.07**	0.43**	0.015	602.08**	482.44**	0.28	466.88
Tester	3	27.80**	298.12**	0.97	3687.03**	6524.59**	0.19	0.033	1576.93**	1604.46**	0.37	484.80
Year*Line	32	9.03**	17.11**	1.59	428.84	289.52	0.45**	0.024	395.22**	262.33	0.37	723.27*
Year*Tester	3	22.10**	28.79*	0.87	1523.67**	609.41	0.82**	0.003	1205.82**	77.81	0.45	290.05
Line*Tester	94	7.18**	10.14*	1.36	584.49**	387.92**	0.35**	0.014	223.30**	214.73	0.34	514.33
Year*Line*Tester	94	5.3**	6.76	0.99	401.73	260.52	0.45**	0.021	240.27**	229.98	0.29	429.80
Error	259	1.51	7.59	1.4	369.45	235.93	0.22	0.018	142.08	212.43	0.34	461.41
Zimbabwe 2018												
Rep	1	4.62*	32.25**	3.98	11150.89**	6595.97**	1.48**	0.30**	600.22	5.12	7.41	40.44
Site	7	1149.62**	8012.63**	108.62**	203931.89**	93895.25**	11.17**	1.66**	66361.61**	883.61**	49.69**	6909.50**
Line	32	16.15**	219.53**	2.38**	5695.34**	4238.37**	1.62**	0.17**	451.76**	74.02**	33.19**	563.92**
Tester	3	63.21**	1348.61**	15.92**	41038.23**	40356.22**	8.79**	1.85**	1464.44**	379.67**	4.39	2010.81**
Site*Line	224	2.39**	8.12**	1.58**	360.24*	259.59**	0.25**	0.04*	273.05**	47.18**	11.76	149.03**
Site*Tester	21	5.07**	30.54**	3.51**	361.79	713.88**	0.42**	0.17**	1035.82**	76.56**	13.92	399.01**
Line*Tester	94	7.58**	19.55**	1.65*	1124.33**	531.50**	0.50**	0.12**	170.30	32.76	12.10	105.59*
Site*Line*Tester	658	1.50**	4.49	1.23	278.91	150.94	0.13*	0.04*	171.16	33.11**	10.48	87.62*
Error	1039	1.11	4.39	1.24	296.92	187.29	0.11	0.03	184.17	26.83	10.95	78.14

† DF= degrees of freedom; GY = Grain yield; DA = Days to anthesis; ASI = anthesis silking interval; PH = plant height; EH = ear height; EA = ear aspect; EPP= ear per plant; RL = root lodging; SL = stalk lodging; HC = hick cover; ER = ear rot; *P<0.05, **P<0.01

5.4.2 Analysis of variance for general and specific combining ability of 130 hybrids evaluated across 13 locations

The combined ANOVA for grain yield and other agronomic traits of the inbred lines (Table 5.3) showed significant ($P < 0.05$) site mean squares for all the traits. The GCA of line was significant ($P < 0.05$) for all the measured traits while the GCA of the testers was also significant ($P < 0.01$) for all the measured traits, except husk cover. Site x line effect was only significant ($P < 0.05$) for anthesis-silking interval, ear aspects, husk cover and root lodging, while site x tester effect was significant for the majority of the traits measured, except days to pollen shed, plant height, husk cover and ear rot. The line x tester SCA was significant for grain yield, anthesis-silking interval, plant and ear heights, ear aspect, husk cover, root lodging and ear per plant. However, site x line x tester was only significant for root lodging. Across the 13 locations, percentage sum of squares due to SCA was found to be higher than that due to GCA for grain yield, anthesis-silking interval, ears per plant and husk cover. On the other hand, GCA sum of squares primarily explained variation for days to pollen shed, plant and ear height, ear aspect, root and stacking lodging and ear rot.

5.4.3 Performance of lines in hybrid generation

Across the 13 locations, the grain yield ranged from 5.14 t ha⁻¹ for line 32 to 6.87 t ha⁻¹ for line 11 (Table 5.4). For ears per plant, line 4 recorded the least number of ears and lines 2 and 30 the most ears (1.15). Ear rots ranged from 8.86% for line 30 to 22.66% for line 14. Generally, all the lines displayed good performance for ear aspect with the exception of lines 32 and 16. Root lodging ranged from 3.82 to 14.13% for lines 8 and 11, respectively, while stalk lodging ranged from 2.78 to 10.34% for line 8 and line 18, respectively. With the exception of lines 5, 7, 14 and 19, all the lines recorded a husk cover score below 2.

5.4.4 Performance of testers in hybrid generation

Among the four testers, non-QPM tester 4 (CML444) produced the highest grain yield (6.57 t ha⁻¹) and QPM tester 2 (CZL059) had lowest grain yield of 5.49 t ha⁻¹ (Table 5.5). For ear aspect, all the non-QPM testers performed better than the QPM testers and a similar trend was observed for root and stalk logging. QPM tester 2 recorded the highest number of ears per plant, followed by non-QPM tester 4.

Table 5.3 Mean squares from analysis of variance for general and specific combining ability for grain yield and other agronomic traits of 130 QPM hybrids across 13 locations in South Africa and Zimbabwe during 2018 and 2019 cropping seasons

Source	DF	GY t ha ⁻¹	DA	ASI	PH	EH cm	ER	EA Scale (1-5)	HC	EPP	RL	SL %
Rep	1	0.08	33.42	0.27	9851.68**	2831.28**	7.97	0.40	1.72	0.09	6.32	117.30
Site	12	1386.42**	9176.85**	168.02**	157807.42**	65344.70**	25867.33**	10.04**	178.37**	2.57**	619**	13639.82**
Line	32	14.78**	302.86**	2.05**	5841.34**	4947.64**	562.90**	1.01**	19.08**	0.14**	777.32**	228.37**
Tester	3	121.49**	1697.53**	16.22**	43271.07**	49665.48**	2167.99**	5.77**	2.84	1.62**	650.20**	1213.84**
Site*Line	256	4.56	9.08	1.66**	403.94	286.42	168.89	0.33**	9.13**	0.04	345.96**	135.02
Site*Tester	24	18.21**	43.61	3.48**	605.12	786.79**	316.33	0.73**	7.99	0.20**	1337.72**	241.62*
Line*Tester	94	10.05*	20.46	1.68**	1419.75**	652.69*	136.78	0.41**	8.90*	0.11**	201.52*	108.35
Site*Line*Tester	752	2.66	4.69	1.19	311.63	180.62	128.98	0.17	7.43	0.04	210.01**	84.85
Error	2209	4.16	44.84	1.19	800.28	338.93	281.57	0.19	6.80	1.06	142.43	143.89
%GCA SS		47.00	88.49	42.07	70.36	83.36	65.60	56.51	42.52	47.53	58.61	51.81
%SCA SS		53.00	11.51	57.93	29.64	16.64	34.40	43.49	57.48	52.47	41.39	48.19

†DF= degree of freedom; GY= Grain yield; DA = Days to anthesis; ASI = anthesis silking interval; PH = plant height; EH = ear height; EA = ear aspect; RL= root lodging; SL = stalk lodging; ER = ear rot; EPP = ear per plant; GCA = general combining ability; SCA = specific combining ability; SS = sum of squares; *P<0.05, **P<0.01

Table 5.4 Mean values of lines generated from 130 crosses across 13 locations

Cross	GY t ha ⁻¹	DA	ASI	PH	EH cm	RL	SL %	EA	HC Scale (1-5)	ER	EPP	
1	5.90	72.24	1.06		229.50	117.63	7.03	4.58	2.90	1.46	10.52	1.11
2	6.14	71.99	1.47		224.91	117.92	7.71	7.98	2.96	1.05	14.20	1.15
3	6.09	73.62	1.46		234.18	128.75	7.00	7.16	2.77	0.79	10.35	1.07
4	6.30	70.71	1.35		220.48	111.50	6.64	6.98	2.75	1.20	11.37	0.99
5	6.11	71.27	1.31		226.53	117.54	10.94	9.14	2.78	2.47	14.14	1.08
6	6.43	70.81	1.34		216.13	113.19	8.32	9.60	2.85	1.09	14.11	1.10
7	6.33	70.83	1.61		219.04	116.96	6.15	4.87	2.82	2.37	12.94	1.05
8	6.24	73.88	1.16		241.96	131.25	3.82	2.78	2.87	0.82	13.84	1.13
9	6.47	73.67	1.54		232.65	127.89	10.73	4.83	2.76	1.16	11.39	1.05
10	6.56	74.21	1.38		237.73	133.42	13.03	6.26	2.72	0.79	11.12	1.02
11	6.87	75.09	1.42		246.70	138.53	14.13	7.34	2.70	0.90	10.95	1.08
12	5.61	73.79	1.33		234.01	122.35	5.59	4.63	2.83	0.86	13.26	1.05
13	6.62	75.27	1.38		226.88	123.25	5.31	4.79	2.78	0.76	12.33	1.11
14	6.64	72.69	1.48		224.21	119.52	5.70	5.56	2.90	2.07	22.66	1.09
15	6.31	72.16	1.29		238.64	126.01	6.94	5.95	2.78	1.07	10.15	1.02
16	5.21	73.96	1.37		221.88	119.95	8.11	6.97	3.04	0.82	14.07	1.04
17	6.04	75.13	1.56		219.59	119.52	4.57	5.24	2.97	1.08	10.16	1.00
18	5.35	74.75	1.25		222.21	122.50	9.04	10.34	2.98	1.68	9.14	1.01
19	5.78	70.43	1.40		220.05	110.13	6.65	5.18	2.76	2.00	12.10	1.01
20	5.85	71.18	1.01		231.94	125.56	8.96	4.95	2.77	1.16	20.83	1.02
21	5.91	70.64	1.30		225.39	126.19	11.92	5.24	2.85	0.86	14.87	1.02
22	5.88	75.48	1.31		221.78	127.38	5.84	7.23	2.75	1.24	9.80	1.07
23	5.93	74.80	1.43		232.45	119.43	6.38	5.43	2.88	1.28	14.56	1.05
24	6.19	75.99	1.27		235.73	122.61	6.13	3.82	2.99	1.12	12.05	1.07
25	6.01	75.08	1.38		220.55	121.76	7.60	8.23	2.92	0.80	9.40	1.07
26	6.11	72.81	1.47		224.59	113.42	8.67	6.75	2.70	1.01	11.02	1.01
27	5.62	69.88	1.06		218.62	111.92	7.98	4.11	2.99	1.05	15.56	1.08
28	6.77	75.82	1.54		243.36	144.41	11.21	6.77	2.63	0.85	12.83	1.06
29	6.09	70.82	1.17		219.00	112.19	8.14	6.79	2.66	1.24	10.62	1.08
30	6.04	72.20	1.21		214.68	113.53	5.03	4.80	2.84	0.78	8.86	1.15
31	6.26	75.73	1.20		223.87	121.63	5.55	7.75	2.77	1.06	13.36	1.08
32	5.14	67.91	0.96		219.83	108.08	7.53	2.93	3.01	1.22	14.29	1.02
35	6.20	71.66	1.21		231.00	122.92	7.25	7.71	2.71	1.25	12.93	1.02
R-Square	0.65	0.51	0.54		0.55	0.62	0.72	0.43	0.50	0.42	0.40	0.51
SE	2.04	6.70	1.09		28.29	18.41	11.93	12.00	0.44	2.61	16.78	0.20
Mean	6.10	72.98	1.33		227.30	121.55	7.74	6.18	2.83	1.19	12.65	1.06

† GY= Grain yield; DA = Days to anthesis; ASI = anthesis silking interval; PH = plant height; EH = ear height; RL = root lodging; SL = stalk lodging; HC = husk cover; EA = ear aspect; ER = ear rot; EPP = ear per plant.

Table 5.5 Average performance of testers for grain yield and other agronomic traits across 13 locations during the 2018 and 2019 cropping seasons

Tester	Tester	GY	DA	ASI	PH	EH	RL	SL	HC	EA	ER	EPP
		t ha ⁻¹			Cm		%		Scale (1-5)			
1	CZL15049	6.15	70.94	1.31	218.37	109.57	8.92	6.48	1.16	2.88	14.84	1.03
2	CZL059	5.49	74.84	1.42	232.01	126.78	7.83	7.64	1.22	2.90	10.77	1.10
3	CML395	6.15	73.81	1.47	235.10	127.94	7.70	6.64	1.15	2.71	11.66	1.02
4	CML444	6.57	72.43	1.12	223.99	122.24	6.52	4.03	1.24	2.83	13.20	1.09
R-Square		0.65	0.51	0.54	0.55	0.62	0.72	0.43	0.42	0.50	0.40	0.51
SE		2.04	6.70	1.09	28.29	18.41	11.93	12.00	2.61	0.44	16.78	0.20
Mean		6.10	72.98	1.33	227.30	121.55	7.74	6.1	1.19	2.83	12.65	1.06

†GY = Grain yield; DA = Days to anthesis; ASI = anthesis silking interval; PH = plant height; EH = ear height; RL = root lodging; SL = stalk lodging; HC = husk cover; EA = ear aspect; ER = ear rot; EPP = ear per plant; SE = Standard error.

Non-QPM tester 3 (CML395) displayed the poorest husk cover. Ear rot was most common in QPM tester 1 followed by non-QPM tester 4, while QPM tester 2 recorded the lowest amount of ear rots.

5.4.5 General combining ability effects of lines for grain yield and other agronomic traits across 13 locations

For grain yield, lines 11, 13, 14 and 28 had positive and significant GCA while lines 16, 18 and 32 had significant ($P<0.05$) negative GCA for grain yield (Table 5.6). A total of 15 lines, representing 45.45% of the total lines, had significant and negative GCA for days to pollen shed. For anthesis-silking interval, only lines 20 and 32 were negative and significant ($P<0.05$). Lines 11, 26, 28 and 29 showed significant and negative GCA effects for ear aspect. Five lines representing 15.15% of the total, recorded positive and significant GCA for ears per plant. None of the lines had negative and significant GCA effects for root lodging while lines 10, 11 and 21 showed positive and significant GCA for root lodging. Lines 8 and 32 had negative and significant ($P<0.05$) GCA for stalk lodging while lines 5, 6 and 18 recorded positive and significant GCA. For ear rot, lines 14 and 20 had positive and significant GCA while line VL0510130 exhibited negative and significant GCA effects.

5.4.6 General combining ability effects of testers for grain yield and other agronomic traits across 13 locations

QPM tester 2 had negative and significant GCA for grain yield while non-QPM tester 4 had positive and significant ($P<0.01$) GCA for grain yield (Table 5.7). For days to pollen shed, testers 1 and 4 recorded negative effects while testers 2 and 3 had significant positive GCA effects. Tester 3 had significant positive effects for anthesis-silking interval, while tester 4 had a significant negative effect. QPM tester 2 recorded positive and significant GCA effects for ear aspect and ears per plant. Non-QPM tester 3 had negative and significant GCA effects for ear aspect and ear per plant. None of the testers displayed neither positive and significant nor significant negative GCA effects for root lodging. QPM testers 1 and 2 had positive and significant GCA values for husk cover, while the non-QPM tester had negative and significant GCA effects for husk cover. Tester 1 recorded positive and significant GCA effects for ear rot, while tester 2 had negative and significant effects for ear rot.

Table 5.6 General combining ability effects of 33 lines for grain yield and other traits evaluated at 13 locations during the 2018 and 2019 seasons in South Africa and Zimbabwe

Line	Name	GY	DA	ASI	PH	EH	EPP	EA	HC	ER	RL	SL
1	CZL0920	-0.20	-0.74*	-0.27	2.20	-3.92*	0.05*	0.07	0.26	-2.13	-0.71	-1.60
2	CZL1330	0.04	-0.99*	0.14	-2.38	-3.63	0.09**	0.13	-0.14	1.56	-0.02	1.80
3	CZL15041	-0.01	0.64	0.13	6.89**	7.20**	0.01	-0.06	-0.40	-2.29	-0.74	0.99
4	CZL15055	0.19	-2.26**	0.02	-6.82**	-10.05**	-0.07**	-0.07	0.01	-1.28	-1.10	0.81
5	CZL15073	0.01	-1.71**	-0.02	-0.76	-4.01*	0.02	-0.05	1.28**	1.50	3.20	2.97*
6	CZL15073	0.33	-2.17**	0.01	-11.17**	-8.36**	0.04	0.02	-0.11	1.46	0.58	3.42**
7	TL135470	0.23	-2.15**	0.28	-8.25**	-4.59*	-0.01	-0.01	1.18**	0.29	-1.58	-1.31
8	VL06378	0.14	0.91**	-0.17	14.66**	9.70**	0.07**	0.04	-0.38	1.19	-3.92	-3.39**
9	TL155805	0.37	0.70*	0.21	5.35*	6.34**	-0.01	-0.07	-0.04	-1.26	2.99	-1.35
10	TL147078	0.46	1.24**	0.06	10.44**	11.87**	-0.04	-0.11	-0.40	-1.52	5.29**	0.08
11	TL147070	0.77**	2.11**	0.10	19.41**	16.98**	0.02	-0.13*	-0.29	-1.70	6.39**	1.16
12	TL13609	-0.50	0.81*	0.00	6.72**	0.80	-0.01	0.00	-0.34	0.61	-2.15	-1.55
13	TL145743	0.52*	2.29**	0.05	-0.41	1.69	0.05*	-0.05	-0.43	-0.32	-2.43	-1.38
14	TL156614	0.54*	-0.28	0.15	-3.09	-2.03	0.03	0.08	0.88**	10.02**	-2.04	-0.61
15	CZL1477	0.21	-0.81*	-0.04	11.34**	4.46*	-0.04	-0.05	-0.13	-2.50	-0.80	-0.22
16	CZL15074	-0.89**	0.97**	0.04	-5.42*	-1.61	-0.02	0.21**	-0.37	1.43	0.38	0.79
17	CZL0616	-0.06	2.15**	0.23	-7.71**	-2.03	-0.06*	0.14*	-0.12	-2.49	-3.16	-0.94
18	CZL083	-0.75*	1.77**	-0.08	-5.09*	0.95	-0.05*	0.16*	0.49	-3.50*	1.30	4.17**
19	CML572	-0.32	-2.54**	0.08	-7.24**	-11.43**	-0.05	-0.07	0.81*	-0.55	-1.09	-0.99
20	EBL167787	-0.25	-1.80**	-0.32*	4.64	4.01*	-0.04	-0.06	-0.03	8.18**	1.22	-1.22
21	CZL0520	-0.20	-2.33**	-0.03	-1.90	4.64*	-0.04	0.02	-0.33	2.23	4.19*	-0.94
22	CZL99005	-0.22	2.51**	-0.02	-5.51*	5.82**	0.01	-0.08	0.05	-2.85	-1.90	1.05
23	CML502	-0.17	1.82**	0.10	5.15*	-2.12	-0.01	0.05	0.09	1.91	-1.36	-0.75
24	CML144	0.09	3.02**	-0.06	8.44**	1.05	0.01	0.16*	-0.07	-0.59	-1.61	-2.36
25	CML159	-0.10	2.101**	0.05	-6.75*	0.21	0.01	0.09	-0.40	-3.25	-0.14	2.06
26	CML181	0.01	-0.17	0.14	-2.71	-8.13**	-0.05*	-0.13*	-0.18	-1.63	0.93	0.58
27	CML197	-0.48	-3.09**	-0.27	-8.68**	-9.64**	0.02	0.16*	-0.14	2.91	0.24	-2.07
28	CML312SR	0.67*	2.84**	0.21	16.06**	22.86**	0.00	-0.20**	-0.34	0.18	3.47	0.59
29	CML488	-0.01	-2.16**	-0.16	-8.30**	-9.36**	0.02	-0.17*	0.05	-2.03	0.41	0.62
30	CML491	-0.06	-0.77*	-0.12	-12.61**	-8.02**	0.09**	0.01	-0.41	-3.78*	-2.71	-1.38
31	LH51	0.16	2.76**	-0.13	-3.43	0.08	0.02	-0.06	-0.14	0.71	-2.19	1.58
32	CZL00025	-0.96**	-5.07**	-0.37*	-7.46**	-13.47*	-0.04	0.18**	0.03	1.64	-0.21	-3.25**
35	CML444	0.10	-1.31**	-0.12	3.70	1.37	-0.04	-0.12	0.06	0.29	-0.49	1.53
SE		0.25	0.35	0.15	2.33	1.96	0.02	0.07	0.35	1.51	2.16	1.35

†GY = Grain yield; DA = Days to anthesis; ASI = anthesis silking interval; PH = plant height; EH = ear height; EA = ear aspect; RL = root lodging; SL = stalk lodging; ER = ear rot; EPP = ear per plant; SE = Standard error; *P<0.05, **P<0.01

Table 5.7 General combining ability effects of four testers for grain yield and other traits evaluated at 13 locations during the 2018 and 2019 seasons

Tester	Status	GY	DA	ASI	PH	EH	RL	SL	HC	EA	ER	EPP
		t ha ⁻¹			cm			%		Scale (1-5)		
1	QPM	0.05	-2.04**	-0.02	-8.93**	-11.98**	1.18	0.31	0.007**	0.055	2.19**	-0.03
2	QPM	-0.61**	1.87**	0.09	4.72**	5.23**	0.09	1.47**	0.006**	0.068*	-1.88**	0.04**
3	Non-QPM	0.05	0.83**	0.14*	7.81**	6.38**	-0.04	0.46	-0.004**	-0.118**	-0.98	-0.04**
4	Non-QPM	0.47**	-0.54*	-0.21**	-3.30**	0.69	-1.22	-2.15**	-0.008**	-0.001	0.56	0.03
R-Square		0.15	0.24	0.07	0.87	1	1.3	0.55	0.001	0.030	0.63	0.01

†GY= Grain yield; DA = Days to anthesis; ASI = anthesis silking interval; PH = plant height; EH = ear height; RL = root lodging; SL = stalk lodging; HC = husk cover, EA = ear aspect; ER = ear rot; EPP = ear per plant; *P<0.05, **P<0.01

5.4.7 Specific combining ability effects among the crosses for grain yield and other measured traits across the 13 locations

The SCA values for the crosses ranged from -3.00 to 1.17 for yield. Thirty crosses, representing 23.08% of the total, showed both positive and negative SCA effects (Table 5.8). Of these, 17 crosses had positive and significant effects while 13 crosses showed negative and significant SCA effects. Hybrid 22 x 2 (entry 85) showed the highest SCA effects for grain yield. Twelve hybrids showed significant and negative SCA effects for days to pollen shed. For anthesis-silking interval, only four crosses showed significant negative SCA effects while for ear aspect, only nine crosses of the 130, had negative and significant SCA effects (Table 5.8). Only eight hybrids had positive and significant SCA effects for ears per plant with hybrid 18 x 1 having the highest value. Across the 13 locations, only hybrid 10 x 1 out of the 130 crosses recorded significant and negative SCA effects for root lodging, while for stalk lodging, three crosses had positive and significant SCA effects and 6 x 4 had negative and significant SCA effects for stalk lodging. The SCA of ear rot, ranged from -5.33 for 21 x 1 to 6.82 for 8 x 4. Of all the hybrids, only three had significant and negative SCA effects and three also recorded positive and significant SCA values for ear rot.

5.4.8 Heterotic groupings of the 33 inbred lines based on grain yield across the 13 locations from the combined analysis using specific combining ability

For an inbred line to be grouped in a heterotic group, the line must have significant ($P < 0.05$) positive SCA effects with one of the testers or also significant ($P < 0.05$) negative SCA effects with at least one of the other testers (Table 5.9). In addition, the line must display a mean yield equal to or greater than one standard error above the grand mean of all testcrosses involving the positive SCA tester. This will enable planned crosses to be made. Based on this rule, 16 of the 33 inbred lines could be classified into a heterotic group. The testers met the criteria for grouping the inbred lines into a heterotic group. Each testers had at least negative and a positive SCA with lines. Having satisfied the criteria for grouping, four lines were grouped with QPM tester CZL15049, six with QPM tester CZL059 while non-QPM testers CML395 and CML444 could discriminate only three lines each (Table 5.9).

Table 5.8 Specific combining ability effects of 33 QPM inbred lines crossed with four testers evaluated for grain yield and other traits across 13 locations in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons

ENTRY	GY	DA	ASI	PH	EH	ER	EA	HC	EPP	RL	SL
1	-0.17	-0.74	-0.23	-1.97	-2.21	0.09	-0.09	-0.37	0.04	0.72	0.30
2	0.70*	-0.49	0.04	3.52	3.67	1.95	-0.11	-0.45	0.01	-3.43	1.46
3	-0.27	0.31	0.03	-1.67	-2.33	-2.75	0.16	1.58**	-0.07	-0.39	0.46
4	-0.23	0.80	0.15	-0.17	0.54	0.83	0.04	-0.76	0.02	3.09	-2.15
5	-0.39	0.20	0.17	-4.37	-5.25*	-1.65	-0.11	-0.06	-0.06	-2.77	0.30**
6	0.13	0.26	0.09	0.18	1.06	-0.69	0.13	-0.34	0.00	-0.86	1.46
7	-0.33	-0.01	0.04	0.94	0.96	1.44	0.01	-0.22	0.00	2.52	0.46
8	0.62	-0.56	-0.30	2.97	2.91	1.01	-0.03	0.62	0.04	1.10	-2.15
9	-0.15	-0.65	-0.13	-3.31	-4.59	-1.01	-0.10	0.00	-0.01	0.56	0.30
10	-0.23	-1.25**	0.17	-12.63**	-7.19**	1.12	0.12	-0.07	-0.02	0.63	1.46
11	-0.20	0.98*	0.20	-1.30	-1.63	3.97	0.06	-0.02	0.01	-2.29	0.46
12	0.62	0.81	-0.25	16.95	13.10**	-3.96	-0.08	0.08	0.02	1.09	-2.15
13	-0.95**	-0.10	0.29	-7.83*	-2.21	0.51	0.11	1.27*	0.05	1.25	0.30
14	0.42	-0.23	0.02	3.91	0.30	0.44	-0.09	-0.53	-0.03	-1.73	1.46
15	0.02	0.03	-0.33	-6.55	-6.66**	-2.00	0.06	-0.27	-0.01	0.57	0.46
16	0.55	0.18	0.02	10.19**	8.25**	1.16	-0.08	-0.48	-0.01	-0.09	-2.15
17	-0.61	-0.23	0.14	-2.43	-1.09	-0.84	-0.05	0.50	0.02	4.65	0.30
18	0.37	-1.17**	0.17	2.58	-1.44	4.02	0.01	-0.12	-0.01	1.54	1.46
19	-0.16	1.24**	-0.03	-1.63	0.77	0.66	0.05	-0.65	-0.04	-2.13	0.46
20	0.44	0.04	-0.29	1.19	1.45	-3.72	-0.01	0.27	0.03	-4.06	-2.15
21	-0.47	1.08**	0.26	-8.01*	-5.59*	-0.25	0.07	-0.33	0.03	0.53	0.30
22	-0.02	-0.10	-0.24	3.75	5.46*	-1.51	-0.17*	0.05	-0.03	-2.65	1.46
23	0.72*	-0.87*	0.10	-2.82	-1.27	1.88	0.06	0.25	0.05	0.60	0.46
24	-0.19	-0.22	-0.13	6.79	1.08	0.00	0.03	0.02	-0.05	1.52	-2.15*
25	-0.68*	1.13**	0.30	0.25	2.14	-0.43	0.07	-0.27	-0.04	2.18	0.30
26	-0.28	-0.96*	0.26	-1.43	-5.38*	1.14	-0.08	0.28	0.00	0.40	1.46
27	0.17	0.23	-0.52**	-3.43	-3.23	0.45	0.03	-0.07	0.00	-2.96	0.46
28	0.83*	-0.51	-0.05	4.32	6.16*	-1.05	-0.01	0.06	0.04	0.38	-2.15
29	0.00	-0.62	-0.06	-2.08	0.44	-3.40	0.04	0.04	-0.09*	-0.84	0.30
30	-0.16	0.06	-0.07	0.41	-0.46	-1.33	0.03	-0.07	0.04	0.17	1.46
31	0.37	0.28	0.08	0.74	2.69	-1.98	-0.02	0.05	-0.04	2.36	0.46
32	-0.17	0.16	0.05	0.65	-2.99	6.82**	-0.06	-0.02	0.09*	-1.69	-2.15
33	0.33	0.33	-0.09	7.30*	3.76	1.58	-0.06	-0.13	-0.06	-1.28	0.30
34	-0.45	0.12	-0.10	-2.19	0.05	-0.33	-0.06	-0.31	0.09*	-1.71	1.46
35	0.10	-0.04	0.17	-3.36	-6.16*	1.39	0.13	-0.27	-0.04	4.12	0.46
36	0.06	-0.51	0.02	-2.04	2.04	-2.53	-0.01	0.71	0.00	-1.14	-2.15
37	0.41	0.52	-0.02	6.03	1.83	0.87	0.03	-0.01	0.02	-6.49*	0.30
38	-0.34	-0.50	0.06	-2.60	-2.53	0.89	-0.08	-0.01	-0.03	1.54	1.46
39	0.00	0.61	0.01	-0.42	-0.01	-0.39	0.10	0.04	0.00	4.32	0.46
40	-0.03	-0.74	-0.06	-3.29	0.40	-1.26	0.05	-0.02	0.01	0.62	-2.15
41	1.08**	-0.24	0.02	-1.98	-2.24	0.92	-0.10	0.01	-0.04	-2.57	0.30

†GY= grain yield; DA = days to anthesis; ASI - anthesis silking interval; PH = plant height; EH = ear height; EA = ear aspect; RL = root lodging; SL = stalk lodging; ER = ear rot; EPP = ear per plant; SE = Standard error; *P<0.05, **P<0.01

Table 5.8 Specific combining ability effects of 33 QPM inbred lines crossed with four testers evaluated for grain yield and other traits across 13 locations in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons (continued)

ENTRY	GY	DA	ASI	PH	EH	ER	EA	HC	EPP	RL	SL
42	-0.12	0.09	-0.10	-2.21	0.59	-0.80	-0.03	-0.12	0.03	3.15	1.46
43	0.00	0.27	0.17	5.80	4.66	1.04	0.06	-0.07	-0.01	0.60	0.46
44	-0.92**	-0.23	-0.10	-1.90	-3.33	-1.05	0.07	0.17	0.01	-1.19	-2.15
45	-0.42	-2.14**	-0.15	-10.01**	-6.43**	0.55	-0.02	0.04	0.03	0.32	0.30
46	0.32	0.77	-0.04	5.62	3.42	1.91	-0.05	-0.13	-0.06	-1.21	1.46
47	-0.11	0.03	0.11	-4.76	-3.14	1.05	0.04	0.05	0.00	1.96	0.46
48	0.25	1.22**	0.07	8.87**	5.83*	-3.39	0.02	0.04	0.03	-1.07	-2.15
49	0.21	1.77**	0.07	5.56	4.97	3.95	-0.08	0.08	-0.03	-3.40	0.30
50	-0.84**	-1.02**	-0.24	-7.06*	-7.69**	2.78	0.19	-0.03	0.00	2.14	1.46
51	0.18	0.17	-0.17	0.41	-0.05	-1.35	-0.01	0.02	-0.01	0.07	0.46
52	0.48	-1.03**	0.33	0.80	2.45	-5.28*	-0.11	-0.06	0.04	1.18	-2.15
53	-0.34	0.69	-0.11	-11.85**	-0.50	0.18	0.08	-0.50	-0.01	2.08	0.30
54	0.46	-0.87*	0.54**	4.89	0.05	1.71	0.05	0.31	0.11**	-3.01	1.46
55	-0.47	0.09	-0.20	1.20	-0.97	-4.55	-0.13	-0.68	-0.02	-0.59	0.46
56	0.39	-0.03	-0.23	5.48	1.10	2.77	0.00	0.87	-0.08*	1.52	-2.15
57	-0.33	0.10	0.16	-6.40	-4.05	4.16	0.15	0.45	0.02	0.00	0.30
58	0.24	0.13	-0.65**	3.24	0.70	-2.44	0.00	-0.28	-0.01	-0.16	1.46
59	0.70**	-1.07**	0.11	5.36	4.53	-0.79	-0.01	-0.23	-0.02	-0.15	0.46
60	-0.58	0.73	0.38	-2.49	-1.49	-0.82	-0.14	0.06	0.00	0.30	-2.15
61	0.51	0.08	0.12	11.99**	7.50**	-2.71	-0.12	-0.10	0.06	-0.32	0.30
62	-0.16	0.90*	-0.35	-6.33	-1.89	-0.01	0.18	-0.05	-0.06	-1.55	1.46
63	-0.54	0.13	0.03	-9.49**	-6.02*	4.95*	0.07	-0.06	-0.01	1.07	0.46
64	0.23	-1.22**	0.19	3.54	0.10	-2.11	-0.14	0.21	0.01	0.79	-2.15
65	0.50	-0.05	0.16	5.13	1.54	2.20	-0.10	-0.03	0.03	-0.50	0.30
66	-1.11**	0.28	0.04	-6.47	-4.18	-2.25	0.25	0.01	-0.08*	-0.84	1.46
67	0.08	-0.26	-0.20	-1.39	2.48	0.23	-0.04	0.09	0.03	0.67	0.46
68	0.56	-0.08	0.00	2.45	-0.15	-0.07	-0.12	-0.06	0.02	0.67	-2.15
69	0.94**	-0.40	-0.42*	14.66**	11.68	-0.82	-0.21**	-0.79	0.20**	1.19	0.30
70	-2.27**	3.03**	0.85**	-30.00**	-18.60**	2.40	0.72**	1.72**	-0.31**	1.75	1.46
71	0.67*	-0.39	-0.28	12.29	9.35**	-2.43	-0.29**	-0.63	0.11**	-2.34	0.46
72	0.69*	-2.16	-0.16	2.77	-2.74	0.96	-0.21**	-0.31	-0.02	-0.60	-2.15
73	-0.23	-0.24	0.00	-6.45	-1.64	1.65	0.13	-0.85	0.05	2.41	0.30
74	0.69*	-1.53**	0.19	6.67	-0.34	3.53	-0.10	2.50**	-0.03	0.95	1.46
75	0.28	0.85**	0.11	0.91	-2.62	-0.25	0.07	-0.41	0.03	-4.19	0.46
76	-0.70*	0.80	-0.31	-1.42	4.29	-4.82*	-0.11	-1.24*	-0.05	0.83	-2.15
77	-0.26	0.40	-0.07	-5.43	-3.04	2.06	0.06	0.56	-0.02	2.94	0.30
78	-1.19**	0.83*	-0.23	7.20*	5.99*	-3.07	-0.02	-0.43	0.04	-2.30	0.46
79	0.87*	0.52	0.39	2.66	1.96	-0.76	0.02	-0.11	0.02	-0.56	-2.15
80	-0.32	0.39	-0.16	2.56	-2.90	-5.33**	0.16	0.03	0.00	2.49	0.30
81	0.63*	0.38	-0.16	4.68	6.10*	1.31	-0.30**	-0.21	0.08	1.34	1.46
82	-0.23	-0.40	0.33	-4.18	-3.10	0.70	0.18*	-0.01	-0.02	-2.22	0.46
83	-0.04	-0.48	-0.01	-3.34	-0.42	3.44	-0.04	0.19	-0.05	-1.62	-2.15

†GY= grain yield; DA = days to anthesis; ASI - anthesis silking interval; PH = plant height; EH = ear height; EA = ear aspect; RL = root lodging; SL = stalk lodging; ER = ear rot; EPP = ear per plant; SE = Standard error; *P<0.05, **P<0.01

Table 5.8 Specific combining ability effects of 33 QPM inbred lines crossed with four testers evaluated for grain yield and other traits across 13 locations in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons (continued)

ENTRY	GY	DA	ASI	PH	EH	ER	EA	HC	EPP	RL	SL
84	1.10**	-0.98*	0.02	7.36*	2.63	-2.42	-0.13	-0.07	-0.02	0.59	0.30*
85	1.17**	-0.31	-0.10	13.98**	13.64**	-1.97	-0.28**	-0.27	0.09*	-1.98	1.46
86	0.77*	-1.51	-0.14	9.64	2.95	-0.09	-0.21**	-0.33	0.04	2.77	0.46
87	-3.00**	2.68	0.21	-31.27**	-19.54**	4.59*	0.62**	0.67	-0.11**	-1.38	-2.15
88	-0.36	-1.88	-0.14	-3.59	-1.83	2.08	0.07	0.30	-0.05	-2.17	0.30
89	0.43	-0.74	-0.07	4.86	0.32	0.26	-0.16	-0.49	0.06	-1.76	1.46
90	-0.05	1.10	0.39	-1.19	3.80	-2.15	0.07	0.73	0.01	0.82	0.46
91	0.02	1.40	-0.18	-0.35	-2.60	-0.07	0.02	-0.54	-0.03	3.11	-2.15
92	-0.48	-0.49	0.02	2.06	-0.47	1.74	-0.02	0.58	-0.07	-1.98	0.30
93	0.37	-0.55	0.02	9.52**	6.22	0.66	-0.01	-0.41	0.00	4.97	1.46
94	0.07	-0.09	0.01	-5.98	-2.32	-3.75	0.00	0.28	-0.01	-1.49	0.46
95	0.08	1.02	-0.06	-5.89	-3.75	1.45	0.03	-0.44	0.08	-1.50	-2.15
96	0.51	0.58	0.19	9.31**	3.70	-1.91	-0.09	0.02	0.02	-0.36	0.30
97	-1.55**	1.17	-0.24	-15.47**	-4.64	-0.36	0.23**	0.16	-0.13**	-0.59	1.46
98	0.25	-0.52	-0.17	0.80	-0.16	0.43	-0.13	-0.02	0.08	1.17	0.46
99	0.83**	-1.34	0.22	5.08	0.79	1.95	-0.01	-0.16	0.03	-0.23	-2.15
100	-0.07	0.42	0.13	-5.30	-3.73	0.90	-0.02	-0.19	-0.01	-1.42	0.30
101	-0.08	-1.37	-0.03	1.14	-3.31	-1.13	-0.11	-0.36	-0.07	-1.57	1.46
102	0.32	-0.37	-0.19	5.53	5.37*	0.51	0.00	0.46	0.02	0.65	0.46
103	-0.13	1.20	0.08	-1.65	1.35	-0.17	0.13	0.09	0.06	2.33	-2.15
104	-0.05	0.11	-0.23	1.08	-0.20	-0.68	0.05	0.03	-0.03	0.00	0.30
105	0.64*	-0.13	0.04	4.15	-0.59	-2.54	-0.08	0.07	0.04	4.16	1.46
106	-0.50	0.63	0.07	-3.75	0.12	-0.47	0.05	-0.14	-0.01	-2.59	0.46
107	-0.05	-0.72	0.11	-1.77	0.36	3.80	-0.03	0.04	-0.01	-1.58	-2.15
108	0.95**	0.49	-0.29	-1.18	1.51	2.79	-0.01	0.08	0.00	-5.67	0.30
109	-0.02	0.32	-0.10	5.52	1.99	-1.63	-0.06	-0.01	0.10**	0.78	1.46**
110	-0.19	-0.88	0.47*	3.01	3.84	1.07	0.10	-0.06	-0.05	4.49	0.46
111	-0.71*	-0.04	-0.10	-7.63*	-7.66**	-2.12	-0.03	-0.02	-0.05	0.40	-2.15
112	-0.46	-0.32	-0.31	-9.83**	-7.42**	-0.37	0.09	-0.41	-0.01	4.21	0.30
113	0.78	-0.30	0.19	8.71**	7.17**	-2.91	-0.10	-0.28	0.06	0.66	1.46
114	-0.27	0.74	0.15	4.83	1.14	3.27	-0.08	0.92	-0.02	-2.03	0.46
115	-0.02	-0.23	-0.04	-4.00	-1.21	0.12	0.09	-0.23	-0.04	-2.84	-2.15
116	0.28	0.26	0.04	6.79	2.37	0.33	0.01	0.07	-0.05	-2.53	0.30
117	0.26	-0.76	-0.31	0.08	2.33	3.03	0.05	-0.13	0.15**	-0.12	1.46
118	-0.33	0.12	0.22	-4.41	-4.73	-3.30	-0.05	0.03	-0.04	-1.60	0.46
119	-0.17	0.27	0.04	-2.74	-0.30	0.05	-0.01	0.03	-0.07	4.25	-2.15
120	1.03**	0.81	0.32	5.87	3.06	-3.67	0.02	-0.16	-0.05	2.15	0.30
121	-1.30**	-0.71	-0.34	-7.45*	-5.17	-0.96	0.17*	-0.23	0.05	0.36	1.46
122	0.33	-0.26	-0.11	3.64	4.77	4.41	-0.15	0.25	0.02	-0.54	0.46
123	-0.03	0.04	0.12	-2.35	-2.97	0.34	-0.05	0.15	-0.03	-1.97	-2.15
124	-0.30	1.17	0.10	5.37	8.73**	-0.10	0.03	0.08	0.00	4.25	0.30
125	0.26	0.18	-0.33	-0.54	-2.76	-0.84	-0.05	-0.17	0.02	-3.52	0.46
126	-0.54	0.40	0.32	-0.39	-1.06	-0.82	0.08	0.12	0.02	-0.64	-2.15
127	-0.52	0.26	0.08	1.41	1.93	-3.44	0.12	0.14	0.07	-0.46	0.30
128	0.41	0.51	-0.08	4.32	3.23	1.06	-0.14	-0.17	-0.08	-0.62	1.46
129	-0.14	-0.46	0.26	-4.73	-3.90	0.25	-0.02	-0.01	-0.03	2.31	0.46
130	0.28	-0.43	-0.27	-1.29	-1.57	2.24	0.04	0.04	0.03	-1.24	-2.15
SE	0.33	0.44	0.22	3.55	2.70	2.28	0.08	0.55	0.04	2.91	1.85

†GY= grain yield; DA = days to anthesis; ASI - anthesis silking interval; PH = plant height; EH = ear height; EA = ear aspect; RL = root lodging; SL = stalk lodging; ER = ear rot; EPP = ear per plant; SE = Standard error; *P<0.05, **P<0.01

Table 5.9 Classification of 33 maize inbred lines into heterotic groups based on the specific combining ability across 13 locations in Zimbabwe and South Africa

CZL15049	CZL059	CML395	CML444
4 (QPM)	19 (non-QPM)	20 (non-QPM)	7 (QPM)
11 (QPM)	31 (QPM)	6 (QPM)	22 (non-QPM)
18 (QPM)	13 (QPM)	15 (QPM)	25 (QPM)
28 (non-QPM)	17 (QPM)		
	21 (non-QPM)		
	27 (QPM)		

5.4.9 Estimation of yield differences of QPM and non-QPM hybrids and the performance of the parents for grain yield, days to anthesis, plant height and tryptophan

From the group which was made up of lines 16 (QPM), 19 (non-QPM) and 2 (QPM) (Table 5.10), the non-QPM genotype (line 2 x CML395) produced the highest grain yield of 7.51 t ha⁻¹ however, a QPM genotype involving the cross between line 16 x CZL059 produced 33.18% more grain yield than non-QPM hybrids in that group. Line 2 produced the highest grain yield in that category and was found to have positive GCA as well as positive SCA with the non-QPM testers (Table 5.10). In the group containing lines 1 (QPM), 27 (QPM) and 11 (QPM), the QPM line 11 hybrids were the best in this study. Line 11 x CZL15049 gave a grain yield of 8.90 t ha⁻¹. This hybrid yielded 62.11% more than non-QPM hybrids in this group. Line 11 took 81 days to flower. It was noticed that non-QPM testers combined better with the lines than QPM testers. In the group consisting of lines 30, 31 and 13, the QPM hybrids were inferior in terms grain yield to the non-QPM hybrids where the QPM hybrid from line 13 x CZL15049 yielded 30.56% less than the non-QPM hybrid in this group. QPM line 31 combined well with QPM CZL15049 (Table 5.10).

Table 5.10 Grain yield differences between QPM and non-QPM hybrids and the performance of the parents for grain yield, days to anthesis, plant height and tryptophan

Line	Grain yield (t ha ⁻¹)				GCA Line	Lines				SCA			
	QPM tester		Non-QPM tester			GY t ha ⁻¹	DA	PH cm	TRP %	QPM tester		Non-QPM tester	
	CZL15049	CZL059	CML444	CML395						CZL15049	CZL059	CML444	CML395
L16 QPM(P1)	5.93	4.49	4.78	6.20	-0.89	2.67	78.49	151.55	0.079	0.51	-0.16	-0.54	0.23
L19 non-QPM(P2)	5.83	6.11	6.21	5.90	-0.32	1.69	72.91	149.48	0.035	-0.23	0.69	0.28	-0.70
L2 QPM(Res L1)	6.08	5.98	5.91	7.51	0.04	3.15	77.27	172.76	0.081	-0.39	0.13	-0.33	0.62
% over L16	2.53	33.18	23.64	21.13	-104.49	17.98	-1.55	14.00	2.530	-176.47	-181.25	-38.89	169.57
% over L19	4.29	-2.13	-4.83	27.29	-112.50	86.39	5.98	15.57	131.430	69.57	-81.16	-217.86	-188.57
L26 QPM(P1)	6.36	5.39	6.90	6.75	0.01	2.80	72.75	145.71	0.078	-0.07	-0.08	0.32	-0.13
L20 non-QPM(P2)	5.71		4.52	7.35	-0.25	1.22	77.77	159.02	0.036	-0.26		-1.19	0.87
L3 QPM(Res L1)	5.97	5.46	6.18	7.76	-0.01	2.79	76.72	189.28	0.090	-0.15	-0.23	-0.20	0.62
% over L26	-6.13	1.30	-10.43	14.96	-200.00	-0.36	5.46	29.90	15.380	114.29	187.50	-162.50	-576.92
% over L20	4.55		36.73	5.58	-96.00	128.69	-1.35	19.03	150.000	-42.31		-83.19	-28.74
L16 QPM(P1)	5.93	4.49	4.78	6.20	0.01	2.67	78.49	151.55	0.079	0.51	-0.16	-0.54	0.23
L19 non-QPM(P2)	5.83	6.11	6.21	5.90	-0.32	1.69	72.91	149.48	0.035	-0.23	0.69	0.28	-0.70
L4 QPM(Res L1)	5.10	6.35	6.77	7.63	0.19	3.57	71.28	158.18	0.080	-0.95	0.42	0.02	0.55
% over L16	-14.00	41.43	41.63	23.06	1800.00	33.71	-9.19	4.37	1.270	-286.27	-362.50	-103.70	139.13
% over L19	-12.52	3.93	9.02	29.32	-159.38	111.24	-2.24	5.82	128.570	313.04	-39.13	-92.86	-178.57
L1 QPM(P1)	5.79	6.23	5.63	6.56	-0.20	2.88	78.94	159.53	0.074	-0.17	0.70	-0.27	-0.23
L19 non-QPM(P2)	5.83	6.11	6.21	5.90	-0.32	1.69	72.91	149.48	0.035	-0.23	0.69	0.28	-0.70
L5 QPM(Res L1)	5.65	6.51	6.26	7.21	0.01	2.95	72.45	160.25	0.066	-0.61	0.37	-0.16	0.44
% over L1	-2.42	4.49	11.19	9.91	-105.00	2.43	-8.22	0.45	-10.810	258.82	-47.14	-40.74	-291.30
% over L19	-3.09	6.55	0.81	22.20	-103.13	74.56	-0.63	7.20	88.570	165.22	-46.38	-157.14	-162.86
L1 QPM(P1)	5.79	6.23	5.63	6.56	-0.20	2.88	78.94	159.53	0.074	-0.17	0.70	-0.27	-0.23
L22 non-QPM(P2)	7.29	6.82	6.62	3.08	-0.22	2.31	80.40	147.57	0.042	1.10	1.17	0.77	-3.00
L6 QPM(Res L1)	6.22	5.77	7.46	6.92	0.33	2.22	72.44	133.17	0.091	-0.47	-0.02	0.72	-0.19
% over L1	7.43	-7.38	32.50	5.49	-265.00	-22.92	-8.23	-16.52	22.970	176.47	-102.86	-366.67	-17.39
% over L22	-14.68	-15.40	12.69	124.68	-250.00	-3.90	-9.90	-9.76	116.670	-142.73	-101.71	-6.49	-93.67

† GY = grain yield; DA = days to anthesis; PH = plant height, TRP = tryptophan; GCA = general combining ability; SCA = specific combining ability; QPM = quality protein maize; non-QPM = non quality protein maize

Table 5.11 Grain yield differences between QPM and non-QPM hybrids and the performance of the parents for grain yield, days to anthesis, plant height and tryptophan (continued)

Line	Grain yield (t ha ⁻¹)				GCA Line	Lines				SCA			
	QPM tester		Non-QPM tester			GY t ha ⁻¹	DA	PH cm	TRP %	QPM tester		Non-QPM tester	
	CZL15049	CZL059	CML444	CML395						CZL15049	CZL059	CML444	CML395
L16 QPM(P1)	5.93	4.49	4.78	6.20	-0.89	2.67	78.49	151.55	0.079	0.51	-0.16	-0.54	0.23
L22 non-QPM(P2)	7.29	6.82	6.62	3.08	-0.22	2.31	80.40	147.57	0.042	1.10	1.17	0.77	-3.00
L7 QPM(Res L1)	5.45	5.46	6.44	7.58	0.23	3.23	72.33	148.55	0.076	-0.68	-0.28	0.17	0.83
% over L16	-8.09	21.60	34.73	22.26	-125.84	20.97	-7.85	-1.98	-3.800	-233.33	75.00	-131.48	260.87
% over L22	-25.24	-19.94	-2.72	146.10	-204.55	39.83	-10.04	0.66	80.950	-161.82	-123.93	-77.92	-127.67
L23 QPM(P1)	5.47	5.77	6.41	6.89	-0.17	1.23	81.13	166.19	0.081	-0.36	0.43	-0.05	0.02
L28 non-QPM(P2)	8.20	6.35	6.85	6.75	0.67	3.71	72.27	146.27	0.035	0.95	-0.02	-0.19	-0.71
L8 QPM(Res L1)	6.48	5.89	7.17	6.87	0.14	1.18	77.06	173.87	0.089	0.00	-0.16	0.37	-0.17
% over L23	18.46	2.08	11.86	-0.29	-182.84	-4.07	-5.02	4.62	9.880	-100.00	-137.21	-840.00	-950.00
% over L28	-20.98	-7.24	4.67	1.78	-79.10	-68.19	6.63	18.87	154.290	-100.00	700.00	-294.74	-76.06
L1 QPM(P1)	5.79	6.23	5.63	6.56	-0.20	2.88	78.94	159.53	0.074	-0.17	0.70	-0.27	-0.23
L27 non-QPM(P2)	5.49	5.70	5.89	6.12	-0.48	0.75	85.02	203.66	0.038	-0.13	-0.05	0.64	-0.50
L9 QPM(Res L1)	6.48	5.89	7.17	6.87	0.37	1.89	76.28	159.33	0.079	0.33	-0.45	0.10	0.06
% over L1	11.92	-5.46	27.35	4.73	-285.00	-34.38	-3.37	-0.13	6.760	-294.12	-164.29	-137.04	-126.09
% over L27	18.03	3.33	21.73	12.25	-177.08	152.00	-10.28	-21.77	107.890	-353.85	800.00	-84.38	-112.00
L1 QPM(P1)	5.79	6.23	5.63	6.56	-0.20	2.88	78.94	159.53	0.074	-0.17	0.70	-0.27	-0.23
L27 QPM(P2)	5.49	5.70	5.89	6.12	-0.48	0.75	85.02	203.66	0.038	-0.13	-0.05	0.64	-0.50
L10 QPM(Res L1)	7.53	6.19	6.91	7.27	0.46	1.71	80.74	180.75	0.089	0.41	-0.34	0.00	-0.03
% over L1	30.05	-0.64	22.74	10.82	-330.00	-40.63	2.28	13.30	20.270	-341.18	-148.57	-100.00	-86.96
% over L27	37.16	8.60	17.32	18.79	-195.83	128.00	-5.03	-11.25	134.210	-415.38	580.00	-100.00	-94.00
L1 QPM(P1)	5.79	6.23	5.63	6.56	-0.20	2.88	78.94	159.53	0.074	-0.17	0.70	-0.27	-0.23
L27 QPM(P2)	5.49	5.70	5.89	6.12	-0.48	0.75	85.02	203.66	0.038	-0.13	-0.05	0.64	-0.50
L11 QPM(Res L1)	8.90	6.23	7.56	6.86	0.77	2.76	81.99	191.38	0.075	1.08	-0.12	0.00	-0.92
% over L1	53.71	0.00	34.28	4.57	-485.00	-4.17	3.86	19.96	1.350	-735.29	-117.14	-100.00	300.00
% over L27	62.11	9.30	28.35	12.09	-260.42	268.00	-3.56	-6.03	97.370	-930.77	140.00	-100.00	84.00
L1 QPM(P1)	5.79	6.23	5.63	6.56	-0.20	2.88	78.94	159.53	0.074	-0.17	0.70	-0.27	-0.23
L29 non-QPM(P2)	5.73	6.63	5.93	6.54	-0.01	3.73	78.44	152.97	0.042	-0.46	0.78	-0.27	-0.02
L12 QPM(Res L1)	5.25	5.47	5.83	6.72	-0.50	1.76	74.94	161.34	0.076	-0.42	0.32	-0.11	0.25
% over L1	-9.33	-12.20	3.55	2.44	150.00	-38.89	-5.07	1.13	2.700	147.06	-54.29	-59.26	-208.70
% over L29	-8.38	-17.50	-1.69	2.75	4900.00	-52.82	-4.46	5.47	80.950	-8.70	-58.97	-59.26	-1350.00

†GY = grain yield; DA = days to anthesis; PH = plant height, TRP = tryptophan; GCA = general combining ability; SCA = specific combining ability; QPM = quality protein maize; non-QPM = non quality protein maize

Table 5.12 Grain yield differences between QPM and non-QPM hybrids and the performance of the parents for grain yield, days to anthesis, plant height and tryptophan (continued)

Line	Grain yield (t ha ⁻¹)				GCA Lines	Lines				SCA			
	QPM tester		Non-QPM tester			GY t ha ⁻¹	DA	PH cm	TRP %	QPM tester		Non-QPM tester	
	CZL15049	CZL059	CML444	CML395						CZL15049	CZL059	CML444	CML395
L30 non-QPM(P1)	6.63	5.89	5.91	6.52	-0.06	2.88	78.94	159.53	0.074	0.28	0.26	-0.33	-0.17
L31 QPM(P2)	7.56	4.65	6.81	7.25	0.16	3.73	78.44	152.97	0.042	1.03	-1.30	0.33	-0.03
L13 QPM(Res L1)	5.25	5.47	5.83	6.72	0.52	2.96	78.74	155.77	0.077	0.21	-0.84	0.18	0.48
% over L30	-20.81	-7.13	-1.35	3.07	-966.67	2.78	-0.25	-2.36	4.050	-25.00	-423.08	-154.55	-382.35
% over L31	-30.56	17.63	-14.39	-7.31	225.00	-20.64	0.38	1.83	83.330	-79.61	-35.38	-45.45	-1700.00
L30 non-QPM(P1)	6.63	5.89	5.91	6.52	-0.06	3.20	79.97	170.37	0.042	0.28	0.26	-0.33	-0.17
L19 non-QPM(P2)	5.83	6.11	6.21	5.90	-0.32	1.69	72.91	149.48	0.035	-0.23	0.69	0.28	-0.70
L14 QPM(Res L1)	6.73	6.86	6.27	7.75	0.54	2.86	76.52	170.48	0.082	-0.34	0.46	-0.47	0.39
% over L30	1.51	16.47	6.09	18.87	1000.00	-10.63	-4.31	0.06	95.240	-221.43	76.92	42.42	-329.41
% over L19	15.44	12.27	0.97	31.36	-268.75	69.23	4.95	14.05	134.290	47.83	-33.33	-267.86	-155.71
L23 QPM(P1)	5.47	5.77	6.41	6.89	-0.17	1.23	81.13	166.19	0.081	-0.36	0.43	-0.05	0.02
L28 non-QPM(P2)	8.20	6.35	6.85	6.75	0.67	3.71	72.27	146.27	0.035	0.95	-0.02	-0.19	-0.71
L15 QPM(Res L1)	5.82	6.14	7.25	6.51	0.21	1.34	75.54	185.98	0.083	-0.33	0.24	0.70	-0.58
% over L23	6.40	6.41	13.10	-5.52	-223.53	8.94	-6.89	11.91	2.470	-8.33	-44.19	-1500.00	-3000.00
% over L28	-29.02	-3.31	5.84	-3.56	-68.66	-63.88	4.52	27.15	137.140	-134.74	-1300.00	-468.42	-18.31
L24 QPM(P1)	5.58	6.02	6.91	7.01	0.09	3.25	78.24	162.94	0.085	-0.48	0.37	0.07	0.08
L32 non-QPM(P2)	4.71		5.18	5.27	-0.96	1.87	75.35	181.83	0.042	-0.30		0.26	-0.54
L17 QPM(Res L1)	6.89	4.51	6.56	7.05	-0.06	2.59	79.62	158.54	0.094	0.50	-1.11	0.08	0.56
% over L24	23.48	-25.08	-5.07	0.57	-166.67	-20.31	1.76	-2.70	10.590	-204.17	-400.00	14.29	600.00
% over L32	46.28		26.64	33.78	-93.75	38.50	5.67	-12.81	123.810	-266.67		-69.23	-203.70
L25 QPM(P1)	6.96	4.16	6.36	7.68	-0.10	1.70	77.01	159.08	0.084	0.51	-1.55	0.25	0.83
L21non-QPM(P2)	6.02	6.04	5.73	6.51	-0.20	2.39	73.94	165.81	0.040	-0.32	0.63	-0.23	-0.04
L18 QPM(Res L1)	6.34	2.38	6.34	6.96	-0.75	3.16	80.76	184.36	0.086	0.94	-2.27	0.67	0.69
% over L25	-8.91	-42.79	-0.31	-9.38	650.00	85.88	4.87	15.89	2.380	84.31	46.45	168.00	-16.87
% over L21	5.32	-60.60	10.65	6.91	275.00	32.22	9.22	11.19	115.000	-393.75	-460.32	-391.30	-1825.00

† GY = grain yield; DA = days to anthesis; PH = plant height, TRP = tryptophan; GCA = general combining ability; SCA = specific combining ability; QPM = quality protein maize; non-QPM = non quality protein maize

5.5 Discussion

Successful crop enhancement through genetic manipulation in breeding programmes depends on the ability of the parental material to transfer traits of interest to their offspring for inbred or heterozygous crops. It depends on combining ability, especially SCA for hybrids. Also, it is essential that germplasm used in breeding programmes are carefully selected in order to determine their integral potential. GCA and SCA identifies breeding values of genotypes (Alamerew and Warsi 2015). The SCA is mainly due to non-additive or over dominant and epistatic gene action effects, while GCA is due to additive gene action. Variances due to SCA and GCA were accessed in order to ascertain the type of gene action primarily controlling the inheritance of grain yield and yield related characteristics. The results from this study, involving QPM and non-QPM lines crossed with QPM and non-QPM testers, showed variation and significant differences for GCA for lines and testers and SCA effects for single cross hybrids. This indicates the presence of both additive and non-additive gene actions conditioning the inheritance of grain yield and most of the measured characters. The variance due to GCA sum of squares and SCA sum of squares as percentage of total sum of squares was estimated to quantify gene effects that determined the inheritance of the traits measured. Non-additive gene effects primarily controlled grain yield. These findings differ from earlier reports by Abbas et al. (2016) and Chiuta and Mutengwa (2020), who found GCA effects to be predominant in the inheritance of grain yield under optimal conditions. However, these results are consistent with those of Asefa et al. (2008) who found SCA to be a more important contributor to grain yield than GCA. These differences might be due to the genetic background of the materials used, as well as the conditions under which the studies were carried out, since environment plays an important role in the performance genotypes.

Positive and significant GCA is important for grain yield improvement of inbreds but SCA is most important for superior hybrid performance. Lines or testers with positive GCA values suggests that they will contribute positively to grain yield, while lines and testers with negative GCA are undesirable as they may not contribute positively to the traits of interest.

The significant effect of site, site $\times$ GCA_{Line} and site $\times$ GCA_{Tester} for grain yield and most of the characters measured in this study means that the site had a large effect on GCA and that there was a site with GCA interaction for both lines and testers and GCA effects

changed ranking between sites. However, the absence of significant site $\times$ line $\times$ tester effect for grain yield and most other measured traits suggested that the performance of the hybrids was consistent across the 13 locations. The substantial GCA_{Line} , GCA_{Tester} and $SCA_{Line \times Tester}$ mean squares for ears per plant and ear aspect emphasized the importance of both additive and non-additive gene action in the expression of these secondary traits.

The positive and significant GCA effects recorded for lines 11, 13, 14 and 28 suggests that these lines have the prospects to be utilized in breeding superior QPM hybrids if they also have superior SCA. Using these parents should lead to progenies with high grain yield (Fasahat et al. 2016). Since ear rot is an important trait in breeding for QPM genotypes, lines with negative and significant GCA effect need to be selected and used in making crosses to overcome the issues surrounding soft kernels of QPM genotypes. Lines 18 and 30 have the potential to pass kernel hardness to their progeny, thereby preventing kernel rots (Vancetovic et al. 2015).

Several studies have used the SCA and other grouping methods to classify lines into well-defined groups to allow successful crosses to be carried out (Badu-Apraku et al. 2013; Annor and Badu-Apraku 2016; Fan et al. 2016). The SCA method of grouping lines under testers could classify 48.48% of the lines. However, in this study, since it does not involve molecular studies, only the SCA method was used, hence, the efficiency of the grouping could not be estimated.

The high grain yield displayed by the superior QPM hybrid (line 11 $\times$ CZL15049) might have been due to the increased days the parental line took to flower (above 80 days). The longer maturity allows the hybrid more time for photosynthate accumulation which is partitioned into grain yield, thereby translating into higher grain yield. This observation differed from the study of Akinwale et al. (2011) who reported positive and non-significant association between days to maturity and grain yield in rice and Pratap et al. (2018) who also found significant negative association between days to 50% flowering and grain yield in rice. However, this finding is in accordance with Egli (1993) who reported on the effects of photosynthesis and flowering on yield components and seeds of cowpea. From the yield comparison analysis for the hybrids studied, it was established that tryptophan content negatively affects the yield potential of the QPM hybrids.

5.6 Conclusions

Significant variations for grain yield and agronomic traits were found for lines, testers, and line x tester at Potchefstroom, Cedara, and Zimbabwe trials and across the 13 testing locations for the 2018 and 2019 cropping seasons. Inbred lines and testers having positive and significant GCA effects for grain yield have the potential to transfer high yielding traits to their first filial generation. Non-additive genetic effects controlled more than 50% of inheritance of grain yield and also controlled the inheritance of anthesis-silking interval, husk cover and ears per plant. On the other hand, additive genetic effects controlled the inheritance of ear rot, plant and ear heights, days to pollen shed, ear aspect as well as root and stalk lodging. This suggested that both additive and dominance gene actions played an important role in the inheritance of traits measured in this study. Inbred lines 11 and 14 and non-QPM tester CML444 showed desirable GCA effects for grain yield, indicating that these lines in combination with the tester should be considered when targeting the development of superior maize genotypes with QPM traits. Inbred lines 1, 2, 8, 13 and 30 were prolific while QPM tester CZL059 was the only tester to display positive significant GCA for ears per plant, which is a major contributor to grain yield. The SCA grouping method showed that QPM testers were superior to non-QPM testers because they have more lines grouped under them for grain yield. Based on the SCA values, crosses 31 x 1 (both QPM), 28 x 1 (non-QPM x QPM), 27 x 2 (both QPM), 25 x 4 (both QPM), 22 x 2 (non-QPM x QPM) and 11 x 1 (both QPM) were identified as the best hybrids across locations. These crosses might be considered for further evaluation and commercialization in Southern Africa under rainfed conditions.

References

- Ababulgu D, Shimelis H, Laing M and Beyene A (2018) Phenotypic characterization of elite quality protein maize (QPM) inbred lines adapted to tropical-highlands and the association studies using SSR markers. *Australia Journal of Crop Science* 12: 22-31.
- Abbas G, Ahsan M, Saleem M and Ahmad R (2016) Inheritance study of different agronomic traits in mung × mash interspecific recombinant inbred lines. *Journal of Animal and Plant Sciences* 26: 149-155.
- Abuali AI, Abdelmulla AA, Khalafalla MM, Atif Elsadig Idris AE and Osman AM (2012) Combining ability and heterosis for yield and yield components in maize. *Australian Journal of Basic and Applied Sciences* 6: 36-41.

- Agbaje SA, Badu-Apraku B and Fakorede MAB (2008) Heterotic patterns of early maturing maize inbred lines in *Striga*-free and *Striga*-infested environments. *Maydica* 53: 87-96.
- Akinwale MG, Gregorio G, Nwilene F, Akinyele BO, Ogunbayo SA and Odiyi AC (2011) Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *African Journal of Plant Science* 5: 207-212.
- Alamerew S and Warsi MZK (2015) Heterosis and combining ability of subtropical maize inbred lines. *Africa Crop Science Journal* 23: 123-133.
- Ali F, Irfan AS, Rahman H, Mohammad N, Durrishahwar, Muhammad YK, Ihteram U and Jianbing Y (2012) Heterosis for yield and agronomic attributes in diverse maize germplasm. *Australian Journal of Crop Science* 6: 455-462.
- Amegbor IK, Badu-Apraku B and Annor B (2017) Combining ability and heterotic patterns of extra-early maturing white maize inbreds with genes from *Zea diploperennis* under multiple environments. *Euphytica* 213: 1-16.
- Annor B and Badu-Apraku B (2016) Gene action controlling grain yield and other agronomic traits of extra-early quality protein maize under stress and non-stress conditions. *Euphytica* 212: 213-228.
- Asefa B, Mohammed H and Zelleke H (2008) Combining ability of transitional highland maize inbred lines. *East African Journal of Sciences* 2: 19-24.
- Badu-Apraku B, Oyekunle M, Fakorede MAB, Vroh I, Akinwale RO and Aderounmu M (2013) Combining ability, heterotic patterns and genetic diversity of extra-early yellow inbreds under contrasting environments. *Euphytica* 192: 413-433.
- Bekele A and Rao TN (2014) Estimates of heritability, genetic advance and correlation study for yield and its attributes in maize (*Zea mays* L.). *Journal of Plant Science* 2: 1-4.
- Chiuta NE and Mutengwa CS (2020) Combining ability of quality protein maize inbred lines for yield and morpho-agronomic traits under optimum as well as combined drought and heat-stressed conditions. *Agronomy* 10: 1-14.
- de Abreu VM, Von Pinho ÉV de R, Mendes-Resende MP, Balestre M, Lima AC, Heloisa Oliveira Santos HO and Von Pinho RG (2019) Combining ability and heterosis of maize genotypes under water stress during seed germination and seedling emergence. *Crop Science* 59: 33-43.
- Egli DB (1993) Cultivar maturity and potential yield of soybean. *Field Crops Research* 32: 147-158.

- Fan XM, Yin XF, Zhang YD, Bi YQ, Liu L, Chen HM and Kang MS (2016) Combining ability estimation for grain yield of maize exotic germplasm using testers from three heterotic groups. *Crop Science* 56: 2527-2535.
- Fasahat P, Rajabi A, Rad JM and Derera J (2016) Principles and utilization of combining ability in plant breeding. *Biometrics and Biostatistics International Journal* 4: 1-24.
- Gangashetty PI, Motagi BN, Pavan R and Roodagi MB (2016) Breeding crop plants for improved human nutrition through biofortification: Progress and prospects. In: Jaiwal PK, Chhillar AK, Chaudhary D, Jaiwal R (eds), *Advances in Plant Breeding Strategies: Agronomic, Abiotic and Biotic Stress Traits*. Springer International Publishing, Switzerland Vol.2, pp. 35-68.
- Haydar FMA and Paul NK (2014) Combining ability analysis for different yield traits in maize. *Bangladesh Journal of Plant Breeding and Genetics* 27: 1-5.
- He K, Chang L, Dong Y, Cui T, Qu J, Liu X, Xu S, Xue J and Liu J (2018) Identification of quantitative trait loci for agronomic and physiological traits in maize (*Zea mays* L.) under high-nitrogen and low-nitrogen conditions. *Euphytica* 214: 1-17.
- Kaur N, Singh B and Sharma S (2019) Comparison of quality protein maize (QPM) and normal maize with respect to properties of instant porridge. *LWT-Food Science and Technology* 99: 291-298.
- Kempthorne O (1957) *An introduction to genetic statistics*. John Wiley and Sons, New York.
- Muraya MM, Ndirangu CM and Omolo EO (2006) Heterosis and combining ability in diallel crosses involving maize (*Zea mays* L.) S1 lines. *Australian Journal of Experimental Agriculture* 46: 387-393.
- Nduwumuremyi A, Tongoona P, Habimana S and Husbandry A (2013) *Journal of Plant Breeding and Genetics* 1: 117-129.
- Pratap A, Bisen P, Loitongbam B, Sandhya and Singh PK (2018) Assessment of genetic variability for yield and yield components in rice (*Oryza sativa* L.) germplasms. *International Journal of Bio-resource and Stress Management* 9: 087-092.
- Qi X, Li ZH, Jiang LL, Yu XM, Ngezahayo F and Liu B (2010) Grain-yield heterosis in *Zea mays* L. shows positive correlation with parental difference in CHG methylation. *Crop Science* 50: 2338-2346.
- Saif-ul-Malook, Ali Q, Ahsan M, Muhammad Khalid Shabaz MK, Waseem M and Aamir A (2016) Combining ability analysis for evaluation of maize hybrids under drought stress. *Journal of the National Science Foundation of Sri Lanka* 44: 223-230.

- SAS Institute (2011) Statistical Analysis Software (SAS) user's guide
- Sharief AE, El-Kalla SE, Gado HE and Abo-Yousef HAE (2009) Heterosis in yellow maize. *Australia Journal of Crop Science* 3: 146-154.
- Sharma JR (2006) Statistical and biometrical techniques in plant breeding. 1st edition. New Age International, Mohan lal Printers, Delhi, pp. 265-285.
- Singh RK and Chaudhary BD (1985) Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, pp. 103-157.
- Sprague GF and Tatum LA (1942) General versus specific combining ability in single crosses of corn. *Journal of the American Society of Agronomy* 34: 923-928.
- Tilahun B, Azimach G, Keno T, Chibsa T, Garoma B, Abebe B, Tulu D, Tafa Z and Chalchisa D (2019) Test cross performance and combining ability of newly introduced quality protein maize (*Zea mays*) inbred lines for grain yield and agronomic traits evaluated in mid-altitude agro-ecological zones of Ethiopia. *South African Journal of Plant and Soil* 36: 173-180.
- Vacaro E, Fernandes J, Neto B, Pegoraro DG, Nuss CN and Conccicao LH (2002) Combining ability of twelve maize populations. *Pesquisa Agropecuária Brasileira* 37: 67-72.
- Vancetovic J, Bozinovic S, Ignjatovic-Micic D, Delic N, Kravic N and Nikolic N (2015) A diallel cross among drought tolerant maize populations. *Euphytica* 205: 1-16.
- Wegary D, Vivek B and Labuschagne M (2013) Association of parental genetic distance with heterosis and specific combining ability in quality protein maize. *Euphytica* 191: 205-216.
- Wegary D, Vivek BS and Labuschagne MT (2014) Combining ability of certain agronomic traits in quality protein maize under stress and nonstress environments in Eastern and Southern Africa. *Crop Science* 54: 1004-1014.

CHAPTER SIX

COMBINING ABILITY ANALYSIS OF QUALITY TRAITS FOR QUALITY AND NON-QUALITY PROTEIN MAIZE INBRED LINES

6.1 Abstract

Breeding and identification of maize hybrids with enhanced quality traits is important for addressing malnutrition among the increasing human population, as well as for feed supplement formulation for the animal and poultry industries. The objectives of this study were to estimate the combining ability of QPM lines with QPM and non-QPM testers for quality traits and to quantify trait performance of the hybrids produced. A total of 135 hybrids were analysed for quality traits, including tryptophan, protein, starch, oil, fibre and moisture content across six environments in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons. The results showed significant variations for quality traits among the hybrids. Hybrids L12 x CZL15049 (61%), L18 x CZL15049 (61%) and L2 x CZL059 (60%) had high quality index while hybrids 45 and 57 had high tryptophan content. Hybrids L13 x CML444 (51) and L10 x CZL15049 (37) had high values for starch and oil contents, respectively. Combining ability estimates were significant for both lines and testers used in this study. Both additive and non-additive gene action played an important role in the inheritance of the quality traits analysed, but additive genetic effects were predominant. Inbred lines 15, 1, 8 and 12; and QPM testers CZL15049 and CZL059 showed desirable GCA effects for tryptophan. The SCA for hybrids 127 and 87 were high for protein content. The superior hybrids identified for various quality traits will be important for the food and animal feed industries to enhance human and animal nutrition. Inbred lines and testers identified for good GCA effects for quality traits should be utilised by other maize improvement programmes for development of superior QPM hybrids in SSA. Promotion and adoption of these superior QPM hybrids for good quality traits would contribute significantly to the fight against malnutrition in SSA.

Keywords: Combining ability, quality traits, quality index, non-quality protein maize

6.2 Introduction

The crucial role maize (*Zea mays* L.) plays as the main staple food for millions of people in the world cannot be underestimated, with global production of 1060 million metric ton from about 187 million hectare in 2016 (FAOSTAT 2016; Hossain et al. 2019). Undernourishment is a chronic problem worldwide, particularly in rural communities of SSA where people rely chiefly on maize, which is a high carbohydrate source, as staple food. Most people have little access to varied diets containing protein. Breeding for biofortified crops with enriched nutritional quality can help improve nutritional deficiencies in SSA and other developing worlds. This could be achieved if nutritionally enhanced crops are accepted, produced and are made available in large quantities for consumption by both humans and animals (De Groote et al. 2010; 2014). Globally, an estimated population of about two billion are suffering from deficiency of essential micronutrients and its related issues and over 800 million people are reported to be malnourished (Global Nutrition Report 2017; Hossain et al. 2019). Some of the visible symptoms of malnutrition are stunted growth and underweight. Black et al. (2013) and Zimmerman et al. (2018) reported that more than 85% of the countries in the world are plagued by malnutrition in one form or another. This causes about 45% of deaths among children below the age of five.

Even though normal endosperm maize, which is generally cultivated, is rich in many nutrients, carbohydrates and oil, it provides little or no essential amino acids for humans and other monogastric animals. The endosperm of normal maize is deficient in two essential amino acids, lysine and tryptophan, even though the endosperm contains about 10% protein with about 73% starch and 4% oil (Annor and Badu-Apraku 2016). The deficiency of essential amino acids can negatively affect human and animal growth (Prasanna et al. 2001). As a result, infants who are constantly fed normal endosperm maize with little or no protein supplements from animal or legume products, suffer from malnutrition, and this often leads to the development of pellagra and other health related diseases (Babu and Prasanna 2014). The development, adoption and cultivation of quality protein maize (QPM) with higher concentrations of tryptophan and lysine could significantly reduce malnutrition and its related diseases, as well as death, in low income countries in the developing world (Mbuya et al. 2011). QPM can supply about 70 to 80% of human protein requirements, depending on the variety, while non-QPM genotypes can only supply a maximum of 46% (Babu and Prasanna 2014). The biological value of protein,

which measures how effectively the body absorbs and utilises amino acids, is 80% for QPM, which is comparable to 86% for egg, while for normal endosperm maize it is 40 to 57% (Babu and Prasanna 2014; Teklewold et al. 2015).

For a maize genotype or the grain to be classified as QPM, it must have a QI equal or above 0.80, where QI is referred to as the proportion of tryptophan to protein present in the grain (Wegary et al. 2011; Masindeni 2013; Wegary et al. 2014; Twumasi-Afriye et al. 2016; Tandzi et al. 2017). Ignjatovic-Micic et al. (2013) and Tandzi et al. (2017) observed that the QI of hybrid maize resulting from hybridizing QPM and non-QPM lines was in the range of 0.71 to 0.74, which was superior to the normal hybrids with 0.57 to 0.62, however it was less than the QPM threshold which is 0.80. The hybrids between QPM and non-QPM lines express the QI regardless of isolation from non-QPM maize while the QPM lines may show reduced QI in non-isolated fields. Consumption of maize products with enhanced lysine and tryptophan content could help alleviate the growing challenge posed by malnutrition in several parts of the world (Menkir et al. 2008; Mpofu et al. 2012). Several authors have reported on the nutritional advantages of QPM in feeding experiments involving livestock, especially monogastric animals, and children (Akuamoah-Boateng 2002; Mpofu et al. 2012; Kostadinovic et al. 2016). Children who were fed with meals made from QPM were healthier than those fed with food products from normal maize (Gunaratna et al. 2010; Tandzi et al. 2017). Studies have shown that within some Southern African countries, for example Lesotho, Malawi and Zambia, consumption of about 100 g of a QPM food product per day is essential for children of school going age to obtain adequate amounts of lysine (Nuss and Tanumihardjo 2011; Tandzi et al. 2017).

Even though the University of Illinois started selections for high protein and high oil contents much earlier than breeding for *o2*, genetic enhancement of nutritional value in maize commenced in 1963 with Mertz et al. (1964) who identified mutant *o2* maize that contains an amount of protein equal to that in normal endosperm maize (Premlatha and Kalamani 2010), but about twice the normal levels of lysine and tryptophan, which increases the protein quality in normal maize (Badu-Apraku and Lum 2010). Several studies of QPM inbred lines for combining ability under varying environmental conditions to identify QPM donors and testers using several mating designs have been reported (Živanović et al. 2006; Mbuya et al. 2011; Amin et al. 2014; Sarika et al. 2018). QPM genotypes with higher amino acid contents had lower grain yield. Therefore, the major aim

of some breeding programmes presently is to improve both grain yield and nutritional value of QPM genotypes instead of focusing only on quality traits (Li and Vasal 2016). Even though there are variations between QPM and non-QPM genotypes for insect attacks, kernel rots and moisture content, there are no differences in some of the physico-chemical properties such as starch and oil contents (Zhang et al. 2008; Li and Vasal 2016; Synrem et al. 2017).

With increasing technological advancement, some quality traits of maize can be screened non-destructively by using NIR techniques which require less time, are cost effective and accurate (Paulsen and Singh 2004; Bastianelli et al. 2007; Alander et al. 2013; Sharma and Carena 2016). A “ $r=0.90$ ” correlation was reported between laboratory analysis and NIR results (Sharma and Carena 2016) for protein, starch and gluten content in maize. Even though several studies have been conducted on QPM for grain yield and nutritional characteristics to address hidden hunger in resource limited populations, important information on the combining ability of genotypes for these quality traits is lacking for the recently released QPM inbred lines developed by the CIMMYT Zimbabwe maize breeding programme. Information on combining ability of lines used in crop development will identify superior lines to be crossed to develop hybrids with improved yield and quality traits. The objectives of this study were to identify the combining ability of QPM and non-QPM lines with QPM and non-QPM testers for quality trait performance of the hybrids.

6.3 Materials and methods

6.3.1 Genetic material

The genetic material and experimental design used for this study were the same as described in Chapters four and five.

6.3.2 Quality characteristics

Tryptophan, moisture, protein, oil, fibre and starch were analysed as described in Chapter 3 in the materials and methods section.

6.3.3 Quality index

Protein QI was calculated as the concentration of tryptophan over protein content expressed as:

$$\text{Quality index (QI)} = \frac{\% \text{ tryptophan concentration}}{\% \text{ protein in endosperm}} \times 100$$

6.4 Results

6.4.1 Analysis of variance for quality traits at Potchefstroom, Cedara and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons and combined analysis across six locations/years.

The ANOVA of separate and combined locations for the measured quality traits for the 135 hybrids evaluated at six locations is presented in Table 6.1. For the Cedara trials, the effect of hybrids (entry) on tryptophan, protein, starch, oil, fibre and moisture was significant ($P < 0.01$). There was significant interaction between year x genotype for all the traits measured at Cedara except for oil. The Potchefstroom trials also had significant differences among the hybrids for all the traits, except for moisture. There was significant year x genotype interaction for the traits analysed, except for oil and fibre. In the Zimbabwe trials, the effect of genotype was significant for all the traits analysed except for starch, while site x entry interaction was significant for only tryptophan (Table 6.1).

The combined ANOVA of the 135 hybrids showed significant ($P < 0.05$) variations for all the quality traits analysed across the six locations (Table 6.1). The effect of sites, genotypes (entry) as well as site x entry interaction was significant ($P < 0.01$) for all the quality traits measured, except for oil and fibre.

6.4.2 Mean values of measured quality traits of QPM and non-QPM hybrids and five commercial checks

Tryptophan values of the hybrids ranged from 0.03% for genotype 110 to 0.09% for genotype 45 across the six environments with a mean of 0.06% (Table 6.2). Protein content had an average value of 8.48% and ranged from 6.82% for genotype 69 to 10.04% for genotype 127. Oil content ranged from 3.77 to 6.78% for genotypes 135 and 37, respectively, with a mean value of 5.27% while starch ranged from 63.78 to 68.24% for genotypes 37 and 51, respectively, with an average value of 66.15% (Table 6.2). Fibre content ranged from 2.17% for genotype 34 to 2.96% for genotype 37 with a mean value 2.50% while moisture content ranged from 13.63% for genotype 87 to 17.99% for genotype 37 with a mean value 15.61%. QI was used to rank the hybrids, which ranged

from 0.37 for genotype 110 to 1.17 for genotypes 45 and 69 (Table 6.3). Genotype 109 with the highest tryptophan value outperformed the best QPM check genotypes 131 and 132 by 15%.

6.4.3 Estimates of combining ability for quality traits

6.4.3.1 Analysis of variance for general and specific combining ability of lines and testers evaluated at Potchefstroom, Cedara and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons

The ANOVA for combining ability for the seed samples from Cedara during the 2017/2018 and 2018/2019 cropping seasons showed significant line GCA and tester GCA for all the traits measured, except tester GCA for moisture content (Table 6.4). Line x tester (SCA effect) was significant for all the quality traits, except oil. Apart from protein and starch, other quality traits showed significant site x line x tester effects (Table 6.4).

Analysis of the Potchefstroom trials showed significant ($P < 0.01$) GCA for lines and testers for all the quality traits (Table 6.4). The SCA for line x tester was significant only for tryptophan, protein, oil and fibre. Site x line x tester effect was only significant for tryptophan, protein and starch (Table 6.4).

The ANOVA for combining ability from two sites in Zimbabwe showed significant ($P < 0.01$) line GCA and significant tester GCA for all the traits that were analysed. The site x line x tester effect was significant only for tryptophan, while site effect was significant for all the quality traits (Table 6.4). The SCA for line x tester was also significant for all quality traits (Table 6.4).

Table 6.1 Analysis of variance of 135 hybrids, including the checks, for quality traits from seeds samples obtained from Cedara, Potchefstroom, Zimbabwe and across six sites during 2017/2018 and 2018/2019 cropping seasons

Source	DF	Tryptophan %	Moisture %	Protein %	Oil %	Fibre %	Starch %
Cedara							
Year	1	0.00280*	1871.07**	12.65**	29.79**	1.81**	111.66**
Rep (Year)	2	0.00005	0.16	0.56	0.02	0.029	1.98
Block (Year*Rep)	104	0.00003*	0.69	0.59*	0.54	0.01	1.62
Entry	134	0.00075**	1.01**	1.12**	1.26**	0.06**	4.00**
Year*Entry	134	0.00011**	0.89*	0.53*	0.68	0.02*	1.86*
Error	164	0.00002	0.60	0.37	0.75	0.01	1.32
Potchefstroom							
Year	1	0.00003	4496.04**	78.44**	36.99**	4.02**	74.97**
Rep (Year)	2	0.00009*	2.00	2.41**	0.95	0.01	8.46*
Block (Year*Rep)	104	0.00003*	1.46	0.58*	0.63	0.02	1.79
Entry	134	0.00102**	1.66	1.63**	1.31**	0.08**	4.71**
Year*Entry	134	0.00013**	1.76**	0.77**	0.58	0.03	2.29**
Error	164	0.00002	1.39	0.42	0.58	0.03	1.43
Zimbabwe							
Site	1	0.00901**	67.63**	11.01	8.59**	4.02**	25.92**
Rep (Site)	2	0.00002	60.63**	1.40*	0.079	0.01	1.41*
Block (Site*Rep)	104	0.00005	3.66	0.35	0.09	0.02	0.42
Entry	134	0.00096**	9.88**	3.21**	1.08**	0.08**	2.2388
Site*Entry	134	0.00014**	2.82	0.29	0.08	0.03	0.36
Error	164	0.00004	3.81	0.32	0.10	0.0272	0.40
Across six locations							
Year	5	0.00748**	3600.05**	403.99**	34.78**	2.02**	1617.87**
Rep (Site)	6	0.00005	20.93**	1.46*	0.35	0.02	3.95*
Block (Site*Year)	312	0.00004**	1.94	0.51*	0.42	0.02	1.28**
Entry	134	0.00208**	5.18**	3.66**	2.31**	0.17**	6.19**
Year*Entry	670	0.00016**	2.53**	0.68**	0.51	0.02	1.73**
Error	492	0.00003	1.93	0.37	0.48	0.02	1.05

*P<0.05; **P<0.01

Table 6.2 Statistics and ranges for tryptophan and five other quality traits analysed for 135 QPM and non-QPM seed samples from Cedara, Potchefstroom, Zimbabwe and across six sites during the 2017/2018 and 2018/2019 cropping seasons

Traits	R ²	CV	SE	Mean	Range	R ²	CV	SE	Mean	Range
Cedara 2017/2018 and 2018/2019						Potchefstroom 2017/2018 and 2018/2019				
Tryptophan (%)	0.98	8.28	0.01	0.056	0.025-0.092	0.98	8.70	0.01	0.056	0.024-0.097
Moisture (%)	0.96	5.79	0.77	13.35	11.90-14.81	0.96	8.35	1.18	14.11	11.89-16.21
Protein (%)	0.85	8.30	0.60	7.28	5.99-9.21	0.88	7.89	0.65	8.24	6.73-10.30
Oil (%)	0.76	16.85	0.87	5.15	3.78-6.74	0.80	15.09	0.76	5.05	2.89-6.72
Fibre (%)	0.88	4.85	0.12	2.48	2.22-2.29	0.85	6.51	0.16	2.51	2.10-3.08
Starch (%)	0.85	1.76	1.15	65.41	62.77-68.14	0.85	1.87	1.20	63.90	59.875-67.846
Zimbabwe 2017/2018						Across six locations 2017/2018 and 2018/2019				
Tryptophan (%)	0.97	9.84	0.01	0.064	0.034-0.112	0.98	9.07	0.01	0.059	0.033-0.090
Moisture (%)	0.81	10.09	1.95	19.36	15.47-24.56	0.96	8.91	1.39	15.61	13.63-17.99
Protein (%)	0.92	5.75	0.57	9.91	7.40-12.62	0.95	7.18	0.61	8.48	6.82-10.04
Oil (%)	0.93	5.64	0.32	5.61	3.39-7.69	0.82	13.11	0.69	5.27	3.77-6.78
Fibre (%)	0.84	6.56	0.16	2.51	2.18-3.01	0.85	6.04	0.15	2.50	2.17-2.96
Starch (%)	0.88	0.91	0.63	69.14	66.19-71.95	0.95	1.55	1.03	66.15	63.78-68.24

†R² = coefficient of determination, CV = coefficient of variation, SE = standard error

Table 6.3 Mean values from analysis of variance for tryptophan, moisture, protein, oil, starch and fibre contents of 135 hybrids seed across six sites during the 2017/2018 and 2018/2019 cropping seasons

Entry	Trpt %	Mois %	Prot %	Oil %	Starch %	Fibre %	QI	Rank	Entry	Trpt %	Mois %	Prot %	Oil %	Starch %	Fibre %	QI	Rank
69	0.080	16.19	6.82	5.80	66.64	2.60	1.17	1	88	0.078	15.90	8.27	6.06	64.49	2.66	0.94	35
45	0.090	15.84	7.67	6.07	65.52	2.81	1.17	2	131	0.077	14.86	8.21	4.60	67.13	2.38	0.94	36
6	0.088	16.09	7.67	4.93	67.55	2.44	1.14	3	46	0.076	14.65	8.16	6.14	65.37	2.47	0.94	37
26	0.083	15.79	7.34	4.84	66.84	2.63	1.12	4	97	0.076	15.13	8.17	5.03	66.51	2.37	0.93	38
37	0.086	17.99	7.84	6.78	63.78	2.96	1.09	5	92	0.078	16.22	8.34	5.43	65.12	2.60	0.93	39
101	0.079	14.98	7.26	5.31	67.37	2.49	1.09	6	13	0.073	17.73	7.77	5.62	65.43	2.78	0.93	40
70	0.082	15.66	7.54	5.70	66.08	2.47	1.09	7	104	0.075	16.39	8.11	5.32	65.94	2.74	0.93	41
121	0.081	15.45	7.70	4.56	67.36	2.32	1.05	8	5	0.079	15.83	8.54	5.28	65.86	2.67	0.92	42
120	0.083	16.06	7.86	4.84	67.07	2.50	1.05	9	38	0.074	15.76	7.96	5.79	66.06	2.50	0.92	43
62	0.079	15.50	7.54	4.93	67.54	2.47	1.05	10	29	0.082	15.17	8.99	6.09	63.90	2.75	0.92	44
100	0.074	16.11	7.06	5.27	66.79	2.74	1.04	11	33	0.076	16.68	8.50	5.98	65.70	2.47	0.90	45
57	0.088	15.21	8.40	5.63	63.92	2.72	1.04	12	93	0.071	15.38	8.00	5.91	65.45	2.55	0.89	46
105	0.077	15.11	7.42	5.16	67.25	2.42	1.04	13	53	0.069	17.16	7.82	4.87	66.16	2.80	0.88	47
49	0.078	17.52	7.54	5.22	65.60	2.88	1.04	14	41	0.077	15.06	8.71	6.32	65.23	2.53	0.88	48
2	0.080	15.14	7.85	5.67	66.15	2.54	1.02	15	17	0.073	15.04	8.51	5.09	66.54	2.58	0.86	49
50	0.077	16.14	7.57	4.71	66.79	2.57	1.02	16	34	0.072	14.36	8.94	6.03	65.84	2.16	0.81	50
30	0.080	15.51	7.85	5.88	65.65	2.62	1.01	17	117	0.054	16.05	7.48	5.95	66.88	2.49	0.72	51
61	0.079	16.33	7.84	5.35	65.93	2.80	1.01	18	55	0.061	15.61	8.56	5.07	66.21	2.62	0.71	52
21	0.078	15.71	7.71	5.64	65.59	2.60	1.01	19	3	0.056	15.89	8.22	5.52	66.74	2.41	0.69	53
22	0.077	15.60	7.62	5.03	66.69	2.32	1.01	20	73	0.058	15.77	8.51	4.96	66.04	2.53	0.68	54
89	0.081	16.40	8.08	5.83	64.77	2.57	1.00	21	67	0.056	16.62	8.26	5.03	66.65	2.48	0.68	55
132	0.078	15.76	7.82	5.26	67.08	2.52	1.00	22	116	0.055	15.17	8.42	6.54	65.44	2.49	0.66	56
65	0.083	16.39	8.32	6.01	64.28	2.64	1.00	23	81	0.051	15.44	7.88	6.05	66.35	2.52	0.65	57
1	0.074	15.39	7.44	5.83	65.69	2.72	0.99	24	112	0.055	14.72	8.52	4.64	67.26	2.45	0.65	58
14	0.074	14.37	7.46	5.20	66.23	2.63	0.99	25	71	0.050	16.48	7.85	5.06	67.39	2.49	0.64	59
10	0.070	15.15	7.07	5.05	67.27	2.44	0.99	26	12	0.053	15.99	8.30	5.31	65.99	2.50	0.64	60
96	0.077	15.39	7.78	5.74	66.08	2.56	0.99	27	82	0.056	14.83	8.73	4.95	66.93	2.60	0.64	61
9	0.077	16.43	7.91	5.93	64.97	2.75	0.97	28	74	0.054	15.31	8.45	4.94	66.21	2.44	0.63	62
58	0.079	14.89	8.11	5.45	65.49	2.58	0.97	29	78	0.058	14.84	9.14	4.01	67.07	2.29	0.63	63
54	0.073	16.09	7.51	5.21	66.64	2.55	0.97	30	52	0.051	15.50	8.02	4.77	66.96	2.40	0.63	64
18	0.074	14.34	7.71	4.82	67.84	2.49	0.96	31	51	0.049	15.19	7.87	4.87	68.24	2.55	0.62	65
25	0.072	17.87	7.56	5.37	65.99	2.88	0.96	32	109	0.057	15.48	9.20	6.21	63.96	2.45	0.61	66
66	0.075	15.22	7.94	6.13	65.45	2.34	0.95	33	63	0.052	15.28	8.57	4.90	66.99	2.47	0.61	67
42	0.085	14.91	9.03	6.19	65.23	2.31	0.94	34	94	0.054	15.36	8.85	5.28	66.01	2.55	0.61	68
SE	0.005	1.39	0.61	0.69	0.15	1.03	-		SE	0.005	1.39	0.61	0.69	0.15	1.03	-	

† QI = Quality index used to rank the hybrids; SE = Standard error; trypt = tryptophan; moist = moisture; prot = protein

Table 6.3 Mean values from analysis of variance for tryptophan, moisture, protein, oil, starch and fibre contents of 135 hybrids seed across six sites during the 2017/2018 and 2018/2019 cropping seasons (continued)

Entry	Trpt %	Mois%	Prot %	Oil %	Starch%	Fibre%	QI	Rank	Entry	Trpt %	Mois%	Prot %	Oil %	Starch%	Fibre%	QI	Rank
108	0.056	16.93	9.29	6.28	64.19	2.48	0.61	69	84	0.042	17.70	8.28	5.32	65.85	2.62	0.51	103
60	0.057	14.73	9.44	5.69	63.85	2.55	0.61	70	122	0.045	14.85	8.85	4.89	66.62	2.37	0.51	104
39	0.052	15.60	8.53	5.04	66.74	2.38	0.60	71	103	0.041	14.73	8.18	5.52	66.65	2.42	0.50	105
27	0.051	16.83	8.62	4.94	65.91	2.73	0.59	72	129	0.045	16.52	9.02	4.83	66.54	2.51	0.50	106
85	0.046	15.56	7.80	4.99	66.74	2.43	0.59	73	124	0.043	14.51	8.53	5.10	66.61	2.74	0.50	107
28	0.052	16.48	8.85	4.74	65.88	2.47	0.59	74	43	0.045	15.76	9.10	5.56	65.95	2.48	0.50	108
4	0.051	14.56	8.78	5.46	66.22	2.47	0.58	75	115	0.044	15.07	8.95	4.78	67.00	2.29	0.49	109
31	0.051	15.68	8.93	5.00	66.03	2.53	0.57	76	56	0.043	16.99	8.69	4.66	66.10	2.45	0.49	110
59	0.055	15.29	9.58	5.09	64.56	2.55	0.57	77	77	0.046	15.52	9.46	5.53	65.16	2.45	0.49	111
24	0.050	15.58	8.68	4.98	66.53	2.33	0.57	78	64	0.041	16.33	8.40	4.72	67.11	2.43	0.49	112
113	0.047	14.85	8.22	5.51	66.69	2.42	0.57	79	72	0.045	15.05	9.19	5.19	65.99	2.36	0.49	113
102	0.048	16.69	8.55	5.38	66.06	2.64	0.56	80	114	0.042	15.33	8.77	4.58	67.40	2.34	0.48	114
11	0.049	14.72	8.73	5.37	66.55	2.54	0.56	81	95	0.044	15.97	9.06	5.51	65.63	2.47	0.48	115
23	0.046	16.63	8.30	5.50	66.14	2.49	0.56	82	111	0.045	15.87	9.36	5.45	65.92	2.29	0.48	116
91	0.049	15.98	8.81	5.73	65.50	2.48	0.56	83	125	0.044	14.59	9.27	4.32	67.04	2.47	0.48	117
80	0.051	13.95	9.13	5.95	65.57	2.69	0.56	84	130	0.042	16.53	8.87	4.81	66.13	2.25	0.47	118
48	0.048	15.31	8.55	6.06	65.75	2.47	0.56	85	134	0.044	14.95	9.32	4.48	66.10	2.38	0.47	119
133	0.049	16.62	8.90	4.78	66.46	2.49	0.55	86	40	0.043	16.01	9.18	5.77	65.36	2.46	0.47	120
16	0.051	15.97	9.38	4.91	65.36	2.36	0.55	87	106	0.043	14.64	9.24	4.56	66.25	2.38	0.47	121
15	0.047	16.45	8.68	4.97	66.03	2.64	0.55	88	19	0.039	15.89	8.49	4.55	67.57	2.53	0.46	122
118	0.047	15.80	8.65	5.13	66.74	2.46	0.54	89	119	0.041	16.26	8.94	5.73	66.10	2.32	0.46	123
7	0.048	15.32	8.81	4.76	67.18	2.46	0.54	90	86	0.040	16.19	8.67	4.35	67.21	2.41	0.46	124
32	0.048	16.03	8.84	5.72	65.20	2.54	0.54	91	126	0.043	14.20	9.54	4.66	65.99	2.41	0.45	125
47	0.047	15.37	8.74	5.17	66.74	2.31	0.54	92	8	0.043	15.37	9.50	5.03	66.36	2.34	0.45	126
76	0.046	16.05	8.49	4.80	66.67	2.47	0.54	93	20	0.041	14.87	9.03	4.82	66.31	2.42	0.45	127
135	0.049	14.97	9.09	3.77	67.89	2.48	0.54	94	36	0.043	14.83	9.84	5.44	65.36	2.34	0.44	128
68	0.048	15.29	9.27	5.41	65.33	2.40	0.52	95	79	0.040	15.24	9.21	5.08	66.52	2.36	0.44	129
90	0.045	15.44	8.53	5.20	66.55	2.67	0.52	96	127	0.043	14.83	10.04	5.25	64.88	2.53	0.43	130
107	0.046	13.96	8.89	4.62	67.15	2.43	0.52	97	83	0.039	15.04	9.13	4.86	66.48	2.39	0.43	131
35	0.046	15.77	8.87	5.64	65.95	2.31	0.51	98	44	0.040	14.52	9.54	5.71	65.34	2.38	0.42	132
99	0.047	15.31	9.17	5.63	65.83	2.29	0.51	99	87	0.041	13.63	9.88	4.35	65.47	2.56	0.42	133
98	0.044	16.06	8.55	5.05	66.57	2.41	0.51	100	123	0.036	14.90	8.81	4.90	66.49	2.37	0.40	134
128	0.047	15.10	9.20	5.21	65.49	2.35	0.51	101	110	0.034	16.03	8.86	5.43	66.10	2.64	0.38	135
75	0.043	15.85	8.52	4.14	67.29	2.46	0.51	102									
SE	0.005	1.39	0.61	0.69	0.15	1.03	-		SE	0.005	1.39	0.61	0.69	0.15	1.03	-	

† QI = Quality index used to rank the hybrids; SE = Standard error; trpt = tryptophan; moist = moisture; prot = protein

Table 6.4 Mean squares from analysis of variance for general and specific combining ability for six quality traits of 33 inbred lines and four testers at Potchefstroom, Cedara and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons

Source	DF	Tryptophan (%)	Moist (%)	Protein (%)	Oil (%)	Fibre (%)	Starch (%)	Quality Index
Cedara								
Rep	1	0.000007	0.07	0.07	0.005	0.03	0.39	0.00
Year	1	0.002731**	1799.64**	12.94**	29.611**	1.84**	105.62**	1.38**
GCA [†] Line	32	0.000808**	1.82**	1.96**	2.496**	0.11**	8.57**	0.22**
GCA [†] Tester	3	0.020580**	1.39	10.11**	15.019**	1.55**	38.30**	5.60**
Year*Line	32	0.000148**	1.30*	0.62	0.529	0.02*	1.94	0.04**
Year*Tester	3	0.000390**	1.69*	2.17*	1.368	0.19**	5.26*	0.02
SCA [†] Line*Tester	94	0.000380**	0.96*	0.80*	0.755	0.03**	2.83**	0.09**
Year*Line*Tester	94	0.000162**	0.87*	0.49	0.702	0.02*	1.80	0.04**
Error	259	0.000025	0.59	0.45	0.680	0.01	1.45	0.01
Potchefstroom								
Rep	1	0.00001	0.16	0.69	1.69	0.005	0.09	0.01
Year	1	0.00004	4291.63**	70.92**	35.92**	3.938**	70.82**	0.38**
GCA [†] Line	32	0.00101**	2.64*	3.70**	2.68**	0.124**	11.76**	0.24**
GCA [†] Tester	3	0.03915**	6.24**	13.30**	10.60**	1.566**	41.75**	7.65**
Year*Line	32	0.00017**	2.76*	0.96*	0.81	0.037*	3.17*	0.04**
Year*Tester	3	0.00048**	1.77	7.99**	0.49	0.275**	8.98**	0.12**
SCA [†] Line*Tester	94	0.00037**	1.53	0.90**	0.71	0.045**	2.06	0.07**
Year*Line*Tester	94	0.00017**	1.53	0.64*	0.64	0.025	2.27*	0.03**
Error	259	0.00003	1.42	0.49	0.57	0.025	1.66	0.01
Zimbabwe								
Rep	1	0.000008	124.75**	2.33*	0.0003	0.005	1.80*	0.01
Site	1	0.008371**	67.04**	9.81**	7.8667**	3.938**	23.11**	1.25**
GCA [†] Line	32	0.001469**	17.01**	4.28**	3.1268**	0.124**	5.16**	0.22**
GCA [†] Tester	3	0.019617**	110.72**	77.99**	13.6516**	1.566**	16.72**	4.35**
Site*Line	32	0.000151**	3.89	0.46	0.0701	0.037*	0.41	0.02**
Site*Tester	3	0.000225**	8.15	0.38	0.1511	0.275**	0.81	0.01
SCA [†] Line*Tester	94	0.000453**	7.66**	1.18**	0.2618**	0.045**	1.03**	0.07**
Site*Line*Tester	94	0.000195**	3.18	0.27	0.0902	0.025	0.32	0.02**
Error	259	0.000043	3.81	0.34	0.0973	0.027	0.41	0.01

†GCA = general combining ability; SCA = specific combining ability; *P<0.05, **P<0.01

6.4.3.2 Analysis of variance of general and specific combining ability of 33 lines and four testers analysed for six quality traits across six environments

The combined ANOVA showed significant genotype effects for all the quality traits and QI ($P < 0.05$). GCA of lines as well as testers were significant for all the traits ($P < 0.01$). The SCA of line x tester was also significant for all the quality traits and QI (Table 6.5). Similar observations were recorded for site, site x line and site x tester for all the traits analysed. Apart for oil and fibre contents, all quality traits showed significant site x line x tester effects across the six environments. The percentage sum of squares for GCA was higher than for SCA for all the quality traits analysed and calculated QI, indicating dominance of additive effects over non-additive gene effects for the traits (Table 6.5).

6.4.3.3 General combining ability effects of 33 lines for six quality traits across six

The GCA effects for the lines varied for the quality traits analysed (Table 6.6). For tryptophan, only lines 1, 2, 6, 7, 8, 12, 13, 15, 17 and 18 recorded positive and significant GCA, while lines 19, 20, 21, 22, 28, 29, 30, 32 and 35 had significant and negative GCA. Lines 4, 7, 10 and 14 had significant and positive GCA for moisture content (Table 6.6). For protein content, 14 lines (42.42% of entries) had positive and significant GCA effects while 13 lines (33.39% of entries) had negative but significant GCA effects (Table 6.6). Eight lines (24.24% of entries) recorded positive and significant GCA effects and nine lines (33.39% of entries) had negative and significant GCA for oil content. For fibre content, nine lines had positive and significant GCA effects while 10 lines recorded significant but negative GCA effects. Lines 5, 13, 16, 19, 26, 27, 29 and 31 showed positive and significant GCA effects for starch while nine lines also recorded negative and significant GCA effects for starch (Table 6.6). Inbred lines 1, 3, 6, 7, 12, 13, 15, 16, 17, 18 and 31 showed positive and significant GCA effects for QI.

Table 6.5 Mean squares from combined analysis of variance for general and specific combining ability for six quality traits of 33 inbred lines and four testers across six sites during the 2017/2018 and 2018/2019 cropping seasons

Source	DF	Tryptophan %	Moisture %	Protein %	Oil %	Fibre %	Starch %	Quality Index
Rep	1	0.000007	36.83**	2.28*	0.61	0.0004	0.06	0.02
Site	5	0.007482**	3452.19**	385.05**	33.72**	2.0014**	1560.82**	1.28**
GCA _{Line}	32	0.002509**	11.28**	7.92**	6.95**	0.3305**	18.38**	0.58**
GCA _{Tester}	3	0.076647**	43.48**	77.95**	35.99**	4.6677**	83.86**	17.09**
Site*Line	160	0.000249**	3.63**	0.81**	0.55*	0.0256*	2.53**	0.04**
Site*Tester	15	0.000758**	17.30**	6.80**	1.06*	0.1514**	5.59**	0.13**
SCA _{Line} *Tester	94	0.000754**	3.99**	1.39**	0.67*	0.0781**	2.71**	0.15**
Site*Line*Tester	470	0.000198**	2.35*	0.58**	0.50	0.0211	1.52*	0.04**
Error	779	0.000032	2.05	0.42	0.45	0.02098	1.17	0.01
%GCA SS		81.41	56.72	78.86	84.01	77.00	76.73	83.06
%SCA SS		18.59	43.28	21.14	15.99	23.00	23.27	16.94

†GCA = general combining ability; SCA = specific combining ability; *P<0.05, **P<0.01

Table 6.6 General combining ability effects of 33 lines for quality traits across six sites during the 2017/2018 and 2018/2019 cropping seasons in South Africa and Zimbabwe

Line	Name	Tryptophan %	Moisture%	Protein %	Oil %	Fibre %	Starch %	Quality Index
1	CZL0920	0.007*	-0.47	0.29**	-0.34*	0.03	0.07	0.12**
2	CZL1330	0.006*	0.32	-0.25*	0.24	-0.03	0.40	0.05
3	CZL15041	0.004	-0.02	-0.03	-0.50**	0.07**	0.31	0.09**
4	CZL15055	0.002	0.54*	-0.20	-0.18	0.10**	-0.14	0.03
5	CZL15073	-0.002	-0.51	-0.50**	0.05	-0.01	0.84**	-0.03
6	CZL15073	0.005*	0.27	0.01	-0.33*	-0.07*	0.08	0.09**
7	TL135470	0.006*	0.88**	-0.27*	-0.47**	0.19**	0.11	0.12**
8	VL06378	0.007*	-0.03	0.37**	0.21	0.11**	-0.98**	0.05
9	TL155805	0.001	-0.20	0.51**	0.64**	-0.16**	-0.54*	-0.05
10	TL147078	0.004	0.78*	0.48**	-0.09	0.07**	-0.51*	0.05
11	TL147070	0.003	-0.40	0.65**	0.63**	-0.08**	-0.83**	-0.03
12	TL13609	0.006*	-0.41	0.54**	-0.14	0.01	-0.28	0.09**
13	TL145743	0.006*	0.27	-0.38*	-0.72**	0.09**	0.78**	0.14**
14	TL156614	0.003	0.59*	-0.26*	-0.39*	0.07**	0.32	0.05
15	CZL1477	0.011**	-0.54	0.09	0.30*	0.08**	-1.41**	0.10**
16	CZL15074	0.003	0.18	-0.16	-0.48**	0.02	0.75**	0.07**
17	CZL0616	0.006*	0.48	0.35*	-0.06	-0.04	-0.60**	0.07**
18	CZL083	0.006*	0.39	0.24*	-0.57**	0.01	0.31	0.15**
19	CML572	-0.010**	-0.14	-0.67**	0.14	-0.07**	0.58*	-0.14**
20	EBL167787	-0.010**	-0.09	-0.36**	0.57**	-0.13**	0.42	-0.17**
21	CZL0520	-0.009**	-0.93**	0.15	0.26*	0.03	0.19	-0.14**
22	CZL99005	-0.016**	0.32	-0.53**	0.23	0.01	0.02	-0.21**
23	CML502	0.004	0.42	0.44**	-0.02	0.09**	-0.93**	0.05
24	CML144	0.004	0.08	0.32*	0.01	0.04	-0.59*	0.04
25	CML159	0.002	-0.3	-0.07	-0.17	-0.10**	0.32	0.03
26	CML181	0.001	0.09	0.14	-0.71**	0.06	0.52*	0.08**
27	CML197	0.002	-0.49	-0.44**	-0.03	-0.03	0.55*	0.04
28	CML312SR	-0.011**	0.42	0.50**	0.76**	-0.02	-1.13**	-0.17**
29	CML488	-0.011**	-0.59*	-0.34*	0.15	-0.12**	0.95**	-0.15**
30	CML491	-0.009**	0.20	0.43**	0.08	-0.07**	0.12	-0.12**
31	LH51	0.004	-0.46	-0.40**	-0.24	-0.13**	0.66*	0.07**
32	CZL00025	-0.016**	-1.25**	-0.58**	0.71**	0.06*	0.22	-0.24**
35	CML444	-0.015**	0.29	-0.29*	0.80**	-0.09**	-0.43	-0.23**
SE		0.002	0.27	0.11	0.13	0.02	0.23	0.03

*P<0.05, **P<0.01; SE = standard error

6.4.3.4 General combining ability effects of testers for quality traits across six locations

QPM testers CZL15049 and CZL059 had positive and significant GCA effects for tryptophan while the two non-QPM testers CML395 and CML444 had negative and significant GCA effects for tryptophan (Table 6.7). Only QPM tester CZL15049 recorded positive and significant GCA effects for moisture content.

Similar to the tryptophan content, the two QPM testers exhibited positive and significant GCA effects for protein while the two non-QPM testers also exhibited negative and significant GCA effects for protein content (Table 6.7). For oil content, non-QPM tester CML444 had positive and significant GCA effects while the two QPM testers CZL15049 and CZL059 recorded negative and significant GCA effects for oil content. QPM tester CZL15049 had positive and significant GCA values for fibre content while QPM tester CZL059 and non-QPM tester CML444 recorded negative and significant SCA effects. QPM tester CZL15049 recorded significant and positive GCA effects for starch content while non-QPM tester CML395 had negative and significant GCA effects (Table 6.7). The QPM testers used in the study showed positive and significant GCA effect for QI while the non-QPM testers showed negative and significant GCA for QI.

Table 6.7 General combining ability effects of four testers for six quality traits across six sites during the 2017/2018 and 2018/2019 cropping seasons

Tester	Name	Tryptophan	Moisture	Protein	Oil	Fibre	Starch	QI
1	CZL15049	0.012**	0.42*	0.35**	-0.25*	0.15**	-0.58**	0.17**
2	CZL059	0.013**	-0.23	0.14**	-0.52**	-0.05**	0.17	0.20**
3	CML395	-0.010**	0.08	-0.34**	0.22	-0.01	0.51**	-0.15**
4	CML444	-0.014**	-0.28	-0.15**	0.52*	-0.10**	-0.08	-0.21**
SE		0.001	0.18	0.045	0.11	0.02	0.10	0.02

*P<0.05, **P<0.01; SE = standard error; QI = quality index

6.4.3.5 Specific combining ability effects among the crosses for quality traits across six locations

The SCA values of tryptophan for the crosses ranged from -0.013 to 0.018 for entries 113 and 78, respectively (Table 6.8). A total of 21 hybrids (6 QPM hybrids and 15 non-QPM hybrids) representing 16.15% of the total crosses had significant and positive SCA effects for tryptophan. For moisture content, 11 crosses had significant and positive GCA effects

and 11 crosses again showed negative and significant SCA effects. Ten crosses had positive and significant SCA effects for oil content, while four crosses showed negative and significant SCA effects. Hybrid (L7 x CML444 (non-QPM) (27) showed the highest SCA effects for oil content. Seventeen hybrids (13.08% of hybrids) showed significant and positive SCA effects for protein content with hybrid L35 x CZL15049 (non-QPM) (127) being the highest. For fibre content, a total of 20 crosses showed significant negative SCA effects while 22 crosses also had positive and significant SCA effects. Hybrids L10 x CML444 (non-QPM) (39) and (L10 x CZL15049 (QPM) (37) recorded the least and the highest SCA values for fibre content, respectively. Only eight hybrids had positive and significant SCA effects for starch content with L15 x CZL059 (QPM) (58) being the highest, while 13 crosses recorded significant and negative SCA effects with L10 x CZL15049 (QPM) (37) recording the lowest value (Table 6.8). The genetic analysis for QI indicated that, 25 hybrids recorded positive and significant SCA. Hybrid 78 (L20 x CML444 non-QPM) recorded the highest SCA value of 0.24 for QI (Table 6.8).

Table 6.8 Specific combining ability effects of 33 lines with four testers for quality traits across six locations in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons

Entries	Pedigree	Tryp %	Moist %	Oil %	Prot %	Fibre %	Starch %	QI
1	L1 x CZL15049 (QPM)	-0.001	0.27	-0.07	-0.33	0.03	-0.21	0.02
2	L1 x CZL059 (QPM)	0.002	0.04	-0.02	0.25	0.06	-0.28	0.01
3	L1 x CML444 (non-QPM)	0.003	0.15	0.14	0.05	-0.09*	0.00	0.03
4	L1 x CML395 (non-QPM)	-0.004	-0.45	-0.06	0.07	0.00	0.48	-0.07
5	L2 x CZL15049 (QPM)	0.002	0.08	-0.06	-0.01	0.04	0.05	0.00
6	L2 x CZL059 (QPM)	0.012**	0.71	-0.14	-0.17	0.03	0.21	0.17**
7	L2 x CML444 (non-QPM)	-0.007*	-0.65	0.13	-0.17	-0.02	0.07	-0.07
8	L2 x CML395 (non-QPM)	-0.007*	-0.12	0.05	0.37*	-0.05	-0.34	-0.11**
9	L3 x CZL15049 (QPM)	0.004	0.35	0.36*	0.01	-0.01	-0.71*	0.04
10	L3 x CZL059 (QPM)	-0.005	-0.15	-0.49**	-0.31	-0.02	0.83*	-0.01
11	L3 x CML444 (non-QPM)	-0.004	-0.72	0.05	0.43*	-0.04	0.16	-0.09*
12	L3 x CML395 (non-QPM)	0.005	0.54	0.08	-0.10	0.07	-0.30	0.05
13	L4 x CZL15049 (QPM)	-0.003	0.87	0.18	-0.30	0.05	0.15	-0.02
14	L4 x CZL059 (QPM)	0.000	-0.90	-0.15	-0.16	0.07*	0.05	0.03
15	L4 x CML444 (non-QPM)	-0.005	0.08	0.10	0.12	0.03	-0.14	-0.07
16	L4 x CML395 (non-QPM)	0.007*	-0.04	-0.13	0.38*	-0.16**	-0.07	0.06
17	L5 x CZL15049 (QPM)	0.005	-0.93*	0.04	0.20	-0.03	0.20	0.03
18	L5 x CZL059 (QPM)	0.005	0.21	-0.25	-0.03	0.02	0.49	0.08
19	L5 x CML444 (non-QPM)	-0.006	0.79*	0.02	-0.21	0.01	-0.11	-0.05
20	L5 x CML395 (non-QPM)	-0.005	-0.06	0.18	0.07	-0.01	-0.59	-0.07
21	L6 x CZL15049 (QPM)	0.004	-0.27	0.05	0.02	0.01	-0.18	0.05
22	L6 x CZL059 (QPM)	-0.001	-0.23	-0.31	-0.25	-0.08*	0.70*	0.03
23	L6 x CML444 (non-QPM)	-0.004	0.59	0.39*	0.13	0.08*	-0.66*	-0.06
24	L6 x CML395 (non-QPM)	-0.001	-0.08	-0.14	0.13	-0.01	0.13	-0.04
25	L7 x CZL15049 (QPM)	-0.003	0.59	-0.10	-0.14	0.08*	0.36	-0.01
26	L7 x CZL059 (QPM)	0.006	-0.56	-0.29	-0.32	-0.03	0.56	0.13**
27	L7 x CML444 (non-QPM)	-0.005	0.08	0.50**	0.28	0.08*	-0.701*	-0.10*
28	L7 x CML395 (non-QPM)	0.001	-0.10	-0.11	0.20	-0.11**	-0.22	-0.02
29	L8 x CZL15049 (QPM)	0.006	-0.60	0.06	0.38*	0.00	-0.60*	0.03
30	L8 x CZL059 (QPM)	0.001	-0.20	-0.04	-0.14	-0.01	0.32	0.03
31	L8 x CML444 (non-QPM)	-0.004	-0.06	-0.16	0.05	0.00	0.16	-0.05
32	L8 x CML395 (non-QPM)	-0.004	0.87*	0.13	-0.26	0.02	0.11	-0.03
33	L9 x CZL15049 (QPM)	0.007*	0.14	-0.14	0.08	-0.03	0.23	0.07
34	L9 x CZL059 (QPM)	-0.002	-0.47	-0.11	0.51*	-0.08*	-0.20	-0.10
35	L9 x CML444 (non-QPM)	-0.003	0.10	0.31	-0.43*	0.02	-0.13	0.01
36	L9 x CML395 (non-QPM)	-0.003	0.25	-0.07	-0.13	0.10**	0.08	0.01
37	L10 x CZL15049 (QPM)	0.012**	1.28**	0.43**	-0.14	0.24**	-1.15**	0.16**
38	L10 x CZL059 (QPM)	-0.004	-0.94*	-0.13	0.02	-0.01	0.65*	-0.06
39	L10 x CML444 (non-QPM)	-0.003	-0.67	-0.32	-0.07	-0.22**	0.58	-0.02
40	L10 x CML395 (non-QPM)	-0.006	0.35	0.02	0.21	-0.01	-0.09	-0.09
41	L11 x CZL15049 (QPM)	0.002	-0.39	-0.11	-0.08	-0.06	0.46	0.03
42	L11 x CZL059 (QPM)	0.011**	0.14	0.15	0.48*	-0.08*	-0.42	0.06
SE		0.003	0.38	0.17	0.19	0.04	0.30	0.05

†SE = standard error; Tryp = tryptophan; Moist = moisture; Prot = protein; QI = quality index; *P<0.05, **P<0.01

Table 6.9 Specific combining ability effects of 33 lines with four testers for quality traits across six locations in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons (continued)

Entries	Pedigree	Tryp %	Moist %	Oil %	Prot %	Fibre %	Starch %	QI
43	L11 x CML444 (non-QPM)	-0.006	0.80*	0.06	-0.30	0.07*	0.05	-0.03
44	L11 x CML395 (non-QPM)	-0.008**	-0.53	-0.11	-0.07	0.07*	-0.10	-0.07
45	L12 x CZL15049 (QPM)	0.012**	-0.14	-0.01	-0.31	0.11**	0.17	0.19**
46	L12 x CZL059 (QPM)	-0.003	-0.07	0.11	0.05	-0.01	-0.06	-0.05
47	L12 x CML444 (non-QPM)	-0.007*	-0.13	-0.25	0.32	-0.15**	-0.04	-0.12**
48	L12 x CML395 (non-QPM)	-0.003	0.35	0.14	-0.02	0.06	-0.07	-0.04
49	L13 x CZL15049 (QPM)	0.002	0.86*	-0.11	-0.15	0.14	-0.32	0.08
50	L13 x CZL059 (QPM)	0.001	0.40	-0.25	0.21	0.02	-0.22	0.01
51	L13 x CML444 (non-QPM)	-0.003	-1.06*	0.37*	0.22	-0.04	0.38	-0.06
52	L13 x CML395 (non-QPM)	-0.001	-0.19	-0.02	-0.25	-0.12**	0.16	-0.03
53	L14 x CZL15049 (QPM)	-0.004	0.29	-0.21	0.01	0.04	0.20	-0.06
54	L14 x CZL059 (QPM)	-0.001	-0.06	0.01	0.00	-0.03	0.20	0.00
55	L14 x CML444 (non-QPM)	0.010**	-0.30	0.34*	-0.01	0.05	-0.42	0.13**
56	L14 x CML395 (non-QPM)	-0.006	0.10	-0.15	0.03	-0.05	0.01	-0.08
57	L15 x CZL15049 (QPM)	0.006	-0.05	0.05	-0.23	0.00	-0.40	0.07
58	L15 x CZL059 (QPM)	-0.003	0.08	-0.20	-0.26	0.00	0.84**	-0.02
59	L15 x CML444 (non-QPM)	-0.004	-0.14	-0.11	0.48*	-0.01	-0.11	-0.07
60	L15 x CML395 (non-QPM)	-0.001	0.13	0.25	0.04	0.02	-0.35	0.00
61	L16 x CZL15049 (QPM)	0.003	0.20	0.02	-0.06	0.10**	-0.40	0.04
62	L16 x CZL059 (QPM)	0.003	0.10	-0.03	0.09	-0.08*	0.26	0.05
63	L16 x CML444 (non-QPM)	0.001	-0.40	0.18	0.22	-0.05	-0.22	-0.01
64	L16 x CML395 (non-QPM)	-0.007*	0.11	-0.18	-0.21	0.04	0.35	-0.09
65	L17 x CZL15049 (QPM)	0.003	0.32	0.35*	-0.12	0.08*	-0.62*	0.04
66	L17 x CZL059 (QPM)	-0.001	-0.47	0.12	0.14	-0.13**	-0.22	-0.02
67	L17 x CML444 (non-QPM)	0.001	0.89*	-0.33	-0.37*	0.02	0.81**	0.05
68	L17 x CML395 (non-QPM)	-0.004	-0.73	-0.15	0.38*	0.03	0.02	-0.08
69	L18 x CZL15049 (QPM)	0.005	-0.08	0.09	-0.70*	-0.02	0.49	0.15**
70	L18 x CZL059 (QPM)	0.005	0.10	0.05	0.35	0.04	-0.64*	0.04
71	L18 x CML444 (non-QPM)	-0.004	0.35	-0.14	-0.40*	0.02	0.36	-0.06
72	L18 x CML395 (non-QPM)	-0.006	-0.36	-0.01	0.77**	-0.04	-0.22	-0.15**
73	L19 x CZL15049 (non-QPM)	-0.004	-0.47	-0.09	0.25	-0.07	0.25	-0.08
74	L19 x CZL059 (non-QPM)	-0.009**	0.11	0.10	0.39*	-0.02	-0.62*	-0.15**
75	L19 x CML444 (non-QPM)	0.004	0.24	-0.18	-0.23	0.00	0.35	0.07
76	L19 x CML395 (non-QPM)	0.008**	0.13	0.16	-0.38*	0.10*	0.01	0.14**
77	L20 x CZL15049 (non-QPM)	-0.010**	-0.13	0.25	0.38*	-0.05	-0.36	-0.15**
78	L20 x CML444 (non-QPM)	0.018**	-0.34	-0.46**	-0.26	-0.10**	0.16	0.24**
79	L20 x CML395 (non-QPM)	0.005	0.25	0.34*	-0.61**	0.11	0.35	0.10*
80	L21 x CZL15049 (non-QPM)	-0.010**	-1.24**	0.07	0.58**	-0.06	0.06	-0.17**
81	L21 x CZL059 (non-QPM)	-0.011**	0.83*	0.33	-0.21	0.03	-0.08	-0.12**
82	L21 x CML444 (non-QPM)	0.017**	0.40	-0.11	-0.23	0.08*	-0.14	0.22**
83	L21 x CML395 (non-QPM)	0.003	0.03	-0.30	-0.12	-0.06	0.15	0.05
84	L22 x CZL15049 (non-QPM)	-0.013**	1.06*	0.05	-0.03	-0.08*	0.15	-0.16**
85	L22 x CZL059 (non-QPM)	-0.010**	-0.21	0.12	-0.26	-0.03	0.35	-0.12**
86	L22 x CML444 (non-QPM)	0.008**	0.22	0.06	-0.32	-0.04	0.36	0.13**
SE		0.003	0.38	0.17	0.19	0.04	0.30	0.05

†SE = standard error; Tryp = tryptophan; Moist = moisture; Prot = protein; QI = quality index; *P<0.05, **P<0.01

Table 6.10 Specific combining ability effects of 33 lines with four testers for quality traits across six locations in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons (continued)

Entries	Pedigree	Tryp %	Moist %	Oil %	Prot %	Fibre %	Starch %	QI
87	L22 x CML395 (non-QPM)	0.014**	-1.05*	-0.24	0.64**	0.15**	-0.88**	0.14**
88	L23 x CZL15049 (QPM)	0.001	-0.22	-0.09	0.08	-0.07*	-0.03	0.01
89	L23 x CZL059 (QPM)	0.005	0.83*	0.06	0.09	0.00	-0.52	0.05
90	L23 x CML444 (non-QPM)	-0.008**	-0.16	-0.08	-0.05	0.09*	0.33	-0.08
91	L23 x CML395 (non-QPM)	0.001	-0.44	0.10	-0.09	-0.02	0.21	0.02
92	L24 x CZL15049 (QPM)	0.002	0.22	-0.34*	0.04	-0.08*	0.12	0.03
93	L24 x CZL059 (QPM)	-0.003	0.14	0.32	-0.07	0.05	-0.37	-0.03
94	L24 x CML444 (non-QPM)	0.004	-0.93*	0.00	0.16	0.03	0.06	0.04
95	L24 x CML395 (non-QPM)	-0.004	0.59	0.01	-0.09	-0.01	0.19	-0.05
96	L25 x CZL15049 (QPM)	0.005	-0.29	-0.12	-0.41*	-0.05	0.60*	0.10*
97	L25 x CZL059 (QPM)	0.003	-0.46	-0.26	0.32	0.05	0.05	-0.01
98	L25 x CML444 (non-QPM)	-0.008**	0.28	-0.07	0.06	0.01	-0.36	-0.11**
99	L25 x CML395 (non-QPM)	0.000	0.48	0.44*	0.06	-0.01	-0.30	0.01
100	L26 x CZL15049 (QPM)	0.002	-0.10	-0.22	-0.24	0.02	0.30	0.06
101	L26 x CZL059 (QPM)	0.006	0.18	-0.15	-0.13	-0.02	0.42	0.10*
102	L26 x CML444 (non-QPM)	-0.002	0.34	0.28	0.38*	0.08*	-0.75*	-0.09
103	L26 x CML395 (non-QPM)	-0.006	-0.40	0.09	0.03	-0.07*	0.01	-0.09
104	L27 x CZL15049 (QPM)	0.002	0.71	0.12	-0.16	0.05	0.03	0.03
105	L27 x CZL059 (QPM)	0.005	-0.13	0.04	-0.41*	0.02	0.22	0.11**
106	L27 x CML444 (non-QPM)	-0.007*	-0.48	-0.02	0.68**	-0.11**	-0.82**	-0.13**
107	L27 x CML395 (non-QPM)	-0.001	-0.09	-0.14	-0.08	0.04	0.56	-0.03
108	L28 x CZL15049 (non-QPM)	-0.005	0.62	0.17	0.13	-0.10**	-0.05	-0.07
109	L28 x CZL059 (non-QPM)	-0.004	-0.76*	0.16	0.59**	0.00	-1.13	-0.11**
110	L28 x CML444 (non-QPM)	-0.003	0.32	-0.24	-0.47*	0.174**	0.56	0.01
111	L28 x CML395 (non-QPM)	0.011**	-0.17	-0.09	-0.22	-0.07*	0.61*	0.16**
112	L29 x CZL15049 (non-QPM)	-0.005	-0.79	-0.41*	0.14	-0.04	0.65	-0.05
113	L29 x CZL059 (non-QPM)	-0.013**	0.62	0.47**	0.12	0.09*	-0.57	-0.19**
114	L29 x CML444 (non-QPM)	0.007*	0.04	-0.12	-0.15	-0.06	0.07	0.09
115	L29 x CML395 (non-QPM)	0.010**	0.14	0.04	-0.08	0.01	-0.16	0.14**
116	L30 x CZL15049 (non-QPM)	-0.007*	-0.78*	0.31	0.29	-0.10**	-0.25	-0.12**
117	L30 x CZL059 (non-QPM)	-0.010**	0.17	-0.02	-0.28	0.10**	0.24	-0.10**
118	L30 x CML444 (non-QPM)	0.010**	0.36	-0.33	0.05	0.03	-0.08	0.12**
119	L30 x CML395 (non-QPM)	0.006	0.26	0.03	-0.03	-0.02	0.08	0.09*
120	L31 x CZL15049 (QPM)	0.009**	0.28	-0.22	-0.14	-0.06	0.51	0.14**
121	L31 x CZL059 (QPM)	0.006	0.23	-0.19	-0.01	0.02	0.03	0.07
122	L31 x CML444 (non-QPM)	-0.006	-0.24	0.24	0.15	-0.01	-0.28	-0.09
123	L31 x CML395 (non-QPM)	-0.010**	-0.27	0.16	0.02	0.05	-0.27	-0.14**
124	L32 x CZL15049 (non-QPM)	-0.013**	-0.45	0.10	-0.30	0.00	0.51	-0.15**
125	L32 x CML444 (non-QPM)	0.012**	0.42	-0.01	-0.12	-0.04	0.01	0.16**
126	L32 x CML395 (non-QPM)	0.014**	-0.18	0.04	-0.07	-0.01	-0.36	0.18**
127	L35 x CZL15049 (non-QPM)	-0.013**	-0.89	-0.14	0.91**	-0.06	-0.40	-0.21**
128	L35 x CZL059 (non-QPM)	-0.012**	-0.28	0.28	0.35	-0.01	-0.60*	-0.18**
129	L35 x CML444 (non-QPM)	0.012**	0.16	-0.01	-0.32	0.11**	0.33	0.17**
130	L35 x CML395 (non-QPM)	0.012**	1.02*	-0.14	-0.91**	-0.03	0.67*	0.20**
SE		0.003	0.38	0.17	0.19	0.04	0.30	0.05

†SE = standard error; Tryp = tryptophan; Moist = moisture; Prot = protein; QI = quality index; *P<0.05, **P<0.01

6.5 Discussion

Development of QPM genotypes with increased lysine and tryptophan and good quality traits is important to alleviate poor nutritional status in the increasing population that depends on maize products. Understanding of gene action and mode of quality trait inheritance of QPM genotypes is essential in any breeding programme because of its implications in speeding up the breeding progress by selecting superior lines for hybrid formation. In the present study, there was large variability among the QPM and non-QPM hybrids for six quality traits. The high values for QI and other quality characteristics, combined with acceptable yield, in a number of hybrids, showed that QPM hybrids with superior quality traits with increased grain yield can be identified for commercialisation across southern Africa and to a larger extent, SSA. Fifty of the 130 single cross hybrids developed had QI above 0.80. The QI values recorded in this study were more than the values reported by other studies (Masindeni 2013; Twumasi-Afriye et al. 2016; Tandzi et al. 2017). This suggested that good improvement has been attained in developing QPM materials in SSA.

The significant genotype x site interactions observed for all the quality traits analysed indicate that the environment plays an important role in the inheritance of the quality traits, and that genotypes do not react the same in all environments. This indicates that genotypes must be selected that are stable for the required traits across different environments. Kaya and Akcura (2014), Nehe et al. (2019), and Anandan et al. (2020) also found interaction between environment and quality traits in rice and wheat cultivars. Singh et al. (2019) reported on the influence of the environment on oil content, suggesting both genetic and environmental factors contribute to inheritance of quality traits.

The tryptophan values obtained from the present study for both QPM and non-QPM genotypes fall within the range reported by several authors (Zilic et al. 2011; Li and Vasal 2016; Sarika et al. 2018; Singh et al. 2019) suggesting the tryptophan contents from the QPM lines and testers were indeed transferred to the progenies.

The protein content recorded for the materials analysed indicated the presence of genetic variability for protein synthesis. It is interesting to note that the best genotype with the highest protein content of 10.04% is a non-QPM hybrid 127, which is a product of non-QPM inbred line 35 by a QPM tester. This is consistent with Marta et al. (2017) who

recorded similar protein content in Indonesian maize hybrids. Superior genotypes with enhanced nutritional traits could be beneficial to the food industries where they use maize for meal and feed for both humans and animals, as well as by companies that use maize for manufacturing of bread and biscuits.

Generally, the starch content of the maize genotypes fell within the starch content of maize as previously reported (Li and Vasal 2016; Sharma and Carena 2016; Lu et al. 2019). Non-QPM based hybrids had higher starch content than their QPM counterparts, suggesting that QPM genotypes have the potential to contribute to health benefits because of their increased protein content with decreased starch. Although non-QPM hybrid L13 x CML444 (51) was observed to have the highest starch content of 68.24%, the figure is far below the reported values for non-QPM or normal maize genotypes having 70 to 75% of starch (Boyer and Hannah 2001; Laude and Carena 2014). The reason for such low values could be that genetic materials used were largely QPM. This observation is in line with previous findings (Hossain et al. 2019; Kaur et al. 2019) that reported low starch contents for QPM genotypes.

Oil from maize is very important for human and animal consumption. The oil content values in this study were higher than those previously reported (Boyer and Hannah 2001; Blumenthal et al. 2008). Interestingly, a QPM hybrid had higher oil contents than the non-QPM hybrids. QPM hybrid L10 x CZL15049 (37) recorded an oil content of 6.78%, far above the range of 3.10 to 5.70% reported by Clark et al. (2006) and Synrem et al. (2017). Such hybrids could be exploited by oil producing companies for manufacturing edible oil to serve as source of fat and poly-unsaturated fatty acids to form part of human and animal nutrition (Cuevas-Rodríguez et al. 2006; Blumenthal et al. 2008).

Fibre from maize consists of non-digestible sugars and lignin that are fundamental and integral in plants (Zilic et al. 2011). The fibre contents of the maize hybrids were significantly lower than the values report by Marta et al. (2017). While the range of fibre recorded in this study across six locations was 2.17 to 2.96%, Marta et al. (2017) reported a range of 3.11 to 4.15%. This difference is probably due to the genetic materials used in the current study. The QPM genotypes generally produced less fibre than non-QPM hybrids. This study could be important to the livestock farmers to include maize genotypes with low fibre in their feed formulation corroborating the study by Dei (2017).

QPM genotypes in the present study retained more moisture than the non-QPM genotypes. In fact, this is a known characteristic of QPM genotypes, suggesting there is a need to ensure that grains from QPM genotypes are dried to the required moisture before storage to avoid post-harvest losses and also to keep the seeds viable for longer durations (Bhandari et al. 2018; Kaur et al. 2019).

In the current study, there was larger contribution of GCA sum of squares for all the quality traits analysed than the SCA sum of squares. This indicated that the quality traits measured were determined predominantly by additive genetic effects. This is in line with results reported in several studies involving QPM and non-QPM genetic materials for quality traits, particularly tryptophan, protein, starch and oil contents (Mathur and Mathur 1986; Pixley and Bjarnason 1993; Njeri et al. 2017; Darshan and Marker 2019). With the predominance of additive genetic effects and the large genetic variability for the quality traits, selection methods such as recurrent selection using half-sibs can be used to improve this germplasm.

Inbred line CZL1477 (15), with significant positive GCA effects for tryptophan across the six sites, is the only inbred line having the favourable alleles to be used by breeding programmes with the aim of developing hybrids with high tryptophan. On the other hand, the two QPM testers (CZL15049 and CZL059) were superior contributors of tryptophan content due to displaying significant positive GCA effects. The 14 inbred lines that showed significant GCA effects for protein content across the six sites denotes their ability to transfer this trait to their progeny. Therefore, lines with high and stable protein content with significant positive GCA effects are good genetic materials to be used in QPM inbred line recycling programmes (Njeri et al. 2017). Similarly, lines and testers having positive and significant GCA effects for oil content are desirable as contributors in breeding for high oil contents. This agrees with the studies by Laude and Carena (2014), Kostadinovic et al. (2016) and Synrem et al. (2017). For nutritional benefits, it is desirable to select lines with negative and significant GCA effects for starch and fibre. However, industries with the aim of producing genotypes with high starch content could select lines with significant positive GCA effects for starch and lines with low GCA for fibre contents (Cuevas-Rodríguez et al. 2006; Mamun et al. 2015; Ai and Jane 2016).

The crosses showing positive and significant specific combinations for tryptophan, protein, and oil contents are desirable for commercial hybrid production and vice versa for the hybrids with negative and significant SCA effects for starch and fibre contents. Even though only 10 inbred lines recorded significant GCA for tryptophan, several hybrids were found to have positive and significant SCA, with hybrids L20 x CML444 (78) and L21 x CML444 (82) being the superior genotypes. Similarly, non-QPM hybrid L35 x CZL15049 (127) was the best genotype for protein content. These findings were similar with the results reported by Wegary et al. (2013), Williams and Kucheryavskiy (2016), Synrem et al. (2017) and Tilahun et al. (2018) on significant SCA effects for quality traits.

The genetic analysis for QI indicated that the majority of the QPM lines recorded positive and significant GCA, while the non-QPM lines recorded negative and significant GCA. Some of the QPM lines such as 5, 9 and 11 recorded non-significant negative GCA. Lines with significant GCA values could be selected for hybrid development with enhanced quality traits. These lines could also be useful in the development of populations. Interestingly, some of the hybrids that are classified as non-QPM for example 78 (L20 x CML444; non-QPM) and 82 (L21 x ML444; non-QPM) showed significant and positive SCA effects for QI, more than the QPM hybrids. This may be linked to one of the parents being QPM for those hybrids, implying that heterosis for QI could be achieved when QPM lines are crossed with non-QPM lines because of the genetic distance the lines and testers. Inheritance of QI traits for the genetic materials studies was controlled additive genetic effects. The observed result is consistent with the study reported by Machida et al. (2010) and Ignjatovic-Micic et al. (2013) who also detected the predominance of GCA over SCA.

6.6 Conclusions

A total of 135 hybrids were analysed for quality traits, including tryptophan, protein, starch, oil, fibre and moisture contents across six environments in South Africa and Zimbabwe. Combining ability of the inbred lines and testers for quality traits were determined. Several hybrids had a QI above 1.00, and the best three hybrids for QI were QPM hybrids L12 x CZL15049 (45), L18 x CZL15049 (69) and L2 x CZL059 (6). For tryptophan, hybrids L12 x CZL15049 (45) and L15 x CZL15049 (57) outperformed the best check, QPM (entry 132) by 15.38 and 12.82%, respectively. Hybrids 45 and 57 were identified as the crosses with the highest tryptophan content, while hybrids L13 x CML444

(51) and L10 x CZL15049 (37) recorded the highest values for starch and oil contents, respectively. Additive gene action was predominant in controlling the inheritance of tryptophan, protein, starch, oil and fibre contents. Inbred lines 1, 2, 6, 7, 8, 12, 13, 15, 17 and 18 and QPM testers CZL15049 and CZL059 showed desirable GCA effects for tryptophan, suggesting this line and testers should be considered for QPM inbred development for high tryptophan content. Several lines had good GCA effects for protein and oil. Based on the SCA values, crosses 78, 82, 87 and 126 were identified as the best hybrids across the six locations for tryptophan content. Hybrids 127 and 87 were identified for superior protein content. The superior hybrids identified for various quality traits will be important for the food and animal feed industries to enhance human and animal nutrition. It is also recommended that these hybrids should be further evaluated across several other locations since the environment was found to interact with these quality traits. Inbred lines and testers with good GCA effects for quality traits could be utilised by other maize improvement programmes for development of superior QPM hybrids. Promotion and adoption of these superior QPM hybrids for quality traits from the present study would contribute significantly to fight against malnutrition in SSA.

References

- Ai Y and Jane JL (2016) Macronutrients in Corn and Human Nutrition. *Comprehensive Reviews in Food Science and Food Safety* 15: 581-598.
- Akuamoa-Boateng A (2002) Quality Protein Maize: Infant Feeding Trials in Ghana. Ghana Health Service, Ashanti, Ghana.
- Alander JT, Bochko V, Martinkauppi B, Saranwong S and Mantere T (2013) A review of optical nondestructive visual and near-infrared methods for food quality and safety. *International Journal of Spectroscopy* 2013: 1-36.
- Amin MN, Amiruzzaman M, Ahmed A and Ali MR (2014) Evaluation of inbred lines of maize (*Zea mays* L.) through line × tester method. *Bangladesh Journal Agricultural Research* 39: 675-683.
- Anandan A, Sabesan T, Eswaran R, Rajiv G and Muthalagan N (2020) Appraisal of environmental interaction on quality traits of rice by additive main effects and multiplicative interaction analysis. *Cereal Research Communications* 37: 131-140.

- Annor B and Badu-Apraku B (2016) Gene action controlling grain yield and other agronomic traits of extra-early quality protein maize under stress and non-stress conditions. *Euphytica* 212: 213-228.
- Babu R and Prasanna B (2014) Molecular Breeding for Quality Protein Maize (QPM). In: Tuberosa R, Graner A and Frison E (eds), *Genomics of Plant Genetic Resources*. Springer, Dordrecht, pp. 490-505. doi: 10.1007/978-94-007-7575-6
- Badu-Apraku B and Lum AF (2010) The pattern of grain yield response of normal and quality protein maize cultivars in stressed and non-stressed environments. *Agronomy Journal* 102: 381-394.
- Bastianelli D, Fermet-Quinet E, Davrieux F, Hervouet C and Bonnal L (2007) Calibration strategies for prediction of amino acid content of poultry feeds. *Proceedings of the 12th International Conference on Near Infrared Spectroscopy*, 9-15th April 2005, Auckland, pp. 314-318.
- Black RE, Victoria CG, Walker SP, Bhutta ZA, Christian P, De-Onis M, Ezzati M, Grantham-McGregor S, Katz J, Martorell R and Uauy R (2013) Maternal and child undernutrition and overweight in low-income and middle-income countries. *The Lancet* 382: 427-445.
- Bhandari G, Ghimire TB, Kaduwal S, Shrestha J and Acharya R (2018) Effects of storage structures and moisture contents on seed quality attributes of quality protein maize. *Journal of Maize Research and Development* 3: 77-85.
- Blumenthal J, Baltensperger D, Cassman KG, Mason S and Palvilista A (2008) Importance and effects of nitrogen on crop quality and health. *Agronomy and Horticulture Faculty Publications*. University of Nebraska - Lincoln.
- Boyer CD and Hannah LC (2001) Kernel mutants of corn. In: Hallauer AR (ed), *Specialty corns*. CRC Press LLC, Boca Raton, pp. 1-32.
- Caprita R, Caprita A and Cretescu I (2011) Effective extraction of soluble non-starch polysaccharides and viscosity determination of aqueous extracts from wheat and barley. *Proceedings of the World Congress on Engineering and Computer Science* 2: 1-3.
- Clark D, Dudley JW, Rocheford TR and Ledeaux JR (2006) Genetic analysis of corn kernel chemical composition in the random mated 10 generation of the cross of generations 70 IHO x ILO. *Crop Science* 46: 807-819.

- Cuevas-Rodríguez EO, Verdugo-Montoya NM, Angulo-Bejarano PI, Milán-Carrillo J, Mora-Escobedo R, Bello-Pérez LA, Garzón-Tiznado JA and Reyes-Moreno C (2006) Nutritional properties of tempeh flour from quality protein maize (*Zea mays* L.). LWT - Food Science and Technology 39: 1072-1079.
- Darshan SS and Marker S (2019) Heterosis and combining ability for grain yield and its component characters in quality protein maize (*Zea mays* L.) hybrids. Electronic Journal of Plant Breeding 10: 111-118.
- De Groote H, Gunaratna N, Ergano K and Friesen D (2010) Extension and adoption of biofortified crops: Quality protein maize in East Africa. Paper presented at the Joint 3rd African Association of Agricultural Economists (AAAE) and 48th Agricultural Economists Association of South Africa (AEASA) Conference, Cape Town, South Africa.
- De Groote H, Gunaratna N, Okuro J, Wondimu A, Chege C and Tomlins K (2014) Consumer acceptance of quality protein maize (QPM) in East Africa. Journal of the Science of Food and Agriculture 94: 3201-3212.
- Dei HK (2017) Assessment of Maize (*Zea mays* L.) as Feed Resource for Poultry In: Manafi M (ed), Poultry Science, pp. 1-32. <http://dx.doi.org/10.5772/65363>
- FAOSTAT (2016) <http://www.fao.org/faostat/en/#data/QC/visualize>
- Global Nutrition Report (2017) <http://www.globalnutritionreport.org>
- Gunaratna NS, De Groote H, Nestel P, Pixley KV and McCabe G (2010) Evaluating the impact of biofortification: A meta-analysis of community-based studies on quality protein maize (QPM). Food Policy 35: 202-210.
- Hossain F, Sarika K, Muthusamy V, Zunjare RU and Gupta HS (2019) Quality protein maize for nutritional security. In: Qureshi AMI, Dar ZA and Wani SH (eds), Quality Breeding in Field Crops. Springer, Switzerland, pp. 217-237. doi: 10.1007/978-3-030-04609-5_11
- Ignjatovic-Micic D, Kostadinovic M, Stankovic G, Markovic K, Vancetovic J, Bozinovic S and Andjelkovic V (2013) Biochemical and agronomic performance of quality protein maize hybrids adapted to temperate regions. Maydica 58: 311-317.
- Kaur N, Singh B and Sharma S (2019) Comparison of quality protein maize (QPM) and normal maize with respect to properties of instant porridge. LWT - Food Science and Technology 99: 291-298. <https://doi.org/10.1016/j.lwt.2018.09.070>

- Kaya Y and Akcura M (2014) Effects of genotype and environment on grain yield and quality traits in bread wheat (*T. aestivum* L.). Food Science and Technology 34: 386-393.
- Kostadinović M, Ignjatović-Mićić D, Vancetović J, Ristić D, Bozinović S, Stanković G and Mladenović-Drinić S (2016) Development of high tryptophan maize near isogenic lines adapted to temperate regions through marker assisted selection - impediments and benefits. PLoS One 11:1-17.
- Laude TP and Carena MJ (2014) Diallel analysis among 16 maize populations adapted to the northern U.S. Corn Belt for grain yield and grain quality traits. Euphytica 200: 29-44.
- Li JS and Vasal SK (2016) Maize: Quality Protein Maize. In: Wrigley C, Corke H, Seetharaman K and Faubion J (eds), Encyclopedia of Food Grains: Second Edition. Elsevier, pp. 420-424. doi: 10.1016/B978-0-12-394437-5.00223-0
- Lu X, Chen J, Zheng M, Guo J, Qi J, Chen Y, Miao S and Zheng B (2019) Effect of high-intensity ultrasound irradiation on the stability and structural features of coconut-grain milk composite systems utilizing maize kernels and starch with different amylose contents. Ultrason-Sonochemistry 55: 135-148.
- Machida L, Derera J, Tongoona P and MacRobert J (2010) Combining Ability and Reciprocal Cross Effects of Elite Quality Protein Maize Inbred Lines in Subtropical Environments. Crop Science 50: 1708-1717.
- Mamun AA, Heim HP and Bledzki AK (2015) The use of maize, oat, barley and rye fibres as reinforcements in composites. In: Faruk O and Sain M (eds), Biofiber Reinforcements in Composite Materials. Woodhead Publishing, pp. 454-487. doi: 10.1533/9781782421276.4.454
- Marta H, Suryadi E and Ruswandi D (2017) Chemical composition and genetics of Indonesian maize hybrids. American Journal of Food Technology 12: 116-123.
- Masindeni DR (2013) Evaluation of South African high quality protein maize (*Zea mays* L.) inbred lines under optimum and low nitrogen conditions and the identification of suitable donor parents. PhD Thesis in Plant Breeding, University of the Free State, South Africa.
- Mathur PN and Mathuw JR (1986) Combining ability for yield, protein, lysine and tryptophan in pearl millet (*Pennisetum americanum* L.). Field Crops Research 15: 181-189.

- Mbuya K, Nkongolo KK and Kalonji-Mbuyi A (2011) Nutritional analysis of quality protein maize varieties selected for agronomic characteristics in a breeding program. *International Journal of Plant Breeding and Genetics* 5: 317-327.
- Menkir A, White WS, Maziya-Dixon B, Rocheford T and Weiping L (2008) Carotenoid diversity in tropical adapted yellow maize inbred lines. *Food Chemistry* 109: 521-529.
- Mertz ET, Bates ET and Nelson OE (1964) Mutant genes that change protein composition and increase lysine content of maize endosperm. *Science* 145: 279-280.
- Mpofu IDT, Sibanda S, Shonihwa A and Pixley K (2012) The nutritional value of quality protein maize for weaner pigs. *Journal of Petroleum and Environmental Biotechnology* 3: 1-4. doi: 10.4172/2157-7463.1000129
- Nehe A, Akin B, Sanal T, Evlice AK, Unsal R, Dincer N, Demir L, Geren H, Sevim I, Orhan S, Yaktubay S, Ezici A, Guzman C and Morgounov A (2019) Genotype x environment interaction and genetic gain for grain yield and grain quality traits in Turkish spring wheat released between 1964 and 2010. *PLoS ONE* 14: 1-18. e0219432. <https://doi.org/10.1371/journal.pone.0219432>
- Njeri SG, Makumbi D, Warburton ML, Diallo A, Jumbo MDB and Chemining'wa G (2017) Genetic analysis of tropical quality protein maize (*Zea mays* L.) germplasm. *Euphytica* 213: 1-19. doi 10.1007/s10681-017-2048-4
- Nurit E, Tiessen A, Pixley K and Palacios-Rojas N (2009) Reliable and inexpensive colorimetric method for determining protein-bound tryptophan in maize kernels. *Journal of Agricultural and Food Chemistry* 57: 7233-7238.
- Nuss ET and Tanumihardjo SA (2011) Quality protein maize for Africa: Closing the protein inadequacy gap in vulnerable populations. *Advances in Nutrition* 2: 217-224.
- Paulsen MR and Singh M (2004) Calibration of a near-infrared transmission grain analyzer for extractable starch in maize. *Biosystems Engineering* 89: 79-83.
- Pixley K V and Bjarnason MS (1993) Combining ability for yield and protein quality among modified-endosperm *opaque-2* tropical maize inbreds. *Crop Science* 33: 1229-1234.
- Prasanna BM, Vasal SK, Kassahun B and Singh NN (2001) Quality Protein Maize. *Current Science* 81: 1308-1319.
- Premlatha M and Kalamani A (2010) Heterosis and combining ability studies for grain yield and growth characters in maize (*Zea Mays* L.). *Indian Journal of Agricultural Research* 44: 62-65.

- Sarika K, Hossain F, Muthusamy V, Zunjare RU, Baveja A, Goswami R, Bhat JS, Saha S and Gupta HS (2018) Marker-assisted pyramiding of *opaque2* and novel *opaque16* genes for further enrichment of lysine and tryptophan in sub-tropical maize. *Plant Science* 272: 142-152.
- Sarika K, Hossain F, Muthusamy V, Zunjare RU, Baveja A, Goswami R, Bhat JS, Saha S and Gupta HS (2018) Marker-assisted pyramiding of *opaque2* and novel *opaque16* genes for further enrichment of lysine and tryptophan in sub-tropical maize. *Plant Science* 272:142-152.
- Sharma S and Carena MJ (2016) Grain quality in maize (*Zea mays* L.): breeding implications for short-season drought environments. *Euphytica* 212: 247-260.
- Singh AA, Agrawal SB, Shahi JP and Agrawal M (2019) Yield and kernel nutritional quality in normal maize and quality protein maize cultivars exposed to ozone. *Journal of the Science of Food and Agriculture* 99: 2205-2214.
- Synrem GJ, Marker S and Ramteke PW (2017) Gene action and combining ability analysis for grain yield and quality parameters in sub-tropical maize (*Zea mays* L.). *Vegetos* 30: 139-147.
- Tandzi LN, Mutengwa CS, Ngonkew ELM, Woïin N and Gracen V (2017) Breeding for quality protein maize (QPM) varieties: a review. *Agronomy* 7: 1-16.
- Teklewold A, Wegary D, Tadesse A, Tadesse B, Bantte K, Friesen D and Prasanna BM (2015) Quality protein (QPM) maize: a guide to the technology and its promotion in Ethiopia. CIMMYT, Addis Ababa, Ethiopia.
- Tilahun B, Azimach G, Keno T, Chibsa T, Garoma B, Abebe B, Tulu D, Tafa Z and Chalchisa D (2018) Test cross performance and combining ability of newly introduced quality protein maize (*Zea mays* L.) inbred lines for grain yield and agronomic traits evaluated in mid-altitude agro-ecological zones of Ethiopia. *South African Journal of Plant and Soil* 36: 173-180.
- Twumasi-Afriye S, Rojas PN, Friesen D, Teklewold A, Gissa DW, De Groote H and Prasanna BM (2016) Guidelines for the quality control of Quality Protein Maize (QPM) seed and grain. CIMMYT, Addis Ababa, Ethiopia.
- Vanous A, Gardner C, Blanco M, Martin-Schwarze A, Wang J, Li X, Lipka AE, Flint-Garcia, S, Bohn M, Edwards J and Lübberstedt T (2019) Stability analysis of kernel quality traits in exotic-derived doubled haploid maize lines. *Plant Genome* 12: 1-14.

- Wegary D, Labuschagne MT and Vivek BS (2011) Protein quality and endosperm modification of quality protein maize (*Zea mays* L.) under two contrasting soil nitrogen environments. *Field Crops Research* 121: 408-415.
- Wegary D, Vivek B and Labuschagne M (2013) Association of parental genetic distance with heterosis and specific combining ability in quality protein maize. *Euphytica* 191: 205-216.
- Wegary D, Vivek BS and Labuschagne MT (2014) Combining ability of certain agronomic traits in quality protein maize under stress and nonstress environments in Eastern and Southern Africa. *Crop Science* 54: 1004-1014.
- Williams PJ and Kucheryavskiy S (2016) Classification of maize kernels using NIR hyperspectral imaging. *Food Chemistry* 209:131-138.
- Zhang J, Lu XQ, Song XF, Yan JB, Song TM, Dai JR, Rocheford, T and Li JS (2008) Mapping quantitative trait loci for oil, starch, and protein concentrations in grain with high-oil maize by SSR markers. *Euphytica* 162: 335-344.
- Zilic S, Milasinovic M, Terzic D, Barac M and Ignjatovic-Micic D (2011) Características y composición del grano de híbridos de maíz de especialidad. *Spanish Journal of Agricultural Research* 9: 230-241.
- Zimmerman AO, Millear AI, Stubbs RW, Shields C, Pickering BV, Earl L, Graetz N , Kinyoki DK, Ray SE, Bhatt S, Browne AJ, Burstein R, Cameron E, Casey DC, Deshpande A, Fullman N, Gething PW, Gibson RS, Henry NJ, Herrero M, Krause LK, Letourneau ID, Levine AJ, Liu PY, Longbottom J, Mayala BK, Mosser JF, Noor AM, Pigott AM, Piwoz EG, Rao P, Rawat R, Reiner Jr RC, Smith DL, Weiss DJ, Wiens KE, Mokdad AH, Lim SS, Murray CJL, Kassebaum NJ and Hay SI (2018) Mapping child growth failure in Africa between 2000 and 2015. *Nature* 555: 41-47.
- Živanović T, Vuckovic S, Prodanovic S and Todorovic G (2006) Evaluation of inbred lines as sources of new alleles for improving elite maize hybrid. *Cereal Research Communications* 34: 941-948.

CHAPTER SEVEN

HERITABILITY AND TRAIT ASSOCIATIONS IN QUALITY AND NON-QUALITY PROTEIN MAIZE GENOTYPES

7.1 Abstract

Exploitation of variance components, correlations and path analysis can be useful to the plant breeder in making informed decision on traits to be considered in breeding for high grain yield and enhanced quality traits in maize breeding programmes. This study was conducted to i) estimate the heritability of grain yield and its related characters as well as quality traits ii) estimate the heterosis of the hybrids for the measured traits and iii) determine the association among grain yield, agronomic and quality traits and. Data was obtained from field and laboratory experiments for grain yield and agronomic characters across 13 locations and for quality traits across six locations. Genotypic variance was larger than the environmental variance for grain yield and a majority of the agronomic traits and all the quality traits analysed in the study. Broad sense heritability estimates were more than 80% for the traits measured. Apart from mid parent (MPH) and better parent (BPH) heterosis for tryptophan, of which a majority of the hybrids were inferior to their parents, most hybrids displayed vigour over their parents for grain yield, as high as 268.75% and 799.76% for MPH and BHP, respectively. The first four principal components accounted for more than 90% of the variations for grain yield and agronomic and quality traits, and combinations of traits. The study revealed significant genotypic and phenotypic correlations for grain yield vs. plant height ($r_G = 0.41$; $r_P = 0.34$), grain yield vs. ears per plant ($r_G = 0.24$; $r_P = 0.24$), grain yield vs. protein ($r_G = 0.38$; $r_P = 0.25$) and tryptophan vs. oil content ($r_G = 0.58$; $r_P = 0.25$). Negative r_G and r_P correlations were recorded for grain yield vs. ear aspect, protein vs. tryptophan and grain yield vs. tryptophan. Path analysis identified ear aspect, ears per plant and starch as the major traits contributing to grain yield. It is recommended that ear aspect should be considered a key secondary trait in breeding for QPM hybrids. Furthermore, with the negative association between grain yield and tryptophan; as well as protein and tryptophan, it might be possible that gene stacking for grain yield and tryptophan might lead to development of hybrids with high grain yield at the same time with increased tryptophan content.

Keywords: Path coefficient analysis, variance components, heterosis, principal components

7.2 Introduction

Heritability and heterosis of traits are some of the important components considered in breeding superior hybrids. Combinability is far more important than heritability in breeding superior hybrids. Heterosis, or hybrid vigour, is the increased performance of the F_1 individuals obtained from crossing two genetically diverse breeding lines (Duvick and Brown 1981). Mather and Jinks (1971) and de Franca (1983) defined heterosis as the extent to which the average of any F_1 generation performs better than its better parent, or an average of its parents. However commercially, performance of a hybrid compared to a commercial check hybrid is important since farmers do not grow inbreds and require new hybrids better than their current ones. The two main theories used to elucidate the manifestation of heterosis are: (i) the dominance theory proposed by Lee and Tracy (2009) and Ram (2014) who stated that the recessive and deleterious alleles present in the parental lines are transferred to the F_1 progeny and subsequent generations. In this model, additive genetic effects of favourable genes increase the superior phenotype of the F_1 over each parent and (ii) the overdominance theory of Shull (1911), East and Hays (1912) and Ram (2014), which states that heterosis is a result of heterozygosity or the fitness of heterozygotes over their homozygous parents. According to this model, novel alleles are interchanged between contrasting parents with differing alleles and this results in expression of superiority of the F_1 's to the homozygous parents. It is important to note that, epistasis influences heterosis of hybrids, however, this is often neglected in genetic analysis and also not estimated statistically probably due to the interactive nature of genes at different loci (Kaeppler 2012; Kerwin et al. 2017). Hence, it is important to consider epistasis when selecting superior hybrids.

Even though the importance of heterosis in maize production has been reported, the inherent mechanisms and most importantly, the physiological and biochemical mechanisms of these phenomena are yet to be fully elucidated (Blum 2013). Even though the expression of superiority of hybrids over their parents is based on how diverse the two parents are, this is often not replicated. For example inbreds B73 and Mo17 which produced one of the most successful hybrids in the USA are fairly closely related (Personal communication: Vernon Gracen). Hence, two parental lines which manifest relatively large

magnitudes of heterosis in their crosses can be said to combine well specifically. In maize, it is estimated that heterosis above 10% of the best hybrid over the best commercial check is usually accepted (Lippman and Zamir, 2006; Chairi et al. 2016). In studies by Saleh et al. (2002) and Ram (2014) high levels of hybrid vigour for grain yield, grain weight per ear and cob weight were observed, while heterosis above 10% was obtained in normal endosperm maize for plant and ear heights, number of kernel rows per ear as well as number of kernels per ear row. Nigussie and Zelleke (2001) noted that hybridizing maize genotypes obtained from dissimilar genetic backgrounds often resulted in better expression of hybrid vigour.

In most breeding programmes, increased yield is the primary objective. As a result of interactions between genotype and the environment, the full expression of grain yield and other traits, which are quantitatively inherited, are variable under varying environmental conditions (Qi et al. 2010; Gangashetty et al. 2016). For selection of grain yield and quality traits to be efficient, it is important to consider traits that contribute to yield and quality. The polygenic nature of grain yield often leads to variability across varied environmental conditions (Machikowa and Laosuwan 2011; Wegary et al. 2013). Subsequently, grain yield and quality traits enhancement in maize can be realised via utilisation of the association between grain yield, quality traits and their associated characters (Amini et al. 2013; Adesoji et al. 2015). Correlations have been exploited in several studies for indirect selection of yield and quality traits (Amini et al. 2013; Adesoji et al. 2015; Muturi et al. 2019).

Information on correlations between traits is crucial in maize breeding to aid in the identification of superior genotypes with higher grain yield through indirect selection achieved via selection of secondary traits (Meseke et al. 2013; Matthew 2015). However, it is important to note that correlations among traits are not adequate to describe the significance of each character contributing to grain yield (Sreckov et al. 2011; Matthew 2015). Bizeti et al. (2004) further noted that these inadequacies often lead to observed dissimilarities that are due to more than one indirect cause. As a result, it is important to conduct in-depth studies on trait associations to fully understand the contribution of each character and then rank their importance for targeting selection. One of the ways of achieving this is to use the path coefficient analysis to assess direct and indirect relationship among traits (Udensi and Ikpeme 2012; Adesoji et al. 2015). There is not enough

information reported on the association between grain yield, agronomic characters and quality traits. Therefore, the objectives of this study were to: (i) estimate the heritability of grain yield, its related characters and quality traits, (ii) estimate the heterosis of the hybrids for the traits measured and, (iii) determine the association among grain yield, agronomic and quality traits.

7.3 Materials and methods

7.3.1 Genetic materials

The hybrids evaluated as reported in Chapter 4 (4.3.1) for agronomic traits and Chapter 5 (5.3.1) for quality traits performance and genetic analysis were used in this chapter.

7.3.2 Heritability estimates

Broad sense heritability estimates (H^2) of each trait across environments was computed as follows:

$$H^2 = \sigma_g^2 / \sigma_p^2$$

Where here σ_g^2 = genotypic variance; and σ_p^2 = phenotypic variance. The σ_p^2 was computed as follows:

$$\sigma_p^2 = \sigma_g^2 + \sigma_{gl}^2/l + \sigma_{gt}^2/t + \sigma_{glt}^2/lt + \sigma_e^2/rlt;$$

Where σ_{gl}^2 = genotype $\times$ location interaction variance, σ_{gt}^2 = genotype $\times$ treatment interaction variance, σ_{glt}^2 = genotype $\times$ location $\times$ treatment interaction variance, σ_e^2 = environmental variance, r = no. of replications; l = no. of locations and t = no. of treatments.

Narrow sense heritability (h^2) was computed as follows:

$$h^2 = \sigma_a^2 / \sigma_p^2$$

Where σ_a^2 = additive genetic variance.

7.3.3 Heterosis

7.3.3.1 Mid-parent heterosis

The mid-parent values for grain yield, agronomic characters and quality traits analysed was calculated as the average of the two parents for the agronomic and quality traits across all locations. Mid-parent heterosis (MPH) was calculated as:

$$\text{MPH} = \frac{(F_1 - \text{MP})}{\text{MP}} \times 100$$

Where F_1 is the mean of the F_1 hybrid performance and $\text{MP} = (P_1 + P_2)/2$ in which P_1 and P_2 are the respective means of the inbred parents.

7.3.3.2 Better-parent heterosis

Better-parent heterosis (BPH) was computed as the percentage increase or decrease demonstrated by the F_1 hybrids over better parents as:

$$\text{BPH} = \frac{(F_1 - \text{better parent})}{\text{Better parent}} \times 100$$

7.3.4 Principal component analysis

GenStat 20th edition statistical software (GenStat 2019) was used for the PCA to obtain the Eigenvalues and PC biplot of the traits measured.

7.3.5 Genetic and phenotypic correlation estimations

The raw data obtained for both agronomic and quality traits used to estimate genetic (r_G) and phenotypic (r_P) correlations using META-R (Multi Environment Trial Analysis with R for Windows) Version 6.04 (Alvarado et al. 2015) used the procedure:

$$\text{Genotypic correlation } (r_G) = C_{AXY}/(V_{AX}V_{AY})^{1/2}$$

Where C_{AXY} = additive covariance between characteristic X and Y; V_{AX} = additive variance of characteristic X, and V_{AY} = additive variance of characteristic Y

$$\text{Phenotypic correlation } (r_P) = \text{Cov}_{XY}/(\sigma_X^2\sigma_Y^2)$$

Where Cov_{XY} = phenotypic covariance between characteristic X and Y; σ_X^2 = phenotypic variance of characteristic X, and σ_Y^2 = phenotypic variance of characteristic Y.

7.3.6 Path coefficient analysis

The coefficient values estimated were used to do the path analysis to determine direct and indirect relationships among the variables measured and analysed for agronomic and quality traits, respectively. Independent variables were regressed on the dependent variables. Grain yield was used as the independent variable for agronomic and quality traits combined. The path coefficient analysis was conducted following (Yu et al. 2019):

$$Y = \beta_0 + \beta_1 X_m + \beta_2 X + \varepsilon_1$$

$$X_m = \gamma_0 + \gamma_1 X + \varepsilon_2$$

where, Y denotes the dependent variable; X_m is the mediator in dependent variable; X is the exogenous independent variable matrix; ε_1 and ε_2 are the errors; β_0 and γ_0 are the intercepts; β_1 , β_2 , and γ_1 are the regression coefficients to be estimated.

The predictable coefficient values β_1 , β_2 and γ_1 were used to calculate the impacts of independent variables on dependent variables, where β_2 represents the direct effect of X on Y and the magnitude of the indirect effect of X on Y estimated by $\gamma_1\beta_1$.

7.4 Results

7.4.1 Variance components and heritability for grain yield, agronomic characters and quality traits

The estimates of genotypic variance and its related mechanisms, heritability of grain yield, agronomic characters and quality traits are shown in Table 7.1. Estimates of tester variance was higher than line variance for anthesis-silking interval, plant and ear heights, grain yield and stalk lodging, while line variance was higher for ear rot, husk cover, days to anthesis and root lodging, but values were generally low. Genetic variance was larger for estimates of grain yield, plant and ear heights, ear per plant, ear aspect, ear rot and days to pollen shed than environmental variance. The environmental variance on the other hand was higher for anthesis-silking interval, husk cover and root and stalk lodgings. Broad sense heritability (H^2) estimates for the traits measured were generally higher than 80% (Table 7.1).

For the quality traits studied, the estimates of tester variance was high for tryptophan, protein and fibre while line variance was also high for moisture, oil content and starch. Genetic variances were relatively low for tryptophan, moisture and oil content but relatively high for protein and starch contents. The genotypic variances were higher than the environmental variance for all the traits analysed. Furthermore, additive variances were larger than dominance variances for tryptophan, oil content, moisture, fibre, starch and protein. Broad sense heritability (H^2) estimates were high (above 90%) for all the quality traits analysed in this study (Table 7.1).

7.4.2 Heterosis for grain yield and its secondary traits and quality traits

From the present study, estimates for heterosis were positive for MPH and BPH for grain yield for all the hybrids evaluated except for hybrid 70. Heterosis over the better parent was higher than the MPH for grain yield, and most of the agronomic characters measured. For the agronomic traits, all the hybrids exhibited superiority over their parents, suggesting presence of substantial heterosis of the crosses and the potential of these parents for hybrid development (Table 7.2). For ears per plant, some of the hybrids recorded negative values. All the hybrids showed superiority of BPH for anthesis-silking interval and ear aspect over the parents except hybrid 70.

Estimates of heterosis for quality traits revealed that most of the hybrids performed poorly against their parents, especially for tryptophan, except for a few hybrids such 120, 104, 105 and 121. Apart from hybrids 109 and 37 with negative values of MPH for starch, the rest of the 35 hybrids shown were superior to their mid- and better parents for protein, oil content and starch (Table 7.3). MPH and BPH values for fibre indicated that the hybrids have lower fibre content than their parents by recording negative values, except for hybrids 37 and 61.

Table 7.1 Estimates of variance components and heritability for grain yield, agronomic and quality traits of 130 crosses evaluated across 13 during 2017/2018 and 2018/2019 cropping seasons

Variance components	Agronomic traits										
	ASI	EH	EPP	ER	EA	GY	HC	PH	DA	RL	SL
Line Variance	0.002	56.023	0.001	5.324	0.004	0.025	0.117	54.170	3.720	3.057	1.208
Tester Variance	0.020	67.955	0.001	2.651	0.006	0.176	0.000	54.733	2.535	0.000	1.645
Line x Tester Variance	0.024	24.043	0.003	0.741	0.017	0.430	0.029	52.729	0.682	0.000	0.457
Genotype Variance	0.042	130.616	0.005	7.872	0.025	0.580	0.147	147.695	6.290	2.896	2.867
Additive Variance	0.167	522.463	0.019	31.488	0.101	2.319	0.590	590.780	25.159	11.584	11.467
Dominance Variance	0.097	96.171	0.012	2.964	0.068	1.720	0.116	210.918	2.728	0.000	1.827
Environmental Variance	0.045	6.608	0.001	7.042	0.010	0.131	0.265	9.282	0.235	7.024	4.656
Broad sense heritability (%)	0.854	0.989	0.955	0.830	0.946	0.969	0.727	0.989	0.992	0.623	0.741
Narrow sense heritability (%)	0.541	0.836	0.578	0.759	0.563	0.556	0.608	0.728	0.895	0.623	0.639
	Quality traits										
	Fibre	Moisture	Oil	Protein	Starch	Tryptophan					
Line Variance	0.005	0.132	0.133	0.133	0.305	0.00000					
Tester Variance	0.011	0.059	0.089	0.188	0.195	0.00033					
Line x Tester Variance	0.005	0.128	0.014	0.069	0.099	0.00001					
Genotype Variance	0.018	0.298	0.212	0.344	0.547	0.00026					
Additive Variance	0.074	1.191	0.849	1.375	2.187	0.00102					
Dominance Variance	0.019	0.513	0.056	0.274	0.394	0.00003					
Environmental Variance	0.002	0.236	0.044	0.063	0.152	0.00002					
Broad sense heritability (%)	0.978	0.878	0.954	0.963	0.944	0.98280					
Narrow sense heritability (%)	0.777	0.614	0.895	0.803	0.800	0.95646					

† GY=grain yield; DA = days to anthesis; ASI = anthesis-silking interval; PH = plant height; EH = ear height; EA = ear aspect; RL = root lodging; SL = stock lodging; HC = husk cover; EPP = ear per plant.

Table 7.2 Mid-parent (MPH%) and better parent (BPH%) heterosis for grain yield and selected secondary traits of the 15 top performing, 10 middle and 10 poorest performing genotypes selected from the 130 crosses evaluated across 13 location during 2017/2018 and 2018/2019 cropping seasons

Entry	Grain yield		ASI		Ears per plant		Ear rot		Ear aspect	
	MPH (%)	BPH (%)	MPH (%)	BPH (%)	MPH (%)	BPH (%)	MPH (%)	BPH (%)	MPH (%)	BPH (%)
111	268.75	131.90	821.43	-170.20	7.22	16.36	246.28	126.92	11.67	-7.48
109	281.62	146.28	412.07	-256.06	12.18	40.87	376.44	229.51	5.64	-13.68
48	187.65	130.81	-30.03	-51.57	16.77	34.51	70.11	66.84	-5.24	-13.21
36	199.08	146.66	-55.17	-39.98	14.67	20.16	95.71	70.23	-10.33	-19.68
60	206.21	123.61	-44.16	-44.84	0.88	2.84	150.66	141.76	-19.06	-29.88
110	240.91	109.55	-229.66	-280.20	-0.26	12.77	457.79	285.77	7.84	-11.40
39	177.65	111.42	171.70	-339.47	-10.65	-11.44	112.73	75.10	-20.56	-28.34
59	214.54	121.72	375.39	-361.87	-8.67	-6.96	194.81	176.03	-20.72	-30.69
79	256.15	152.74	-40.05	-52.83	13.14	14.83	308.89	215.01	-13.73	-24.49
103	192.99	132.08	-2.61	-13.54	3.37	7.38	144.30	93.70	-12.54	-24.31
75	150.40	89.91	42.34	-382.26	-4.26	2.09	99.35	49.88	-12.36	-16.56
37	230.77	164.97	-29.08	-36.62	-7.66	-2.17	155.97	162.61	-16.90	-21.74
30	213.37	128.34	-85.70	-90.06	5.71	19.80	218.97	183.63	-16.89	-28.40
127	147.64	105.35	-35.04	-49.79	9.85	15.22	73.04	63.54	-12.79	-16.98
31	222.04	119.13	1080.7	-170.04	-4.27	-1.54	270.67	229.60	-19.77	-31.29
69	111.50	123.42	-63.88	114.82	5.66	20.30	221.28	143.12	-4.59	-11.03
52	161.21	163.46	4.62	29.50	8.61	17.58	233.21	215.98	-0.91	-4.86
3	94.88	72.24	135.70	-265.79	-23.41	-7.89	183.66	109.89	-0.67	-7.61
77	181.41	101.15	-68.56	-68.86	-8.64	-8.18	371.12	303.66	-16.57	-23.13
57	178.26	104.78	-21.88	-37.54	-3.25	-0.38	357.01	289.38	-11.94	-19.75
62	71.11	74.09	29.54	-764.98	-10.38	-0.01	130.53	101.79	9.43	3.94
80	130.31	112.48	-34.74	-44.83	-7.53	-1.12	211.00	204.64	-9.28	-16.20
18	135.59	152.48	-20.44	-23.28	16.66	25.21	292.27	188.63	-11.32	-19.19
8	163.47	158.04	-85.92	-86.04	-1.57	24.71	267.07	227.47	-4.48	-12.03
124	124.64	65.71	-56.33	-59.10	14.28	27.52	289.60	266.50	-4.48	-10.75
7	95.16	80.84	80.04	-191.55	-14.93	3.08	399.99	308.93	-3.81	-10.53
83	145.60	123.66	-26.87	-32.49	-6.61	-1.17	496.58	415.11	-11.76	-22.58
117	86.66	128.26	-28.18	-44.12	-0.60	1.64	405.94	377.32	9.01	8.82
56	168.73	166.42	-46.42	-52.56	-14.25	-4.26	541.52	445.69	-4.81	-11.21
53	136.30	137.13	-26.46	-35.34	-3.04	9.44	504.16	481.59	-4.00	-5.35
26	88.05	111.74	-28.64	-48.24	-27.45	-22.81	457.51	410.91	-5.57	-10.83
87	18.10	5.92	314.24	-147.93	4.95	17.59	407.53	379.48	16.14	9.80
27	98.14	96.63	-46.03	-244.52	-22.54	-8.94	491.98	442.50	-7.19	-12.93
63	61.11	46.33	-490.48	-1063.2	-8.52	-7.24	495.96	421.67	3.83	-2.03
70	-17.13	-24.73	153.03	1151.90	-39.60	-38.66	338.10	302.12	34.69	30.47

Table 7.3 Mid-parent (MPH%) and better parent (BPH%) heterosis for quality traits of the 15 top performing, 10 middle and 10 poorest performing genotypes selected from the 130 crosses evaluated across six location during 2017/2018 and 2018/2019 cropping seasons

Entry	Tryptophan		Protein		Oil		Starch		Fibre		Sum
	MPH %	BPH %	MPH %	BPH %	MPH %	BPH %	MPH %	BPH %	MPH %	BPH %	
120	23.35	66.00	15.53	18.50	11.36	58.73	3.26	3.95	-9.66	-13.38	200.68
104	22.38	97.37	7.02	22.31	11.92	37.72	0.66	0.46	-2.39	-5.05	199.83
105	35.14	102.63	-1.56	13.37	10.98	33.62	2.65	2.85	-10.88	-11.19	199.68
121	28.61	62.00	13.86	17.61	7.40	49.48	3.70	4.40	-13.11	-14.09	187.06
29	-5.52	-3.04	15.98	35.52	34.03	76.93	2.61	7.98	-5.29	-6.12	164.49
73	-2.99	65.71	12.94	28.23	7.96	40.10	0.58	1.02	-9.70	-12.11	153.56
74	-2.67	54.29	12.90	29.16	10.05	39.62	0.82	1.25	-10.26	-10.63	145.42
77	-23.70	27.78	22.36	42.57	19.14	52.14	1.15	2.68	-10.57	-15.05	144.12
30	-3.01	5.32	1.81	19.91	32.48	70.95	5.41	10.95	-7.22	-10.82	143.83
109	2.74	62.86	14.61	40.65	9.29	14.15	-1.02	0.18	-11.55	-13.51	143.46
108	-6.33	60.00	15.00	40.01	8.56	11.24	-0.65	0.55	-13.13	-13.90	128.38
57	5.03	6.02	13.50	26.69	16.48	40.10	4.05	11.19	-4.64	-3.84	123.06
80	-18.12	27.50	23.41	37.67	17.36	32.37	0.54	0.79	-5.59	-6.76	121.52
78	17.85	61.11	7.59	11.91	-3.77	10.30	4.68	5.69	-13.46	-15.13	115.36
2	6.70	8.11	27.19	35.40	11.68	20.18	1.88	2.60	-10.43	-14.41	113.74
101	2.63	4.01	14.85	19.01	2.13	7.16	3.74	4.48	-9.21	-10.43	58.00
27	-26.32	-18.31	18.55	35.19	15.95	29.02	0.32	1.90	-3.72	-8.34	56.30
124	-32.06	2.38	13.97	28.63	7.06	31.45	2.22	2.56	-1.00	-4.98	56.22
28	-26.15	-19.78	30.79	38.76	10.29	23.75	-1.03	-0.80	-13.75	-17.02	55.83
70	1.26	7.96	13.91	15.17	6.21	7.64	1.27	1.50	-8.12	-8.60	54.92
65	-7.04	-1.86	6.58	25.41	12.19	18.66	-0.33	1.06	-2.50	-8.42	54.67
99	-36.84	-27.49	22.07	28.13	27.68	38.89	0.41	1.73	-12.86	-16.97	54.58
62	1.96	4.01	11.64	15.16	0.91	13.78	2.55	3.28	-7.02	-8.87	53.29
66	-11.74	-1.26	2.31	21.33	16.71	21.08	1.47	2.90	-10.57	-13.44	52.80
119	-23.24	-2.38	19.63	24.96	13.38	20.20	-0.40	-0.33	-13.71	-15.67	51.82
47	-32.10	-24.72	16.11	7.04	3.04	10.09	4.34	5.52	-13.94	-14.48	-10.68
43	-34.51	-27.92	5.11	11.46	1.92	18.43	5.42	9.11	-8.16	-8.41	-10.99
71	-32.63	-19.91	5.69	17.39	1.31	7.82	3.84	4.19	-7.42	-7.76	-12.30
24	-35.82	-22.87	11.91	21.23	-3.68	4.48	3.17	6.36	-13.34	-15.63	-15.22
15	-34.00	-24.72	11.86	18.03	0.71	5.81	2.84	3.62	-2.63	-3.06	-15.85
39	-31.32	-16.71	-0.65	4.46	4.92	7.43	4.75	6.37	-7.43	-11.57	-20.75
67	-28.40	-10.30	-3.69	1.08	3.17	7.19	3.90	4.78	-5.16	-8.07	-22.28
64	-42.99	-36.75	19.10	20.80	3.75	8.92	1.11	1.18	-9.38	-11.99	-24.88
23	-40.04	-26.32	0.48	1.58	7.06	17.09	3.97	5.74	-6.07	-7.57	-30.44
19	-39.27	-37.53	4.39	4.91	6.99	19.41	2.99	4.47	-5.00	-6.32	-33.64

7.4.3 Principal component analysis

The agronomic traits for the hybrids showed that the first four principal components (PCs) explained 96.4% of the variation of the traits measured (Table 7.4). The first four PC were significant with PC1 accounting for 80.10% of the variation. The most important traits in PC1 were plant and ear height. The second, third and fourth PCs explained 6.90, 5.30 and 4.10% of the variations, respectively. The most important traits in these PCs were plant height for PC2 and ear rot and ear height for PC3. Root and stalk lodgings were the important traits located on the PC4.

Table 7.4 Estimates of principal component analysis for 135 QPM and non-QPM hybrids for grain yield and other agronomic traits

Traits	Eigenvectors			
	PC1	PC2	PC3	PC4
Grain yield	0.018	0.012	0.019	-0.021
Plant height	0.718	0.657	-0.211	-0.011
Ear height	0.682	-0.610	0.364	0.003
ASI	0.003	0.005	-0.014	0.019
Day to shed	0.095	-0.202	-0.058	-0.067
Root lodging	-0.001	0.111	0.199	0.893
Stalk lodging	0.002	-0.146	-0.191	0.427
Husk cover	-0.006	0.009	0.023	-0.007
Ears per plant	0.001	-0.002	0.000	-0.003
Ear rot	-0.105	0.347	0.861	-0.119
Ear aspect	-0.006	-0.001	0.008	-0.001
Eigenvalue	273.987	23.479	18.174	14.102
Proportion (%)	80.10	6.90	5.30	4.10
Cumulative (%)	80.10	87.00	92.30	96.40

PC = principal component

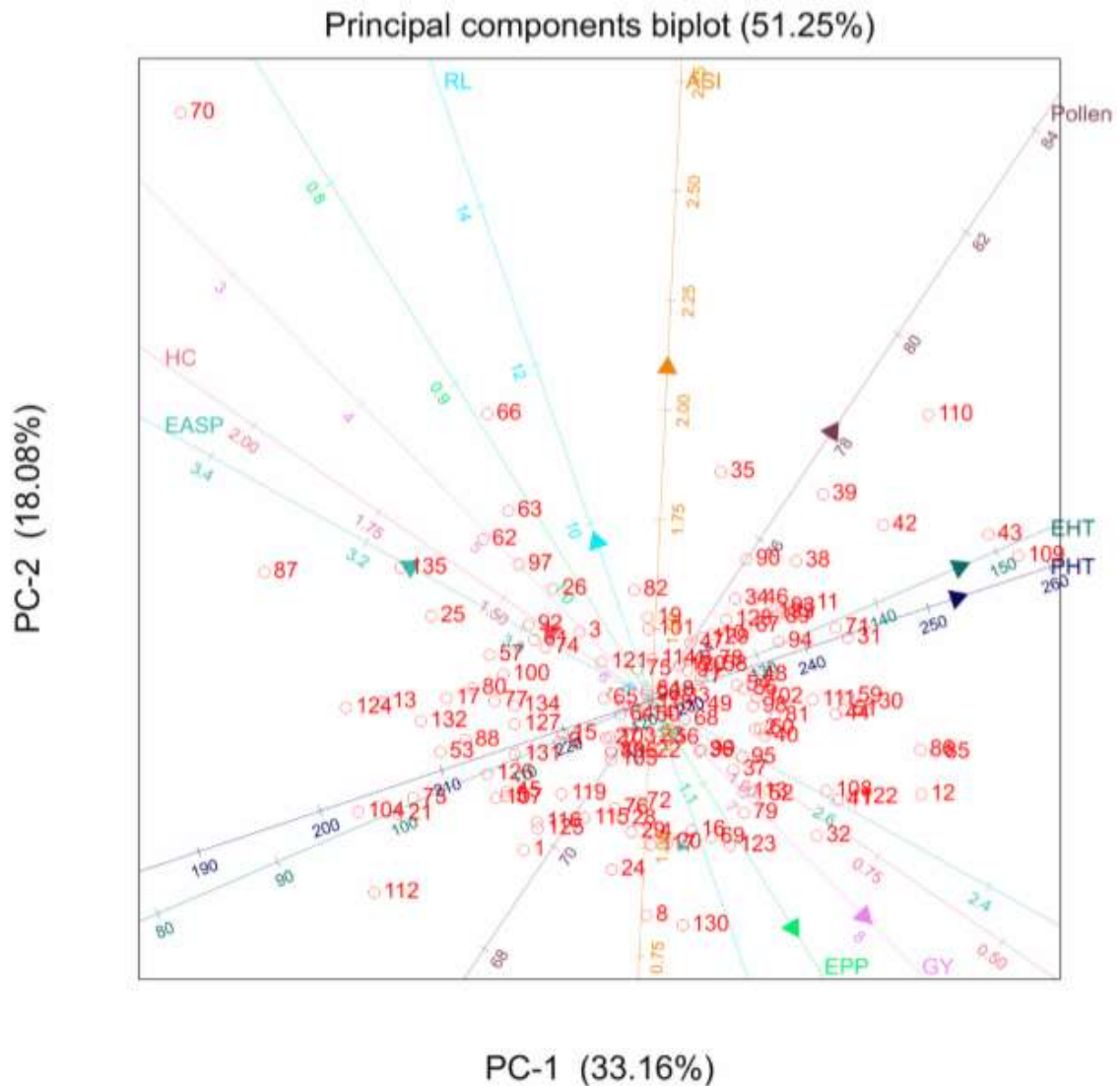


Figure 7.1 Principal component analysis biplot of genotype by grain yield and other agronomic traits of 135 QPM and non-QPM hybrids evaluated across 13 locations.

GY = Grain yield; EPP = ears per plant; PHT = plant height; EHT = ear height; EASP = ear aspect; HC = husk cover; SL = stalk lodging; RL = root lodging; ASI = anthesis-silking interval

The graphical view of the principal component analysis (PCA) biplot showed that the hybrids varied with regards to the agronomic traits measured. Genotypes 43 and 109 recorded high values for ear and plant height, respectively. Genotypes 123 and 69 were identified as the most prolific hybrids, while genotype 79 had higher grain yield. The angle forming between ears per plant and grain yield is less than 60° suggesting the strong correlation between the two traits. Similarly, ear and plant heights are strongly correlated

based on the angle between the traits. Grain yield and ear aspect are in directly opposite of one another, suggesting the negative correlation between the two traits (Figure 7.1).

The PCA conducted for quality traits showed that the first three PCs accounted for 99.70% of the total variation (Table 7.5). However, only the first three PCs were significant for the traits of which PC1 accounted for 63.70% of the variation and most important traits located on this axis were grain moisture and starch contents. The second PC explained 20.50% of the variation, with protein, oil content and starch as the most important traits on this axis, while the third PC explained 15.0% of the variation. The traits important on this PC were protein, oil and starch contents.

The PCA biplot for quality traits indicated significant variations among the hybrids for the quality traits analysed. Strong positive correlation was detected between fibre and tryptophan with hybrid 53 being the most superior genotype for these traits. Hybrid 42 was the best genotype for oil content. Protein and tryptophan were not positively correlated and similar observations were made between protein and oil content (Figure 7.2).

Table 7.5 Principal component analysis of 135 QPM and non-QPM hybrids for quality traits

Traits	Eigenvectors			
	PC1	PC2	PC3	PC4
Tryptophan	0.002	-0.003	-0.011	-0.002
Moisture	0.982	-0.065	0.157	0.077
Protein	-0.048	0.811	0.534	0.205
Oil	0.048	0.185	-0.602	0.756
Starch	-0.172	-0.551	0.568	0.557
Fibre	0.030	-0.026	-0.063	-0.266
Eigenvalue	3.562	1.149	0.837	0.029
Proportion (%)	63.663	20.540	14.961	0.521
Cumulative (%)	63.66	84.20	99.16	99.68
Principal component				

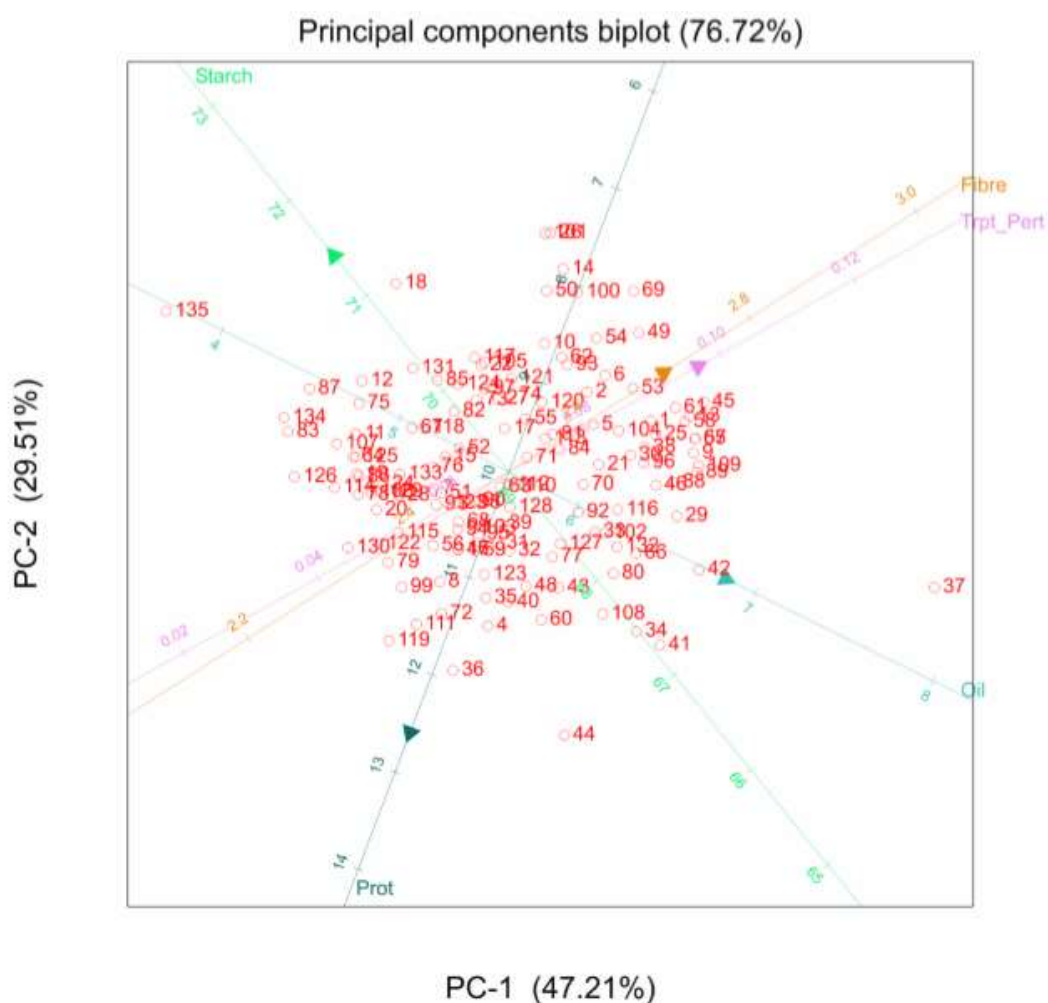


Figure 7.2 Principal component analysis biplot of genotype by quality traits of 135 QPM and non-QPM hybrids evaluated across six locations.

Trypt_pert = tryptophan; prot = protein

When the agronomic traits were combined with the quality traits, six significant PCs were identified and these explained 98.40% of the variation for the measured traits (Table 7.6). The first PC explained 78.80% of the variation and the traits located on this PC were ear height and ear rot. PC2 accounted for 6.80% of the variation and the traits contributing through PC2 were plant and ear height, and ear rot. The third and fourth PCs accounted for 5.3 and 4.10% of variation, respectively. The essential traits found on these PCs were ear height and ear rot for PC3, and ear rot, root and stalk lodgings for PC4 (Table 7.6).

The agronomic data set and the data obtained from quality traits were combined to observe the associations between these traits. Most of the traits taken from the agronomic data set

were clustered together showing positive correlations when combined with quality traits and similar observation was also made for quality traits. Some of the agronomic traits showing positive correlations were grain yield, plant height, ear height and ear per plant with angles among them less than 90°. However, oil content was highly correlated with anthesis-silking interval with an angle less than 45° between the two traits. Tryptophan content also showed a highly positive correlation with stalk lodging (Figure 7.3).

Table 7.6 Principal component analysis of 135 QPM and non-QPM hybrids for grain yield, agronomic and quality traits

	Eigenvectors					
	PC1	PC2	PC3	PC4	PC5	PC6
Grain yield	0.018	0.013	0.020	-0.020	-0.002	0.215
Plant height	0.718	0.657	-0.211	-0.014	0.068	-0.040
Ear height	0.681	-0.609	0.365	0.007	-0.038	0.069
ASI	0.003	0.005	-0.014	0.019	0.006	0.010
Days to anthesis	0.095	-0.201	-0.059	-0.065	0.108	-0.266
Root lodging	-0.001	0.112	0.194	0.892	-0.363	-0.027
Stalk lodging	0.002	-0.144	-0.195	0.429	0.849	-0.041
Husk cover	-0.006	0.010	0.023	-0.007	0.034	0.024
Ears per plant	0.001	-0.002	0.000	-0.003	0.005	0.002
Ear rot	-0.105	0.348	0.859	-0.112	0.317	-0.096
Ear aspect	-0.006	-0.001	0.008	-0.001	-0.002	-0.034
Tryptophan	0.000	0.001	-0.001	0.001	0.001	0.000
Moisture	-0.010	0.043	0.031	0.014	0.107	0.912
Protein	0.007	-0.010	0.046	-0.017	-0.128	0.045
Oil	0.006	0.010	-0.026	0.030	0.010	0.022
Starch	-0.007	-0.014	0.021	-0.024	0.016	-0.171
Fibre	-0.002	0.009	-0.004	0.003	0.006	0.019
Eigenvalue	274.053	23.527	18.247	14.127	8.378	3.628
Proportion (%)	78.80	6.800	5.30	4.10	2.40	1.00
Cumulative (%)	78.80	85.60	90.80	94.90	97.30	98.40

PC = Principal component

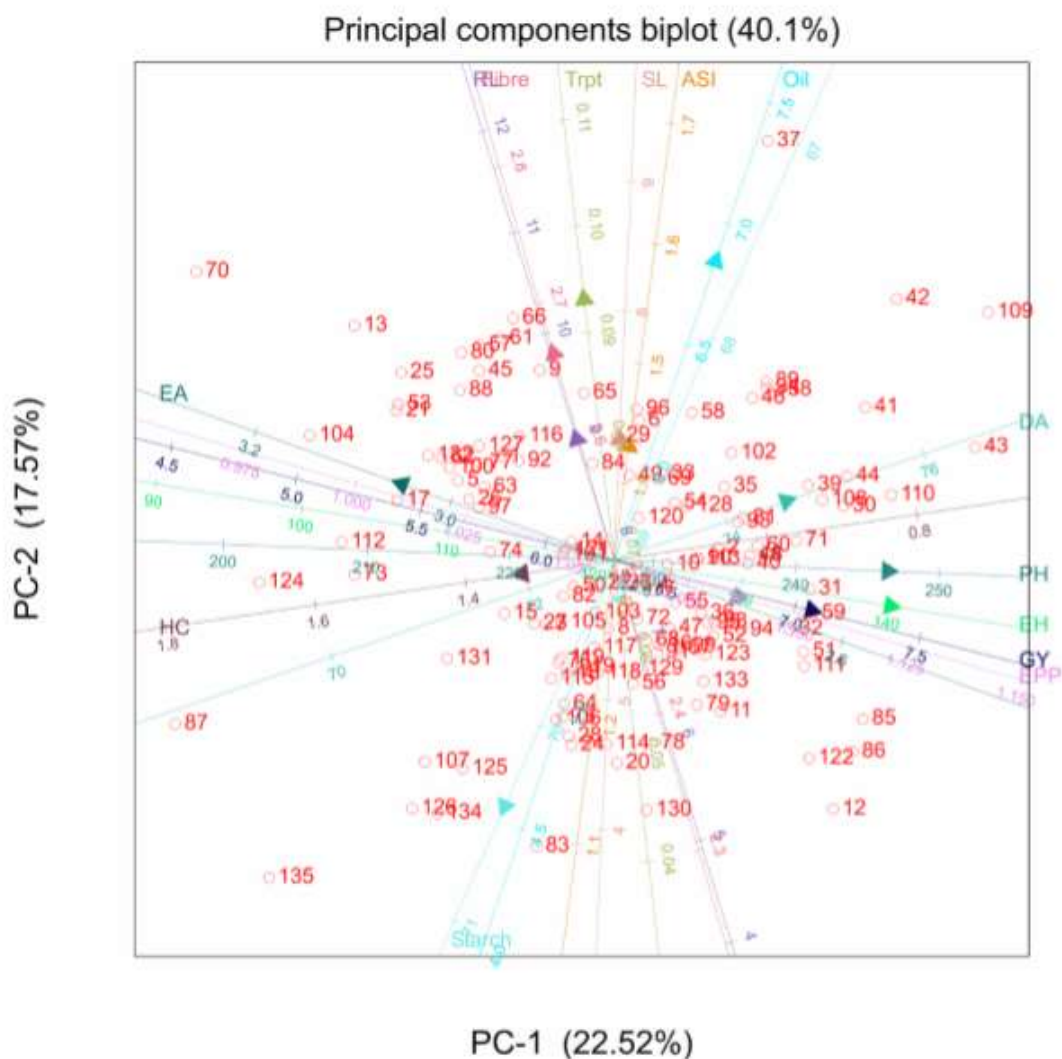


Figure 7.3 Combined principal component analysis biplot of 135 genotypes by grain yield, agronomic and quality traits.

GY = grain yield; EPP = ears per plant; PHT = plant height; EHT = ear height; EASP = ear aspect; HC = husk cover; SL = stalk lodging; RL = root lodging; ASI = anthesis-silking interval; Trypt_pert = tryptophan; prot = protein.

7.4.4 Genotypic and phenotypic correlation between grain yield and other agronomic traits of 135 QPM and non-QPM hybrids evaluated across 13 locations during the 2017/2018 and 2018/2019 cropping seasons

The estimates for genotypic and phenotypic correlations are presented in Table 7.7. For genotypic correlation, grain yield was significantly and positively correlated with plant height, ear height, ear rot and ears per plant while it was negatively correlated with husk cover, stalk lodging and ear aspect. Ears per plant were also found to be positively and significantly correlated with plant and ear height but negatively with anthesis-silking

interval, root lodging and husk cover. Ear aspect was significantly and positively correlated with husk cover and negatively correlated with plant and ear height, stalk lodging and husk cover. However, no significant correlation was observed between grain yield and days to pollen shed and grain yield vs. anthesis-silking interval. Similar to the genotypic correlation for the agronomic traits, grain yield was significantly and positively correlated with plant height, ear height and ears per plant phenotypically. Grain yield showed negative and significant phenotypic correlation with ear aspect ($r_p = -0.61$) and also showed negative correlation with stalk lodging and husk cover (Table 7.7).

For the genotypic correlation, tryptophan content showed significant positive association with moisture, oil and fibre contents but strong negative correlation with protein and starch contents. Protein had a significant and negative relationship with fibre and starch but correlated poorly with oil. Oil content showed a strong positive correlation with fibre and also a highly negative relation with starch ($r_G = -0.78$) (Table 7.8). For the phenotypic relationships among the quality traits analysed, tryptophan exhibited positive correlation with oil content and fibre but did not correlate with moisture, while a significant negative correlation was recorded between tryptophan and protein ($r_p = -0.559$) and tryptophan and starch ($r_p = -0.299$). Protein showed a negative and significant relationships with all the quality traits analysed at phenotypic level, except for oil content (Table 7.8). Oil content showed a negative correlation with starch but positively correlated with starch, while fibre exhibited a negative relationship with starch.

The genotypic relationship between agronomic and quality traits examined showed that grain yield had positive association with moisture and protein content but negatively with protein and starch contents (Table 7.9).

Table 7.7 Phenotypic correlation (r_P) above diagonal and genotypic correlation (r_G) coefficients below diagonal between grain yield and agronomic traits of 135 QPM and non-QPM hybrids evaluated at 13 environments during the 2017/2018 and 2018/2019 growing seasons

Traits	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	ER	EA
GY	-	-0.15	-0.12	0.34**	0.28**	-0.03	-0.19*	0.24*	-0.12	0.08	-0.61**
DA	-0.15	-	0.30**	0.46**	0.62**	-0.1	0.15	0.07	-0.18*	-0.39**	0.03
ASI	-0.15	0.52**	-	0.14	0.13	0.19*	0.29**	-0.25**	0.19*	-0.1	0.03
PH	0.41**	0.48**	0.25*	-	0.86**	0.1	0.02	0.19*	-0.23*	-0.27**	-0.54**
EH	0.33**	0.66**	0.25*	0.87**	-	0.09	0.05	0.23*	-0.24*	-0.33*	-0.46**
RL	0.01	-0.20*	0.63**	0.18*	0.17	-	0.33**	-0.19*	-0.03	0.01	-0.05
SL	-0.28**	0.25*	0.63**	0.05	0.09	1.00**	-	-0.02	0.06	-0.18*	-0.06
EPP	0.24*	0.09	-0.42**	0.20*	0.25*	-0.42**	0.01	-	-0.18**	-0.04	-0.1
HC	-0.19*	-0.28**	0.45**	-0.37**	-0.38**	-0.20*	0.13	-0.32**	-	0.23*	0.19*
ER	0.17*	-0.56**	-0.26**	-0.37**	-0.47**	0.03	-0.50**	-0.02	0.47**	-	0.20*
EA	-0.73**	0.04	0	-0.63**	-0.54**	-0.1	-0.18*	-0.12	0.33**	0.15	-

† GY= grain yield; DA= days to anthesis; ASI = anthesis-silking interval; PH = plant height; EH = ear height; EA = ear aspect; RL = root lodging; SL = stock lodging; HC = husk cover; EPP= ear per plant; *P<0.05, **P<0.01

Table 7.8 Phenotypic correlation (r_P) above diagonal and genotypic correlation (r_G) coefficients below diagonal between quality traits of 135 QPM and non-QPM hybrids evaluated at 13 environments during 2017/2018 and 2018/2019 growing seasons

Traits	Tryptophan	Moisture	Protein	Oil	Fibre	Starch
Tryptophan		0.15	-0.56**	0.51**	0.39**	-0.30**
Moisture	0.21*		-0.32**	0.20*	0.48**	-0.20*
Protein	-0.64**	-0.45**		-0.15	-0.40**	-0.30**
Oil	0.58**	0.32**	-0.17		0.29**	-0.69**
Fibre	0.44**	0.64**	-0.48**	0.33**		-0.32*
Starch	-0.35**	-0.29**	-0.21*	-0.78**	-0.36**	

*P<0.05, **P<0.01

Table 7.9 Phenotypic correlation (r_P) above diagonal and genotypic correlation (r_G) coefficients below diagonal between grain yield, agronomic and quality traits of 135 QPM and non-QPM hybrids evaluated during the 2017/2018 and 2018/2019 growing seasons

Traits	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	ER	ESP	Trpt	Mois	Prot	Oil	Fibre	Starch
GY	-	-0.16	-0.14	0.29**	0.19*	0.18*	-0.19*	0.42**	-0.1	0.06	-0.54**	-0.27**	0.26**	0.25*	0.07	-0.06	-0.17
DA	-0.19**	-	0.35**	0.39**	0.60**	0.02	0.22*	-0.04	-0.33**	-0.29**	0.01	-0.10	0.03	-0.07	0.13	-0.27**	0.02
ASI	-0.23**	0.78**	-	0.09	0.14	0.15	0.32**	-0.29**	0.08	-0.09	0.14	0.10	0.19*	-0.24*	0.14	0.18*	-0.01
PH	0.40**	0.43**	0.30**	-	0.82**	0.20*	0.14	0.15	-0.15	-0.17	-0.53**	-0.09	0.01	0.08	0.14	-0.07	-0.09
EH	0.27**	0.65**	0.37**	0.86**	-	0.20*	0.19*	0.14	-0.23*	-0.24*	-0.44**	-0.23*	-0.07	0.18*	0.04	-0.26**	-0.01
RL	NA	NA	NA	NA	NA	-	0.13	-0.03	0.23*	-0.03	-0.18*	-0.18*	0.01	0.14	0.14	-0.07	0.04
SL	-0.28**	0.47**	1.00**	0.37**	0.43**	NA	-	-0.08	0.03	-0.20**	-0.13	0.19*	0.04	-0.26**	-0.02	-0.09	0.21*
EPP	0.64**	-0.08	-0.76**	0.19*	0.20*	NA	-0.16	-	-0.20*	0.05	-0.34**	-0.10	0.01	0.05	-0.04	-0.17	0.07
HC	-0.16	-0.68**	0.21*	-0.24*	-0.41**	NA	0.06	-0.63**	-	0.18*	0.06	0.11	-0.05	-0.01	-0.10	0.16	0.06
ER	0.29**	-0.47**	-0.35**	-0.20*	-0.39**	NA	-0.88**	0.31**	0.36**	-	0.28**	-0.03	0.12	0.06	-0.03	0.16	-0.09
ESP	-0.83**	0.01	0.27**	-0.83**	-0.74**	NA	-0.68**	-0.58*	-0.02	0.11	-	0.19*	-0.02	-0.14	0.05	0.14	-0.08
Trpt	-0.39**	-0.12	0.16	-0.12	-0.26**	NA	0.42**	-0.18*	0.24*	-0.04	0.35**	-	0.15	-0.56**	0.51**	0.39**	-0.30**
Mois	0.50**	0.05	0.38**	0.02	-0.10	NA	0.05	0.06	-0.06	0.15	-0.07	0.21*	-	-0.32**	0.20*	0.48**	-0.20*
Prot	0.38**	-0.04	-0.45**	0.11	0.23*	NA	-0.54**	0.15	-0.01	0.07	-0.31**	-0.64**	-0.45**	-	-0.15	-0.40**	-0.30**
Oil	0.04	0.14	0.21*	0.14	0.03	NA	-0.16	-0.09	-0.23*	-0.05	0.13	0.58**	0.32**	-0.17*	-	0.29**	-0.69**
Fibre	-0.10	-0.31**	0.28**	-0.09	-0.31**	NA	-0.19*	-0.26**	0.31**	0.24**	0.20*	0.44**	0.64**	-0.48**	0.33**	-	-0.32**
Starch	-0.25*	0.01	0.01	-0.12	-0.02	NA	0.44**	0.04	0.16	-0.13	-0.08	-0.35**	-0.29**	-0.21*	-0.78**	-0.36**	-

† GY= grain yield; DA = days to anthesis; ASI = anthesis-silking interval; PH = plant height; EH = ear height; EA = ear aspect; RL = root lodging; SL = stock lodging; HC = husk cover; EPP = ear per plant; Trpt = tryptophan; Mois- = moisture and Prot = protein; *P<0.05, **P<0.01; NA – not applicable

Ear aspect recorded significant positive association with tryptophan and fibre contents but was negatively correlated with protein content. There was no association between plant height and all the quality traits analysed in this study. However, ear height was significantly and negatively correlated with tryptophan and fibre content (Table 7.9). For phenotypic relationship, grain yield showed negative and significant associations with tryptophan, moisture and protein content. Ears per plant, ear rot and husk cover had no relationships with the quality traits at phenotypic level. Ear aspect showed a weak positive ($r_p=0.19$) correlation with tryptophan (Table 7.9).

7.4.5 Path coefficient analysis for grain yield and agronomic traits

The path coefficient analysis using the stepwise regression model for grain yield and agronomic traits measured identified ear aspect, ears per plant, stalk lodging and ear rot as the traits which contributed to grain yield most directly and accounted for 68% of the variation in grain yield (Figure 7.4). Ear aspect recorded the highest direct effect (-0.64) on grain yield while ear rot had the least direct effect on grain yield. Plant and ear height, anthesis-silking interval, husk cover, days to anthesis and stalk lodging are ranked as the second order of traits. With the exception of husk cover and anthesis-silking interval, the rest of the second order traits contributed to grain yield indirectly via ear aspect. Anthesis-silking interval and root lodging contributed to grain yield through ears per plant, while husk cover contributed to grain yield through ear rot. However, none of the second order traits contributed through stalk lodging to grain yield.

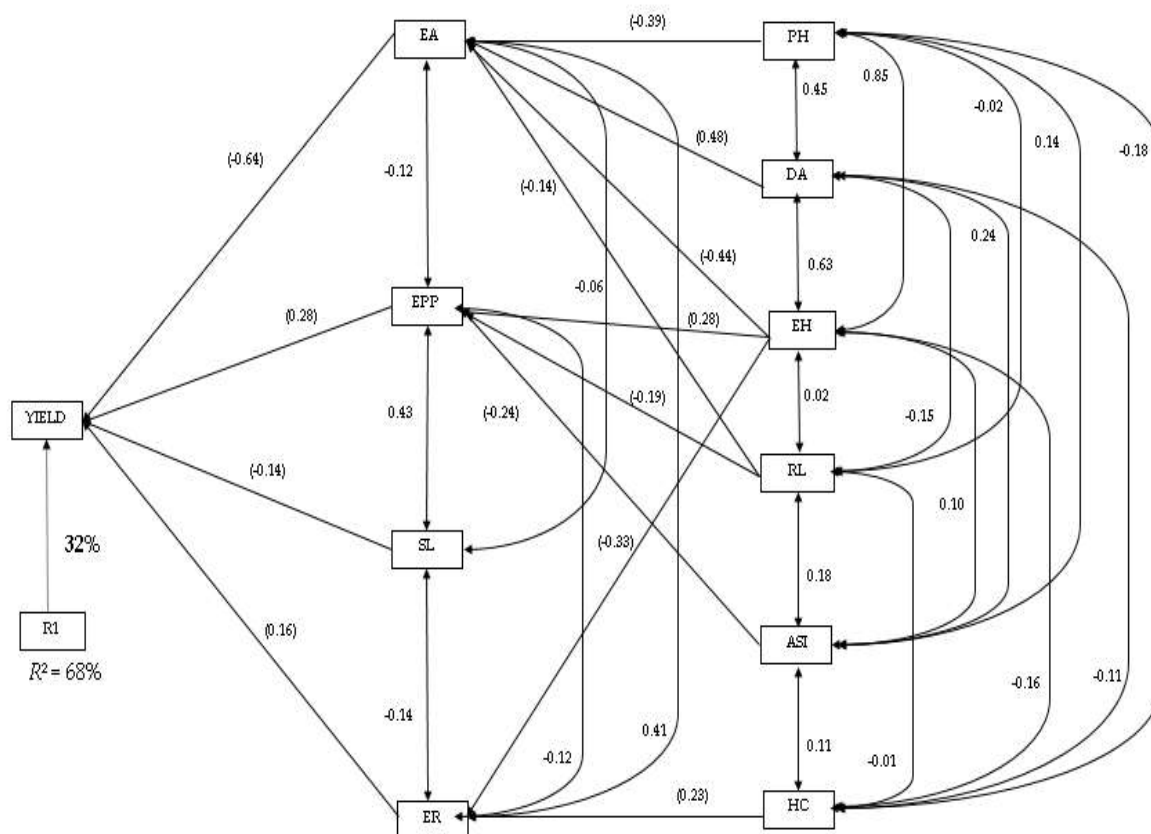


Figure 7.4 Path analysis showing the relationship of grain yield and agronomic traits of 135 QPM and non-QPM maize hybrids

Yield = grain yield; ER = ear rot; EPP = ear per plant, EA = ear aspect, HC = husk cover, ASI = anthesis-silking interval; EH, ear height; PH = plant height; DA = days to anthesis; RL = root lodging and SL = stalk lodging of 135 QPM and non-QPM maize hybrids. Values in parenthesis are correlation coefficients and other values are direct path coefficients. R1 represent the residual effects.

The path analysis represented in Figure 7.5 shows the stepwise regression model for grain yield, secondary traits related to grain yield and quality traits examined in this study. The first order traits identified contributing directly to grain yield were ear aspect, ear per plant, starch and tryptophan, these contributed 71% of the variation of grain yield (Figure 7.5). Ear aspect contributed the highest direct effect (-0.49) for grain yield while tryptophan recorded the least effect with the contribution of -0.23. Plant and ear heights, protein, fibre and oil content were the other traits contributing to grain yield indirectly. Oil content, fibre and protein contributed to grain yield through starch while ear height, protein and fibre also contributed to grain yield indirectly through ears per plant. Only plant height

contributed to grain yield through ear aspect while oil content also contributed to grain yield via tryptophan for the secondary order traits. Husk cover was identified as the only third order trait contributing to grain yield through plant height and ear aspect and also through oil content and tryptophan.

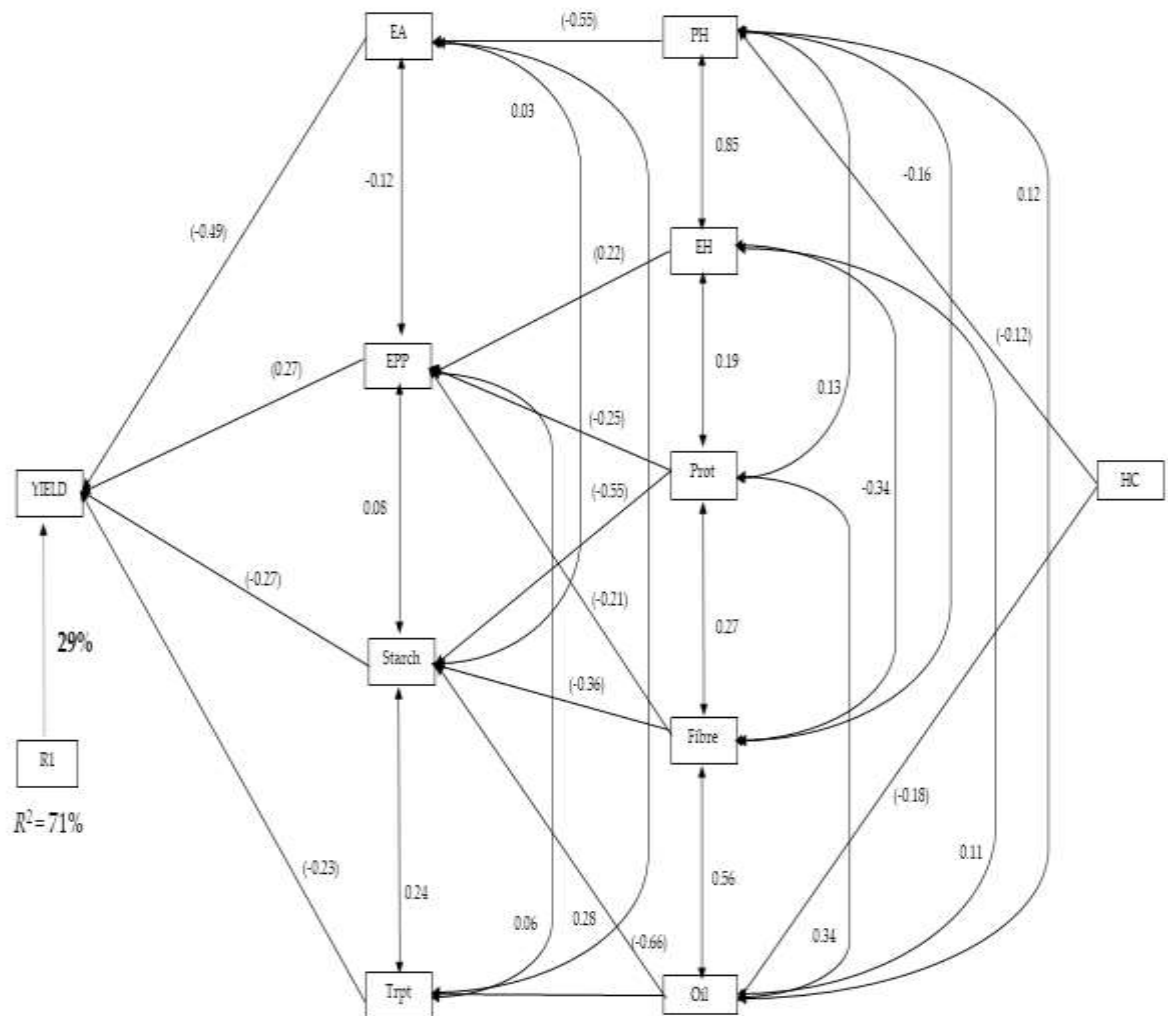


Figure 7.5 Path analysis showing the relationship of grain yield, agronomic and quality traits of 135 QPM and non-QPM maize hybrids

Yield = grain yield; ER = ear rot; EPP = ear per plant, EA = ear aspect, HC = husk cover, ASI = anthesis-silking interval; EH, ear height; PH = plant height; DA = days to anthesis; Trypt = tryptophan; prot = protein. Values in parenthesis are correlation coefficients and other values are direct path coefficients. R1 represent the residual effects.

7.5 Discussion

7.5.1 Heritability and variance components for agronomic and quality traits

The present study showed substantial phenotypic and genotypic variations among the QPM and non-QPM hybrids evaluated. High values for broad sense heritability suggested selection will be possible for superior inbred genotypes, confirming earlier findings (Halilu et al. 2016; Saif-ul-Malook et al. 2016; Ababulgu et al. 2018). However, the heritability estimates in this study were higher than the previous estimates. Dutta et al. (2017) and Mastrodomenico et al. (2018) indicated that phenotypic variance and heritability are indicators for direct selection. For the genotypes studied, the magnitude of genotypic variances (σ^2_g) were greater than environmental variances (σ^2_e) for most of the traits measured except for husk cover, root and stalk lodgings. This finding is consistent with the work by Halilu et al. (2016) and Ababulgu et al. (2018), suggesting the recently developed QPM inbred lines by CIMMYT are suitable germplasm for developing superior hybrids for grain yield and other phenotypic traits measured.

The high broad sense heritability (H^2) values recorded for the various quality traits in the present study indicates that the identification and selection of inbreds with increased tryptophan, protein, starch, oil content and low fibre is possible to reduce malnutrition. The higher values further indicates the genetic variability among the genetic material studied, hence some of the genotypes can be selected for synthetic cultivar or population development from which other superior quality traits such as tryptophan, protein and oil content could be developed.

Assefa et al. (1999) and Aman et al. (2016) suggested that selection based only on traits with high H^2 is easy because of the limited influence of the environment on these genotype. However, H^2 solely is not adequate to select for promising individuals and it is important to include other genetic components (Johnson et al. 1995; Muturi et al. 2019). This study showed that σ^2_g was greater than σ^2_e for protein, tryptophan, oil content, starch and fibre. This corroborates the findings of Bekele and Rao (2014), Setimela et al. (2017), and Sharma et al. (2017). This implied that quality traits are controlled by additive gene effects as the result of inheritance from their parents.

7.5.2 Heterosis of grain yield, agronomic characters and quality traits

Hybrid vigour for grain yield is of utmost importance to the breeder because of the economic usefulness of the trait. Flint-Garcia et al. (2009) and Ige et al. (2018) noted that better progress was attained when the parental lines were developed from populations or parents with maximum variability in their progenies. The majority of the crosses in the current study had high positive values for MPH and BPH for grain yield, plant and ear height, and ears per plant as a manifestation of diversity among the parents. MPH and BPH recorded in this study is consistent with studies by Ige et al. (2018) and Chakrabarty et al. (2019) under optimal conditions but the values recorded in this study were far higher than their values. The negative heterosis value obtained for anthesis-silking interval in the current study implies that the crosses flowered earlier than their analogous parents. Moreover, it is expected that superior hybrids should display negative values for ear aspect and ear rot. This was observed for ear aspect whereby most hybrids performed better than their corresponding parents, however, all the hybrids performed poorly in terms of ear rot compared to their parents.

Heterosis for the quality traits analysed indicated that only a few crosses were better than their parents for both MPH and BPH probably because of the additive nature of such traits. A deeper insight into this further revealed that hybrids with high grain yield tend to have low tryptophan suggesting the two traits might not be inherited together since they are both controlled by poly genes. However, this development of inbreds with high tryptophan and good SCA could result in hybrids with high tryptophan and yield. From the study, most of the hybrids displayed superiority over their parents for protein, starch, fibre and oil content, corroborating the findings of Werle et al. (2014) and Darshan and Marker (2019). The presence of MPH for crosses showing positive values for tryptophan, protein and oil content and negative values for fibre implied that promising genes of interest exist for quality traits improvement.

7.5.3 Principal component analysis for agronomic and quality traits

For the PC biplot of the agronomic traits, PC1 and PC2 accounted for 51.25% of the variations for the traits measured with a strong association between grain yield and ear per plant; and plant and ear height, suggesting that for high grain yield to be attained, prolificacy of a genotype is a major contributor coupled with plant and ear heights.

For quality traits, a large contribution from maturity and protein content were observed to PC1 and PC2. This result is partly consistent with Liu et al. (2019) in which major amino acids such as leucine and lysine were located on the first PC. The strong association between tryptophan and fibre as evident in the PC biplot suggested that the two traits can be selected for without affecting each other. Similarly, the angle between tryptophan and oil content is less than 90° suggesting the existence of a strong relationship between the traits. However, with the position of tryptophan and protein, the two traits cannot be selected together within the same breeding objective to improve protein and tryptophan at the same time (Sarika et al. 2018).

For the combined agronomic and quality traits, the characters used different pathways. While the agronomic traits were located on the first four PCs, the quality traits used were mainly located on the fifth and sixth PCs. This shows how divergent the traits are and further evident in the PCA biplot especially for grain yield and tryptophan.

7.5.4 Correlation coefficients and path analysis of grain yield, agronomic and quality traits

Genetic and phenotypic correlations showed similar trends for the traits analysed, hence the discussion applies to both phenotypic and genotypic correlations. The substantial negative relationship between grain yield and anthesis-silking interval; and grain yield and ear aspect indicated that these traits are inversely interrelated therefore could be considered as essential traits in breeding for QPM genotypes aiming at high grain yield with reduced days to maturity. This confirms previous reports by Izzam et al. (2017) and Singh and Kumar (2017). The manifestation of positive and significant correlation between grain yield and number of ears per plant, grain yield and plant height, and grain yield with ear height, indicated that these traits can be used for selecting high yielding QPM genotypes, corroborating the findings of various studies (Babu and Prasanna 2014; Tulu 2014; Izzam et al. 2017; Bhusal and Lal 2017). Husk cover has significant implications for ear rot at genotypic and phenotypic levels signifying closed tip of cobs should be considered as an important secondary trait to prevent exposure of kernel from adverse environmental conditions and also from insect attack which consequently affects grain yield and its quality. Grain yield was negatively associated with tryptophan and starch content. The inverse association between grain and tryptophan indicated that the traits cannot be

selected together, implying pleiotropy, thereby as one increases, the other decreases. The strong positive relationship between grain yield and protein implied the traits can be selected together. The strong negative correlation between protein and tryptophan content, and starch and oil content implied that simultaneous improvement of these traits will be difficult. The correlation between grain yield and protein content varied from the study conducted by Gupta et al. (1974) who recorded strong negative association between grain yield and protein but agrees with the study by Mutiga et al. (2017) who also reported positive and significant association between grain yield and protein.

Because of the polygenic nature of grain yield, selection based only on correlation may not be efficient in selecting superior genotypes, therefore, it is crucial to access other pathways through which grain yield is inherited. Bocianowski et al. (2016) and Raza et al. (2018) indicated that path coefficient analysis assists plant breeders in detecting favourable traits which aid in selection to enhance grain yield. The path coefficient analysis was conducted for grain yield against other agronomic traits and how the combination between agronomic and quality traits are related to grain yield. The study identified ear aspect as a major contributor to grain yield and it also serves as a channel through which several secondary traits contribute to grain yield indirectly. Identification of ear aspect in this study is consistent with the results of Badu-Apraku et al. (2017) who reported on ear aspect as a major trait which contributes to grain yield. Ears per plant was also identified as a direct and indirect means through which ear height, protein and fibre content contributed to grain yield. It was interesting that tryptophan content contributed directly to grain yield even though the correlation analysis showed that the traits are inversely related. Also, starch and husk cover contributed indirectly to grain yield through tryptophan. This, indeed suggests for the use of path analysis to identify other essential traits rather than relying on correlations only for the selection of secondary traits as utilized by several authors on other crops apart from maize [Barrera et al. 2019 (tomato); John et al. 2019 (groundnut); Kanwar and Nag 2019 (rice)]

7.6 Conclusions

This study was conducted to determine various associations among grain yield and agronomic traits; associations among quality traits and among the two trait sets by exploiting variance components and multivariate analysis such as correlations, principal

component and path analyses. Mid- and better parent heterosis were high for grain yield, plant and ear height and ear aspect over the parental lines. Only few hybrids were found to be superior to their two parents for tryptophan. However, the crosses showed vigour over the parents for protein, starch, oil and fibre contents. All the traits studied were highly heritable with genetic variance dominating environmental variance. The present study showed that the relationship between grain yield and secondary traits ear aspect, ears per plant, ear rot and earliness are important contributors to grain yield. Path analysis identified ears per plant as a medium through which several secondary traits contributed to grain yield indirectly. For efficient selection to be realised, breeders should explore several genetic analyses before choosing a particular genotype. It is strongly recommended that ear aspect should be considered a key secondary trait in breeding for QPM hybrids. Also with the negative association between grain yield and tryptophan; and protein and tryptophan, it is recommended that gene pyramiding should be considered for these traits. There might be a possibility that, the full potentials of QPM hybrids would be realised if all these traits are incorporated into a specific genetic material.

Reference

- Ababulgu D, Shimelis H, Laing M and Beyene A (2018) Phenotypic characterization of elite quality protein maize (QPM) inbred lines adapted to tropical-highlands and the association studies using SSR markers. *Australia Journal of Crop Science* 12: 22-31.
- Adesoji AG, Abubakar IU and Labe DA (2015) Character association and path coefficient analysis of maize (*Zea mays* L.) grown under incorporated legumes and nitrogen. *Journal of Agronomy* 14: 158-163.
- Alvarado G, López M, Vargas M, Pacheco Á, Rodríguez F, Burgueño J and Crossa J (2015) META-R (Multi Environment Trial Analysis with R for Windows) Version 6.04", hdl:11529/10201, CIMMYT Research Data and Software Repository Network, V23
- Aman J, Bantte K, Alamerew S and Tolera B (2016) Evaluation of quality protein maize (*Zea mays* L.) hybrids at Jimma. *Journal of Forensic Anthropology* 1: 1-6.
- Amini Z, Khodambashi M and Houshmand S (2013) Correlation and path coefficient analysis of seed yield related traits in maize. *International Journal of Agriculture and Crop Sciences* 5: 2217-2220.

- Assefa K, Ketema S, Tefera H, Nguyen HT, Blum A, Ayele M, Bai G, Simane B and Kefyalew T (1999) Diversity among germplasm lines of the Ethiopian cereal tef (*Eragrostis tef* (Zucc.) Trotter). *Euphytica* 106: 87-97.
- Babu R and Prasanna B.M (2014). Molecular breeding for quality protein maize (QPM). In: Tuberosa R, Graner A and Frison E (eds), *Genomics of Plant Genetic Resources*. Springer. pp. 490-505. doi: 10.1007/978-94-007-7575-6
- Badu-Apraku B, Fakorede MAB, Annor B and Talabi AO (2017) Improvement in grain yield and low-nitrogen tolerance in maize cultivars of three eras. *Experimental Agriculture* 54: 1-19.
- Barrera SF, Ribeiro LP, Rodrigues EV, Lopes BL and Eduardo TP (2019) Correlations and path analysis in cherry tomato genotypes. *Functional Plant Breeding Journal* 1: 37-44.
- Bekele A and Rao TN (2014) Estimates of heritability, genetic advance and correlation study for yield and its attributes in maize (*Zea mays* L.). *Journal of Plant Sciences* 2: 1-4.
- Bhargava A, Shukla S, Rajan S and Ohri D (2007) Genetic diversity for morphological and quality traits in quinoa (*Chenopodium quinoa* Willd) germplasm. *Genetic Resources and Crop Evolution* 54: 167-173.
- Bhusal TN and Lal GM (2017) Relationship among heterosis, combining ability and SSR based genetic distance in single cross hybrids of maize (*Zea Mays* L). *Vegetos- An International Journal of Plant Research* 30: 1-10.
- Bizeti HS, Carvalho CGP, Souza JRP and Destro D (2004) Path analysis under multicollinearity in soybean. *Brazilian Archives of Biology and Technology* 47: 669-676.
- Blum A (2013) Heterosis, stress, and the environment: a possible road map towards the general improvement of crop yield. *Journal Experimental Botany* 64: 4829-4837.
- Bocianowski J, Górczak K, Nowosad K, Wojciech Rybiński W and Piesik D (2016) Path analysis and estimation of additive and epistatic gene effects of barley SSD lines. *Journal of Integrative Agriculture* 15: 1983-1990.
- Chairi F, Elazab A, Sanchez-Bragado R, Aras JL and Serret MD (2016) Heterosis for water status in maize seedlings. *Agricultural Water Management* 164:100-109.
- Chakrabarty S, Islam AKMA, Mian MAK and Ahamed T (2019) Combining ability and heterosis for yield and related traits in chili (*Capsicum annuum* L.). *Open Agriculture Journal* 13: 34-43.

- Darshan SS and Marker S (2019) Heterosis and combining ability for grain yield and its component characters in quality protein maize (*Zea mays* L.) hybrids. *Electron Journal of Plant Breeding* 10: 111-118.
- De Franca JGE (1983) Genetic and combining ability analysis of some agronomic and grain quality characters in sorghum (*Sorghum bicolor* (L.) Moench). MSc Thesis, Department of Genetics and Plant Breeding, Andhra Pradesh Agricultural University.
- Dutta R, Kumar A, Chandra S and Ngachan SV (2017) Genetic divergence, path coefficient, principal component and cluster analyses of maize genotypes in the mid-altitudes of Meghalaya. *Maydica* 62: 1-5.
- Duvick DN and Brown WL (1981) Current breeding methods in maize: Sneep J and Hendricksen T (eds), Wageningen, Holand: Pudoc. *Plant Breeding Perspectives*, pp. 190-203.
- East EM and Hayes HK (1912) Heterozygosis in evolution and in plant breeding. U. S. Department Agriculture Bulletin.
- Flint-Garcia SA, Buckler ES, Tiffin P, Ersoz E and Springer NM (2009) Heterosis is prevalent for multiple traits in diverse maize germplasm. *PLoS One* 4: 1-11.
- Gangashetty PI, Motagi BN, Pavan R and Roodagi MB (2016) Breeding crop plants for improved human nutrition through biofortification: Progress and prospects. In: Jaiwal PK, Chhillar AK, Chaudhary AK and Jaiwal R (eds), *Advances in Plant Breeding Strategies: Agronomic, Abiotic and Biotic Stress Traits*, 2nd edn. Springer Netherlands, vol.2, pp. 35-68. doi 10.1007/978-3-319-22518-0_2
- GenStat (2019) VSN International. GenStat for Windows 20th edition. VSN International
- Gupta D, Kovács I and Gáspár L (1974) Protein quality traits and their relationships with yield and yield components of *opaque-2* and analogous normal maize hybrids and inbred lines. *Theoretical and Applied Genetics* 45: 341-348.
- Halilu AD, Ado SG, Aba DA and Usman IS (2016) Genetics of carotenoids for provitamin A biofortification in tropical-adapted maize. *The Crop Journal* 4: 313-322.
- Ige SA, Bello OB and Alake O (2018) Combining ability and heterosis of tolerance to low soil nitrogen in tropical maize cultivars derived from two breeding eras. *Open Agriculture* 3: 339-346.
- Izzam A, Rehman H, Sohail A, Ali S, Manzoor and Hussain Q (2017) Genetic variability and correlation studies for morphological and yield traits in maize (*Zea mays* L.). *Pure and Applied Biology* 6: 1243-1243.

- John K and Santhoshi MVM and Rajasekhar P (2019) Correlation and path analysis for yield and yield attributes in groundnut (*Arachis hypogaea* L.). *Legume Research* 42: 518-522.
- Johnson HW, Robinson HF and Comstock RE (1955) Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* 47: 314-318.
- Kanwar SS and Nag YK (2019) To study correlation and path analysis in rice breeding lines. *International Journal of Current Microbiology and Applied Sciences* 8: 2481-2487.
- Lee EA and Tracy WF (2009) Modern Maize Breeding. In: Bennetzen JL and Hake S (eds), *Handbook of Maize: Genetics and Genomics*. Springer Science + Business Media, LLC, pp. 141-160. doi: 10.1007/978-0-387-77863-1
- Lippman ZB and Zamir D (2006) Heterosis: Revisiting the magic. *Trends in Genetics* 23: 60-65.
- Liu H, Pandey MK, Xu Z, Rao D, Huang Z, Chen M, Feng D, Varshney RK and Hong Y (2019) Analysis and evaluation of quality traits of peanut varieties with near infra-red spectroscopy technology. *International Journal of Agriculture and Biology* 21:491-498.
- Machikowa T and Laosuwan P (2011) Path coefficient analysis for yield of early maturing soybean. *Sonklanakarin Journal of Science and Technology* 33: 365-368.
- Mastrodomenico A, Hendrix C and Below F (2018) Nitrogen use efficiency and the genetic variation of maize expired plant variety protection germplasm. *Agriculture* 8: 1-17.
- Mather K and Jinks JL (1971) *Biometrical genetics. The study of continuous variation*. Cornell University Press, New York.
- Matthew I (2015) Combining ability, Genetic gains and path coefficient analyses of maize hybrids developed from maize streak virus and downey mildew resistant recombinant inbred lines. Student thesis, University of KwaZulu-Natal Pietermaritzburg, South Africa.
- Meseka S, Fakorede MA, Ajala S, Badu-Apraku B and Menkir A (2013) Introgression of alleles from maize landraces to improve drought tolerance in an adapted germplasm. *Journal of Crop Improvement* 27: 96-112.
- Mutiga SK, Morales L, Angwenyi S, Wainaina J, Harveyb J, Das B and Nelson BJ (2017) Field crops research association between agronomic traits and aflatoxin accumulation in diverse maize lines grown under two soil nitrogen levels in Eastern Kenya. *Field Crops Research* 205: 124-134.

- Muturi PW, Mgonja M and Rubaihayo P (2019) Gene action conditioning resistance traits to spotted stem borer, *Chilo partellus*, in grain sorghum. International Journal of Tropical Insect Science 39: 147-155.
- Nigussie M and Zelleke H (2001) Heterosis and combining ability in a diallel among eight elite maize populations. African Crop Science Journal 9: 471-479.
- Qi X, Li ZH, Jiang LL, Yu XM, Ngezahayo F and Liu B (2010) Grain-yield heterosis in *Zea mays* L. shows positive correlation with parental difference in CHG Methylation. Crop Science 50: 2338-2346.
- Ram L. (2014) Improvement of non-QPM lines through introgression of QPM genes. Student thesis, Department of Genetics and Plant Breeding, Banaras Hindu University Varanasi, India.
- Raza I, Khan A, Masood A and Abid S (2018) Path analysis for potato crisps. International Journal of Scientific and Engineering Research 9: 1565-1570.
- Saif-ul-Malook, Ali Q, Ahsan M, Muhammad Khalid Shabaz MK, Waseem M and MumtazA (2016) Combining ability analysis for evaluation of maize hybrids under drought stress. Journal of the National Science Foundation of Sri Lanka 44: 223-230.
- Saleh G, Abdullah D and Anuar AR (2002) Performance, heterosis and heritability in selected tropical maize single, double and three-way cross hybrids. Journal of Agricultural Sciences 138: 21-28.
- Sarika K, Hossain F, Muthusamy V, Zunjare RU, Baveja A, Goswami R, Bhat JS, Saha S and Gupta HS (2018) Marker-assisted pyramiding of *opaque2* and novel *opaque16* genes for further enrichment of lysine and tryptophan in sub-tropical maize. Plant Science 272: 142-152.
- Setimela PS, Gasura E and Tarekegne AT (2017) Evaluation of grain yield and related agronomic traits of quality protein maize hybrids in Southern Africa. Euphytica 213: 1-14.
- Sharma P, Punia MS, Kamboj MC, Singh N and Chand M (2017) Evaluation of quality protein maize crosses through line x tester analysis for grain yield and quality traits. Agricultural Science Digest 37: 42-45.
- Shull GH (1911) The genotypes of maize. American Naturalist 45: 234-252.
- Singh G and Kumar R (2017) Genetic parameters and character association study for yield traits in maize (*Zea mays* L.). Journal of Pharmacognosy and Phytochemistry 6: 808-813.

- Sreckov Z, Nastasic A, Bocanski J, Djalovic I, Vukosavljev M and Jockovic B (2011) Correlation and path analysis of grain yield and morphological traits in test-cross populations of maize. *Pakistan Journal of Botany* 43: 1729-1731.
- Tulu BN (2014) Correlation and path coefficients analysis studies among yield and yield related traits of quality protein maize (QPM) inbred lines. *International Journal of Plant Breeding and Crop Science* 1: 6-17.
- Udensi O and Ikpe E (2012) Correlation and path coefficient analyses of seed yield and its contributing traits in *Cajanus cajan* (L.) Millsp. *American Journal of Experimental Agriculture* 2: 351-358.
- Wegary D, Vivek B and Labuschagne M (2013) Association of parental genetic distance with heterosis and specific combining ability in quality protein maize. *Euphytica* 191: 205-216.
- Werle AJK, Ferreira FRA, Pinto RJB, Mangolin CA, Scapim CA and Gonçalves LSA (2014) Diallel analysis of maize inbred lines for grain yield, oil and protein. *Crop Breeding and Applied Biotechnology* 14: 23-28.
- Yu R, Zheng Y, Abdel-Aty M and Gao Z (2019) Exploring crash mechanisms with microscopic traffic flow variables: A hybrid approach with latent class logit and path analysis models. *Accident Analysis and Prevention* 125: 70-78.

CHAPTER EIGHT

CONCLUSIONS AND RECOMMENDATIONS

As the world population keeps increasing, millions of people have critical health issues as a result of a poor diet weakening their immune systems and making them susceptible to several chronic diseases. Maize is the most widely grown and cultivated cereal crop in SSA, therefore developing maize genotypes with increased amounts of essential amino acids will contribute significantly to supporting the fight against hunger and malnutrition. In this study, 130 single cross hybrids developed from 33 QPM and non-QPM inbred lines and four testers (two QPM and two non-QPM) as well as five hybrid checks (two QPM and three non-QPM, all single cross hybrids) obtained from the International Maize and Wheat Improvement Center (CIMMYT), Zimbabwe were used. The 135 hybrids together with 40 inbred lines were evaluated in South Africa and Zimbabwe during the 2017/2018 and 2018/2019 cropping seasons. Self-pollinated seeds were used for determination of quality traits, tryptophan, protein, moisture, starch, oil, fibre, amylose and zein proteins.

Promising QPM inbred lines were identified for grain yield, and agronomic and quality traits. The average yield of QPM inbred lines was higher than that of non-QPM lines. The best six performing inbred lines identified included three QPM and three non-QPM lines, although the two top performers were non-QPM lines. Based on the GGE biplot, the most promising and desirable inbred lines in this study were two non-QPM lines and one QPM line across all the environments.

Among the 135 hybrids evaluated, the best performing hybrid was a QPM hybrid involving a cross between line 11 x CZL15049 (entry 41), followed by a non-QPM hybrid, entry 108 (line 28 x CZL15049). The best QPM hybrid outperformed the best non-QPM hybrid by 8.81%. In addition, the best QPM hybrid genotype 41 outperformed best non-QPM check (Pioneer) and best QPM check (CBI) by 50.45 and 52.24%, respectively. In spite of this, there was a substantial yield reduction (13.9%) for QPM versus non-QPM hybrids. The AMMI analyses indicated that the grain yield performance of QPM and non-QPM hybrids was highly affected by environmental effects. The AMMI and GGE biplots identified QPM hybrids 108 and 41 and non-QPM hybrid 12 as the highest yielding and most stable genotypes in this study.

Non-additive genetic effects controlled more than 50% of inheritance of grain yield and also controlled the inheritance of anthesis-silking interval, husk cover and ears per plant. On the other hand, additive genetic effects controlled the inheritance of ear rot, plant and ear heights, days to pollen shed, ear aspect as well as root and stalk lodging. This suggested that both additive and dominance gene effects played an important role in the inheritance measured traits. Inbred lines 11, 14 and 28 and non-QPM tester CML444 showed desirable GCA effects for grain yield, indicating that these lines in combination with the tester could be considered when targeting the development of superior maize genotypes with QPM traits. Lines 1, 2, 8, 13 and 30 were found to be prolific while QPM tester CZL059 was the only tester to display positive significant GCA for ears per plant, which is a major contributor to grain yield. The SCA grouping method showed that QPM testers were superior to non-QPM testers in discriminating between the lines for grain yield. Based on the SCA values, crosses with the entries 41, 85, 99, 105, 105 and 121 were identified as the best hybrids across the 13 locations for grain yield.

The quality traits analysed for the QPM and non-QPM maize genotypes varied significantly, and were also influenced by the environment. Several hybrids had QI above 1, but the best three hybrids for QI were QPM L12 x CZL15049 (45), L18 x CZL15049 (69) and L2 x CZL059 (6). Hybrids L12 x CZL15049 (45) and L15 x CZL15049 (57) outperformed the best check, QPM (entry 132) by 15.38 and 12.82%, respectively for tryptophan. Hybrids 45 and 57 were identified as the crosses with the highest tryptophan content. Additive gene action was predominant in the inheritance tryptophan, protein, starch, oil and fibre contents. Inbred lines 1, 2, 6, 7, 8, 12, 13, 15, 17 and 18 and QPM testers CZL15049 and CZL059 showed desirable GCA effects for tryptophan, suggesting this line and testers should be considered for QPM hybrid development for high tryptophan content. Several lines were found to have good GCA effects for protein and oil. Based on the SCA values, crosses with the entries 78, 82, 87 and 126 were identified as the best hybrids across the six locations for tryptophan. Hybrids 127 and 87 were also identified for superior protein content.

Mid- and better parent heterosis was high for grain yield, plant and ear height and ear aspect. Only a few hybrids were superior to their parents for tryptophan. However, the crosses showed vigour over the parents for grain protein, starch, oil and fibre contents. All the traits studied were highly heritable with additive genetic variance dominating. There

was a strong relationship between grain yield and secondary traits such as ear aspect, ears per plant, ear rot and earliness, which are clearly important contributors to grain yield. Path analysis identified ears per plant as a medium through which several secondary traits contributed to grain yield indirectly.

This study has, therefore, shown that although QPM inbred lines performed somewhat better than non-QPM lines, there was a yield penalty associated with QPM, compared to non-QPM hybrids. There were, however, some excellent QPM hybrids. Superior QPM inbred lines identified in this study could be exploited by breeding programmes in SSA. The high yielding QPM hybrids identified could be further tested for commercial release. Good QPM hybrids can contribute to alleviate poverty, hunger and malnutrition in southern Africa and SSA at large. It is suggested that tropical maize breeding should in the future be more focused on pyramiding of high protein and tryptophan content genes together with high grain yield.

Appendix 1. Grain yield and agronomic performance of 130 hybrids and five checks at Cedara during 2017/2018 and 2018/2019 cropping seasons

Entry	GY	DA	ASI	PHT	EHT	RL	SL	EPP	HC	ER	EASP
1	6.34	80.91	0.59	200.80	102.39	10.29	20.69	0.98	2.04	22.01	2.43
2	5.14	86.80	-0.17	209.94	112.18	-3.31	5.44	0.97	1.97	19.99	2.61
3	7.11	85.30	-0.54	190.62	104.03	10.35	7.28	0.87	1.58	34.37	3.56
4	4.24	83.26	1.52	192.97	117.74	1.06	32.78	0.97	1.84	54.63	2.87
5	6.70	84.35	-0.89	186.95	94.65	0.77	16.23	1.09	2.41	31.12	3.14
6	5.72	84.36	0.53	199.21	116.12	3.06	26.71	1.04	1.26	11.46	2.21
7	5.77	85.25	0.62	197.33	110.92	12.79	19.21	1.01	2.06	38.34	3.17
8	8.44	82.20	0.35	191.52	112.39	10.60	32.30	0.93	1.48	26.51	2.20
9	6.12	82.48	0.73	187.47	99.00	4.17	32.43	0.81	2.20	49.13	2.96
10	4.81	83.78	0.86	187.72	110.26	-8.09	42.59	1.01	1.67	41.09	2.53
11	5.41	88.83	0.50	197.87	120.44	5.12	18.63	0.95	2.22	42.57	2.96
12	7.66	85.85	0.68	221.30	133.57	6.52	27.14	0.94	2.26	19.06	2.56
13	5.09	80.19	0.76	178.51	90.47	0.79	38.44	0.85	2.14	47.52	3.13
14	7.94	83.48	1.21	229.52	114.82	5.12	31.66	1.03	1.81	24.26	2.39
15	8.36	83.82	0.71	187.11	92.81	5.60	9.73	0.95	1.90	5.40	2.40
16	9.38	80.74	0.91	202.56	115.48	17.97	16.66	0.90	1.84	25.71	2.30
17	6.91	78.51	0.85	181.75	104.67	-7.66	13.53	1.02	2.01	27.71	2.54
18	5.59	82.11	0.18	212.46	127.21	7.64	29.71	1.00	2.56	41.44	2.72
19	6.09	84.79	-0.25	199.94	106.35	4.68	29.15	1.00	1.81	42.64	2.84
20	6.64	81.93	0.94	197.74	112.36	5.77	3.39	0.95	2.40	26.41	2.76
21	5.55	82.78	0.16	179.30	88.99	-1.30	50.35	1.04	2.14	62.24	2.66
22	5.24	84.63	0.33	204.17	123.38	-1.80	46.39	1.08	1.95	46.91	2.32
23	7.06	87.47	0.95	200.48	118.41	6.64	32.45	0.98	1.85	38.31	2.74
24	5.88	83.50	0.15	197.25	114.46	-0.42	25.77	1.05	1.86	44.26	2.60
25	4.20	84.39	1.16	193.72	108.16	3.95	13.50	0.86	2.60	33.69	3.12
26	6.49	82.74	0.21	202.26	130.16	8.64	22.20	0.98	2.02	50.72	2.47
27	7.84	84.32	0.30	217.52	123.58	0.65	16.60	1.00	1.91	41.14	3.20
28	8.24	80.83	0.39	188.02	114.22	1.07	4.07	1.04	2.09	32.89	2.83
29	5.62	82.68	0.89	196.50	111.17	8.04	10.50	0.84	2.05	40.50	3.02
30	5.13	87.84	0.82	217.61	121.96	4.13	7.29	1.02	1.66	47.42	3.59
31	7.27	87.14	1.34	222.10	135.17	13.78	4.67	0.94	1.98	42.35	3.18
32	6.92	87.16	1.51	197.45	111.13	4.39	23.90	1.01	2.17	64.37	2.76
33	6.83	84.75	0.61	197.92	114.14	12.16	0.65	0.94	2.33	50.51	2.91
34	5.94	89.20	0.74	199.41	123.49	17.16	7.91	0.91	2.20	38.48	2.91
35	6.93	87.30	-0.15	213.61	122.18	22.37	18.45	0.92	2.41	42.82	2.94
36	6.79	84.00	0.38	208.85	123.10	9.77	19.58	1.01	1.77	41.12	2.79
37	8.48	85.64	0.47	216.91	121.34	2.61	19.91	1.02	1.97	41.09	3.01
38	5.86	85.22	0.97	204.68	117.30	14.33	19.13	1.03	1.69	44.33	2.55
39	8.46	87.64	1.16	221.14	138.15	46.60	5.64	1.03	1.46	20.46	2.71
40	6.62	88.14	0.49	200.52	123.68	37.27	8.01	0.95	2.08	30.20	2.30
41	8.41	86.96	-0.29	220.26	122.38	23.65	12.39	1.00	1.89	39.38	2.55
42	5.91	91.39	0.71	199.70	135.84	20.77	7.65	0.91	1.89	37.81	3.07
43	9.45	88.39	0.82	224.35	142.67	42.27	-0.20	0.95	1.59	28.31	2.38
44	6.29	88.45	0.17	214.52	125.05	15.55	17.93	1.04	2.10	37.51	2.79
45	4.88	80.18	0.10	186.41	102.18	5.28	31.56	0.86	2.31	36.66	2.45
46	6.29	87.91	0.95	220.19	132.42	11.64	18.93	0.91	1.86	35.93	3.03
47	6.73	88.61	-1.02	205.20	123.12	11.43	21.31	0.99	2.09	31.18	2.96
48	7.40	88.62	1.25	210.11	122.48	4.00	2.88	0.92	2.54	17.67	2.48
49	6.09	85.53	0.99	204.51	115.65	6.32	9.48	0.94	2.11	52.10	3.20
50	6.28	90.26	0.34	203.60	111.47	-3.44	31.13	1.07	1.24	42.79	3.07
51	6.73	84.10	0.63	201.48	119.75	3.92	20.75	1.01	1.75	21.84	2.67
52	8.31	87.00	0.30	199.09	122.95	-6.61	26.25	0.97	2.17	29.21	2.78
53	5.81	82.27	1.14	188.95	101.47	6.76	12.67	0.87	2.20	63.05	2.96
54	5.57	85.16	1.05	186.88	104.42	1.59	18.68	1.02	2.02	15.07	3.02
55	8.22	82.10	0.51	205.06	117.15	3.38	13.72	0.95	2.04	23.58	2.51
56	8.13	83.77	0.29	204.63	116.47	12.28	7.61	0.98	1.89	37.27	2.31
57	5.85	83.31	0.76	216.16	120.81	24.37	9.73	0.83	2.08	63.05	3.54

58	5.74	86.73	0.43	217.53	122.47	13.06	12.95	0.96	2.19	24.30	3.32
59	9.07	87.65	0.09	229.69	145.17	3.56	19.90	0.99	1.76	30.87	2.36
60	6.31	87.66	1.07	200.84	111.37	-0.11	21.98	1.02	1.44	24.32	2.53
61	5.19	83.81	0.80	198.76	101.58	-2.55	34.92	0.94	1.94	49.79	3.13
62	5.71	89.16	0.51	172.22	92.26	19.02	16.84	1.06	2.18	26.15	3.12
63	3.45	86.18	1.12	191.54	109.24	7.98	17.04	0.81	2.13	86.65	3.55
64	5.05	86.06	0.84	202.63	117.40	-5.27	31.99	0.94	2.06	28.92	2.59
65	5.84	85.19	1.34	189.19	101.00	-8.63	12.58	0.92	2.48	44.55	2.95
66	6.10	86.60	-0.22	193.33	112.25	1.73	24.60	0.91	1.53	33.94	2.71
67	4.91	86.22	1.34	187.50	113.52	3.08	27.23	0.83	2.02	42.37	3.28
68	6.28	85.71	0.63	192.72	115.56	2.86	10.67	0.98	1.99	26.79	2.67
69	5.99	84.00	-0.48	205.97	118.10	12.06	26.91	0.98	2.29	48.85	2.50
70	0.95	92.49	1.58	172.27	103.11	-1.81	17.90	0.71	2.30	33.67	4.03
71	8.85	84.35	0.80	203.37	129.99	21.28	20.04	0.88	2.06	20.78	2.24
72	9.11	85.94	0.21	192.67	107.07	11.98	9.51	1.00	1.69	30.51	2.25
73	5.55	80.32	2.14	167.03	75.83	6.65	6.53	0.79	2.11	32.81	2.61
74	6.60	83.33	0.87	203.37	107.39	0.70	25.57	0.97	1.94	27.44	2.54
75	6.90	86.62	1.90	194.75	103.02	15.22	15.71	1.00	2.07	16.93	2.62
76	6.70	82.30	0.39	192.41	105.65	2.18	20.78	0.93	1.80	29.65	2.28
77	7.08	79.51	0.64	186.75	98.29	7.49	20.85	1.00	2.13	45.65	2.69
78	6.43	85.01	-0.08	220.21	132.78	7.00	4.33	1.03	1.59	37.20	2.38
79	8.93	82.48	0.50	194.81	110.75	28.99	-1.96	0.99	1.61	49.51	2.45
80	6.35	82.26	0.63	204.02	115.12	6.99	17.87	0.99	2.39	34.03	2.30
81	5.90	84.79	0.37	196.89	134.63	13.53	39.88	0.99	1.91	23.42	2.25
82	4.53	83.72	0.93	195.87	119.33	16.08	12.38	0.90	1.90	45.74	2.69
83	7.20	82.12	0.22	206.97	137.07	23.09	3.57	0.70	2.27	75.92	2.69
84	7.78	88.82	2.07	200.13	113.71	1.56	21.21	0.96	1.93	8.18	2.32
85	7.55	88.17	2.15	200.01	132.98	3.34	22.85	0.98	1.46	35.28	2.35
86	7.37	90.08	0.23	209.08	124.99	7.12	25.40	1.02	2.54	32.35	2.27
87	2.88	89.83	2.24	161.94	100.79	6.61	2.88	0.99	2.14	48.77	3.08
88	6.24	82.62	0.39	191.69	90.97	0.16	9.13	1.08	1.93	34.00	2.68
89	5.05	87.42	1.20	190.35	101.40	5.97	22.59	1.04	2.64	28.85	2.39
90	5.74	88.79	0.91	211.66	114.21	24.74	17.24	1.02	1.97	19.94	2.47
91	6.80	88.60	0.79	191.49	98.07	23.63	-0.73	0.93	1.87	59.33	3.10
92	4.93	85.05	0.01	203.89	105.93	7.80	12.77	0.94	1.87	45.71	2.97
93	5.81	91.37	0.32	209.60	124.01	22.79	11.91	1.06	1.77	34.35	2.63
94	6.16	91.12	-0.12	212.88	121.34	-0.04	5.16	1.05	1.56	16.37	2.14
95	5.27	90.99	0.59	189.27	111.98	16.35	10.60	0.93	1.91	56.24	3.09
96	6.83	86.32	1.40	209.78	128.01	4.02	17.48	0.99	1.82	37.63	2.58
97	5.51	90.92	0.22	180.42	102.58	2.46	45.95	1.02	1.92	26.05	2.82
98	8.01	85.52	1.05	198.80	116.02	8.69	15.67	0.98	1.87	18.16	2.44
99	8.13	84.05	2.53	182.10	106.53	9.33	17.55	0.92	1.99	30.10	2.90
100	8.19	81.09	1.07	186.58	89.11	6.95	28.43	0.97	1.94	36.90	2.09
101	5.94	86.92	0.49	206.13	113.67	5.62	32.32	0.94	1.92	29.59	2.83
102	6.85	85.84	-0.06	203.69	110.19	15.83	15.90	1.03	1.14	19.53	2.39
103	6.59	88.89	2.19	193.96	104.15	18.49	1.61	0.92	1.62	41.89	2.92
104	5.47	80.16	0.23	190.54	92.27	-0.71	9.42	0.95	2.01	25.87	2.74
105	6.30	83.44	0.36	204.29	102.33	6.05	20.44	0.98	2.62	31.22	2.67
106	6.84	80.99	0.39	199.31	110.11	-2.16	22.56	1.08	1.72	36.29	3.05
107	6.57	79.59	1.16	188.16	114.90	23.55	14.77	1.04	2.15	31.44	2.61
108	7.85	85.42	-0.30	195.46	119.37	13.82	3.86	1.07	2.39	45.39	3.11
109	6.27	87.03	1.75	220.81	140.00	3.27	35.94	0.91	1.86	33.01	2.42
110	6.97	89.91	1.13	214.63	132.39	10.73	24.33	0.94	1.50	42.90	3.03
111	7.15	87.79	0.05	205.97	131.85	0.45	10.40	0.96	2.06	19.45	2.84
112	6.70	78.38	0.18	171.31	80.10	-4.29	38.10	1.00	2.27	40.45	2.60
113	6.62	82.42	0.79	209.05	115.77	4.04	22.26	0.95	1.59	23.52	2.46
114	7.33	83.67	0.89	205.67	101.11	5.37	11.73	0.91	1.95	46.28	2.74
115	8.35	83.33	0.36	198.73	111.77	2.82	24.81	1.00	1.45	22.41	2.13
116	9.25	85.07	0.23	180.47	90.27	17.16	19.19	0.80	1.90	39.63	2.60
117	5.26	84.87	0.76	182.64	100.41	3.80	19.65	1.02	2.01	33.53	2.85
118	8.16	87.19	0.49	201.41	113.40	9.11	7.03	0.96	2.30	8.56	2.62

119	7.44	86.73	0.94	185.13	104.89	25.00	16.20	0.92	1.87	48.67	2.78
120	6.84	85.63	2.17	203.43	119.17	10.62	13.59	1.02	1.65	9.12	2.26
121	4.04	86.44	0.41	179.35	98.61	2.07	14.87	0.99	2.36	35.25	2.92
122	6.82	89.90	0.89	212.85	126.22	-15.08	35.94	0.92	1.71	50.16	2.58
123	6.43	87.50	0.52	188.33	112.39	4.17	22.64	0.94	1.79	35.93	2.58
124	5.83	79.70	0.47	185.14	95.15	10.94	2.69	1.02	2.39	33.58	2.74
125	4.56	79.71	0.47	193.48	114.89	11.56	13.53	0.93	2.60	32.60	2.78
126	4.24	80.07	0.59	188.62	87.82	5.66	10.26	0.90	2.35	40.03	2.68
127	5.16	79.54	0.81	186.47	90.32	-1.17	12.17	0.99	2.02	9.15	2.60
128	5.50	85.38	2.17	200.91	120.03	-0.48	64.69	0.95	2.18	24.99	2.18
129	5.32	84.92	2.41	198.40	123.66	12.40	19.77	0.93	2.30	29.35	3.11
130	7.05	81.91	-0.50	215.21	129.89	12.40	21.56	0.91	1.97	25.99	2.14
131	6.52	80.96	0.26	181.42	85.21	9.33	22.98	0.93	2.05	53.75	3.06
132	6.15	79.56	0.07	178.53	85.60	17.81	-0.35	0.97	2.06	18.96	2.42
133	7.13	84.39	2.28	211.24	109.83	3.00	-1.30	0.89	1.85	30.91	2.26
134	6.36	81.61	0.55	189.51	88.41	17.79	-4.55	0.94	1.69	33.15	2.56
135	5.24	79.61	0.31	198.41	114.82	8.80	8.51	0.90	2.26	48.25	3.57
SE	1.10	2.22	1.16	14.59	12.28	10.87	12.12	0.12	0.45	20.53	0.44

Appendix 2. Grain yield and agronomic performance of 130 hybrids and five checks at Potchefstroom during 2017/2018 and 2018/2019 cropping seasons

Entry	GY	DA	ASI	PHT	EHT	RL	SL	EPP	HC	ER	EASP
1	7.69	69.00	0.17	206.00	97.00	1.19	7.33	1.10	2.08	3.68	2.42
2	7.70	73.50	0.17	221.83	129.17	4.55	11.27	1.12	2.42	17.40	2.88
3	6.59	73.67	0.67	226.50	117.33	7.02	17.60	0.95	2.08	3.33	2.75
4	8.11	72.83	0.00	219.00	110.50	0.00	2.50	1.07	2.00	4.26	2.42
5	6.99	69.33	0.50	213.67	93.00	2.58	0.00	1.07	2.42	7.07	2.75
6	6.16	74.33	1.00	210.83	107.83	0.00	24.78	0.98	2.00	5.00	3.08
7	7.41	72.50	1.17	217.50	117.00	5.68	18.33	1.00	2.17	4.42	2.58
8	9.18	71.50	0.17	210.67	108.67	0.98	8.68	1.30	1.83	10.52	2.67
9	7.79	72.33	0.33	211.33	104.83	8.33	4.75	1.07	2.17	6.20	2.75
10	5.34	76.67	1.50	218.83	120.67	3.33	5.65	0.87	2.25	0.00	2.92
11	7.67	76.83	2.17	234.67	135.17	2.63	19.68	1.05	1.75	14.93	2.75
12	8.30	75.17	0.67	235.17	139.33	3.87	3.74	1.22	2.33	4.23	2.75
13	6.61	68.50	0.33	193.17	98.83	8.71	13.25	0.97	2.42	7.12	2.67
14	7.35	73.50	0.50	218.17	112.67	3.61	14.48	0.98	1.75	7.50	2.75
15	7.80	73.17	0.50	217.50	117.83	5.13	20.47	0.82	2.67	9.64	2.50
16	8.80	71.33	0.67	220.67	115.67	2.23	10.46	0.97	2.08	8.89	2.58
17	6.39	68.33	0.67	212.83	106.83	32.53	22.54	0.88	2.17	26.27	2.50
18	7.05	72.83	0.83	223.67	117.83	11.24	28.86	1.05	2.33	20.60	2.67
19	6.84	73.00	1.17	219.67	125.33	2.96	26.23	0.85	2.00	22.59	2.50
20	9.30	71.33	0.17	197.50	105.67	3.03	1.04	1.17	1.92	11.98	2.58
21	9.08	70.33	1.17	196.50	95.17	9.16	15.88	1.05	1.92	12.84	2.75
22	8.13	76.50	1.17	211.17	118.17	1.96	14.34	1.17	2.25	8.03	2.83
23	11.33	72.33	0.33	219.00	117.67	1.00	15.55	1.12	2.08	23.43	2.83
24	8.85	72.00	0.50	217.50	114.83	12.77	2.15	1.02	2.33	11.94	3.08
25	8.19	68.50	1.33	200.00	98.33	11.18	6.07	0.95	2.08	15.28	2.67
26	6.99	72.50	1.83	207.67	107.83	2.56	11.97	1.10	1.92	11.37	2.50
27	7.15	73.83	0.17	219.83	124.67	2.23	1.04	0.97	1.92	18.63	2.67
28	11.23	71.33	0.50	210.67	122.33	1.04	1.04	1.20	1.92	17.66	2.50
29	7.81	70.00	0.50	229.50	115.83	1.39	2.26	0.98	2.42	13.37	2.83
30	5.11	76.33	0.83	229.00	126.50	1.33	2.58	0.93	2.17	13.99	2.83
31	7.50	75.17	1.33	231.00	131.00	1.39	7.78	0.97	2.25	17.10	2.83
32	6.25	75.67	0.50	223.67	122.50	0.00	0.00	1.03	2.25	18.86	2.58
33	8.56	73.00	0.17	224.50	118.17	4.44	3.10	1.03	2.83	7.52	2.58
34	5.46	76.17	1.83	224.17	120.83	4.38	10.14	0.95	2.17	3.06	2.92
35	8.02	76.33	1.67	222.83	138.50	2.71	16.96	1.02	2.17	10.83	2.92
36	7.44	75.50	1.17	209.17	131.00	2.86	9.26	0.97	2.00	3.42	2.75
37	8.11	74.00	0.33	223.83	120.83	2.30	0.00	0.98	2.25	12.71	3.00
38	6.39	75.17	1.67	225.17	128.17	9.72	16.49	0.93	2.08	8.12	2.83
39	6.01	79.17	1.33	222.17	141.17	0.00	23.10	0.80	2.17	10.57	2.75
40	8.13	74.83	0.67	213.67	129.50	0.00	11.67	1.00	2.25	9.76	2.83
41	11.13	75.00	0.50	228.33	125.33	0.00	15.63	1.18	2.50	12.22	2.83
42	6.67	78.33	0.83	240.33	138.83	11.66	18.81	1.08	2.25	6.55	2.75
43	5.74	79.50	1.50	245.50	155.67	0.00	26.92	0.92	2.33	12.14	3.08
44	8.03	76.00	0.67	226.50	128.00	1.67	16.93	1.03	2.08	1.39	2.33
45	7.76	69.33	0.50	211.17	102.50	4.76	0.00	1.03	2.17	15.99	2.42
46	5.24	75.83	1.00	240.50	133.50	1.75	11.70	0.83	2.08	11.25	3.00
47	6.46	74.83	0.83	226.83	120.50	0.00	0.00	0.97	2.50	18.16	2.92
48	7.37	74.17	0.67	241.50	131.33	0.00	1.85	1.03	2.25	13.06	2.92
49	9.58	75.67	1.00	226.50	116.17	0.00	1.33	1.17	2.33	19.50	2.75
50	5.98	76.17	0.33	223.00	123.00	0.00	1.50	1.10	2.17	12.62	3.08
51	6.41	79.17	0.50	223.75	127.33	0.00	11.98	1.03	2.08	9.23	2.75
52	9.63	76.83	0.83	215.67	118.50	3.70	1.85	1.22	2.00	9.62	2.50
53	7.83	70.83	0.50	205.67	106.33	14.72	9.71	0.93	2.42	29.93	2.92
54	8.60	74.17	0.67	225.67	118.33	6.07	7.21	1.22	2.75	31.95	2.92
55	6.48	76.83	0.83	216.17	122.67	3.57	6.54	1.12	2.17	25.43	2.75
56	10.39	72.83	0.50	205.17	106.50	2.78	2.50	1.18	2.58	39.10	2.92
57	9.46	70.83	1.00	215.17	105.33	1.83	8.89	1.08	2.25	10.61	2.92

58	7.04	73.50	0.83	234.83	121.33	0.00	17.54	0.97	2.25	6.27	2.75
59	8.37	73.50	0.50	248.67	148.33	8.51	16.11	0.85	2.25	4.81	2.75
60	7.64	73.17	0.50	232.33	129.67	3.13	6.11	1.03	2.08	11.05	2.50
61	7.29	73.50	0.67	225.17	122.00	5.45	4.55	1.20	1.92	11.30	2.83
62	4.71	77.33	1.00	207.83	119.67	1.28	10.09	0.85	2.00	25.83	3.33
63	5.36	78.17	0.67	220.00	128.83	3.38	8.45	0.93	1.67	7.84	2.67
64	7.92	73.50	1.00	216.67	119.83	0.00	10.96	1.07	2.00	8.45	2.75
65	9.70	72.67	0.83	209.67	111.83	3.57	17.69	1.12	2.00	15.19	2.83
66	5.25	78.33	1.67	197.67	112.17	5.00	5.77	0.87	2.50	9.52	3.42
67	7.66	76.33	0.67	219.33	133.83	2.39	17.51	0.97	2.08	9.21	2.92
68	9.25	75.17	0.83	207.83	106.50	3.03	2.56	1.00	2.00	4.55	2.92
69	9.01	71.67	0.33	220.67	117.00	7.44	23.45	1.27	2.42	2.32	2.58
70	2.90	79.40	2.17	176.67	94.17	12.88	21.73	0.60	2.67	0.00	3.42
71	6.45	77.17	0.83	232.50	138.17	8.17	18.18	1.08	1.92	5.09	2.48
72	6.98	72.33	0.33	210.17	122.33	9.17	18.48	1.05	2.33	18.65	3.00
73	7.77	67.83	0.33	203.17	99.17	10.08	1.96	1.08	2.50	14.58	2.83
74	7.09	71.83	0.83	227.50	109.67	3.19	14.86	0.97	2.25	6.80	2.83
75	7.75	72.33	1.00	217.17	116.33	1.17	6.33	1.00	2.33	13.21	2.83
76	6.70	70.83	0.33	203.50	111.67	0.00	6.79	1.07	2.08	7.61	2.75
77	8.22	68.17	0.17	211.17	108.17	13.28	8.83	1.08	2.33	12.10	2.50
78	5.62	73.50	0.33	237.17	142.33	1.85	8.16	1.07	1.92	12.61	2.58
79	8.45	72.50	0.83	226.83	132.67	8.54	11.28	1.07	2.33	15.86	2.67
80	8.17	68.83	0.50	210.33	115.33	14.68	6.35	0.90	2.33	8.57	2.83
81	6.61	74.00	0.50	226.17	132.83	4.71	6.86	1.23	1.83	6.16	2.67
82	7.99	73.00	0.50	230.33	135.33	4.39	6.07	0.93	2.17	11.30	2.83
83	8.01	71.33	0.50	212.50	123.00	6.67	2.08	0.97	2.42	8.07	2.67
84	9.49	72.83	0.50	216.33	115.17	2.56	11.31	1.03	2.42	10.33	2.50
85	6.77	77.17	0.33	224.17	126.67	5.58	3.77	1.00	2.17	0.00	2.42
86	8.68	75.33	0.83	227.50	130.33	2.83	8.81	1.10	2.08	10.94	2.58
87	5.14	77.83	0.33	167.17	99.50	0.93	6.17	0.90	2.00	3.61	3.25
88	6.49	71.00	0.17	213.83	99.33	2.96	17.23	0.92	2.25	24.19	2.50
89	6.39	76.17	1.33	231.00	115.33	0.00	11.59	1.18	2.00	1.52	2.33
90	6.11	78.00	1.50	228.83	128.33	1.52	14.76	0.97	2.17	10.29	2.92
91	7.73	76.17	1.00	221.83	110.50	0.88	0.88	1.00	2.17	4.26	2.17
92	7.39	74.50	1.17	222.17	109.83	1.28	1.00	0.92	2.00	11.89	2.67
93	6.78	76.83	1.00	240.67	130.50	1.04	1.11	0.98	2.08	4.64	2.83
94	7.37	77.67	1.00	237.33	132.67	0.00	1.67	0.90	2.08	2.02	2.83
95	9.88	76.33	0.50	219.67	117.17	0.88	1.75	1.22	1.92	8.15	2.83
96	8.26	72.50	0.83	214.83	111.33	12.52	5.36	1.12	2.17	5.27	2.83
97	4.05	79.50	1.17	202.00	119.33	5.40	21.22	0.87	2.33	7.56	3.17
98	7.41	76.00	1.00	222.50	127.50	5.23	7.24	1.08	1.67	2.58	2.42
99	8.64	73.50	1.17	218.00	124.83	1.11	5.09	1.08	1.75	5.35	2.75
100	7.65	71.83	0.67	207.00	97.17	3.03	11.28	0.87	2.00	7.41	2.25
101	5.53	75.17	0.67	220.67	120.67	3.00	6.90	0.85	1.75	4.70	2.75
102	7.54	74.83	1.00	230.17	127.83	2.56	14.24	0.87	2.25	6.94	2.50
103	9.03	74.67	0.83	197.17	112.50	9.21	5.51	1.03	2.17	3.07	2.83
104	7.67	67.33	0.33	198.33	88.83	0.00	1.96	0.95	2.50	22.45	3.00
105	6.48	72.83	0.83	204.50	105.50	5.27	3.36	0.98	2.25	8.94	2.92
106	6.18	70.83	0.50	216.17	113.17	0.00	2.04	0.95	2.33	16.70	3.00
107	7.94	67.17	0.33	200.33	100.33	1.52	1.67	1.03	2.42	20.97	2.83
108	9.70	75.67	0.83	234.50	138.33	3.03	9.04	1.03	2.33	20.61	3.00
109	5.46	78.83	1.33	231.83	147.50	2.78	22.89	0.90	2.17	1.67	3.08
110	6.83	78.67	3.67	251.83	169.67	8.09	9.64	0.80	2.33	14.07	3.08
111	6.66	78.33	1.00	209.67	129.33	2.78	9.31	0.88	2.67	17.97	2.75
112	8.12	69.00	0.00	191.83	85.83	17.22	0.00	0.98	2.25	9.22	2.58
113	6.91	72.67	1.17	218.50	118.67	18.06	6.13	1.00	2.00	0.00	2.50
114	8.43	72.17	0.83	233.33	124.17	2.86	12.67	1.02	2.33	16.27	2.42
115	8.72	71.33	0.33	195.67	104.33	1.52	3.33	1.07	2.08	5.99	2.58
116	7.59	71.00	0.67	205.17	99.50	4.57	2.08	1.17	2.25	6.15	2.83
117	6.53	73.33	0.50	203.17	112.67	0.00	6.41	1.23	1.75	1.45	2.50
118	7.64	74.00	0.33	220.83	116.67	2.08	18.54	1.13	2.00	4.46	2.67
119	7.88	73.00	0.83	206.17	117.83	7.50	1.11	1.22	2.33	6.11	2.67

120	9.76	74.00	0.33	213.50	114.33	5.18	9.89	0.93	2.50	11.36	2.92
121	4.69	77.33	0.50	202.83	114.83	2.38	16.35	1.08	2.08	10.81	3.00
122	6.35	77.00	0.67	226.33	132.50	6.84	10.26	1.12	1.92	19.34	2.33
123	8.64	76.33	0.33	208.50	117.17	1.17	4.55	1.07	2.33	2.22	2.58
124	6.89	66.33	0.50	201.33	98.00	0.00	1.52	0.90	2.58	22.27	2.67
125	9.28	68.33	0.50	217.83	110.33	0.00	4.22	1.00	2.67	18.90	2.75
126	6.43	67.83	1.00	202.83	103.00	1.11	3.33	1.00	2.67	24.36	2.92
127	7.61	69.83	0.33	215.50	107.83	2.67	6.48	1.00	2.58	17.23	2.92
128	7.27	73.33	0.33	231.00	126.00	1.00	14.24	1.02	2.33	5.09	2.75
129	8.42	72.00	0.50	225.17	124.67	4.72	13.13	0.98	2.00	6.77	2.42
130	8.79	71.00	0.67	214.00	112.17	0.00	6.46	0.98	2.25	10.30	2.42
131	8.77	68.33	0.67	213.50	103.17	6.24	9.06	1.02	2.00	27.16	2.58
132	6.53	71.00	1.00	198.50	98.83	0.00	1.00	1.02	2.08	10.68	2.67
133	8.07	73.83	1.67	234.17	122.67	4.22	11.03	1.07	2.08	3.94	2.08
134	7.70	70.83	0.33	218.17	111.67	0.00	0.98	0.90	2.25	28.10	3.00
135	7.23	70.00	0.71	215.50	116.86	3.06	4.76	0.91	2.50	25.39	2.86
SE	1.27	1.63	0.81	10.30	8.27	8.33	11.15	0.17	0.42	10.37	0.41

Appendix 3. Grain yield and agronomic performance of 130 hybrids and five checks at eight locations in Zimbabwe during 2017/2018 cropping season

Entry	GY	PHT	EHT	DA	ASI	RL	SL	HC	EPP	ER	EASP
1	4.78	231.77	107.12	66.70	1.21	9.44	2.21	0.56	1.14	11.63	3.13
2	5.58	255.09	132.12	70.21	1.88	8.05	1.77	0.50	1.21	6.98	2.86
3	4.78	248.72	126.44	70.84	1.53	7.45	0.92	3.63	1.03	8.40	2.98
4	6.28	235.31	121.97	68.98	1.26	10.78	0.07	-0.13	1.29	7.61	3.11
5	5.31	222.07	108.36	66.13	2.25	12.94	1.09	-0.47	1.06	10.76	2.91
6	5.55	248.01	131.79	71.52	2.28	8.75	2.94	0.27	1.34	13.21	3.36
7	5.16	249.40	131.10	70.44	1.99	9.22	4.97	-0.95	1.22	13.79	2.99
8	6.13	231.36	121.31	67.93	1.19	7.68	2.79	2.20	1.29	11.22	3.13
9	5.11	229.91	113.61	67.80	1.77	10.71	1.67	-0.80	1.03	6.67	2.77
10	5.54	242.85	139.13	70.78	1.95	5.96	-0.15	0.10	1.19	3.42	2.92
11	5.65	254.74	136.74	71.41	2.09	3.87	0.27	0.77	1.14	2.80	2.61
12	7.10	260.22	145.51	69.74	1.21	4.30	0.47	-0.61	1.14	1.01	2.64
13	4.59	218.32	102.04	66.28	2.36	9.44	5.25	2.30	1.06	11.48	3.04
14	5.18	235.52	117.24	69.32	1.69	12.57	0.52	-0.20	0.98	5.92	2.89
15	5.52	229.00	109.95	67.75	1.66	11.32	0.70	0.02	0.93	8.16	2.87
16	6.38	235.44	124.95	66.76	1.33	5.28	-0.25	0.04	1.05	10.14	2.73
17	4.97	223.51	107.19	66.69	1.86	16.73	3.31	2.51	1.13	11.07	3.05
18	5.96	239.84	118.68	68.22	2.27	7.69	0.72	2.37	1.19	8.14	2.94
19	5.62	242.57	127.65	70.94	2.04	11.29	1.76	2.18	1.00	3.10	2.73
20	6.08	242.03	126.54	67.43	1.53	6.02	1.31	2.85	1.20	4.55	2.85
21	5.15	205.82	97.75	66.08	1.82	12.07	4.79	-0.12	1.13	10.31	3.17
22	4.80	231.09	123.19	68.38	1.34	12.06	6.07	1.35	1.16	6.73	2.84
23	5.77	228.22	119.74	66.81	2.29	10.93	3.79	1.35	1.09	7.54	2.78
24	6.11	226.18	116.53	65.55	1.15	8.39	-0.11	0.17	1.15	8.08	2.71
25	4.88	221.24	109.38	66.30	2.33	7.86	2.12	1.74	1.03	7.18	3.04
26	4.50	230.50	117.28	68.51	2.34	11.90	3.37	2.53	1.06	8.20	3.09
27	5.67	224.00	118.23	68.17	1.72	3.81	0.26	2.81	1.07	6.20	2.81
28	6.05	228.27	126.40	66.83	1.79	8.04	0.59	2.90	1.07	7.29	3.03
29	6.02	238.32	121.93	69.06	0.85	5.96	1.76	-0.40	1.07	8.50	2.91
30	5.80	270.85	149.26	72.90	1.19	3.81	3.23	0.31	1.35	1.01	2.85
31	6.33	260.63	142.54	71.95	1.44	5.32	0.66	0.43	1.08	4.10	2.61
32	6.58	259.38	136.63	69.36	0.95	2.16	0.51	1.09	1.33	9.22	2.81
33	5.73	241.71	121.58	68.98	1.80	14.65	0.88	-0.08	0.97	8.98	2.71
34	5.31	245.73	137.35	72.15	1.56	10.53	0.77	0.05	1.25	3.94	2.83
35	6.01	249.57	125.96	70.28	2.47	20.99	-0.62	0.75	0.94	7.60	2.64
36	6.69	235.47	128.86	69.19	1.57	9.03	-1.20	1.87	1.20	0.55	2.82
37	6.41	237.50	120.96	69.28	1.93	6.02	0.35	-0.29	1.07	6.18	2.59
38	5.76	252.52	144.88	72.96	1.69	17.32	-0.59	0.60	1.06	7.03	2.60
39	6.42	257.81	139.59	71.11	1.91	20.82	2.59	0.46	1.03	3.81	2.47
40	6.73	246.88	140.95	68.28	1.35	9.94	-0.69	0.37	1.11	8.54	2.78
41	7.15	247.64	126.21	68.79	2.10	9.36	1.70	0.20	1.05	9.56	2.66
42	5.68	264.96	147.50	74.21	1.86	17.43	-0.02	0.32	1.20	4.06	2.76
43	6.89	278.74	149.82	71.43	1.95	11.24	1.93	-0.20	1.09	5.51	2.47
44	5.94	251.23	140.19	69.49	1.84	8.33	0.31	0.74	1.18	6.89	2.82
45	4.25	229.52	109.51	66.62	1.66	13.74	1.26	-0.55	1.13	10.03	2.99
46	5.06	251.64	131.10	73.23	1.57	8.45	1.72	0.14	1.17	0.88	2.73
47	4.85	245.05	121.89	70.84	2.21	4.09	0.93	-0.11	1.01	3.42	2.75
48	5.74	247.27	130.80	71.38	1.60	7.34	2.30	0.42	1.12	0.92	3.00

49	6.20	230.72	119.30	72.16	1.91	5.18	1.58	-0.37	0.99	13.38	2.79
50	4.43	235.02	123.55	72.16	1.50	7.05	0.47	0.23	1.17	4.44	3.04
51	7.07	247.27	131.61	72.73	2.12	3.27	3.71	0.72	1.08	3.09	2.48
52	6.50	232.30	127.70	69.49	2.09	7.76	1.89	-0.48	1.26	6.03	2.94
53	6.28	206.47	109.12	68.88	1.57	9.87	7.34	1.83	1.13	14.72	3.12
54	5.77	248.75	133.86	70.49	2.98	-0.17	3.48	1.03	1.32	17.63	3.11
55	5.46	248.12	126.35	69.89	2.00	3.18	0.41	0.96	0.99	9.07	2.57
56	6.38	241.93	128.37	69.39	1.58	3.55	1.56	3.80	0.94	19.98	3.03
57	4.62	228.40	108.82	66.85	1.76	15.15	0.36	0.96	1.04	9.00	2.95
58	5.55	253.88	136.21	70.59	1.10	8.23	0.20	0.59	1.05	7.92	2.96
59	6.17	258.94	136.86	66.93	2.12	7.85	2.15	0.54	1.01	3.76	2.64
60	5.94	248.88	132.83	67.71	1.71	4.89	1.76	0.17	1.06	1.78	2.63
61	5.04	224.16	111.80	69.53	2.07	18.92	1.69	0.67	1.08	4.02	3.07
62	3.96	230.65	125.73	73.28	1.67	9.04	1.61	0.25	1.07	2.99	3.42
63	4.77	223.65	116.02	70.91	2.19	11.61	3.69	0.51	1.05	4.06	3.06
64	5.13	230.74	120.38	68.33	1.77	12.98	1.44	1.02	1.16	7.73	3.05
65	5.80	228.70	114.43	70.32	1.98	6.58	0.35	0.54	0.95	8.44	2.86
66	3.24	228.56	124.64	74.38	2.64	8.86	2.21	0.53	1.00	0.88	3.46
67	6.19	244.65	133.78	72.40	1.99	9.90	2.33	0.63	1.07	-0.73	2.55
68	6.09	232.80	130.64	71.80	1.50	5.30	-1.35	0.52	1.09	10.54	2.93
69	5.47	240.38	126.47	69.68	0.89	13.40	5.11	-0.04	1.20	3.17	2.89
70	2.49	216.41	118.49	77.02	2.40	14.89	4.84	3.44	0.76	3.80	3.87
71	5.57	253.27	140.24	71.87	1.87	9.34	-0.11	0.40	1.12	3.23	2.64
72	5.90	233.46	122.17	68.20	1.29	7.46	7.21	1.30	0.99	2.78	2.78
73	4.89	213.84	101.09	65.08	1.66	13.70	3.74	-0.19	1.13	9.07	3.03
74	5.20	231.37	118.33	67.85	2.23	10.93	1.24	6.24	1.09	8.91	2.73
75	5.29	240.22	112.43	68.91	2.00	4.90	1.28	0.77	1.01	3.98	2.52
76	4.85	230.99	121.51	67.45	1.38	9.55	3.33	-0.39	1.04	3.38	2.69
77	4.45	229.47	114.20	67.79	1.74	12.42	2.33	1.19	0.94	4.50	2.97
78	3.57	249.33	131.60	69.04	1.47	8.03	2.07	0.09	0.99	13.86	2.77
79	6.13	245.27	128.36	67.05	1.70	3.39	1.10	-0.70	1.13	15.23	2.85
80	4.87	226.68	106.63	66.36	1.35	19.72	5.22	0.13	0.98	10.77	3.26
81	5.71	242.24	138.16	69.40	1.48	15.50	2.19	0.20	1.17	16.04	2.69
82	4.88	236.41	130.65	68.13	2.31	8.41	2.83	0.73	1.02	6.21	2.88
83	5.36	224.03	130.05	65.97	1.55	5.78	0.30	0.39	1.03	13.91	2.92
84	5.94	226.05	117.37	68.77	1.87	12.15	8.05	1.53	1.04	8.36	2.87
85	6.31	251.91	154.50	74.65	1.00	1.33	3.51	0.59	1.35	2.90	2.67
86	5.61	255.67	147.66	71.05	1.48	4.97	5.41	-1.02	1.11	3.98	2.35
87	2.29	199.64	111.01	74.78	0.76	3.15	2.59	1.25	0.96	13.53	3.61
88	4.79	226.09	106.98	67.68	2.05	7.36	0.51	1.06	1.04	14.75	3.31
89	5.56	262.62	135.21	73.15	2.05	4.06	-0.47	0.89	1.12	8.05	2.91
90	5.92	247.04	131.47	73.33	1.83	0.32	3.23	1.44	1.03	7.60	2.87
91	6.22	245.30	127.72	72.01	1.48	9.85	-0.02	-0.34	1.08	10.13	3.24
92	5.38	239.84	114.82	69.62	1.76	6.12	6.56	2.08	1.02	12.95	3.22
93	5.70	257.92	133.34	73.86	1.59	10.60	2.39	0.57	1.22	8.76	3.17
94	6.23	247.17	127.23	72.83	1.91	11.92	-0.22	0.95	1.12	7.27	2.96
95	5.98	240.38	126.36	73.17	1.24	0.17	-0.18	0.20	1.22	12.64	2.95
96	6.06	229.70	116.09	70.54	1.71	7.85	6.73	0.37	1.06	5.25	2.98
97	3.29	218.63	126.77	74.08	1.38	10.29	4.91	-0.61	1.07	2.26	3.26
98	5.48	241.69	131.94	71.37	1.52	4.99	3.35	0.55	1.10	1.15	2.84
99	6.87	234.95	124.89	70.28	1.46	5.10	4.42	-0.21	1.21	9.31	2.99
100	5.05	216.75	104.45	67.94	2.43	11.71	3.82	-1.19	0.92	11.05	3.03
101	5.00	241.69	115.35	69.25	2.16	5.32	1.73	0.74	1.06	3.95	2.59

102	6.08	249.72	128.09	69.35	2.00	6.72	3.10	1.18	1.04	10.67	2.69
103	5.55	228.47	114.72	69.22	1.32	5.72	-0.11	0.41	1.15	5.39	2.88
104	4.35	218.82	101.81	65.35	1.32	17.45	0.86	0.79	1.07	14.91	3.21
105	4.91	242.06	124.57	68.94	1.29	8.86	3.99	-0.04	1.24	5.66	3.04
106	4.92	234.32	125.59	69.08	1.78	6.32	3.16	0.57	1.08	4.84	2.79
107	5.27	220.73	115.92	66.44	1.43	10.58	-0.13	1.33	1.16	17.69	3.05
108	7.38	243.81	135.88	70.21	1.46	8.15	0.25	-0.30	1.08	10.93	2.54
109	6.43	270.56	154.91	74.64	2.12	16.46	2.22	-0.55	1.41	3.54	2.32
110	6.35	265.26	153.79	71.21	1.90	19.57	-0.67	-0.55	1.02	4.82	2.32
111	6.30	245.94	143.74	70.97	1.17	16.08	0.82	0.41	1.12	3.21	2.48
112	4.59	209.16	97.07	65.87	1.10	13.19	2.44	0.46	1.04	11.72	2.83
113	5.91	239.85	126.73	69.84	1.49	-0.79	3.04	-0.36	1.28	2.65	2.77
114	4.79	240.64	121.47	69.52	2.07	8.69	3.52	2.61	1.05	3.75	2.50
115	5.13	227.09	117.63	66.10	1.70	9.67	2.93	0.57	1.11	10.81	2.97
116	5.25	225.04	114.21	67.41	1.42	5.17	1.99	-1.61	1.03	9.61	3.02
117	5.49	235.08	125.67	70.08	1.09	8.06	3.34	0.47	1.44	9.00	3.25
118	4.51	223.72	118.42	69.22	2.25	-1.49	2.80	-0.30	1.06	-0.40	2.70
119	5.42	214.49	115.85	68.49	1.04	10.76	0.28	-0.43	1.08	4.32	2.97
120	6.43	233.15	113.90	71.66	2.01	10.77	2.80	-1.44	1.03	10.02	2.97
121	4.41	233.40	128.20	74.53	1.31	11.66	3.25	0.79	1.24	4.67	3.09
122	6.60	243.50	132.55	72.86	1.11	3.69	0.91	0.90	1.16	7.06	2.50
123	6.35	229.25	125.61	71.12	1.49	-1.14	-0.45	1.40	1.18	13.76	2.68
124	3.78	227.02	107.80	64.74	1.63	18.64	2.40	0.89	1.06	11.52	3.49
125	3.97	235.71	111.22	66.88	0.88	3.06	0.35	-1.57	0.95	3.81	2.86
126	4.91	231.93	122.57	65.94	1.48	4.79	0.36	-0.14	1.11	5.59	3.19
127	4.97	229.68	112.74	67.72	1.95	13.74	5.66	0.66	1.09	4.25	2.96
128	5.50	252.15	135.26	71.30	1.34	14.34	0.32	0.92	0.93	12.21	2.74
129	5.40	245.82	125.56	67.94	2.13	12.94	0.10	-0.16	1.02	2.20	2.53
130	6.39	234.50	125.35	67.26	0.61	6.50	0.80	1.25	1.15	17.65	2.89
131	4.42	243.92	122.60	66.74	1.46	10.24	1.35	0.24	1.07	23.79	3.41
132	4.92	219.43	112.23	67.05	2.25	7.14	-0.62	3.21	1.10	15.61	3.33
133	4.89	254.80	121.75	67.95	2.38	6.05	2.40	0.34	1.10	8.16	2.58
134	4.29	231.29	120.40	67.16	1.46	15.68	-0.45	0.22	1.00	12.67	2.99
135	3.54	238.01	112.44	66.18	2.47	16.09	1.11	0.74	0.97	14.90	3.45
SE	1.00	15.05	11.58	2.02	1.07	11.58	5.11	3.36	0.17	8.34	0.30

Appendix 4. Grain yield and agronomic performance of 130 hybrids and five checks at 13 locations in South Africa and Zimbabwe during 2017/2018 and 2018/2019 cropping seasons

Entry	GY	DA	ASI	PHT	EHT	RL	SL	HC	EPP	ER	EASP
1	5.64	69.42	0.83	221.96	105.60	7.70	5.87	1.20	1.10	10.99	2.88
2	5.93	73.77	1.11	241.15	129.07	5.45	4.42	1.18	1.13	11.78	2.87
3	5.51	73.63	1.11	234.08	120.80	7.10	4.34	2.91	1.01	11.54	3.03
4	6.35	72.16	0.95	223.96	117.80	7.03	5.23	0.68	1.18	16.05	2.95
5	5.99	69.63	1.33	214.11	103.11	8.21	3.75	0.60	1.07	12.50	2.88
6	5.70	74.10	1.75	232.40	124.11	5.50	11.54	0.77	1.21	10.75	3.13
7	5.79	73.27	1.52	233.58	123.63	9.04	9.65	0.27	1.14	16.89	2.91
8	7.24	70.80	0.88	220.55	116.11	6.66	9.49	2.04	1.25	13.54	2.90
9	5.77	71.09	1.29	219.20	109.31	7.48	6.41	0.28	0.99	13.26	2.79
10	5.23	73.98	1.73	228.51	131.76	2.67	7.48	0.84	1.09	9.03	2.82
11	6.00	75.04	1.80	241.26	134.09	4.77	6.46	1.25	1.08	9.67	2.68
12	7.51	73.82	1.00	247.59	141.11	4.64	3.56	0.55	1.12	5.26	2.65
13	5.08	68.82	1.58	208.48	100.89	7.55	11.69	2.30	1.01	14.78	2.92
14	6.14	72.37	1.25	230.36	114.40	8.45	7.29	0.57	0.99	9.44	2.76
15	6.64	71.65	1.20	219.28	107.59	8.36	7.49	0.92	0.90	9.07	2.70
16	7.36	70.07	1.15	226.45	120.73	5.56	5.12	0.83	1.01	12.92	2.66
17	5.49	69.01	1.42	214.14	105.49	16.36	8.67	2.38	1.06	17.57	2.82
18	6.26	71.44	1.58	233.43	122.20	8.11	12.28	2.38	1.11	15.27	2.84
19	6.12	73.50	1.38	231.65	123.76	8.93	11.30	2.15	0.95	14.66	2.74
20	6.91	70.50	1.09	226.52	121.83	5.00	2.68	2.55	1.16	10.98	2.78
21	6.12	69.38	1.36	199.59	94.47	9.55	13.80	0.73	1.09	19.24	3.02
22	5.69	72.48	1.15	223.06	123.10	8.09	14.49	1.57	1.15	13.34	2.78
23	7.27	71.39	1.62	221.18	119.56	7.72	11.86	1.55	1.07	16.34	2.81
24	6.76	69.73	0.77	220.21	117.36	9.06	3.23	0.96	1.09	15.49	2.81
25	5.45	69.49	1.98	211.91	107.12	9.00	5.02	1.94	0.98	12.80	2.94
26	5.27	71.40	2.01	221.68	118.44	8.74	9.89	2.29	1.06	15.32	2.87
27	6.19	72.23	1.17	221.59	120.67	3.67	4.55	2.45	1.01	16.27	2.79
28	7.45	69.97	1.25	217.71	122.60	5.75	0.89	2.52	1.11	14.23	2.85
29	6.36	71.37	0.69	228.41	117.44	5.03	3.63	0.65	1.03	13.52	2.88
30	5.59	76.06	1.06	252.84	139.50	3.25	3.51	0.96	1.21	10.36	2.90
31	6.89	74.96	1.50	246.87	137.75	5.73	2.83	1.06	1.03	12.78	2.76
32	6.66	73.59	0.94	241.22	129.49	2.69	4.13	1.54	1.23	20.30	2.75
33	6.59	72.39	1.26	231.99	119.96	11.20	2.22	0.93	0.99	15.18	2.71
34	5.40	75.52	1.60	234.22	130.99	9.69	4.12	0.90	1.14	8.73	2.86
35	6.57	74.33	2.06	239.53	128.90	17.25	5.83	1.34	0.94	13.17	2.77
36	6.92	72.65	1.23	225.61	127.75	8.30	4.08	1.90	1.11	7.93	2.81
37	7.22	73.08	1.24	231.37	120.93	5.73	4.87	0.62	1.05	12.17	2.76
38	5.88	75.55	1.53	239.41	137.69	15.04	7.21	1.14	1.06	12.66	2.66
39	6.62	75.40	1.69	244.44	139.30	20.79	8.39	1.03	0.97	7.79	2.60
40	7.00	72.66	1.11	232.85	134.49	10.96	3.73	1.07	1.08	12.46	2.75
41	8.61	73.02	1.27	239.55	124.66	8.98	7.06	1.03	1.09	14.08	2.63
42	6.01	77.86	1.46	249.59	144.40	16.84	6.11	0.90	1.13	10.17	2.76
43	7.10	75.88	1.70	262.83	150.24	15.38	8.39	0.62	1.05	10.48	2.63
44	6.58	73.90	1.33	240.68	136.04	7.76	5.17	1.21	1.13	9.04	2.64
45	5.20	69.46	1.04	218.23	106.20	10.22	6.33	0.54	1.07	16.69	2.81
46	5.23	76.22	1.32	243.59	130.30	6.87	7.85	0.82	1.06	8.42	2.87
47	5.63	74.50	1.47	233.85	122.28	4.05	1.84	0.77	1.00	9.68	2.80
48	6.47	74.75	1.37	237.91	129.28	4.82	3.78	1.16	1.07	5.85	2.90
49	7.02	74.76	1.60	225.34	117.83	3.18	3.40	0.68	1.05	20.21	2.86
50	5.07	75.86	0.98	227.12	121.17	3.19	3.90	0.82	1.14	11.54	3.05
51	6.88	75.96	1.51	235.07	130.47	1.97	9.69	1.18	1.07	6.88	2.58

52	7.49	73.87	1.49	222.65	124.43	4.81	7.37	0.52	1.20	10.86	2.84
53	6.50	71.21	1.22	203.24	106.17	10.99	8.92	2.04	1.05	26.26	3.09
54	6.61	73.42	2.17	232.67	124.66	1.34	5.81	1.58	1.27	19.36	3.04
55	6.20	73.39	1.46	235.45	126.14	2.75	2.27	1.40	1.00	14.55	2.56
56	7.45	72.47	1.11	230.56	124.20	5.13	3.11	3.19	0.99	27.19	2.83
57	5.68	70.11	1.48	223.58	109.45	13.65	3.42	1.43	1.02	16.03	3.05
58	5.91	73.86	0.96	243.80	130.93	7.04	6.03	1.21	1.01	10.41	2.98
59	7.11	71.68	1.29	251.35	139.51	6.36	7.17	1.10	0.98	6.68	2.60
60	6.28	72.00	1.39	237.40	128.30	4.22	5.21	0.79	1.03	7.90	2.61
61	5.83	72.72	1.58	218.66	111.97	12.89	6.86	1.26	1.08	12.94	3.04
62	4.28	76.73	1.29	215.17	118.95	9.14	6.77	1.02	1.03	12.06	3.39
63	4.63	74.84	1.80	218.13	117.29	9.47	6.91	1.03	0.99	17.62	3.16
64	5.97	72.42	1.37	222.19	119.87	8.81	8.37	1.36	1.11	11.78	2.88
65	6.75	73.31	1.58	218.71	112.47	3.36	4.09	1.18	0.97	15.74	2.82
66	4.21	77.20	1.96	217.14	121.10	6.16	8.86	1.14	0.94	7.46	3.39
67	6.31	75.37	1.46	231.13	131.69	7.13	8.46	1.17	1.01	6.68	2.73
68	6.74	74.72	1.21	221.61	123.96	5.42	1.32	1.06	1.02	11.82	2.83
69	6.31	72.19	0.61	230.98	123.48	12.32	11.85	0.87	1.17	9.64	2.70
70	2.31	79.68	2.25	201.79	111.21	12.00	9.24	3.01	0.71	3.80	3.78
71	6.28	74.66	1.52	240.60	137.77	10.97	7.94	1.01	1.09	6.33	2.54
72	6.78	71.81	0.85	222.74	119.62	7.70	10.75	1.57	1.02	10.94	2.74
73	5.70	67.94	1.48	203.36	96.67	11.95	4.66	0.77	1.09	13.80	2.87
74	5.95	71.27	1.70	225.37	113.58	7.30	9.21	4.69	1.05	11.63	2.71
75	6.16	72.71	1.76	227.40	111.72	5.30	6.35	1.35	1.01	9.39	2.64
76	5.75	70.74	0.94	220.60	117.98	5.96	7.63	0.53	1.03	8.34	2.68
77	5.65	69.91	1.22	218.97	110.31	11.10	8.00	1.58	0.95	6.30	2.80
78	4.48	72.61	0.97	240.40	134.82	6.94	3.62	0.76	1.00	15.85	2.67
79	7.18	70.72	1.21	231.13	125.67	8.83	2.13	0.33	1.12	18.62	2.72
80	5.88	69.42	1.21	218.85	110.08	16.65	8.24	1.01	0.98	13.40	3.00
81	5.91	72.90	1.15	231.67	138.10	12.37	10.18	0.84	1.15	16.68	2.63
82	5.53	71.89	1.67	228.28	129.43	9.60	5.17	1.20	0.97	13.51	2.84
83	6.45	69.56	1.09	219.56	129.23	8.16	0.77	1.18	0.96	22.96	2.79
84	7.07	72.81	1.63	220.62	117.49	9.38	10.08	1.74	1.03	8.11	2.71
85	6.49	77.23	0.97	238.89	146.96	3.12	6.88	1.11	1.19	7.35	2.58
86	6.54	74.98	1.13	242.97	140.28	4.42	9.69	0.18	1.10	10.75	2.41
87	2.94	77.51	0.91	186.37	107.17	3.50	3.06	1.59	0.94	15.73	3.45
88	5.38	70.86	1.29	218.06	102.43	5.08	5.93	1.45	1.04	19.29	3.03
89	5.56	75.98	1.73	242.17	125.02	3.31	6.11	1.42	1.11	9.86	2.70
90	6.09	76.78	1.75	237.41	128.66	4.79	8.24	1.71	1.02	9.41	2.85
91	6.69	75.47	1.26	231.57	119.42	8.70	-0.11	0.58	1.04	16.23	2.98
92	5.63	73.02	1.36	229.39	111.84	6.67	6.07	2.06	0.98	17.44	3.07
93	5.85	77.52	1.23	244.99	129.97	10.48	4.23	1.09	1.14	12.24	2.95
94	6.59	76.90	1.42	238.43	126.94	6.62	0.62	1.29	1.08	8.60	2.85
95	6.70	76.85	1.06	228.58	122.29	3.22	3.31	0.85	1.15	18.58	2.96
96	6.64	73.80	1.46	222.64	117.85	8.11	8.06	1.02	1.05	10.05	2.89
97	3.90	77.98	1.11	210.58	121.78	7.01	14.18	0.45	1.01	8.08	3.21
98	6.15	74.52	1.24	231.98	129.12	5.27	6.04	1.04	1.06	4.28	2.67
99	7.42	72.90	1.68	222.14	120.96	5.96	7.15	0.65	1.14	10.99	2.93
100	6.07	70.82	1.96	208.56	99.94	9.04	9.21	0.00	0.93	13.48	2.70
101	5.33	73.62	1.67	231.33	115.43	4.53	7.10	1.21	0.99	9.20	2.63
102	6.63	73.04	1.41	237.64	124.98	7.33	8.30	1.44	1.01	10.88	2.55
103	6.49	73.18	1.39	216.41	113.06	9.55	0.91	1.01	1.10	9.34	2.85
104	5.19	68.31	0.91	207.40	96.92	10.71	4.50	1.36	1.04	18.54	3.09
105	5.42	72.11	1.02	229.08	117.42	6.73	6.98	0.84	1.12	11.82	3.01
106	5.70	71.23	1.26	225.34	119.47	2.78	6.17	1.12	1.05	12.04	2.88
107	5.93	68.81	1.15	211.90	111.93	10.34	1.07	1.66	1.09	19.98	2.91

108	7.95	73.99	0.99	233.50	132.83	7.69	1.72	0.71	1.06	18.13	2.68
109	6.17	77.62	1.86	255.13	151.23	11.89	10.99	0.42	1.21	8.39	2.49
110	6.47	75.74	2.23	252.93	152.96	15.41	6.31	0.43	0.95	11.93	2.59
111	6.55	75.03	0.96	233.21	139.88	10.49	4.05	1.18	1.05	8.51	2.58
112	5.70	68.25	0.66	200.59	91.93	11.38	8.33	1.20	1.02	15.23	2.76
113	6.31	72.19	1.35	230.83	122.57	4.94	6.24	0.43	1.15	6.05	2.69
114	5.69	72.59	1.51	231.89	117.53	7.74	6.45	2.47	1.01	14.10	2.54
115	6.41	70.07	1.13	216.11	114.35	7.65	6.88	1.11	1.07	11.21	2.75
116	6.39	70.95	1.09	213.03	104.91	6.48	6.24	-0.18	1.02	14.63	2.93
117	5.75	73.28	1.00	221.14	118.69	5.60	6.34	0.96	1.33	11.43	3.05
118	5.64	73.17	1.68	219.75	116.73	1.58	7.07	0.62	1.03	2.26	2.67
119	6.26	72.35	1.02	207.52	113.68	11.76	3.95	0.55	1.11	12.95	2.90
120	7.37	74.36	1.71	225.18	114.38	9.25	4.89	0.01	1.01	9.87	2.88
121	4.45	76.85	1.01	219.72	121.13	7.85	9.17	1.30	1.16	9.94	3.03
122	6.62	76.53	0.84	233.63	131.82	1.63	7.22	1.30	1.11	15.92	2.46
123	7.03	74.70	1.04	217.64	122.00	-0.28	3.76	1.63	1.12	14.31	2.62
124	4.77	67.26	1.19	214.42	103.99	13.10	1.68	1.54	1.01	17.41	3.17
125	5.05	69.14	0.67	225.14	111.72	3.38	3.48	0.01	0.95	12.04	2.83
126	5.12	68.72	1.20	217.46	112.33	4.31	0.41	0.92	1.03	14.57	3.00
127	5.65	70.14	1.45	219.13	107.65	9.69	6.15	1.30	1.06	8.86	2.89
128	6.03	73.86	1.33	237.59	129.83	9.39	12.16	1.55	0.95	12.74	2.62
129	6.17	71.55	1.73	233.79	124.78	10.78	4.01	0.78	1.00	7.95	2.61
130	7.05	70.26	0.42	226.83	122.46	4.96	5.14	1.56	1.07	18.46	2.65
131	5.65	69.47	1.09	226.53	112.45	9.05	6.63	0.93	1.07	29.79	3.17
132	5.56	69.81	1.57	208.40	105.10	6.71	1.26	2.77	1.09	14.19	3.02
133	5.83	71.73	2.29	243.16	121.16	5.60	2.67	0.99	1.06	10.26	2.42
134	5.29	70.22	1.08	222.51	114.79	10.90	0.25	0.98	0.97	18.81	2.97
135	4.71	68.65	1.63	226.09	112.78	12.38	0.63	1.40	0.95	22.07	3.35
SE	1.03	1.85	1.14	13.06	10.11	9.68	6.89	2.44	0.22	12.32	0.32

Appendix 5. Grain yield of 130 hybrids and five checks at 13 locations in South Africa and Zimbabwe during 2017/2018 and 2018/2019 cropping seasons

Entry	Site1	Site2	Site3	Site4	Site5	Site6	Site7	Site8	Site9	Site10	Site11	Site12	Site13
1	6.80	4.34	1.64	3.10	4.84	8.39	4.37	5.82	10.40	8.73	3.96	6.79	6.01
2	7.61	5.53	1.94	3.40	6.29	7.68	4.80	4.38	8.22	12.77	2.11	6.13	7.01
3	7.85	4.62	2.36	3.22	4.46	6.76	3.84	7.21	7.71	8.38	3.69	8.05	5.77
4	7.79	5.66	1.12	3.19	6.92	10.77	5.27	4.75	10.40	10.23	3.70	2.92	7.17
5	7.31	5.39	1.45	3.60	5.90	7.37	4.09	6.53	7.07	9.57	4.34	6.61	6.27
6	8.41	5.47	1.98	3.74	5.15	9.72	3.48	4.17	7.49	9.25	1.75	6.95	5.99
7	7.88	5.91	1.39	3.11	5.04	7.09	3.99	4.35	8.87	9.66	3.70	8.29	6.92
8	9.49	6.73	1.40	3.49	7.63	9.16	4.52	8.27	11.69	11.70	4.16	8.60	7.26
9	7.77	4.09	2.39	2.80	5.42	8.50	4.70	6.30	10.66	8.68	4.02	7.46	5.18
10	6.79	4.66	1.56	2.59	6.21	8.65	4.89	4.29	5.76	7.98	2.28	5.64	6.92
11	7.84	5.52	1.78	3.13	6.98	7.87	4.78	6.79	9.33	10.07	3.62	3.16	6.47
12	9.36	6.90	1.78	4.42	8.63	11.06	5.51	8.10	11.64	10.19	3.07	5.73	7.00
13	7.24	4.64	2.50	2.56	5.55	7.42	3.72	4.47	7.12	8.48	4.22	6.24	6.00
14	6.97	5.44	2.43	2.28	7.16	8.09	4.28	7.13	8.23	10.49	3.34	7.65	5.81
15	7.17	5.35	1.48	2.61	7.27	9.40	5.49	9.72	8.48	10.45	4.46	6.11	4.79
16	7.76	7.10	3.42	3.51	6.94	9.10	5.13	10.16	11.21	10.74	4.46	7.70	7.95
17	6.36	5.79	2.20	2.67	5.61	7.07	4.15	3.89	7.55	8.72	2.90	9.87	5.42
18	8.43	6.59	2.55	2.86	5.61	6.37	4.41	4.44	8.50	9.42	3.23	6.52	7.31
19	8.79	4.30	3.87	3.66	7.38	6.38	4.49	4.21	4.85	12.48	3.18	6.75	7.62
20	8.85	6.15	3.06	3.66	7.44	8.27	5.29	6.34	14.70	9.64	3.55	7.10	7.15
21	7.24	4.91	2.01	2.50	5.92	7.56	4.33	3.57	12.79	9.31	5.14	7.27	5.67
22	7.72	5.47	1.51	2.57	5.25	7.93	4.84	4.36	9.92	9.37	5.12	5.99	5.27
23	8.53	4.02	1.80	2.82	5.11	9.91	6.00	7.09	18.08	11.00	4.91	7.18	7.28
24	8.96	6.27	3.37	3.63	6.45	8.22	5.43	5.40	11.29	10.36	4.89	6.81	6.18
25	7.26	4.71	3.39	2.76	5.74	7.56	4.04	3.59	11.03	9.69	3.86	4.83	5.70
26	7.07	5.55	1.05	2.26	4.11	5.01	5.00	7.36	11.17	5.95	3.85	7.06	5.29
27	8.20	6.03	2.85	2.44	7.44	8.20	5.56	8.83	9.31	9.18	2.96	7.35	6.82
28	8.78	5.20	2.35	3.54	8.27	9.43	5.05	6.85	16.43	12.05	5.20	10.62	5.47
29	9.04	6.47	1.46	3.46	6.40	8.40	4.58	7.17	10.00	8.97	4.46	5.40	5.99
30	8.40	7.08	1.08	4.26	6.55	8.15	4.92	4.90	4.78	8.35	2.19	5.67	4.83
31	7.76	7.44	3.24	5.72	5.16	9.25	4.56	7.17	6.95	12.53	3.03	7.03	6.86
32	11.28	6.90	2.01	5.00	7.65	10.70	4.64	3.64	7.50	7.22	4.05	9.64	4.88
33	9.72	5.10	2.11	4.50	7.58	9.25	5.73	6.95	11.53	9.96	4.21	6.88	5.57
34	8.83	5.73	1.46	2.77	5.38	6.58	4.56	6.15	5.94	7.81	2.64	6.58	5.87
35	8.80	4.02	2.02	5.41	7.77	9.27	5.33	6.56	9.80	11.11	3.16	6.74	6.21
36	10.39	6.08	1.61	4.36	7.62	11.93	5.34	5.42	10.42	7.93	3.97	8.90	7.15
37	10.72	5.75	1.92	4.26	8.10	7.67	4.01	8.25	7.36	12.66	4.31	8.88	7.45
38	8.34	4.70	1.65	3.44	6.94	8.25	4.79	5.47	6.85	10.35	1.98	4.08	6.12
39	9.31	4.80	2.16	5.56	8.19	9.28	5.43	7.04	6.27	7.97	3.80	8.75	7.40
40	9.53	6.51	1.90	4.34	8.09	10.06	5.11	6.57	8.32	12.55	3.54	6.79	7.79
41	11.08	5.99	2.05	4.16	6.40	11.19	5.29	7.91	15.55	13.96	3.89	8.31	8.31
42	9.80	7.05	1.39	4.27	5.94	8.68	5.22	7.29	7.07	9.83	3.11	4.75	5.36
43	10.33	6.93	1.72	5.16	5.78	10.84	5.44	7.69	7.73	7.81	1.70	10.91	8.04
44	6.51	6.95	1.92	3.96	7.60	9.50	5.31	4.23	8.47	12.39	3.23	6.71	6.72
45	6.46	4.40	2.04	2.40	4.80	4.98	4.81	4.10	9.57	9.05	4.67	5.05	5.81
46	7.17	5.63	2.44	3.57	5.72	5.90	3.76	6.49	6.79	6.75	2.20	6.41	6.19
47	6.04	4.74	2.38	2.98	6.44	5.96	4.24	5.70	7.04	9.58	2.77	8.46	5.75
48	7.15	6.06	1.44	3.49	6.23	9.03	5.15	8.31	10.09	8.84	3.17	7.01	6.33
49	9.78	5.98	1.48	3.69	6.17	8.56	5.16	4.79	12.05	11.94	4.77	7.63	7.50

50	6.52	5.01	1.30	2.09	4.29	8.91	3.87	6.53	6.64	8.57	2.73	5.74	4.88
51	11.11	6.19	2.38	4.53	7.92	10.47	4.51	5.39	8.47	7.95	2.81	8.05	9.33
52	10.42	6.46	2.81	4.28	6.83	9.29	5.79	6.43	10.90	12.26	5.72	11.16	6.13
53	7.76	6.09	1.95	3.25	7.20	9.94	4.06	4.35	8.92	10.52	4.04	8.55	5.90
54	7.51	6.02	2.49	3.30	5.97	9.28	4.28	6.73	11.47	10.72	3.61	6.13	6.78
55	6.79	5.32	1.93	4.54	5.84	9.34	4.55	7.13	5.61	9.14	4.68	10.09	5.90
56	8.06	5.64	1.33	3.24	7.92	11.23	5.02	5.32	16.56	10.69	3.91	10.75	7.80
57	7.11	4.66	1.25	3.64	6.30	5.25	4.16	6.42	13.37	10.37	4.66	5.20	6.16
58	7.79	6.29	2.49	4.15	4.89	8.58	4.56	7.74	8.79	8.95	3.38	3.58	6.05
59	9.78	5.33	1.66	5.16	6.59	8.88	5.23	6.21	8.13	11.54	5.43	12.05	5.85
60	8.74	7.21	2.15	4.27	4.88	7.36	4.46	2.95	9.03	8.94	4.95	8.97	6.87
61	7.07	4.87	1.84	3.33	5.90	8.28	3.65	6.49	9.43	7.92	4.52	5.66	6.06
62	6.11	3.84	1.37	2.38	3.26	7.03	3.64	6.58	3.82	9.32	0.98	4.43	4.87
63	5.68	4.18	1.41	2.63	5.12	9.89	4.02	3.47	7.34	5.73	3.03	3.57	5.27
64	7.21	5.87	2.05	3.68	5.96	9.03	4.08	4.39	9.46	10.85	3.44	5.34	5.44
65	8.80	4.82	1.36	2.96	5.75	9.40	4.62	6.22	10.10	14.72	4.27	6.04	6.72
66	4.91	3.50	1.55	2.01	3.30	4.26	3.55	8.84	7.74	7.13	0.88	4.56	3.99
67	10.19	5.18	1.86	4.17	6.37	8.80	4.59	3.94	10.80	9.53	2.66	4.35	7.88
68	10.88	6.23	1.33	4.72	7.97	9.17	4.58	6.30	14.25	10.59	2.92	6.73	6.34
69	6.48	5.39	1.21	3.24	6.20	10.46	4.80	4.27	10.15	11.28	5.61	7.46	5.90
70	11.18	1.36	1.12	0.48	1.50	2.83	1.06	1.59	2.24	5.99	0.49	0.43	1.75
71	7.19	5.87	1.47	3.64	5.07	7.50	4.83	7.36	5.93	8.22	5.21	11.02	5.67
72	6.76	5.76	2.57	3.37	7.29	8.59	5.11	5.83	7.54	8.98	4.43	11.43	7.05
73	5.78	3.88	0.96	2.38	5.79	8.38	4.58	5.31	10.84	8.39	4.09	5.98	6.54
74	7.82	5.17	1.99	2.75	5.86	7.11	4.17	6.92	10.36	7.62	3.29	7.56	5.55
75	8.85	3.93	1.73	2.95	7.06	6.96	4.28	8.44	7.05	10.71	5.50	5.17	6.84
76	8.06	4.90	1.83	2.97	6.13	4.97	4.53	5.76	5.66	10.54	3.92	7.34	5.65
77	5.73	4.54	1.35	3.11	4.90	5.17	4.68	4.97	8.89	10.40	5.38	9.72	4.41
78	4.99	5.04	1.75	3.30	4.35	4.22	3.78	3.82	5.86	6.86	4.13	9.05	4.14
79	10.17	7.03	2.20	3.74	7.33	8.64	5.03	6.98	11.19	9.40	4.77	9.49	7.54
80	6.78	4.20	1.21	2.79	4.96	7.92	3.85	4.23	10.37	10.28	3.87	6.97	5.86
81	8.89	5.77	1.00	3.65	7.19	7.79	4.55	5.53	5.83	9.70	4.29	7.39	5.46
82	7.71	5.33	2.30	3.47	5.24	6.53	5.13	2.95	10.20	10.28	3.50	4.89	6.89
83	7.12	5.48	1.28	3.03	5.96	6.39	5.13	6.34	9.90	9.07	5.06	9.41	8.22
84	9.51	5.18	2.70	3.34	7.70	7.65	5.62	4.42	10.98	13.02	4.48	11.24	5.64
85	8.02	6.71	2.82	3.42	6.54	7.99	5.52	5.42	8.55	9.01	2.74	9.50	7.49
86	8.05	6.47	2.43	3.63	7.30	5.97	5.20	3.57	9.24	11.58	5.24	11.34	7.16
87	3.50	2.77	1.14	1.23	3.05	3.45	3.22	2.08	7.92	5.09	2.43	4.01	3.73
88	7.09	4.82	1.85	3.57	5.85	8.37	4.00	6.46	7.62	8.07	3.77	6.37	5.27
89	8.01	6.37	2.40	3.11	6.56	8.26	5.57	6.91	6.55	9.85	2.77	3.69	4.74
90	9.31	4.84	2.57	4.05	6.91	9.00	5.33	5.42	6.57	9.19	2.58	5.21	6.15
91	9.03	6.11	1.34	3.55	7.15	10.37	5.50	5.65	9.70	8.67	4.82	6.49	5.13
92	7.31	4.78	4.92	3.41	5.30	8.26	4.17	5.07	9.81	8.64	3.73	4.30	5.25
93	8.29	5.44	1.93	3.93	5.72	9.21	4.90	7.47	9.14	8.22	2.98	3.82	6.31
94	7.65	6.35	2.40	3.83	6.44	10.73	4.46	5.56	10.13	9.31	2.67	6.36	6.25
95	7.92	5.96	1.33	3.29	6.75	9.45	5.26	4.77	15.21	11.05	3.40	7.47	5.82
96	7.84	5.22	1.06	3.50	7.10	9.81	4.95	4.73	12.32	10.09	2.36	9.08	7.31
97	5.86	3.68	0.72	2.24	3.44	2.48	4.30	7.59	5.18	6.10	0.88	3.15	4.28
98	7.96	4.93	2.06	4.40	6.74	7.00	5.14	7.49	8.04	10.34	3.84	6.94	7.16
99	8.65	6.45	1.48	3.65	8.55	11.86	5.64	9.15	12.75	8.88	4.28	6.51	7.17
100	7.23	4.22	1.69	2.91	5.77	6.67	4.13	9.30	10.28	9.19	3.49	7.83	6.49
101	8.57	5.66	1.25	3.69	4.35	8.26	4.78	5.76	6.26	7.02	3.30	7.26	4.21
102	8.52	5.12	1.93	4.33	6.57	10.18	5.42	3.74	8.75	10.79	3.08	8.92	6.95

103	6.30	5.98	2.37	3.01	6.92	8.28	4.15	5.48	9.97	12.70	4.42	7.33	7.07
104	7.32	4.11	1.19	3.05	4.95	8.45	4.53	4.90	9.68	9.74	3.59	6.70	4.88
105	7.24	4.64	2.27	2.84	4.66	9.29	4.38	6.16	7.96	8.47	3.03	6.77	5.68
106	7.01	5.54	1.56	3.21	3.62	5.57	4.42	6.26	5.99	9.23	3.33	5.73	5.72
107	6.69	5.87	1.77	2.76	5.28	8.71	4.94	5.19	9.66	10.93	3.22	8.01	5.56
108	11.79	5.79	2.47	4.83	8.10	11.47	6.12	7.44	9.86	14.77	4.49	6.91	7.03
109	9.16	7.06	4.01	4.08	4.44	9.67	4.97	6.07	7.58	7.30	1.50	5.67	8.38
110	10.12	6.78	2.83	4.18	7.99	7.58	4.13	9.06	8.61	10.46	1.44	5.44	7.70
111	8.85	7.24	1.48	4.47	7.74	7.08	4.39	8.29	8.40	8.44	3.14	7.79	7.74
112	6.22	5.26	2.46	2.37	4.82	5.87	3.94	5.21	8.56	9.52	6.28	8.63	4.83
113	8.75	6.97	1.34	4.44	4.67	10.14	5.13	5.12	8.36	9.34	3.02	8.05	6.05
114	7.52	4.88	1.60	3.36	4.73	4.95	4.38	8.52	11.29	9.58	4.43	5.98	5.14
115	8.03	4.38	2.18	3.15	6.05	6.25	4.18	8.63	11.17	10.05	4.95	8.89	7.20
116	8.67	5.02	2.32	3.36	4.99	8.49	3.87	7.64	8.02	10.43	4.33	10.28	5.42
117	7.49	5.19	2.74	2.32	5.71	7.83	3.93	6.73	7.11	8.74	3.76	6.05	6.39
118	6.13	5.17	0.94	3.94	4.11	4.24	4.63	9.63	8.93	11.23	2.78	7.16	6.10
119	7.76	5.92	1.14	3.57	5.26	8.85	3.68	7.26	9.35	9.44	4.86	8.49	6.95
120	10.27	5.58	1.56	3.94	6.63	11.40	4.69	6.49	11.78	12.94	4.57	7.79	7.80
121	5.66	4.26	1.70	2.60	3.63	7.79	3.50	3.22	4.53	7.69	1.85	4.33	5.78
122	9.46	6.76	2.65	4.41	8.32	9.84	4.46	9.09	5.22	9.55	4.29	4.70	7.68
123	9.27	5.54	1.75	3.45	7.64	9.37	5.20	4.64	11.53	10.13	4.26	7.87	6.57
124	4.21	3.69	3.20	2.14	3.80	4.01	3.81	7.56	7.57	9.43	3.67	5.73	4.83
125	5.53	3.45	3.53	1.92	4.60	6.07	4.15	5.43	13.63	10.35	3.88	3.52	4.91
126	6.85	5.01	1.48	2.26	5.20	7.78	4.74	3.01	8.09	7.97	3.22	4.52	5.79
127	7.25	5.03	2.31	2.71	7.62	6.61	4.76	3.78	10.16	8.61	4.07	6.29	5.39
128	8.61	4.56	2.60	4.71	5.35	6.92	4.26	5.19	8.22	10.14	3.46	6.81	7.21
129	9.43	5.98	1.82	4.68	8.03	4.73	4.92	5.80	9.72	11.29	4.25	3.51	5.32
130	8.99	6.41	2.51	3.96	6.87	9.88	4.62	5.34	9.70	10.99	5.69	7.99	7.49
131	5.68	4.92	2.08	2.70	3.19	6.97	4.71	8.28	10.81	11.42	4.09	3.54	5.62
132	5.74	4.10	2.89	2.85	6.35	8.78	3.96	3.78	5.94	9.34	4.33	7.68	5.38
133	8.03	5.25	1.05	4.23	5.83	6.21	4.78	7.13	7.57	11.35	5.31	6.92	4.11
134	5.86	4.66	1.27	3.27	4.04	6.65	4.42	5.01	11.97	8.90	2.25	7.73	5.13
135	5.08	4.31	2.67	2.17	3.84	4.90	3.56	5.63	9.80	9.74	2.53	4.94	4.71
SE	2.58	0.81	0.88	0.50	0.93	1.62	0.65	0.89	1.71	1.26	0.56	1.28	1.11

Appendix 6. Biochemical analysis of 130 hybrids and five checks obtained from self-pollinated seed samples at Cedara during 2017/2018 and 2018/2019 cropping seasons

ENTRY	Tryptophan	Moisture	Protein	Oil	Fibre	Starch
1	0.069	13.79	6.55	6.16	2.94	63.51
2	0.080	13.32	6.94	5.01	2.55	65.82
3	0.055	13.23	6.87	5.22	2.43	65.88
4	0.045	13.45	6.97	4.57	2.43	66.62
5	0.072	13.38	7.64	4.83	2.59	65.40
6	0.083	13.49	6.74	4.58	2.42	66.68
7	0.047	12.90	7.04	4.33	2.47	67.65
8	0.035	12.40	7.92	4.84	2.37	65.98
9	0.071	13.83	6.94	5.98	2.76	63.74
10	0.064	14.58	6.27	4.48	2.48	66.47
11	0.045	13.30	7.31	5.63	2.58	65.22
12	0.055	14.27	6.91	6.03	2.56	64.70
13	0.048	14.02	7.03	5.40	2.77	63.92
14	0.068	13.53	6.75	5.66	2.55	64.72
15	0.050	14.21	7.54	4.93	2.55	65.47
16	0.054	13.20	8.16	4.57	2.37	64.65
17	0.063	12.80	6.17	5.41	2.59	66.67
18	0.072	13.34	6.47	4.38	2.42	67.53
19	0.040	14.22	6.83	4.07	2.51	67.42
20	0.031	12.53	7.74	4.18	2.35	65.94
21	0.074	12.52	6.24	5.07	2.56	65.99
22	0.075	12.70	6.89	5.69	2.37	65.05
23	0.057	13.28	7.19	4.95	2.45	65.54
24	0.051	12.74	7.65	4.97	2.37	65.45
25	0.065	14.72	6.15	5.04	2.82	66.03
26	0.072	14.49	7.32	4.72	2.63	64.62
27	0.049	12.73	8.20	5.28	2.57	63.98
28	0.060	14.32	7.94	4.97	2.52	64.45
29	0.081	11.97	8.16	5.54	2.69	62.94
30	0.076	13.25	7.70	6.02	2.65	64.21
31	0.058	13.07	7.87	5.27	2.59	64.26
32	0.042	13.87	7.92	5.99	2.58	63.40
33	0.077	13.60	7.20	6.15	2.46	64.39
34	0.039	12.39	7.92	5.81	2.22	64.81
35	0.040	13.31	7.38	5.87	2.28	65.37
36	0.050	11.90	8.83	5.35	2.37	64.27
37	0.088	14.35	7.02	6.19	2.79	62.90
38	0.066	13.42	6.98	6.02	2.40	65.48
39	0.042	14.06	6.94	4.45	2.33	67.07
40	0.035	13.10	7.57	5.72	2.41	64.71
41	0.071	12.82	7.44	5.76	2.63	64.94
42	0.072	14.30	7.64	5.66	2.32	65.70
43	0.049	13.85	7.61	4.93	2.40	65.90
44	0.032	12.55	7.90	5.43	2.40	64.52
45	0.085	13.39	6.79	5.55	2.77	65.51
46	0.060	13.62	6.71	6.70	2.47	64.77
47	0.039	12.35	7.52	5.12	2.43	65.70
48	0.043	13.80	7.58	6.15	2.45	64.69
49	0.087	13.84	6.94	4.51	2.66	64.95

50	0.075	13.59	6.64	4.74	2.55	66.35
51	0.050	12.85	6.27	4.92	2.62	67.40
52	0.040	13.28	6.56	4.60	2.44	66.74
53	0.044	13.35	6.65	4.65	2.85	64.97
54	0.056	13.96	6.34	5.93	2.42	65.96
55	0.055	12.77	7.36	5.55	2.58	64.94
56	0.038	13.66	7.81	3.87	2.42	64.98
57	0.075	12.72	7.74	4.58	2.70	62.77
58	0.076	12.06	7.69	5.49	2.45	64.26
59	0.051	13.92	8.26	4.72	2.59	63.74
60	0.066	14.17	7.61	5.69	2.55	63.44
61	0.077	14.12	7.67	4.92	2.81	63.75
62	0.072	13.25	5.99	5.28	2.42	67.86
63	0.055	14.25	7.66	4.56	2.36	66.10
64	0.035	13.39	6.88	4.75	2.49	66.58
65	0.077	13.34	7.30	6.44	2.55	63.12
66	0.071	14.24	6.15	5.94	2.32	65.53
67	0.051	13.61	6.92	5.19	2.52	66.00
68	0.031	13.23	7.85	5.63	2.32	64.11
69	0.079	13.45	6.33	5.69	2.49	65.10
70	0.092	14.30	6.42	5.77	2.50	64.91
71	0.049	13.11	6.56	4.87	2.37	67.30
72	0.061	13.40	7.95	4.64	2.33	65.45
73	0.061	13.44	7.38	5.05	2.45	65.22
74	0.077	12.18	7.62	4.58	2.37	65.10
75	0.037	13.65	7.33	3.86	2.42	67.54
76	0.041	13.81	6.99	5.02	2.37	66.43
77	0.074	12.75	8.14	5.57	2.40	64.71
78	0.062	13.20	8.05	4.16	2.24	65.70
79	0.028	12.94	7.75	4.70	2.35	65.96
80	0.075	12.54	8.02	5.93	2.69	64.23
81	0.062	13.43	6.65	5.90	2.51	66.31
82	0.060	12.63	7.58	4.92	2.61	66.31
83	0.034	12.62	8.48	4.92	2.46	65.04
84	0.077	13.74	6.63	5.81	2.64	65.22
85	0.079	13.89	6.09	4.65	2.49	66.66
86	0.036	13.62	7.19	3.83	2.31	67.50
87	0.036	12.70	8.81	4.10	2.53	63.57
88	0.072	13.01	7.13	6.10	2.66	63.55
89	0.075	13.89	7.24	5.48	2.49	63.63
90	0.049	12.92	7.32	5.01	2.53	66.10
91	0.051	13.82	7.65	5.43	2.36	64.84
92	0.077	13.62	6.74	5.30	2.75	64.34
93	0.062	12.80	7.29	6.10	2.47	64.67
94	0.047	13.58	7.41	5.38	2.54	65.01
95	0.035	13.94	7.28	5.33	2.39	65.54
96	0.068	13.16	6.90	5.76	2.58	64.77
97	0.070	13.41	7.39	4.49	2.27	66.05
98	0.042	13.98	6.84	5.09	2.42	65.76
99	0.049	13.63	8.27	5.73	2.26	64.18
100	0.075	13.82	6.41	5.76	2.85	65.02
101	0.060	13.21	7.14	5.78	2.42	64.81
102	0.036	12.97	7.38	4.95	2.49	64.82

103	0.045	13.34	6.77	4.10	2.32	67.05
104	0.072	13.06	6.83	5.06	2.48	65.27
105	0.075	13.31	6.43	4.92	2.48	66.53
106	0.044	13.27	7.96	4.82	2.49	65.02
107	0.039	13.55	6.79	4.78	2.45	66.76
108	0.067	14.81	7.92	5.97	2.54	63.02
109	0.068	13.79	7.46	6.66	2.35	63.42
110	0.044	14.44	7.47	4.97	2.25	66.63
111	0.045	13.19	7.41	5.56	2.42	65.90
112	0.077	13.86	6.17	3.95	2.45	68.14
113	0.074	12.91	7.25	4.56	2.25	66.48
114	0.032	12.89	7.61	4.41	2.45	66.82
115	0.046	13.60	7.20	4.80	2.31	66.49
116	0.074	13.29	7.06	6.74	2.46	65.02
117	0.074	13.33	6.66	6.32	2.55	65.37
118	0.043	13.50	7.85	4.12	2.43	66.32
119	0.048	13.11	7.45	5.76	2.23	65.84
120	0.082	13.11	6.50	4.08	2.66	67.07
121	0.074	13.37	7.03	4.26	2.34	66.54
122	0.044	12.57	8.01	4.59	2.31	66.36
123	0.027	13.50	7.06	4.38	2.34	66.99
124	0.079	12.53	6.88	5.40	2.68	65.86
125	0.040	13.08	7.79	4.37	2.49	66.46
126	0.036	12.82	7.11	5.29	2.53	65.49
127	0.075	11.98	9.21	4.90	2.41	63.36
128	0.079	12.97	7.94	5.72	2.27	64.13
129	0.045	13.00	7.58	4.94	2.57	65.87
130	0.047	13.32	7.22	5.28	2.35	65.25
131	0.077	13.14	7.31	3.80	2.45	65.92
132	0.079	13.17	6.68	5.20	2.56	66.53
133	0.051	12.77	7.59	5.03	2.43	66.20
134	0.043	13.10	8.64	3.78	2.33	65.16
135	0.047	13.08	7.88	4.22	2.48	67.13
SE	0.004	0.77	0.60	0.87	0.12	1.15

Appendix 7. Biochemical analysis of 130 hybrids and five checks obtained from self-pollinated seed samples at Potchefstroom during 2017/2018 and 2018/2019 cropping seasons

ENTRY	Tryptophan	Moisture	Protein	Oil	Fibre	Starch
1	0.072	13.23	6.94	5.06	2.57	64.77
2	0.087	13.73	8.22	5.89	2.50	63.35
3	0.057	14.77	7.50	5.93	2.39	65.17
4	0.052	13.84	8.18	5.75	2.55	63.66
5	0.077	14.00	8.28	5.44	2.70	63.27
6	0.071	14.66	7.13	4.54	2.40	66.61
7	0.030	12.90	9.01	4.85	2.51	64.67
8	0.032	13.07	8.80	5.06	2.20	64.34
9	0.074	13.64	7.64	5.63	2.72	63.08
10	0.073	12.40	7.26	4.89	2.39	65.76
11	0.044	14.22	8.24	5.67	2.54	64.00
12	0.048	14.15	8.40	4.98	2.52	62.63
13	0.079	15.95	7.18	5.38	2.75	63.89
14	0.076	13.70	8.00	4.32	2.66	63.77
15	0.037	15.17	8.29	5.03	2.70	63.32
16	0.036	14.24	9.08	4.79	2.33	62.66
17	0.078	13.61	9.30	4.49	2.59	63.36
18	0.080	14.21	7.97	5.12	2.58	64.71
19	0.031	14.71	7.86	4.79	2.55	65.36
20	0.037	13.12	8.72	5.23	2.54	63.49
21	0.086	14.02	7.96	5.71	2.73	62.27
22	0.074	14.55	7.39	3.89	2.28	64.99
23	0.035	14.02	7.70	6.14	2.52	63.93
24	0.040	13.81	8.31	4.72	2.35	64.43
25	0.076	14.83	7.37	5.21	2.95	63.66
26	0.082	14.58	6.98	4.50	2.62	65.36
27	0.037	16.19	8.07	4.49	2.89	64.30
28	0.042	13.93	8.07	4.44	2.50	63.98
29	0.083	13.34	8.74	6.35	2.87	60.70
30	0.077	15.57	6.84	5.42	2.65	64.22
31	0.030	13.66	8.08	4.24	2.47	65.23
32	0.036	14.50	8.05	5.37	2.59	63.57
33	0.072	14.95	7.92	5.61	2.44	64.23
34	0.079	13.49	8.26	5.52	2.10	65.13
35	0.039	14.12	8.57	5.14	2.30	64.13
36	0.037	12.77	8.94	5.04	2.29	63.58
37	0.075	16.21	6.77	6.47	3.08	62.25
38	0.062	14.72	7.87	5.13	2.57	64.13
39	0.052	14.38	8.65	4.74	2.38	64.25
40	0.036	13.80	8.65	5.71	2.45	63.00
41	0.078	13.19	7.92	6.28	2.50	63.32
42	0.072	13.54	9.11	6.19	2.22	62.25
43	0.027	13.79	8.85	5.65	2.48	63.79
44	0.028	13.79	8.11	5.41	2.25	64.21
45	0.097	14.40	7.47	6.29	2.83	62.38
46	0.082	13.43	8.62	5.01	2.46	62.80
47	0.044	13.45	8.28	4.66	2.16	65.61
48	0.048	14.96	7.56	5.70	2.50	64.06
49	0.074	15.66	7.24	5.58	2.98	62.78
50	0.073	14.90	8.01	4.06	2.59	64.01
51	0.049	14.22	7.37	4.03	2.58	67.85

52	0.044	13.96	7.92	4.43	2.37	64.79
53	0.080	14.65	7.74	4.29	2.73	64.65
54	0.079	15.05	7.86	4.02	2.54	64.50
55	0.058	15.10	8.56	4.40	2.58	64.40
56	0.036	15.48	7.55	4.80	2.50	64.45
57	0.098	13.05	8.61	5.87	2.77	60.63
58	0.078	14.29	8.01	4.44	2.60	63.66
59	0.055	13.70	9.66	4.99	2.57	61.14
60	0.057	13.07	9.87	5.18	2.56	60.17
61	0.075	14.47	6.75	5.12	2.75	65.39
62	0.076	14.56	8.05	3.86	2.45	65.15
63	0.045	13.79	8.15	4.34	2.51	65.69
64	0.037	14.57	8.29	4.59	2.43	64.89
65	0.074	15.17	8.64	5.31	2.69	61.43
66	0.077	13.97	8.07	5.81	2.30	62.89
67	0.055	15.17	7.88	5.06	2.46	64.18
68	0.053	14.27	9.20	4.98	2.42	62.55
69	0.078	14.09	6.73	5.72	2.59	65.21
70	0.083	14.79	7.00	5.11	2.45	64.71
71	0.044	13.62	7.69	4.74	2.48	66.06
72	0.030	13.86	8.72	5.05	2.44	63.96
73	0.078	14.54	8.47	4.86	2.64	63.34
74	0.076	13.27	8.33	4.88	2.43	63.89
75	0.036	15.60	8.49	3.80	2.53	64.06
76	0.039	14.88	8.29	4.32	2.48	64.20
77	0.087	13.14	9.34	5.17	2.42	62.36
78	0.053	13.70	8.76	2.89	2.31	65.76
79	0.036	13.17	8.28	5.34	2.35	64.22
80	0.084	13.76	7.99	5.87	2.66	64.32
81	0.073	14.51	7.96	6.41	2.59	63.64
82	0.045	14.06	8.63	4.80	2.51	64.55
83	0.039	13.89	8.74	5.04	2.41	63.82
84	0.075	14.82	7.88	4.93	2.52	63.49
85	0.081	14.38	8.13	5.12	2.41	63.42
86	0.041	14.52	8.52	4.32	2.47	64.41
87	0.038	12.38	10.22	4.43	2.59	61.76
88	0.074	14.37	8.42	5.51	2.60	61.61
89	0.075	14.62	8.07	5.55	2.63	62.68
90	0.035	15.31	7.78	5.17	2.82	64.45
91	0.053	15.22	8.64	5.84	2.61	61.95
92	0.077	14.61	8.33	4.93	2.58	62.49
93	0.078	13.83	8.38	5.68	2.63	62.06
94	0.059	14.94	8.46	4.89	2.59	63.88
95	0.046	13.67	9.28	5.58	2.45	62.44
96	0.082	14.68	7.40	4.99	2.48	64.88
97	0.079	15.20	8.09	5.13	2.50	63.61
98	0.029	14.66	8.59	4.54	2.34	64.86
99	0.047	13.68	8.24	5.57	2.28	64.31
100	0.073	13.02	7.18	4.34	2.68	65.52
101	0.084	14.84	6.88	4.55	2.48	66.36
102	0.038	15.20	7.76	5.13	2.71	65.04
103	0.036	13.35	7.82	6.42	2.47	63.79
104	0.075	14.79	7.54	5.43	2.82	63.88
105	0.077	13.38	7.42	5.26	2.41	65.51
106	0.032	13.00	9.14	3.87	2.29	64.01
107	0.044	11.89	9.28	4.27	2.42	64.26

108	0.080	13.65	8.68	6.72	2.45	61.78
109	0.085	12.47	10.21	5.59	2.46	59.87
110	0.023	14.80	9.38	5.24	2.89	62.48
111	0.038	14.58	9.34	4.93	2.24	63.00
112	0.070	13.45	8.87	4.32	2.42	64.28
113	0.080	14.02	7.81	6.39	2.54	64.47
114	0.047	13.89	8.55	4.22	2.35	65.43
115	0.032	13.14	8.91	4.20	2.27	65.15
116	0.071	14.38	7.79	6.69	2.49	62.64
117	0.077	14.56	7.07	5.96	2.54	64.98
118	0.052	13.92	8.91	5.92	2.50	64.13
119	0.037	13.90	7.98	5.88	2.47	63.93
120	0.087	13.42	8.18	4.93	2.31	64.95
121	0.082	14.08	7.49	3.71	2.34	65.73
122	0.055	13.58	7.98	4.95	2.40	64.44
123	0.031	13.89	8.53	4.64	2.28	63.98
124	0.073	13.67	8.13	5.08	2.78	63.70
125	0.039	12.55	9.41	4.01	2.43	64.82
126	0.038	13.84	10.30	4.06	2.37	62.00
127	0.076	13.91	9.25	5.18	2.61	62.49
128	0.078	13.35	8.97	4.47	2.35	63.43
129	0.037	14.43	8.56	4.90	2.51	64.29
130	0.034	14.52	8.74	4.12	2.18	63.95
131	0.073	13.01	7.82	4.92	2.36	64.91
132	0.071	14.38	6.89	4.41	2.55	66.86
133	0.053	14.49	8.95	4.40	2.50	63.80
134	0.044	14.26	9.20	5.20	2.46	62.53
135	0.056	13.41	9.09	3.72	2.51	64.59
SE	0.005	1.18	0.65	0.76	0.16	1.20

Appendix 8. Biochemical analysis of 130 hybrids and five checks obtained from self-pollinated seed samples at Harare during 2017/2018 cropping season

ENTRY	Tryptophan	Moisture	Protein	Oil	Fibre	Starch
1	0.084	19.14	8.82	6.27	2.65	68.79
2	0.072	18.38	8.39	6.12	2.57	69.30
3	0.060	19.68	10.28	5.41	2.42	69.18
4	0.049	16.39	11.20	6.06	2.43	68.37
5	0.086	20.13	9.71	5.55	2.71	68.93
6	0.110	20.12	9.13	5.67	2.50	69.35
7	0.066	20.16	10.39	5.09	2.41	69.24
8	0.065	20.66	11.78	5.17	2.46	68.76
9	0.086	21.81	9.15	6.19	2.77	68.09
10	0.073	18.47	7.69	5.77	2.45	69.58
11	0.055	16.62	10.63	4.81	2.50	70.43
12	0.055	19.54	9.58	4.92	2.43	70.65
13	0.090	23.22	9.10	6.07	2.82	68.47
14	0.079	15.87	7.63	5.61	2.67	70.21
15	0.052	19.97	10.22	4.95	2.67	69.30
16	0.068	20.46	10.89	5.36	2.37	68.78
17	0.080	18.70	10.07	5.37	2.56	69.60
18	0.070	15.47	8.69	4.96	2.47	71.27
19	0.047	18.74	10.77	4.80	2.51	69.92
20	0.051	18.97	10.64	5.05	2.37	69.50
21	0.073	20.59	8.91	6.12	2.51	68.51
22	0.082	19.54	8.59	5.50	2.30	70.02
23	0.049	22.60	10.00	5.40	2.50	68.95
24	0.057	20.18	10.07	5.26	2.26	69.71
25	0.074	24.07	9.16	5.87	2.87	68.29
26	0.092	18.28	7.73	5.30	2.65	70.55
27	0.063	21.57	9.60	5.06	2.75	69.45
28	0.061	21.18	10.54	4.82	2.40	69.22
29	0.086	20.21	10.07	6.37	2.70	68.07
30	0.083	17.72	9.00	6.21	2.54	68.53
31	0.064	20.32	10.82	5.47	2.54	68.60
32	0.064	19.72	10.55	5.81	2.45	68.63
33	0.082	21.49	10.37	6.17	2.51	68.48
34	0.098	17.19	10.63	6.74	2.18	67.59
35	0.055	19.89	10.66	5.92	2.34	68.35
36	0.045	19.82	11.77	5.92	2.36	68.22
37	0.097	23.41	9.75	7.69	3.01	66.19
38	0.092	19.13	9.03	6.24	2.52	68.58
39	0.056	18.34	10.00	5.94	2.45	68.89
40	0.057	21.15	11.32	5.86	2.53	68.39
41	0.077	19.17	10.76	6.93	2.45	67.43
42	0.109	16.88	10.35	6.74	2.39	67.75
43	0.061	19.64	10.86	6.10	2.57	68.17
44	0.062	17.23	12.62	6.30	2.51	67.30
45	0.088	19.74	8.74	6.37	2.81	68.66
46	0.086	16.89	9.17	6.72	2.47	68.55
47	0.058	20.31	10.44	5.72	2.33	68.90
48	0.050	17.17	10.52	6.33	2.47	68.51

49	0.074	23.06	8.43	5.57	2.98	69.08
50	0.089	19.92	8.07	5.33	2.58	70.02
51	0.048	18.52	9.98	5.67	2.44	69.48
52	0.068	19.27	9.58	5.29	2.38	69.36
53	0.084	23.47	9.07	5.67	2.82	68.86
54	0.083	19.25	8.34	5.68	2.69	69.47
55	0.072	18.95	9.77	5.27	2.69	69.28
56	0.053	21.84	10.72	5.32	2.42	68.88
57	0.088	19.85	8.86	6.43	2.70	68.38
58	0.085	18.31	8.64	6.43	2.69	68.57
59	0.058	18.26	10.83	5.58	2.49	68.80
60	0.047	16.96	10.83	6.19	2.54	67.95
61	0.086	20.40	9.10	6.02	2.85	68.64
62	0.087	18.69	8.57	5.66	2.52	69.60
63	0.057	17.82	9.89	5.79	2.53	69.17
64	0.050	21.02	10.05	4.82	2.36	69.84
65	0.096	20.66	9.02	6.27	2.67	68.30
66	0.078	17.45	9.60	6.64	2.40	67.94
67	0.065	21.07	9.97	4.85	2.46	69.76
68	0.060	18.36	10.77	5.63	2.47	69.34
69	0.083	21.03	7.40	5.98	2.71	69.60
70	0.071	17.88	9.20	6.22	2.46	68.63
71	0.058	22.72	9.31	5.58	2.61	68.81
72	0.044	17.88	10.89	5.87	2.32	68.55
73	0.081	19.32	9.67	4.96	2.51	69.58
74	0.083	20.48	9.41	5.36	2.51	69.64
75	0.055	18.29	9.74	4.75	2.42	70.28
76	0.054	19.47	10.18	5.06	2.55	69.37
77	0.075	20.66	10.89	5.84	2.53	68.41
78	0.055	17.63	10.61	4.96	2.32	69.75
79	0.058	19.61	11.61	5.21	2.38	69.39
80	0.081	15.54	11.38	6.05	2.71	68.17
81	0.077	18.37	9.04	5.86	2.46	69.10
82	0.060	17.80	9.97	5.14	2.67	69.92
83	0.046	18.61	10.18	4.63	2.30	70.58
84	0.087	24.56	10.31	5.22	2.69	68.85
85	0.073	18.40	9.17	5.19	2.38	70.14
86	0.042	20.43	10.30	4.90	2.45	69.73
87	0.050	15.81	10.62	4.50	2.57	71.07
88	0.073	20.31	9.26	6.57	2.72	68.29
89	0.092	20.70	8.94	6.45	2.58	67.99
90	0.050	18.09	10.50	5.41	2.67	69.10
91	0.042	18.90	10.15	5.91	2.46	69.70
92	0.079	20.43	9.94	6.05	2.46	68.52
93	0.076	19.53	8.32	5.96	2.54	69.63
94	0.054	17.58	10.69	5.57	2.50	69.13
95	0.052	20.29	10.62	5.62	2.56	68.92
96	0.075	18.33	9.03	6.48	2.62	68.60
97	0.084	16.78	9.02	5.47	2.33	69.88
98	0.060	19.56	10.22	5.51	2.46	69.09
99	0.044	18.62	11.00	5.59	2.32	69.00
100	0.074	21.49	7.59	5.70	2.69	69.84
101	0.096	16.88	7.78	5.59	2.57	70.93

102	0.070	21.90	10.50	6.07	2.71	68.31
103	0.042	17.52	9.95	6.05	2.46	69.12
104	0.082	21.33	9.97	5.47	2.90	68.67
105	0.077	18.63	8.40	5.32	2.37	69.72
106	0.054	17.65	10.62	4.99	2.37	69.71
107	0.052	16.44	10.59	4.81	2.43	70.43
108	0.086	22.32	11.26	6.15	2.46	67.77
109	0.119	20.16	9.95	6.38	2.53	68.57
110	0.032	18.84	9.73	6.08	2.78	69.21
111	0.052	19.84	11.34	5.85	2.21	68.86
112	0.079	16.85	10.51	5.66	2.48	69.35
113	0.086	17.63	9.59	5.59	2.48	69.12
114	0.048	19.20	10.15	5.11	2.21	69.95
115	0.056	18.47	10.73	5.33	2.30	69.37
116	0.094	17.84	10.42	6.19	2.53	68.66
117	0.076	20.26	8.70	5.58	2.38	70.30
118	0.048	19.98	9.19	5.36	2.44	69.76
119	0.039	21.75	11.39	5.54	2.27	68.54
120	0.079	21.66	8.90	5.52	2.51	69.18
121	0.087	18.91	8.57	5.71	2.29	69.81
122	0.039	18.41	10.56	5.13	2.38	69.05
123	0.054	17.31	10.84	5.68	2.48	68.50
124	0.077	17.31	10.59	4.82	2.75	70.26
125	0.052	18.14	10.61	4.57	2.50	69.85
126	0.053	15.92	11.21	4.63	2.34	70.49
127	0.094	18.59	11.67	5.66	2.58	68.78
128	0.085	18.97	10.70	5.43	2.44	68.91
129	0.061	22.13	10.92	4.66	2.44	69.46
130	0.048	21.74	10.65	5.02	2.21	69.20
131	0.081	18.44	9.50	5.08	2.33	70.58
132	0.082	19.74	9.88	6.17	2.44	67.85
133	0.043	22.60	10.17	4.92	2.55	69.38
134	0.045	17.49	10.13	4.47	2.35	70.61
135	0.044	18.42	10.30	3.39	2.45	71.95
SE	0.006	1.95	0.57	0.32	0.16	0.63

Appendix 9. Biochemical analysis and grain yield of 130 hybrids and five checks obtained from self-pollinated seed samples at across during 2017/2018 and 2018/20121 cropping season

ENTRY	Tryptophan	Grain yield	Moisture	Protein	Oil	Fibre	Starch
1	0.075	5.64	15.39	7.44	5.83	2.72	65.69
2	0.080	5.93	15.14	7.85	5.67	2.54	66.15
3	0.057	5.51	15.89	8.22	5.52	2.41	66.74
4	0.049	6.35	14.56	8.78	5.46	2.47	66.22
5	0.078	5.99	15.83	8.54	5.28	2.67	65.86
6	0.088	5.70	16.09	7.67	4.93	2.44	67.55
7	0.048	5.79	15.32	8.81	4.76	2.46	67.18
8	0.044	7.24	15.37	9.50	5.03	2.34	66.36
9	0.077	5.77	16.43	7.91	5.93	2.75	64.97
10	0.070	5.23	15.15	7.07	5.05	2.44	67.27
11	0.048	6.00	14.72	8.73	5.37	2.54	66.55
12	0.053	7.51	15.99	8.30	5.31	2.50	65.99
13	0.072	5.08	17.73	7.77	5.62	2.78	65.43
14	0.075	6.14	14.37	7.46	5.20	2.63	66.23
15	0.046	6.64	16.45	8.68	4.97	2.64	66.03
16	0.053	7.36	15.97	9.38	4.91	2.36	65.36
17	0.074	5.49	15.04	8.51	5.09	2.58	66.54
18	0.074	6.26	14.34	7.71	4.82	2.49	67.84
19	0.039	6.12	15.89	8.49	4.55	2.53	67.57
20	0.040	6.91	14.87	9.03	4.82	2.42	66.31
21	0.078	6.12	15.71	7.71	5.64	2.60	65.59
22	0.077	5.69	15.60	7.62	5.03	2.32	66.69
23	0.047	7.27	16.63	8.30	5.50	2.49	66.14
24	0.049	6.76	15.58	8.68	4.98	2.33	66.53
25	0.072	5.45	17.87	7.56	5.37	2.88	65.99
26	0.082	5.27	15.79	7.34	4.84	2.63	66.84
27	0.050	6.19	16.83	8.62	4.94	2.73	65.91
28	0.054	7.45	16.48	8.85	4.74	2.47	65.88
29	0.083	6.36	15.17	8.99	6.09	2.75	63.90
30	0.079	5.59	15.51	7.85	5.88	2.62	65.65
31	0.050	6.89	15.68	8.93	5.00	2.53	66.03
32	0.048	6.66	16.03	8.84	5.72	2.54	65.20
33	0.077	6.59	16.68	8.50	5.98	2.47	65.70
34	0.072	5.40	14.36	8.94	6.03	2.16	65.84
35	0.045	6.57	15.77	8.87	5.64	2.31	65.95
36	0.044	6.92	14.83	9.84	5.44	2.34	65.36
37	0.087	7.22	17.99	7.84	6.78	2.96	63.78
38	0.073	5.88	15.76	7.96	5.79	2.50	66.06
39	0.050	6.62	15.60	8.53	5.04	2.38	66.74
40	0.043	7.00	16.01	9.18	5.77	2.46	65.36
41	0.075	8.61	15.06	8.71	6.32	2.53	65.23
42	0.084	6.01	14.91	9.03	6.19	2.31	65.23
43	0.045	7.10	15.76	9.10	5.56	2.48	65.95
44	0.041	6.58	14.52	9.54	5.71	2.38	65.34
45	0.090	5.20	15.84	7.67	6.07	2.81	65.52
46	0.076	5.23	14.65	8.16	6.14	2.47	65.37
47	0.047	5.63	15.37	8.74	5.17	2.31	66.74
48	0.047	6.47	15.31	8.55	6.06	2.47	65.75
49	0.078	7.02	17.52	7.54	5.22	2.88	65.60
50	0.079	5.07	16.14	7.57	4.71	2.57	66.79
51	0.049	6.88	15.19	7.87	4.87	2.55	68.24

52	0.051	7.49	15.50	8.02	4.77	2.40	66.96
53	0.069	6.50	17.16	7.82	4.87	2.80	66.16
54	0.073	6.61	16.09	7.51	5.21	2.55	66.64
55	0.062	6.20	15.61	8.56	5.07	2.62	66.21
56	0.042	7.45	16.99	8.69	4.66	2.45	66.10
57	0.087	5.68	15.21	8.40	5.63	2.72	63.92
58	0.080	5.91	14.89	8.11	5.45	2.58	65.49
59	0.055	7.11	15.29	9.58	5.09	2.55	64.56
60	0.057	6.28	14.73	9.44	5.69	2.55	63.85
61	0.079	5.83	16.33	7.84	5.35	2.80	65.93
62	0.078	4.28	15.50	7.54	4.93	2.47	67.54
63	0.052	4.63	15.28	8.57	4.90	2.47	66.99
64	0.041	5.97	16.33	8.40	4.72	2.43	67.11
65	0.082	6.75	16.39	8.32	6.01	2.64	64.28
66	0.075	4.21	15.22	7.94	6.13	2.34	65.45
67	0.057	6.31	16.62	8.26	5.03	2.48	66.65
68	0.048	6.74	15.29	9.27	5.41	2.40	65.33
69	0.080	6.31	16.19	6.82	5.80	2.60	66.64
70	0.082	2.31	15.66	7.54	5.70	2.47	66.08
71	0.050	6.28	16.48	7.85	5.06	2.49	67.39
72	0.045	6.78	15.05	9.19	5.19	2.36	65.99
73	0.073	5.70	15.77	8.51	4.96	2.53	66.04
74	0.079	5.95	15.31	8.45	4.94	2.44	66.21
75	0.043	6.16	15.85	8.52	4.14	2.46	67.29
76	0.045	5.75	16.05	8.49	4.80	2.47	66.67
77	0.079	5.65	15.52	9.46	5.53	2.45	65.16
78	0.056	4.48	14.84	9.14	4.01	2.29	67.07
79	0.041	7.18	15.24	9.21	5.08	2.36	66.52
80	0.080	5.88	13.95	9.13	5.95	2.69	65.57
81	0.071	5.91	15.44	7.88	6.05	2.52	66.35
82	0.055	5.53	14.83	8.73	4.95	2.60	66.93
83	0.040	6.45	15.04	9.13	4.86	2.39	66.48
84	0.080	7.07	17.70	8.28	5.32	2.62	65.85
85	0.078	6.49	15.56	7.80	4.99	2.43	66.74
86	0.040	6.54	16.19	8.67	4.35	2.41	67.21
87	0.041	2.94	13.63	9.88	4.35	2.56	65.47
88	0.073	5.38	15.90	8.27	6.06	2.66	64.49
89	0.081	5.56	16.40	8.08	5.83	2.57	64.77
90	0.044	6.09	15.44	8.53	5.20	2.67	66.55
91	0.049	6.69	15.98	8.81	5.73	2.48	65.50
92	0.078	5.63	16.22	8.34	5.43	2.60	65.12
93	0.072	5.85	15.38	8.00	5.91	2.55	65.45
94	0.053	6.59	15.36	8.85	5.28	2.55	66.01
95	0.044	6.70	15.97	9.06	5.51	2.47	65.63
96	0.075	6.64	15.39	7.78	5.74	2.56	66.08
97	0.078	3.90	15.13	8.17	5.03	2.37	66.51
98	0.044	6.15	16.06	8.55	5.05	2.41	66.57
99	0.047	7.42	15.31	9.17	5.63	2.29	65.83
100	0.074	6.07	16.11	7.06	5.27	2.74	66.79
101	0.080	5.33	14.98	7.26	5.31	2.49	67.37
102	0.048	6.63	16.69	8.55	5.38	2.64	66.06
103	0.041	6.49	14.73	8.18	5.52	2.42	66.65
104	0.076	5.19	16.39	8.11	5.32	2.74	65.94
105	0.077	5.42	15.11	7.42	5.16	2.42	67.25
106	0.043	5.70	14.64	9.24	4.56	2.38	66.25
107	0.045	5.93	13.96	8.89	4.62	2.43	67.15

108	0.078	7.95	16.93	9.29	6.28	2.48	64.19
109	0.091	6.17	15.48	9.20	6.21	2.45	63.96
110	0.033	6.47	16.03	8.86	5.43	2.64	66.10
111	0.045	6.55	15.87	9.36	5.45	2.29	65.92
112	0.075	5.70	14.72	8.52	4.64	2.45	67.26
113	0.080	6.31	14.85	8.22	5.51	2.42	66.69
114	0.043	5.69	15.33	8.77	4.58	2.34	67.40
115	0.045	6.41	15.07	8.95	4.78	2.29	67.00
116	0.080	6.39	15.17	8.42	6.54	2.49	65.44
117	0.076	5.75	16.05	7.48	5.95	2.49	66.88
118	0.048	5.64	15.80	8.65	5.13	2.46	66.74
119	0.041	6.26	16.26	8.94	5.73	2.32	66.10
120	0.083	7.37	16.06	7.86	4.84	2.50	67.07
121	0.081	4.45	15.45	7.70	4.56	2.32	67.36
122	0.046	6.62	14.85	8.85	4.89	2.37	66.62
123	0.037	7.03	14.90	8.81	4.90	2.37	66.49
124	0.076	4.77	14.51	8.53	5.10	2.74	66.61
125	0.044	5.05	14.59	9.27	4.32	2.47	67.04
126	0.042	5.12	14.20	9.54	4.66	2.41	65.99
127	0.082	5.65	14.83	10.04	5.25	2.53	64.88
128	0.081	6.03	15.10	9.20	5.21	2.35	65.49
129	0.048	6.17	16.52	9.02	4.83	2.51	66.54
130	0.043	7.05	16.53	8.87	4.81	2.25	66.13
131	0.077	5.65	14.86	8.21	4.60	2.38	67.13
132	0.077	5.56	15.76	7.82	5.26	2.52	67.08
133	0.049	5.83	16.62	8.90	4.78	2.49	66.46
134	0.044	5.29	14.95	9.32	4.48	2.38	66.10
135	0.049	4.71	14.97	9.09	3.77	2.48	67.89
SE	0.005	1.03	1.39	0.61	0.69	0.15	1.03

Appendix 10. GCA of 33 lines and four testers for grain yield and agronomic traits for trials evaluated at Cedara during 2017/2018 and 2018/2019 cropping seasons

Line	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	Ear rot	EA
1	-0.715	-1.28	-0.31	-4.21	-6.19	-4.05	-7.50	0.00	-0.08	-4.44	0.13
2	0.252	-1.16	-0.44	-2.80	-4.32	0.32	5.08	0.02	-0.05	-4.93	-0.13
3	-0.537	0.47	-0.25	-1.55	1.93	-3.04	9.55	-0.02	-0.01	6.75	0.19
4	0.926	-3.03	0.19	1.73	-6.35	-2.03	0.91	-0.05	-0.05	-6.58	0.00
5	-0.330	-2.97	-0.13	-1.71	-3.07	0.30	4.92	0.02	0.17	0.11	-0.06
6	-0.512	-1.22	-0.31	-1.71	-3.25	-5.59	12.07	0.04	0.02	5.21	-0.03
7	0.593	-2.10	0.06	0.92	4.43	-6.56	0.23	0.04	-0.08	-5.80	-0.09
8	-0.143	0.90	0.44	7.67	3.81	-2.16	-11.03	0.00	-0.08	2.65	0.35
9	0.303	0.47	0.00	10.79	10.37	7.25	-4.26	0.02	0.17	8.29	0.06
10	0.508	1.40	-0.19	11.89	13.65	17.90	-1.38	-0.01	-0.11	1.40	0.07
11	0.756	3.53	-0.06	12.26	17.25	21.27	-4.88	0.01	-0.08	2.47	0.03
12	-0.030	1.72	0.06	3.92	3.03	-1.19	0.44	-0.06	0.20	7.43	0.03
13	0.495	1.65	0.00	-0.77	2.40	-6.40	2.52	0.02	-0.26	-0.38	0.03
14	0.911	-1.78	0.12	4.01	-0.41	-3.16	-4.59	0.00	-0.11	1.80	-0.09
15	0.170	1.65	-0.19	11.73	6.15	-0.29	0.27	0.01	-0.08	-1.20	0.16
16	-1.479	1.53	-0.25	-7.02	-6.35	-4.25	5.86	-0.01	0.05	16.01	0.38
17	-0.598	1.09	0.25	-10.93	-5.72	-6.39	-5.53	-0.07	0.08	-3.32	0.25
18	-0.299	1.47	0.12	-6.55	0.06	-0.31	-0.23	-0.05	-0.05	-6.65	0.06
19	0.090	-2.97	0.25	-5.77	-12.00	-3.14	-1.72	-0.03	0.24	-2.64	-0.09
20	0.867	-2.07	-0.61	-0.30	-0.05	2.47	-6.70	0.03	-0.07	8.70	-0.09
21	-0.507	-2.47	0.00	5.01	13.25	5.21	1.46	-0.03	-0.08	1.66	-0.25
22	-0.021	3.40	1.25	-3.89	6.62	-1.27	-2.29	0.03	-0.01	-4.90	-0.25
23	-0.695	2.09	-0.06	-3.33	-10.57	4.43	-5.16	0.02	0.11	5.60	0.00
24	-0.867	4.34	-0.31	8.45	0.37	-0.31	-6.61	0.04	-0.17	-3.71	-0.06
25	0.358	2.22	0.37	-9.33	-1.50	-4.22	4.51	0.02	0.02	-1.49	0.03
26	0.482	0.53	0.06	-2.02	-9.00	2.74	2.58	0.02	-0.14	-4.32	-0.28
27	-0.256	-3.78	-0.19	-7.18	-11.66	1.40	-2.76	0.02	0.08	-0.65	0.13
28	0.613	3.28	0.06	10.17	18.18	0.52	1.14	0.01	-0.01	3.23	0.13
29	0.909	-3.78	-0.13	0.29	-7.44	-4.56	5.50	0.01	-0.14	-3.90	-0.31
30	1.434	-0.16	-0.06	-11.86	-11.35	3.94	-5.29	0.01	-0.01	-9.70	-0.12
31	-0.454	2.34	0.25	-4.36	0.37	-4.54	8.83	0.02	-0.01	0.43	-0.14
32	-1.508	-6.41	-0.52	-1.97	-8.59	-3.42	-7.44	-0.05	0.43	-3.33	0.03
35	-0.879	-1.03	0.25	-2.18	3.81	-1.12	7.98	-0.02	0.20	-2.45	-0.09
SE	0.740	1.02	0.31	5.10	4.19	4.89	3.99	0.04	0.15	6.62	0.17
Tester									GCA		
1	-0.007	-2.20	-0.03	-4.48	-9.71	-3.96	0.37	-0.01	0.08	1.71	0.02
2	-0.650	0.99	0.09	3.29	4.43	-1.53	4.75	0.02	-0.05	-2.97	0.01
3	0.234	1.20	0.06	5.83	6.09	3.97	-0.56	-0.01	-0.01	0.43	0.03
4	0.383	0.08	-0.12	-4.45	-0.54	1.44	-4.28	0.00	-0.02	0.64	-0.06
SE	0.354	0.40	0.07	2.94	1.86	2.62	0.66	0.00	0.05	1.28	0.07

Appendix 11. SCA of 130 hybrids for grain yield and agronomic traits for trials evaluated at Cedara during 2017/2018 and 2018/2019 cropping seasons

Entry	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	Ear rot	EA
1	0.556	-1.42	-0.10	6.51	3.15	7.53	7.55	0.03	0.26	3.44	-0.36
2	0.148	0.89	-0.47	6.86	0.89	-2.57	-6.86	0.01	0.02	-7.25	-0.10
3	1.639	-0.32	-0.44	-5.05	-4.53	-1.41	-2.74	-0.03	-0.27	-9.06	0.25
4	-2.304	0.80	1.00	-8.52	0.23	-3.46	1.76	-0.01	-0.01	13.04	0.21
5	-0.145	2.95	0.03	-10.52	-8.10	-1.62	-13.05	0.01	0.61	6.49	0.39
6	-0.511	-0.49	-0.09	4.21	7.14	-6.04	-2.73	0.07	-0.14	-5.26	-0.35
7	-0.637	-0.95	0.19	-3.33	-8.91	9.33	8.99	-0.02	-0.05	-1.85	-0.02
8	1.332	-1.58	-0.13	9.45	9.60	-1.57	6.51	-0.06	-0.42	0.80	-0.03
9	0.956	-0.42	0.59	1.35	-6.22	-1.14	-0.66	0.00	-0.30	-4.31	-0.30
10	-0.319	-2.86	-0.03	-15.79	-10.36	-1.65	7.64	0.03	-0.42	8.69	-0.04
11	-1.192	1.93	-0.25	-0.83	3.59	5.26	-7.27	-0.01	0.17	6.38	0.19
12	0.595	1.30	-0.32	15.07	12.73	-2.38	0.01	-0.02	0.55	-10.58	0.15
13	-2.031	-0.92	0.15	-14.43	-6.07	0.34	9.33	-0.10	0.23	11.47	0.26
14	0.641	0.64	0.53	22.80	4.79	-4.59	2.47	0.06	-0.01	4.49	-0.23
15	0.282	0.43	-0.69	-10.36	-5.62	-7.27	-15.12	0.02	-0.17	-19.48	0.00
16	1.147	-0.20	0.00	1.79	6.63	11.61	3.03	0.01	-0.04	3.70	-0.04
17	0.746	-0.73	0.47	-14.74	-4.35	-4.49	-10.50	0.03	-0.11	-10.70	-0.30
18	-0.012	-0.67	-0.41	14.99	14.64	14.40	1.99	-0.01	0.27	16.87	0.08
19	-0.894	1.36	0.13	1.20	-7.66	-5.38	5.08	0.00	-0.14	2.53	0.19
20	0.199	-0.01	-0.19	-1.65	-2.90	-4.44	3.15	-0.01	-0.01	-8.51	0.02
21	-0.531	0.77	0.15	-16.62	-20.41	3.07	5.28	0.04	-0.21	5.90	-0.08
22	-0.134	-1.92	-0.22	6.24	8.45	-1.02	1.91	-0.05	-0.08	-6.74	-0.32
23	0.943	1.36	0.31	4.32	6.28	-1.23	1.78	-0.04	0.14	1.94	0.16
24	-0.239	-0.26	-0.25	5.85	5.41	-0.73	-9.25	0.05	0.15	-0.92	0.24
25	-2.845	4.14	0.78	-8.62	-5.60	2.38	10.70	-0.07	0.39	6.08	0.36
26	0.799	-0.05	-0.34	6.61	6.51	2.89	-4.08	0.05	-0.11	5.56	-0.38
27	0.795	-0.51	-0.06	1.70	-6.41	-5.55	-4.28	0.00	-0.14	1.08	0.22
28	1.290	-3.64	-0.38	0.10	5.23	0.38	-2.64	0.02	-0.13	-12.54	-0.19
29	-0.036	-1.11	-0.10	-6.62	-1.85	2.97	-2.70	-0.12	-0.24	-9.07	-0.08
30	-0.391	-0.80	-0.22	1.24	-2.24	1.79	-3.53	-0.01	-0.11	-3.36	0.18
31	0.536	0.24	0.31	13.70	13.59	-0.57	-4.60	0.02	0.11	-8.20	0.03
32	-0.069	1.61	0.00	-8.52	-9.77	-4.10	10.54	0.11	0.24	20.81	-0.13
33	0.152	0.08	0.59	2.76	5.34	5.23	-10.12	-0.05	0.01	6.70	0.08
34	0.241	1.39	-0.03	-12.51	-2.55	-8.66	-1.31	0.06	0.27	0.03	-0.04
35	-0.361	0.43	0.00	-0.05	-7.34	14.29	4.73	-0.03	0.11	-11.02	0.06
36	0.007	-1.95	-0.57	9.60	4.29	-10.76	6.42	0.01	-0.38	4.46	-0.10
37	1.594	0.14	-0.47	16.67	12.68	-17.92	1.93	0.04	-0.46	8.80	0.07
38	-1.554	-1.05	0.41	-17.98	-15.21	-9.11	-0.30	-0.05	0.30	-1.20	0.08
39	0.683	0.49	0.44	9.48	7.50	15.43	2.44	0.06	0.01	-5.94	-0.04
40	-0.683	0.36	-0.38	-8.36	-5.24	11.68	-4.36	-0.05	0.15	-1.48	-0.11
41	0.893	0.02	-0.60	4.04	1.59	1.68	-2.31	-0.04	0.01	-1.98	-0.27
42	-0.554	-0.42	0.28	-13.98	-0.05	-7.85	-7.35	-0.05	0.02	-2.74	0.24
43	1.841	-0.39	0.31	14.10	9.53	13.46	4.64	0.03	-0.27	-3.79	-0.28
44	-2.141	0.74	0.00	-4.36	-11.34	-7.20	4.74	0.05	0.24	8.69	0.31
45	-1.860	-2.42	-0.47	-14.74	-8.57	-2.99	7.83	-0.04	0.11	-0.68	-0.14
46	0.658	0.64	0.41	8.74	4.17	4.84	0.81	-0.02	-0.39	12.65	0.24
47	0.406	1.43	-0.56	-11.93	-8.12	3.96	1.88	0.03	-0.30	1.86	-0.03

48	0.837	0.30	0.62	17.73	12.26	-5.71	-10.81	0.02	0.58	-13.65	-0.07
49	-0.745	1.64	0.34	5.57	6.43	2.21	-7.67	0.01	-0.05	9.38	0.11
50	-0.180	2.45	0.47	-10.32	-12.08	1.25	0.69	0.02	-0.05	11.67	0.12
51	-0.481	-2.26	-0.50	-0.36	0.63	-2.46	4.40	0.03	-0.08	-1.41	0.10
52	1.446	-1.89	-0.32	4.92	4.76	-0.92	2.29	-0.06	0.18	-19.46	-0.32
53	-0.921	1.58	0.72	-5.46	-2.01	2.62	-4.60	0.03	0.04	15.06	0.23
54	-0.301	0.64	0.84	-12.61	-11.15	-3.46	7.57	-0.01	-0.08	-6.47	0.24
55	0.994	-1.82	-0.87	10.23	7.81	-5.74	-1.43	-0.03	0.14	-7.96	-0.15
56	0.268	-0.45	-0.69	7.64	5.07	6.68	-1.83	0.01	-0.10	-0.46	-0.32
57	-0.825	-1.86	0.03	11.20	9.56	4.50	0.62	-0.03	0.26	17.02	0.36
58	-0.330	-1.30	-0.34	-2.20	-8.33	9.19	-17.42	-0.04	0.02	-13.44	0.37
59	2.258	0.74	0.19	7.14	9.38	-8.25	0.09	0.01	-0.14	-2.80	-0.53
60	-1.064	2.36	0.12	-16.33	-10.87	-5.35	16.43	0.06	-0.13	-0.61	-0.19
61	1.091	-2.23	-0.16	25.57	15.18	0.06	-1.66	-0.01	-0.49	-6.41	0.01
62	1.162	1.08	-0.28	-20.32	-13.33	5.13	-8.25	0.18	0.14	-21.04	0.02
63	-1.707	0.11	0.00	-4.11	-4.37	-4.93	-2.75	-0.17	0.11	38.47	0.25
64	-0.507	0.99	0.43	-1.33	2.26	-0.17	12.37	0.00	0.24	-10.84	-0.29
65	0.263	0.70	0.34	6.98	0.81	4.71	2.07	0.02	-0.02	5.84	0.01
66	1.477	-1.24	-1.03	14.21	6.67	1.63	-4.01	0.01	-0.14	-10.34	-0.23
67	-1.958	-0.20	0.50	-23.96	-10.00	-3.04	0.39	-0.06	0.20	9.69	0.50
68	0.258	0.67	0.18	2.57	2.26	-3.20	1.26	0.03	-0.04	-5.02	-0.29
69	-0.302	-0.17	-0.78	18.85	13.78	2.79	6.80	0.08	-0.02	10.00	-0.30
70	-4.514	3.39	0.84	-28.29	-18.49	-5.06	-9.82	-0.19	0.61	4.97	1.08
71	2.784	-2.82	0.38	11.67	12.97	2.81	3.03	0.02	-0.17	-8.39	-0.44
72	2.071	-0.45	-0.44	-2.43	-8.52	-0.45	-0.30	0.09	-0.42	-6.40	-0.35
73	-0.909	-0.48	1.09	-16.93	-11.91	-1.04	-4.69	-0.09	-0.17	4.65	0.11
74	1.326	-1.92	-0.78	12.80	7.32	-1.47	1.92	0.02	0.08	10.36	-0.13
75	0.013	2.11	0.50	-1.61	0.78	3.43	0.28	0.05	0.17	-2.79	0.22
76	-0.391	0.24	-0.82	5.54	3.54	-0.82	2.20	0.02	-0.07	-12.04	-0.19
77	0.016	-0.88	-0.05	-9.27	-9.87	-2.40	6.93	0.00	0.00	6.25	0.11
78	-1.137	-0.03	-0.14	18.54	16.20	-10.32	0.71	0.07	-0.28	-8.90	-0.15
79	0.511	1.84	0.29	-6.18	-2.17	11.28	-3.18	-0.04	0.23	-0.14	0.06
80	-0.354	1.27	-0.41	-7.71	-9.41	-6.27	-0.60	0.06	0.14	-11.61	0.26
81	1.143	0.33	-0.03	8.27	14.82	10.29	7.87	0.07	-0.23	-13.27	-0.48
82	-2.278	-0.39	0.75	-10.52	-12.09	-0.83	-1.12	-0.02	0.11	9.81	0.38
83	1.528	-1.26	-0.32	9.76	6.41	-3.09	-6.44	-0.11	-0.01	15.25	-0.16
84	1.387	1.64	-0.16	2.45	0.34	-2.92	7.27	0.00	0.08	-9.96	0.01
85	1.660	-1.55	0.22	13.43	16.20	-5.35	-1.30	-0.04	-0.67	1.31	-0.23
86	0.776	-0.26	-1.00	7.76	0.78	7.33	3.36	0.04	0.55	-3.91	-0.25
87	-3.784	0.11	0.93	-23.83	-17.59	1.03	-9.61	0.01	0.05	12.74	0.46
88	0.647	-2.05	-0.35	7.51	9.40	-6.95	2.39	0.01	-0.17	-12.32	-0.11
89	0.177	-1.49	-0.47	-7.39	-5.36	-6.04	-3.77	-0.03	0.20	7.02	-0.10
90	-0.695	1.05	0.31	4.07	2.34	15.02	5.00	-0.02	0.17	-10.59	-0.12
91	-0.089	2.42	0.50	-4.40	-6.65	-1.93	-3.91	0.04	-0.20	16.07	0.34
92	-0.911	-0.05	-0.10	-4.90	-5.29	-2.79	-3.02	-0.06	0.23	6.63	0.33
93	0.695	-0.24	0.28	6.71	6.20	18.90	-2.01	0.03	-0.14	1.06	-0.04
94	0.123	-0.45	-0.44	3.54	2.03	-11.80	1.50	0.01	-0.17	-10.21	-0.56
95	0.133	0.67	0.25	-5.55	-3.21	-4.22	3.24	0.02	0.08	2.71	0.27
96	0.080	0.33	0.47	19.76	22.21	1.89	-9.42	0.10	-0.21	-2.60	-0.14
97	-0.808	1.14	-0.66	-8.01	-11.30	-2.39	8.88	-0.06	0.05	-1.60	0.12
98	0.150	0.43	-0.62	-6.05	-4.84	0.13	1.27	0.00	0.26	0.67	-0.28

99	0.617	-1.95	0.81	-5.90	-6.34	0.47	-1.02	-0.04	-0.10	3.70	0.31
100	1.623	-1.73	-0.22	-3.18	-5.29	-4.54	7.95	0.00	0.20	-3.92	-0.46
101	0.207	-0.42	-0.59	7.80	4.95	-4.35	5.25	-0.04	-0.05	1.69	0.05
102	-0.857	-1.39	-0.81	3.39	3.91	5.18	-6.11	0.05	-0.33	-8.58	-0.09
103	-0.934	3.49	1.62	-8.21	-3.84	3.81	-7.38	-0.01	0.18	10.99	0.49
104	-0.409	0.83	0.03	-3.65	-3.26	-5.58	-4.19	0.00	-0.27	-12.68	-0.11
105	0.902	0.39	-0.09	6.71	-4.27	9.49	-4.51	-0.04	0.36	6.08	-0.10
106	-0.453	0.43	0.19	-4.58	-4.06	-13.51	5.25	0.00	0.08	11.34	0.25
107	-0.002	-1.70	-0.13	1.32	11.32	9.70	3.16	0.04	-0.17	-4.56	-0.04
108	0.096	0.77	-0.22	-9.12	-4.97	5.35	-6.56	0.09	0.33	5.87	0.26
109	-0.563	0.33	0.16	8.11	9.64	1.20	11.84	-0.07	0.45	4.20	-0.10
110	-0.067	-0.64	0.19	-3.18	-5.78	-2.70	0.61	0.01	-0.58	0.06	0.00
111	0.573	-0.51	-0.13	3.98	0.85	-3.76	-6.18	-0.03	-0.20	-9.94	-0.16
112	-0.454	-1.17	-0.28	-8.62	-6.85	0.37	16.37	0.05	-0.05	-1.59	0.08
113	-0.144	0.14	0.59	12.86	9.01	1.27	-6.13	0.01	-0.05	-3.65	-0.04
114	-0.361	0.18	0.13	-3.30	-5.16	-4.56	-8.12	-0.04	0.05	11.96	0.06
115	0.999	0.80	-0.44	-1.15	2.73	3.00	-2.40	-0.02	0.05	-6.54	-0.10
116	1.063	1.20	-0.60	3.54	2.68	0.50	2.43	-0.09	-0.05	-8.69	-0.11
117	-0.864	-2.49	0.03	1.39	1.67	-10.55	4.18	0.05	-0.17	9.94	0.15
118	0.256	1.05	0.06	-1.77	-3.12	-1.70	-7.71	0.06	0.05	-9.67	-0.12
119	-0.416	0.17	0.50	-3.36	-1.49	11.85	0.81	-0.03	0.18	8.61	0.09
120	1.129	0.70	0.59	12.29	11.59	10.70	-6.05	0.03	-0.17	-22.49	-0.22
121	-1.595	-1.74	-0.53	-13.61	-13.18	0.30	-4.37	0.02	0.45	-0.48	0.29
122	0.647	0.55	0.50	-0.52	3.28	-7.58	4.83	-0.02	-0.20	16.15	-0.23
123	-0.141	0.42	-0.57	1.64	-1.96	-3.33	5.30	-0.03	-0.07	7.01	0.16
124	1.692	1.70	-0.14	6.14	10.55	3.40	-0.45	0.05	0.00	-0.89	-0.14
125	-0.720	-0.45	0.27	-3.54	3.49	-1.31	5.75	0.02	0.10	-0.16	-0.03
126	-1.582	-0.33	-0.05	0.49	-9.88	-3.53	-0.83	-0.04	-0.15	-1.73	0.18
127	-0.547	-0.67	-0.91	4.48	-3.10	-1.40	-3.68	0.05	-0.02	-11.02	0.11
128	1.060	0.89	0.72	-2.67	-1.61	-3.12	14.15	-0.02	-0.14	-5.75	-0.38
129	-1.167	0.68	1.00	-15.21	-3.91	4.75	-1.21	-0.01	0.70	21.47	0.47
130	0.693	-0.95	-0.82	13.20	8.35	-0.14	-9.55	-0.02	-0.54	-4.52	-0.19
SE	0.990	1.11	0.43	8.55	6.88	6.61	6.47	0.06	0.23	8.84	0.29

Appendix 12. GCA of 33 lines and four testers for grain yield and agronomic traits for trials evaluated at Potchefstroom during 2017/2018 and 2018/2019 cropping seasons

Line	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	Ear Rot	EA
1	0.025	-1.45	-0.52	0.51	-5.16	-0.97	0.35	0.04	-0.05	-3.88	-0.13
2	-0.062	-1.78	-0.06	-4.66	-12.04	-1.85	3.62	0.07	-0.09	-4.30	0.02
3	-0.223	1.55	0.40	7.18	6.34	0.38	-0.87	0.03	-0.07	-4.71	0.04
4	0.141	-2.07	-0.27	-5.45	-7.41	0.76	5.34	-0.08	0.04	-2.76	-0.12
5	-0.105	-2.32	-0.06	-4.41	-4.74	8.27	10.34	-0.03	-0.09	9.31	-0.19
6	1.849	-0.91	0.02	-6.78	-7.20	2.06	2.65	0.07	-0.05	3.01	0.13
7	0.891	-2.16	0.19	-8.28	-5.37	0.09	-4.30	0.04	-0.23	4.69	-0.17
8	-0.830	0.59	0.02	10.47	5.30	-3.14	-6.17	-0.04	0.08	4.78	0.02
9	-0.126	1.55	0.44	2.34	8.46	-0.57	0.54	-0.03	0.10	-4.84	0.04
10	-0.336	2.09	0.23	3.39	11.26	-1.16	3.48	-0.09	-0.01	-0.76	0.11
11	0.396	3.51	0.11	17.34	18.30	-0.83	10.25	0.04	0.10	-2.97	0.00
12	-0.789	-0.16	-0.02	12.18	3.30	-2.54	-5.94	-0.05	0.06	3.57	0.06
13	0.401	3.26	-0.10	4.41	2.59	-3.24	-5.16	0.11	-0.05	1.69	0.02
14	0.825	-0.03	-0.14	-4.66	-5.20	2.62	-2.84	0.09	0.29	20.56	0.13
15	0.628	-0.95	-0.06	14.93	7.51	-0.80	2.84	-0.03	0.02	-2.86	-0.02
16	-1.178	1.93	0.07	-0.41	3.92	-1.64	-0.82	-0.01	-0.30	2.31	0.15
17	0.468	1.93	0.23	-9.20	-2.58	-0.67	1.56	-0.03	-0.05	-1.43	0.27
18	-1.161	1.26	0.15	-7.82	-0.74	5.25	11.13	-0.02	0.14	-4.53	0.12
19	-0.169	-2.99	-0.14	-4.99	-9.45	-0.55	-1.84	0.01	0.10	-0.50	0.06
20	-0.067	-2.31	-0.32	7.23	9.06	3.73	0.10	0.05	0.00	2.48	-0.17
21	0.198	-1.91	-0.27	2.01	7.96	3.45	-3.99	-0.01	-0.01	-2.52	0.00
22	0.024	2.09	-0.27	-9.03	-0.74	-1.19	-1.81	-0.01	-0.03	-4.83	-0.06
23	-0.819	1.63	0.23	6.05	-5.29	-2.83	1.79	0.00	-0.05	-0.98	-0.27
24	0.359	2.63	0.15	12.14	3.88	-3.36	-7.94	-0.01	-0.17	-4.37	0.04
25	-0.409	1.68	0.27	-3.49	2.09	1.90	0.40	0.02	-0.21	-5.86	0.04
26	-0.061	0.43	0.02	-4.07	-4.12	0.29	0.16	-0.11	-0.15	-5.52	-0.17
27	-0.430	-4.16	-0.27	-12.99	-16.70	-2.47	-7.07	-0.04	0.18	6.22	0.19
28	-0.334	4.18	0.94	14.14	27.55	0.00	3.39	-0.11	0.18	2.53	0.23
29	0.547	-2.41	-0.18	-7.99	-10.41	5.75	-3.79	0.00	-0.03	-3.18	-0.23
30	-0.085	-0.87	-0.18	-8.99	-6.99	-0.63	-2.29	0.17	-0.11	-6.50	-0.08
31	-0.137	2.47	-0.31	-5.03	1.05	-0.27	0.93	0.03	0.02	-0.12	-0.04
32	0.036	-6.20	-0.10	-10.49	-14.88	-3.79	-6.30	-0.05	0.45	10.80	0.03
35	0.525	-2.16	-0.31	3.59	-0.99	-2.07	0.75	-0.02	0.10	-1.20	-0.12
SE	0.478	0.49	0.22	3.24	2.24	2.41	4.35	0.05	0.14	3.23	0.15
Tester											
1	0.677	-2.68	-0.22	-5.32	-11.28	2.28	-1.73	0.01	0.10	2.07	-0.03
2	-1.284	1.75	0.21	1.56	1.69	0.15	2.63	-0.02	-0.03	-2.71	0.11
3	-0.199	1.31	0.17	9.02	10.82	-1.11	3.10	-0.04	-0.06	0.89	-0.03
4	0.727	-0.26	-0.15	-5.18	-1.12	-1.31	-3.84	0.05	-0.02	-0.40	-0.04
SE	0.261	0.26	0.04		0.94	2.05	2.54	0.03	0.02	0.84	0.10

Appendix 13. SCA of 130 hybrids for grain yield and agronomic traits for trials evaluated at Potchefstroom during 2017/2018 and 2018/2019 cropping seasons

Entry	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	Ear rot	EH
1	-0.507	0.63	0.13	-7.02	-5.22	-4.28	-0.61	0.03	-0.17	-5.56	-0.17
2	1.458	0.63	-0.29	1.94	13.98	1.21	-1.03	0.08	0.30	12.95	0.16
3	-0.734	0.63	0.25	-0.86	-6.99	4.94	4.82	-0.07	-0.01	-4.72	0.17
4	-0.139	0.63	-0.10	5.84	-1.88	-1.88	-3.34	-0.04	-0.13	-2.50	-0.16
5	-1.120	0.63	0.01	5.82	-2.34	-2.01	-11.22	-0.03	0.21	-1.75	0.01
6	0.009	0.63	0.08	-3.90	-0.48	-2.46	9.20	-0.08	-0.07	0.96	0.20
7	0.171	0.63	0.29	-4.69	-0.44	4.48	2.28	-0.05	0.12	-3.22	-0.15
8	1.018	0.63	-0.39	2.68	3.17	-0.02	-0.42	0.17	-0.25	4.17	-0.06
9	-0.167	0.63	-0.62	-8.35	-8.89	1.51	-1.98	0.01	-0.06	-2.21	-0.02
10	-0.649	0.63	0.12	-7.73	-6.02	-1.36	-5.43	-0.16	0.16	-3.63	0.01
11	0.599	0.63	0.83	0.64	-0.65	-0.81	8.12	0.04	-0.32	7.70	-0.01
12	0.295	0.63	-0.35	15.34	15.46	0.65	-0.88	0.12	0.22	-1.71	0.00
13	-1.710	0.63	0.05	-13.89	-1.14	1.51	0.32	0.02	0.08	-3.23	0.07
14	0.997	0.63	-0.21	4.23	-0.27	-1.46	-2.81	0.07	-0.45	1.93	0.01
15	0.357	0.63	-0.17	-3.90	-4.24	1.31	2.70	-0.08	0.49	0.47	-0.09
16	0.434	0.63	0.32	13.47	5.54	-1.37	-0.37	-0.01	-0.13	1.00	0.00
17	-1.682	0.63	0.18	4.73	4.20	17.81	4.60	-0.12	-0.04	3.85	-0.04
18	0.942	0.63	-0.09	8.69	2.23	-1.35	6.57	0.08	0.26	2.95	-0.01
19	-0.358	0.63	0.29	-2.77	0.60	-8.37	3.46	-0.10	-0.05	1.34	-0.03
20	1.176	0.63	-0.39	-10.74	-7.13	-8.09	-14.79	0.13	-0.17	-7.98	0.06
21	-0.945	0.63	0.59	-9.22	-5.01	0.66	5.63	-0.05	-0.33	-3.29	-0.10
22	0.071	0.63	0.16	-1.44	5.02	-4.41	-0.27	0.10	0.14	-3.32	-0.15
23	2.180	0.63	-0.63	-1.07	-4.61	-4.12	0.47	0.07	-0.01	8.49	-0.01
24	-1.229	0.63	-0.14	11.63	4.50	7.87	-5.99	-0.12	0.20	-1.72	0.25
25	-0.873	0.63	0.59	-4.22	-3.68	4.64	2.77	-0.12	0.02	-2.52	0.11
26	-0.118	0.63	0.66	-3.44	-7.15	-1.84	4.31	0.07	-0.01	-1.65	-0.19
27	-1.040	0.63	-0.96	1.27	0.56	-0.91	-7.09	-0.05	0.01	2.01	0.12
28	2.110	0.63	-0.31	6.30	10.17	-1.90	-0.15	0.10	-0.03	2.33	-0.04
29	0.464	0.63	-0.07	6.53	3.16	-1.92	0.84	-0.01	0.04	-4.53	0.09
30	-0.277	0.63	-0.17	-0.86	0.85	0.16	-3.20	-0.02	-0.07	0.88	-0.05
31	1.032	0.63	0.37	-6.32	-3.78	1.47	1.52	0.03	0.04	0.38	0.10
32	-1.141	0.63	-0.14	0.55	-0.33	0.29	0.69	0.01	0.00	3.43	-0.14
33	0.515	0.63	-0.82	9.65	2.32	-1.43	-5.04	0.03	0.44	-0.76	-0.18
34	-0.625	0.63	0.41	2.44	-7.98	0.63	-2.35	-0.02	-0.09	-0.43	0.01
35	0.849	0.63	0.29	-6.36	0.56	0.22	4.00	0.06	-0.07	3.74	0.16
36	-0.661	0.63	0.11	-5.82	5.00	0.58	3.23	-0.07	-0.28	-2.38	0.00
37	0.270	0.63	-0.45	7.94	2.20	-2.98	-11.08	0.04	-0.04	0.35	0.17
38	0.515	0.63	0.46	2.39	-3.44	6.57	1.05	0.03	-0.07	0.54	-0.13
39	-0.952	0.63	0.16	-8.07	0.43	-1.90	7.18	-0.09	0.04	-0.61	-0.07
40	0.245	0.63	-0.18	-2.37	0.71	-1.69	2.69	0.02	0.08	-0.13	0.02
41	2.560	0.63	-0.16	-1.52	-0.34	-5.61	-2.22	0.12	0.11	2.08	0.11
42	0.059	0.63	-0.25	3.60	0.19	8.18	-3.39	0.05	-0.01	1.18	-0.11
43	-1.950	0.63	0.45	1.31	7.89	-2.23	4.25	-0.10	0.10	3.18	0.37
44	-0.591	0.63	-0.06	-3.49	-7.83	-0.35	1.20	-0.07	-0.19	-6.28	-0.37
45	0.376	0.63	-0.03	-13.52	-8.18	0.85	-1.66	0.06	-0.19	-0.69	-0.37
46	-0.181	0.63	0.04	8.94	9.85	-0.02	5.68	-0.11	-0.14	-0.65	0.08
47	-0.046	0.63	-0.09	-12.19	-12.28	-0.52	-6.49	0.04	0.31	2.66	0.14
48	-0.071	0.63	0.07	16.68	10.50	-0.31	2.30	0.02	0.02	-1.16	0.15
49	1.007	0.63	0.55	9.59	6.20	-3.21	-1.10	0.03	0.08	4.69	0.01

50	-0.635	0.63	-0.54	-0.79	0.06	-1.08	-5.29	-0.01	0.05	2.59	0.20
51	-1.294	0.63	-0.34	-7.50	-4.74	0.18	4.71	-0.06	-0.01	-4.40	0.01
52	1.000	0.63	0.32	-1.39	-1.63	4.09	1.53	0.04	-0.13	-2.72	-0.23
53	-1.173	0.63	0.09	-2.18	4.16	5.66	4.95	-0.19	-0.17	-3.74	0.07
54	1.563	0.63	-0.17	10.94	3.19	-0.87	-1.91	0.13	0.30	3.06	-0.07
55	-1.648	0.63	0.04	-6.02	-1.61	-2.11	-3.05	0.04	-0.26	-7.06	-0.09
56	1.336	0.63	0.03	-2.82	-5.83	-2.69	-0.15	0.02	0.12	7.90	0.09
57	0.660	0.63	0.51	-12.27	-9.55	-3.81	-1.54	0.09	-0.06	0.36	0.21
58	0.193	0.63	-0.09	0.52	-6.52	-3.52	2.75	0.00	0.07	0.80	-0.09
59	0.439	0.63	-0.38	6.89	11.35	6.25	0.85	-0.09	0.10	-4.26	0.06
60	-1.214	0.63	-0.06	4.76	4.62	1.07	-2.21	0.00	-0.11	3.27	-0.19
61	0.292	0.63	0.05	13.07	10.70	0.64	-2.23	0.18	-0.08	-4.12	-0.04
62	-0.328	0.63	-0.04	-11.15	-4.61	-1.40	-1.05	-0.14	0.14	15.19	0.33
63	-0.757	0.63	-0.34	-6.44	-4.57	1.96	-3.16	-0.04	-0.17	-6.40	-0.19
64	0.871	0.63	0.32	4.43	-1.63	-1.21	6.29	0.01	0.12	-4.50	-0.10
65	1.053	0.63	0.05	6.36	7.03	-2.21	8.53	0.12	-0.25	3.51	-0.16
66	-1.431	0.63	0.46	-12.52	-5.61	1.35	-7.74	-0.10	0.39	2.62	0.29
67	-0.104	0.63	-0.50	1.68	6.93	0.00	3.53	0.02	-0.01	-1.29	-0.07
68	0.560	0.63	-0.01	4.38	-8.46	0.85	-4.48	-0.03	-0.13	-4.67	-0.06
69	1.999	0.63	-0.37	15.98	10.36	-4.25	4.72	0.26	-0.02	-6.26	-0.26
70	-2.151	0.63	1.04	-34.90	-25.44	3.32	-1.36	-0.38	0.36	-3.80	0.44
71	0.313	0.63	-0.25	13.48	9.43	-0.14	-5.38	0.12	-0.36	-2.31	-0.35
72	-0.084	0.63	-0.43	5.34	5.54	1.07	1.86	0.00	0.02	12.54	0.17
73	-0.236	0.63	-0.07	-4.35	1.24	4.19	-3.79	0.04	0.11	1.96	0.05
74	1.042	0.63	0.00	13.10	-1.23	-0.57	4.75	-0.04	-0.01	-1.04	-0.09
75	0.623	0.63	0.20	-4.69	-3.69	-1.34	-4.26	0.01	0.10	1.77	0.06
76	-1.351	0.63	-0.14	-4.16	3.58	-2.30	3.15	-0.01	-0.19	-2.54	-0.02
77	0.114	0.63	-0.06	-8.57	-8.27	3.11	1.14	0.00	0.04	-3.49	-0.06
78	-1.617	0.63	-0.28	3.09	3.79	-4.93	-4.37	0.03	-0.22	-1.80	0.03
79	0.297	0.63	0.54	6.95	6.07	1.97	5.70	-0.05	0.16	2.74	0.13
80	-0.202	0.63	0.22	-4.18	-0.01	4.79	2.74	-0.12	0.04	-2.02	0.11
81	0.195	0.63	-0.21	4.77	4.52	-3.05	-1.11	0.25	-0.32	0.35	-0.19
82	0.497	0.63	-0.17	1.48	-2.11	-2.12	-2.38	-0.04	0.04	1.89	0.12
83	-0.412	0.63	0.15	-2.16	-2.50	0.37	0.58	-0.09	0.25	-0.05	-0.04
84	1.294	0.63	0.22	12.86	8.53	-2.69	5.53	0.01	0.15	2.04	-0.16
85	0.530	0.63	-0.38	13.81	7.06	2.45	-6.37	0.01	0.03	-3.50	-0.38
86	1.361	0.63	0.16	9.68	1.60	0.97	-1.81	0.13	-0.03	3.83	-0.07
87	-3.107	0.63	-0.01	-36.45	-17.29	-0.73	2.49	-0.16	-0.15	-2.21	0.61
88	-0.870	0.63	-0.62	-4.72	-2.76	-0.66	7.85	-0.11	0.00	12.06	0.05
89	0.993	0.63	0.12	5.56	0.27	-1.49	-2.15	0.19	-0.11	-5.84	-0.26
90	-0.367	0.63	0.33	-4.07	4.14	1.28	0.54	-0.01	0.08	-0.66	0.47
91	0.321	0.63	0.15	3.13	-1.75	0.85	-6.40	-0.06	0.04	-5.40	-0.27
92	-1.140	0.63	0.47	-2.47	-1.43	-1.80	1.35	-0.10	-0.12	3.15	-0.10
93	0.207	0.63	-0.13	9.14	6.27	0.09	-2.90	0.00	0.09	0.68	-0.07
94	-0.289	0.63	-0.09	-1.65	-0.69	0.31	-2.82	-0.07	0.12	-5.54	0.08
95	1.301	0.63	-0.26	-5.12	-4.25	1.39	4.21	0.17	-0.09	1.87	0.09
96	0.490	0.63	0.01	5.82	1.86	4.17	-2.64	0.07	0.08	-1.99	0.07
97	-1.751	0.63	-0.09	-13.90	-3.11	-0.81	8.87	-0.15	0.39	5.09	0.26
98	0.518	0.63	-0.21	-0.86	-4.07	0.27	-5.59	0.08	-0.26	-3.50	-0.34
99	0.821	0.63	0.28	8.84	5.21	-3.64	-0.80	0.00	-0.21	0.56	0.00
100	-0.461	0.63	0.09	-1.43	-6.09	-3.70	3.53	-0.05	-0.14	-0.18	-0.31
101	-0.627	0.63	-0.34	5.35	4.44	-1.60	-5.21	-0.03	-0.26	1.88	0.06
102	0.300	0.63	0.04	7.39	2.47	-0.78	1.66	0.00	0.26	0.53	-0.05
103	0.866	0.63	0.19	-11.41	-0.92	6.07	-0.14	0.08	0.14	-2.06	0.29

104	-0.077	0.63	0.05	-1.18	-1.84	-3.98	1.43	-0.04	0.02	3.12	0.09
105	0.700	0.63	0.12	-1.90	1.85	3.43	-1.52	0.03	-0.09	-5.61	-0.13
106	-0.686	0.63	-0.17	2.31	0.39	-0.59	-3.32	0.01	0.01	-1.45	0.10
107	0.140	0.63	-0.01	0.68	-0.50	1.13	3.25	0.01	0.06	4.11	-0.06
108	1.861	0.63	-0.66	7.86	3.41	-3.42	-1.95	0.12	-0.14	4.96	0.05
109	-0.420	0.63	-0.59	-1.69	-0.40	-1.54	7.54	0.02	-0.18	-9.20	-0.01
110	-0.132	0.63	1.79	10.85	12.64	5.03	-6.18	-0.07	0.01	-0.39	0.14
111	-1.231	0.63	-0.56	-17.12	-15.75	-0.08	0.43	-0.07	0.31	4.80	-0.19
112	-0.605	0.63	-0.37	-12.68	-11.14	5.03	-3.80	-0.04	-0.02	-0.72	0.09
113	0.146	0.63	0.37	7.10	8.73	7.99	-2.03	0.00	-0.14	-5.16	-0.13
114	0.587	0.63	0.08	14.48	5.10	-5.95	4.04	0.04	0.22	7.52	-0.07
115	-0.050	0.63	-0.10	-8.99	-2.79	-7.08	1.64	0.00	-0.07	-1.48	0.11
116	-0.497	0.63	0.30	1.65	-0.89	-1.25	-3.22	-0.03	0.06	-0.46	0.19
117	0.406	0.63	-0.29	-7.23	-0.69	-3.69	-3.25	0.07	-0.30	-0.38	-0.28
118	0.428	0.63	-0.42	2.98	-5.82	-0.35	8.40	-0.02	-0.03	-0.97	0.03
119	-0.259	0.63	0.40	2.51	7.29	5.28	-2.08	-0.02	0.27	1.97	0.04
120	1.725	0.63	0.09	6.03	5.91	-0.99	1.36	-0.13	0.19	-1.64	0.23
121	-1.387	0.63	-0.17	-11.52	-6.56	-1.66	3.46	0.05	-0.09	2.59	0.18
122	-0.812	0.63	0.04	4.52	1.97	4.05	-3.10	0.11	-0.24	7.52	-0.34
123	0.551	0.63	0.03	0.88	-1.42	-1.41	-1.87	-0.03	0.14	-8.31	-0.08
124	-1.321	0.63	0.05	-0.68	5.50	-2.65	0.22	-0.08	-0.16	-1.64	-0.09
125	1.949	0.63	-0.34	1.48	-4.26	0.74	-1.90	0.07	0.08	-3.83	0.01
126	-1.834	0.63	0.49	0.68	0.35	2.05	4.15	-0.01	0.04	2.92	0.18
127	-1.088	0.63	0.09	-0.60	1.45	-1.71	-1.86	-0.01	0.19	5.31	0.32
128	0.532	0.63	-0.34	8.02	6.64	-1.25	1.53	0.04	0.07	-2.04	0.01
129	0.593	0.63	-0.13	-5.27	-3.82	3.73	-0.05	0.03	-0.24	-3.96	-0.17
130	0.041	0.63	0.36	-2.24	-4.38	-0.78	0.22	-0.06	-0.03	0.86	-0.16
SE	0.729	0.63	0.27	4.71	4.13	3.42	5.05	0.07	0.19	4.81	0.17

Appendix 14. GCA of 33 lines and four testers for grain yield and agronomic traits for trials evaluated at eight locations in Zimbabwe during 2017/2018 cropping season

Line	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	ER	EA
1	-0.158	-0.33	-0.17	4.43	-2.88	0.23	-0.85	0.06	0.46	-0.89	0.14
2	0.025	-0.64	0.36	-1.43	-0.31	0.58	0.30	0.11	-0.19	5.38	0.23
3	0.207	0.34	0.13	8.89	8.83	-0.58	-0.46	0.01	-0.62	-3.65	-0.15
4	0.031	-2.14	0.08	-9.47	-11.96	-1.56	-0.92	-0.07	0.01	0.61	-0.07
5	0.132	-1.16	0.02	0.84	-3.98	2.03	-0.29	0.04	2.07	-1.09	0.00
6	-0.028	-2.88	0.08	-15.18	-10.07	1.57	1.55	0.03	-0.16	-0.06	0.00
7	-0.107	-2.16	0.36	-10.54	-6.56	-0.97	-0.57	-0.05	2.02	0.16	0.07
8	0.580	1.03	-0.39	17.98	12.82	-4.65	-0.44	0.12	-0.62	-0.51	-0.04
9	0.578	0.43	0.18	5.12	4.54	3.26	-1.33	-0.01	-0.14	-2.30	-0.15
10	0.751	0.87	0.05	12.71	11.65	4.56	-0.83	-0.03	-0.62	-2.54	-0.23
11	0.917	1.23	0.13	21.96	16.41	5.38	-0.73	0.01	-0.49	-2.26	-0.22
12	-0.502	0.95	-0.01	5.37	-0.70	-2.25	-0.40	0.01	-0.62	-2.20	-0.04
13	0.566	2.09	0.11	-2.13	1.18	-1.13	-0.94	0.03	-0.62	-1.06	-0.10
14	0.334	0.00	0.27	-4.28	-1.24	-3.51	1.22	0.01	1.34	8.12	0.10
15	0.069	-1.38	0.00	9.90	2.90	-0.92	-1.49	-0.05	-0.19	-2.68	-0.11
16	-0.642	0.50	0.10	-6.90	-2.49	2.29	0.13	-0.02	-0.51	-2.55	0.20
17	-0.119	2.50	0.22	-6.35	-0.90	-3.29	-0.72	-0.07	-0.19	-2.67	0.06
18	-0.714	2.04	-0.21	-3.69	1.80	0.23	2.66	-0.07	0.75	-2.33	0.19
19	-0.475	-2.27	0.11	-8.46	-12.02	-0.77	-0.49	-0.07	1.21	-0.04	-0.11
20	-0.605	-1.53	-0.24	4.90	3.13	-0.04	-0.35	-0.09	-0.03	10.19	-0.01
21	-0.264	-2.46	0.05	-5.10	1.24	4.21	-0.40	-0.05	-0.52	4.15	0.09
22	-0.356	2.43	-0.25	-4.60	8.08	-2.32	2.96	0.02	0.09	-1.60	-0.04
23	0.207	1.83	0.10	6.93	1.18	-2.26	-0.59	-0.01	0.13	2.08	0.18
24	0.234	2.83	-0.07	7.04	0.16	-1.28	0.80	0.02	-0.01	1.61	0.25
25	-0.092	2.23	-0.12	-7.32	-0.07	0.12	2.06	0.00	-0.57	-2.71	0.12
26	-0.080	-0.57	0.21	-2.36	-9.42	0.72	0.23	-0.05	-0.20	0.51	-0.08
27	-0.557	-2.52	-0.29	-7.44	-6.48	0.97	-0.02	0.04	-0.32	2.56	0.16
28	1.067	2.23	-0.03	18.26	22.27	5.50	-0.60	0.04	-0.62	-1.46	-0.44
29	-0.447	-1.66	-0.15	-10.57	-9.45	-0.36	1.05	0.03	0.13	-1.13	-0.11
30	-0.419	-0.89	-0.10	-14.16	-7.57	-5.15	-0.05	0.08	-0.62	-1.28	0.08
31	0.426	2.97	-0.15	-2.60	-0.35	-2.32	0.00	0.02	-0.22	1.09	-0.05
32	-1.196	-4.30	-0.43	-7.70	-14.16	1.94	-1.05	-0.03	-0.23	-0.55	0.28
35	0.187	-1.07	-0.14	5.21	1.65	0.26	0.22	-0.05	0.01	1.53	-0.12
SE	0.190	0.35	0.15	2.34	1.98	2.03	0.85	0.02	0.42	1.50	0.06
Tester											
1	-0.168	-1.75	0.05	-11.40	-12.81	2.05	1.05	-0.05	-0.11	2.36	0.09
2	-0.354	2.13	0.05	6.25	6.76	0.47	0.21	0.07	0.06	-1.29	0.07
3	0.101	0.56	0.15	7.84	4.79	-0.64	-0.27	-0.05	-0.05	-2.04	-0.19
4	0.399	-0.81	-0.25	-2.32	1.67	-1.85	-0.98	0.03	0.10	0.89	0.03
SE	0.085	0.21	0.07	0.72	1.01	1.21	0.33	0.02	0.14	0.75	0.02

Appendixn15. SCA of 130 hybrids for grain yield and agronomic traits for trials evaluated at eight locations in Zimbabwe during 2017/2018 cropping season

Entry	GY	DA	ASI	PH	EH	RL	SL	EPP	HC	ER	EA
1	-0.224	-0.64	-0.40	-2.20	-2.42	0.90	-0.26	0.05	-0.61	1.37	0.01
2	0.558	-0.83	0.29	3.28	0.51	-5.39	-0.74	-0.02	-0.85	0.13	-0.21
3	-0.570	0.55	0.07	-1.12	-0.03	-2.13	-0.31	-0.08	2.63	-0.44	0.13
4	0.258	0.79	0.03	-0.34	1.53	6.59	1.29	0.05	-1.18	-0.98	0.07
5	-0.170	-0.45	0.26	-6.65	-5.62	-3.35	-0.02	-0.08	-0.33	-3.65	-0.27
6	0.336	0.29	0.13	0.70	0.12	1.04	-1.55	0.02	-0.49	-0.16	0.22
7	-0.445	0.48	-0.09	4.11	3.96	0.09	2.38	0.03	-0.39	4.01	0.07
8	0.301	-0.46	-0.31	1.46	1.14	2.19	-0.83	0.03	1.20	-0.12	-0.02
9	-0.418	-0.87	-0.13	-2.59	-2.58	0.63	-0.79	-0.02	0.11	0.26	-0.08
10	-0.054	-1.19	0.24	-13.67	-6.84	1.95	0.61	0.02	-0.06	1.00	0.20
11	-0.247	1.00	0.08	-2.14	-3.31	-4.73	-0.81	0.00	0.05	1.96	0.05
12	0.741	0.93	-0.20	18.02	12.31	2.12	0.97	0.00	-0.10	-3.15	-0.17
13	-0.396	0.24	0.42	-3.91	-1.66	1.37	1.05	0.09	1.98	-0.83	0.09
14	0.144	-0.58	-0.02	-0.94	-0.60	-1.12	-0.24	-0.09	-0.69	-1.12	-0.10
15	-0.175	-0.14	-0.31	-6.59	-7.82	2.25	-0.76	0.00	-0.58	1.44	0.12
16	0.448	0.36	-0.09	11.07	9.67	-2.54	-0.06	-0.01	-0.72	0.59	-0.12
17	-0.540	-0.06	0.04	-2.04	-2.26	2.00	0.48	0.07	0.86	-0.14	0.01
18	0.253	-1.63	0.42	-2.81	-6.84	-0.60	-0.91	-0.04	-0.36	1.20	-0.02
19	0.091	1.56	-0.18	-1.90	2.94	1.03	-0.79	-0.03	-1.00	-0.07	0.05
20	0.217	0.00	-0.28	6.38	5.75	-2.46	1.21	0.00	0.50	-0.92	-0.05
21	-0.274	1.47	0.17	-5.40	-2.11	-0.16	-0.14	0.06	-0.36	-0.65	0.18
22	-0.033	-0.41	-0.40	5.08	4.88	-2.40	2.47	-0.08	0.05	0.47	-0.14
23	0.123	-1.09	0.32	-5.26	-1.90	2.83	-0.01	0.06	0.38	-0.61	0.05
24	0.206	-0.10	-0.09	5.21	-1.28	-0.30	-2.34	-0.05	-0.07	0.87	-0.10
25	-0.066	0.94	0.07	4.15	6.25	1.20	-0.46	0.00	-0.55	-1.27	-0.02
26	-0.608	-1.25	0.26	-2.69	-7.70	0.61	1.52	-0.04	0.49	1.09	0.04
27	0.462	0.13	-0.46	-6.47	-3.86	-3.08	-0.67	0.02	-0.09	-0.29	-0.06
28	0.234	0.06	0.13	4.63	4.89	1.24	-0.41	0.02	0.15	0.55	0.04
29	-0.173	-0.12	-0.05	-4.18	0.00	-1.39	1.14	-0.12	0.11	-1.55	0.05
30	-0.053	0.18	0.01	0.67	-0.51	-0.23	0.38	0.08	-0.06	-1.65	0.02
31	0.080	0.56	-0.09	0.14	2.39	3.43	-1.00	-0.08	0.05	-1.31	-0.07
32	0.167	-0.75	0.13	2.99	-2.30	-1.83	-0.53	0.12	-0.10	4.60	-0.01
33	0.299	0.35	0.01	7.55	3.91	-2.85	-0.60	-0.09	-0.38	1.17	-0.06
34	-0.561	0.15	-0.30	-1.35	3.71	-0.85	0.14	0.14	-0.54	-0.38	-0.09
35	-0.063	-0.09	0.16	-3.06	-8.39	3.05	0.10	-0.08	-0.44	3.61	0.13
36	0.346	-0.53	0.13	-3.53	0.36	0.63	0.36	0.03	1.35	-4.33	0.01
37	0.166	0.47	0.26	2.65	-1.01	-4.95	-1.17	0.01	0.11	-0.92	-0.03
38	-0.354	0.34	-0.18	-0.63	0.98	2.33	-0.91	-0.05	-0.06	1.54	-0.10
39	0.180	0.09	-0.15	-0.03	-2.06	3.87	2.21	0.01	0.05	1.09	0.03
40	0.030	-1.03	0.07	-2.37	1.69	-1.28	-0.14	0.02	-0.10	-1.63	0.10
41	0.574	-0.57	0.24	-3.66	-3.91	-2.48	-1.88	-0.09	-0.03	1.21	-0.13
42	-0.086	0.48	-0.13	-1.44	0.90	4.02	0.39	0.04	-0.19	-1.06	-0.07
43	0.276	0.17	0.02	5.41	2.24	-1.55	0.25	0.01	-0.08	1.45	0.02
44	-0.744	-0.21	-0.14	-0.68	0.36	-0.01	1.22	0.03	0.30	-1.52	0.18
45	-0.355	-2.29	-0.12	-7.51	-5.23	0.94	-1.47	0.03	0.11	1.32	0.15
46	0.417	0.89	-0.18	3.59	0.82	-3.17	1.16	-0.04	-0.06	0.18	-0.17
47	-0.268	-0.30	0.35	-0.19	1.54	2.39	-0.80	-0.02	0.05	0.25	0.02

48	0.227	1.57	-0.06	3.72	2.47	-0.19	1.09	0.03	-0.10	-1.67	-0.01
49	0.156	1.94	-0.18	4.05	4.14	-4.87	-1.67	-0.07	0.11	2.31	-0.17
50	-1.089	-1.32	-0.30	-8.60	-9.49	3.57	-0.74	-0.01	-0.06	0.64	0.21
51	0.903	0.50	-0.02	3.56	1.54	0.67	1.74	0.00	0.05	-0.18	-0.04
52	0.051	-1.25	0.50	0.60	3.41	0.61	0.66	0.07	-0.10	-2.69	-0.01
53	0.117	0.79	-0.40	-17.08	-1.87	0.60	3.23	0.05	-0.77	-2.07	0.05
54	0.239	-1.10	0.73	6.99	1.68	-3.71	-1.14	0.13	0.41	3.25	0.04
55	-0.394	-0.09	-0.12	1.65	-2.92	1.26	-1.07	-0.04	-1.04	-2.76	-0.14
56	0.060	0.28	-0.22	8.06	2.70	1.81	-1.02	-0.14	1.40	1.65	0.05
57	-0.571	0.35	0.06	-8.60	-5.39	0.31	-0.72	0.01	0.69	2.38	0.07
58	0.401	0.90	-0.94	5.62	5.66	-1.23	-0.67	-0.01	-0.49	-0.90	-0.06
59	0.404	-1.72	0.27	4.35	0.75	-0.52	0.85	0.00	-0.38	1.01	0.10
60	-0.213	0.34	0.61	-1.75	-1.44	1.42	0.52	-0.01	0.17	-2.41	-0.12
61	0.449	0.47	0.21	8.20	4.38	-0.78	-2.00	0.03	-0.01	-1.26	-0.18
62	-0.427	1.21	-0.48	-1.02	1.99	-3.27	-0.25	-0.10	-0.17	-0.46	0.16
63	-0.171	-0.28	0.18	-11.98	-6.98	2.24	2.14	0.04	-0.06	0.83	0.13
64	0.171	-1.53	0.08	4.43	0.20	1.78	0.10	0.02	0.24	0.97	-0.12
65	0.355	-0.15	0.15	4.21	-0.34	-1.17	-0.57	0.00	0.04	0.79	-0.10
66	-1.629	0.40	0.15	-9.38	-6.35	-2.28	0.39	-0.10	-0.10	-2.05	0.36
67	0.661	-0.16	-0.26	3.10	3.93	1.85	0.06	0.06	0.10	-1.56	-0.17
68	0.636	-0.22	-0.04	1.69	2.36	1.56	0.12	0.04	-0.04	2.89	-0.10
69	0.856	-0.39	-0.35	13.12	11.64	2.83	0.28	0.22	-1.27	-1.48	-0.17
70	-1.758	3.04	0.77	-28.60	-16.06	2.86	-0.19	-0.31	2.51	4.09	0.73
71	0.281	-0.27	-0.45	12.00	8.41	-4.46	-2.53	0.14	-0.84	-0.98	-0.24
72	0.642	-2.52	0.02	3.10	-4.41	-1.27	2.43	-0.05	-0.40	-1.55	-0.33
73	-0.056	-0.20	-0.24	-4.62	-0.16	2.61	0.15	0.09	-1.38	0.78	0.16
74	0.396	-1.77	0.51	2.73	-1.92	2.12	-1.15	-0.04	4.05	3.54	-0.09
75	0.212	0.73	-0.02	3.64	-3.07	-7.17	-1.19	0.03	-0.74	-0.37	0.04
76	-0.530	1.11	-0.25	-2.14	4.73	2.41	2.17	-0.09	-1.93	-3.86	-0.12
77	-0.477	1.07	-0.07	-3.29	0.63	4.22	-0.09	-0.03	0.89	3.09	0.09
78	-1.036	1.06	-0.23	5.91	4.27	0.69	-0.11	0.03	-0.54	-2.08	0.00
79	1.180	-0.13	0.36	3.25	1.45	-4.46	0.40	0.07	-0.29	-2.22	-0.03
80	-0.357	0.43	-0.24	7.65	-2.36	3.82	0.92	0.02	0.00	-5.00	0.15
81	0.670	0.36	-0.18	3.75	4.51	0.75	-0.67	0.01	-0.16	5.32	-0.29
82	0.002	-0.52	0.41	-4.72	-1.21	-2.60	0.31	-0.01	-0.06	-2.03	0.15
83	-0.294	-0.39	0.00	-7.06	-1.34	-2.00	-0.58	-0.03	0.22	1.79	-0.01
84	0.956	-1.90	-0.01	6.52	0.99	2.69	2.59	-0.03	-0.19	-2.20	-0.16
85	1.287	0.03	-0.07	14.19	15.48	-2.79	-1.50	0.14	-0.29	-2.21	-0.25
86	0.546	-1.72	-0.04	10.10	4.00	2.30	1.13	0.00	-0.66	-0.61	-0.25
87	-2.768	3.47	0.11	-31.18	-20.87	-2.23	-2.23	-0.12	1.14	5.10	0.66
88	-0.423	-1.92	0.09	-5.95	-4.30	-1.55	-1.16	-0.03	0.54	1.93	0.12
89	0.290	-0.49	-0.04	7.65	1.76	-0.79	-1.35	0.03	-0.81	0.85	-0.14
90	0.224	1.02	0.43	-1.44	4.04	-2.91	2.04	0.03	1.11	-0.61	-0.04
91	-0.070	1.26	-0.48	-0.65	-1.91	5.21	0.46	-0.03	-0.84	-2.10	0.06
92	-0.126	-1.11	-0.12	5.51	1.09	-1.85	3.50	-0.07	0.93	0.00	-0.08
93	0.351	-0.36	0.01	10.36	6.21	3.31	0.05	0.00	-0.67	0.56	0.01
94	0.193	-0.05	0.16	-9.98	-4.01	0.41	-1.79	0.01	0.45	-1.46	0.11
95	-0.397	1.39	-0.06	-6.26	-3.70	-1.91	-1.78	0.06	-0.71	0.98	-0.05
96	0.623	0.93	0.18	8.00	-0.23	-2.61	1.93	-0.02	0.05	-1.70	-0.13
97	-1.666	0.73	-0.19	-17.93	-3.56	-0.06	-0.05	-0.13	0.10	-2.09	0.24
98	0.176	-0.70	-0.04	3.14	2.47	1.76	-1.93	0.09	-0.01	1.84	-0.01

99	0.889	-1.08	0.05	6.42	0.91	0.88	0.04	0.06	-0.15	2.04	-0.10
100	-0.348	0.97	0.23	-7.27	-2.45	0.21	1.03	0.00	-0.31	2.51	0.19
101	0.046	-1.85	0.23	-2.11	-8.27	-0.86	-0.54	-0.10	-0.48	-2.95	-0.21
102	0.620	-0.03	-0.12	5.36	6.82	0.06	0.01	0.03	0.73	2.78	0.04
103	-0.296	0.78	-0.34	3.64	3.50	0.56	-0.51	0.06	0.06	-2.26	-0.02
104	0.049	-0.20	-0.40	3.12	1.17	2.89	-2.09	-0.03	0.10	0.90	0.08
105	0.552	-0.89	0.04	5.78	-0.59	3.11	1.12	0.06	0.06	-3.54	-0.05
106	-0.448	0.92	0.13	-5.81	1.07	-0.61	1.43	-0.01	-0.25	-3.06	-0.02
107	-0.132	0.04	0.22	-3.47	-2.06	-5.41	-0.48	-0.03	0.09	5.78	-0.01
108	0.817	0.43	-0.16	-2.59	2.42	-9.28	-1.41	-0.06	0.11	1.21	-0.10
109	0.272	0.73	0.02	7.58	0.98	1.55	1.79	0.17	-0.06	-0.25	-0.07
110	-0.240	-1.08	0.05	1.61	2.94	6.08	-0.46	-0.06	0.05	1.88	0.12
111	-0.828	-0.21	0.08	-6.98	-6.75	1.62	0.07	-0.05	-0.10	-2.76	0.06
112	-0.400	-0.37	-0.29	-9.07	-6.17	4.86	-0.04	-0.01	-0.64	0.07	0.09
113	1.250	-0.38	0.02	8.28	6.13	-2.25	-0.87	0.09	-0.39	-1.89	-0.10
114	-0.569	1.31	0.18	3.25	1.22	0.07	0.87	-0.03	1.40	-0.49	-0.13
115	-0.261	-0.69	0.08	-2.84	-1.59	-2.71	0.02	-0.05	-0.36	2.39	0.13
116	0.368	-0.20	0.10	9.52	3.52	-3.78	-0.94	-0.05	0.11	2.89	-0.03
117	0.487	-0.14	-0.40	2.50	3.63	3.83	1.44	0.21	-0.06	2.58	0.15
118	-0.761	-0.02	0.51	-7.84	-4.71	-2.04	-0.04	-0.07	0.05	-2.58	-0.06
119	-0.073	0.23	-0.22	-4.56	-2.84	1.96	-0.47	-0.10	-0.10	-2.80	-0.06
120	0.742	0.94	0.34	4.21	-0.14	1.19	-0.89	-0.03	-0.29	0.27	0.01
121	-1.191	-0.50	-0.35	-4.38	-2.65	1.13	1.92	0.05	-0.46	-2.41	0.13
122	0.683	-0.37	-0.32	4.35	6.19	-0.50	-0.76	0.00	0.54	0.31	-0.06
123	-0.213	-0.19	0.33	-4.56	-3.81	-1.85	-0.28	-0.02	0.20	1.91	-0.08
124	-0.409	0.90	0.18	7.44	9.48	7.05	-0.39	0.02	0.18	0.67	0.11
125	-0.122	0.58	-0.48	-0.55	-3.75	-5.67	0.51	-0.01	-0.34	0.11	-0.07
126	0.198	0.52	0.36	-1.02	0.62	-0.93	0.08	0.05	0.21	-2.00	0.02
127	-0.295	0.22	0.32	1.40	3.36	0.25	2.81	0.11	0.17	-4.82	0.05
128	0.210	0.59	-0.18	4.69	3.16	0.24	-0.97	-0.13	-0.28	3.92	-0.14
129	-0.161	-0.59	0.23	-1.90	-3.93	1.17	-0.65	-0.05	-0.10	-3.47	-0.08
130	0.268	-0.35	-0.37	-4.56	-3.00	-1.69	-1.19	0.07	0.21	4.44	0.17
SE	0.261	0.45	-0.40	3.56	2.62	2.79	1.23	0.04	0.69	2.00	0.08

Appendix 16. GCA of 33 lines and four testers for biochemical traits for self-pollinated seed samples obtained from Cedara during 2017/2018 and 2018/2019 cropping seasons

Line	Tryptophan	Moisture	Protein	Oil	Fibre	Starch
1	0.008	0.11	-0.39	0.06	0.10	0.14
2	0.004	-0.08	0.17	-0.36	-0.03	0.58
3	0.003	0.50	-0.36	0.14	0.10	-0.06
4	-0.003	0.50	-0.24	-0.10	0.06	-0.03
5	-0.002	-0.24	-0.34	-0.57	-0.02	1.29
6	0.008	-0.58	-0.03	-0.15	-0.07	0.05
7	0.006	0.73	0.00	-0.05	0.16	-0.61
8	0.009	-0.18	0.46	0.42	0.17	-1.46
9	-0.005	-0.48	0.57	0.64	-0.14	-0.57
10	0.002	0.42	-0.06	0.15	-0.02	-0.06
11	0.003	-0.04	0.45	0.41	-0.07	-0.35
12	0.001	-0.10	0.03	0.54	0.01	-0.34
13	0.007	0.10	-0.66	-0.54	0.08	0.95
14	-0.007	0.19	-0.35	-0.12	0.05	-0.09
15	0.011	-0.14	0.60	-0.18	0.08	-1.82
16	0.003	0.26	-0.38	0.01	0.04	0.69
17	0.002	0.19	-0.20	0.51	-0.06	-0.57
18	0.015	0.29	-0.59	0.31	0.00	0.43
19	-0.008	-0.12	0.28	-0.65	-0.10	0.63
20	-0.010	-0.16	0.47	-0.37	-0.14	0.52
21	-0.003	-0.41	0.33	0.36	0.08	0.04
22	-0.015	0.16	0.06	-0.54	0.02	0.07
23	0.006	0.05	0.09	0.35	0.04	-1.06
24	0.001	0.11	-0.08	0.29	0.05	-0.56
25	0.002	0.07	-0.08	0.04	-0.10	0.07
26	-0.003	-0.02	-0.47	0.15	0.03	0.09
27	0.004	0.04	-0.33	-0.40	-0.01	0.68
28	-0.003	0.51	0.40	0.51	-0.07	-0.70
29	-0.011	-0.10	-0.12	-0.72	-0.13	1.56
30	-0.007	-0.13	0.18	0.48	-0.08	0.07
31	0.002	-0.47	-0.07	-0.63	-0.06	1.00
32	-0.017	-0.97	0.19	-0.05	0.07	0.20
35	-0.009	-0.32	0.63	-0.06	-0.06	-0.61
SE	0.003	0.28	0.19	0.18	-1.65	0.34
Tester						
1	0.012	0.03	-0.22	0.34	0.16	-0.71
2	0.010	0.15	-0.25	0.26	-0.06	0.08
3	-0.009	-0.04	0.13	-0.34	-0.02	0.60
4	-0.013	-0.13	0.33	-0.23	-0.09	0.04
SE	0.001	0.10	0.11	0.09	0.03	0.17

Appendix 17. SCA of 130 hybrids for biochemical traits for self-pollinated seed samples obtained from Cedara during 2017/2018 and 2018/2019 cropping seasons

Entry	Pedigree	Tryptophan	Moisture	Protein	Oil	Fibre	Starch
1	L1 x CZL15049 (QPM)	-0.003	0.39	0.10	0.37	0.15	-1.40
2	L1 x CZL059 (QPM)	0.009	-0.29	0.14	-0.26	0.05	0.23
3	L1 x CML444 (non-QPM)	0.001	-0.03	0.03	0.24	-0.12	-0.17
4	L1 x CML395 (non-QPM)	-0.007	-0.08	-0.25	-0.37	-0.08	1.33
5	L2 x CZL15049 (QPM)	0.000	0.21	0.16	-0.05	-0.02	0.15
6	L2 x CZL059 (QPM)	0.013	0.22	-0.19	-0.21	0.01	0.10
7	L2 x CML444 (non-QPM)	-0.003	0.09	-0.34	0.03	0.00	0.30
8	L2 x CML395 (non-QPM)	-0.011	-0.52	0.39	0.20	0.01	-0.54
9	L3 x CZL15049 (QPM)	0.001	-0.06	0.17	0.39	0.01	-0.97
10	L3 x CZL059 (QPM)	-0.005	0.21	-0.23	-1.13	-0.03	1.35
11	L3 x CML444 (non-QPM)	-0.005	-0.46	0.42	0.30	0.00	-0.43
12	L3 x CML395 (non-QPM)	0.007	0.30	-0.35	0.43	0.02	0.05
13	L4 x CZL15049 (QPM)	-0.019	0.36	-0.01	-0.23	0.04	0.01
14	L4 x CZL059 (QPM)	0.002	-0.59	-0.36	0.15	0.04	-0.03
15	L4 x CML444 (non-QPM)	0.002	0.28	0.21	-0.11	0.01	0.07
16	L4 x CML395 (non-QPM)	0.015	-0.06	0.17	0.17	-0.09	-0.06
17	L5 x CZL15049 (QPM)	0.003	-0.10	-0.37	0.61	-0.02	0.31
18	L5 x CZL059 (QPM)	0.010	0.12	-0.07	-0.28	-0.02	0.57
19	L5 x CML444 (non-QPM)	-0.002	0.39	0.00	-0.21	0.08	-0.15
20	L5 x CML395 (non-QPM)	-0.011	-0.41	0.46	-0.14	-0.05	-0.74
21	L6 x CZL15049 (QPM)	-0.002	-0.25	-0.27	-0.05	-0.01	0.54
22	L6 x CZL059 (QPM)	-0.002	0.12	-0.29	0.09	-0.03	0.17
23	L6 x CML444 (non-QPM)	0.003	0.32	0.03	0.07	0.08	-0.46
24	L6 x CML395 (non-QPM)	0.000	-0.20	0.54	-0.13	-0.04	-0.26
25	L7 x CZL15049 (QPM)	-0.007	0.37	-0.91	-0.52	0.01	2.08
26	L7 x CZL059 (QPM)	-0.002	0.35	-0.04	-0.61	0.04	0.00
27	L7 x CML444 (non-QPM)	-0.002	-1.05	0.50	1.00	0.00	-1.46
28	L7 x CML395 (non-QPM)	0.010	0.32	0.47	0.12	-0.05	-0.63
29	L8 x CZL15049 (QPM)	0.006	-0.61	0.35	-0.27	-0.08	-0.31
30	L8 x CZL059 (QPM)	0.003	0.10	0.29	-0.13	0.01	0.27
31	L8 x CML444 (non-QPM)	0.001	-0.29	-0.24	0.02	0.00	0.19
32	L8 x CML395 (non-QPM)	-0.010	0.79	-0.38	0.37	0.08	-0.15
33	L9 x CZL15049 (QPM)	0.017	0.44	0.16	-0.15	-0.06	0.01
34	L9 x CZL059 (QPM)	-0.023	-0.38	0.38	-0.30	-0.06	-0.10
35	L9 x CML444 (non-QPM)	-0.003	0.27	-0.70	0.42	0.05	0.30
36	L9 x CML395 (non-QPM)	0.009	-0.34	0.17	0.02	0.07	-0.22
37	L10 x CZL15049 (QPM)	0.018	0.75	0.02	0.34	0.17	-1.53
38	L10 x CZL059 (QPM)	-0.003	-0.58	-0.03	0.12	0.00	1.07
39	L10 x CML444 (non-QPM)	-0.007	0.22	-0.19	-0.38	-0.15	0.76
40	L10 x CML395 (non-QPM)	-0.009	-0.40	0.21	-0.10	-0.01	-0.30
41	L11 x CZL15049 (QPM)	0.003	-0.35	-0.26	-0.21	0.01	0.77
42	L11 x CZL059 (QPM)	0.007	0.81	0.41	0.24	-0.09	-0.19

43	L11 x CML444 (non-QPM)	0.001	0.68	-0.35	-0.01	0.00	0.20
44	L11 x CML395 (non-QPM)	-0.012	-1.14	0.21	-0.03	0.09	-0.80
45	L12 x CZL15049 (QPM)	0.014	0.26	-0.27	-0.52	0.05	1.00
46	L12 x CZL059 (QPM)	-0.008	0.21	-0.39	0.38	0.01	0.07
47	L12 x CML444 (non-QPM)	-0.009	-0.88	0.33	-0.23	-0.07	-0.34
48	L12 x CML395 (non-QPM)	0.002	0.40	0.34	0.36	0.01	-0.74
49	L13 x CZL15049 (QPM)	0.011	0.23	0.11	-0.38	0.00	-0.12
50	L13 x CZL059 (QPM)	0.004	0.01	0.30	-0.14	0.01	-0.07
51	L13 x CML444 (non-QPM)	-0.006	-0.82	-0.18	0.45	0.03	0.18
52	L13 x CML395 (non-QPM)	-0.009	0.57	-0.21	0.06	-0.04	0.00
53	L14 x CZL15049 (QPM)	-0.015	-0.23	-0.24	-0.38	0.10	0.35
54	L14 x CZL059 (QPM)	-0.001	-0.05	0.32	0.08	-0.10	0.19
55	L14 x CML444 (non-QPM)	0.014	-0.05	-0.13	1.00	0.03	-0.86
56	L14 x CML395 (non-QPM)	0.002	0.32	0.07	-0.71	-0.03	0.32
57	L15 x CZL15049 (QPM)	-0.003	-0.28	0.20	-0.33	0.00	-0.98
58	L15 x CZL059 (QPM)	-0.001	-1.03	0.02	-0.03	-0.03	0.94
59	L15 x CML444 (non-QPM)	-0.006	0.62	0.11	-0.05	0.03	0.04
60	L15 x CML395 (non-QPM)	0.009	0.68	-0.32	0.39	0.01	0.00
61	L16 x CZL15049 (QPM)	0.001	0.74	0.45	-0.17	0.12	-1.35
62	L16 x CZL059 (QPM)	0.004	-0.57	-0.31	0.11	-0.07	1.26
63	L16 x CML444 (non-QPM)	0.004	0.20	0.50	0.06	-0.12	-0.71
64	L16 x CML395 (non-QPM)	-0.010	-0.38	-0.62	-0.02	0.07	0.79
65	L17 x CZL15049 (QPM)	0.007	0.06	0.49	0.94	0.01	-1.44
66	L17 x CZL059 (QPM)	0.005	0.04	-0.30	0.05	-0.05	0.23
67	L17 x CML444 (non-QPM)	0.000	0.13	-0.57	-0.41	0.07	1.05
68	L17 x CML395 (non-QPM)	-0.013	-0.24	0.40	-0.59	-0.04	0.16
69	L18 x CZL15049 (QPM)	-0.002	-0.12	-0.40	0.12	-0.08	0.06
70	L18 x CZL059 (QPM)	0.009	0.44	0.38	-0.12	0.07	-0.91
71	L18 x CML444 (non-QPM)	-0.012	-0.15	-0.36	0.10	0.01	0.57
72	L18 x CML395 (non-QPM)	0.005	-0.17	0.40	-0.12	0.01	0.28
73	L19 x CZL15049 (non-QPM)	-0.001	0.25	0.01	0.03	-0.07	0.41
74	L19 x CZL059 (non-QPM)	-0.006	-0.82	0.60	-0.05	0.01	-1.38
75	L19 x CML444 (non-QPM)	-0.003	0.12	-0.01	-0.30	0.00	0.47
76	L19 x CML395 (non-QPM)	0.008	0.43	-0.59	0.31	0.06	0.50
77	L20 x CZL15049 (non-QPM)	-0.010	0.09	0.10	0.50	-0.11	0.18
78	L20 x CML444 (non-QPM)	0.025	0.32	0.17	-0.38	-0.07	-0.58
79	L20 x CML395 (non-QPM)	-0.005	-0.26	-0.50	0.12	0.12	0.47
80	L21 x CZL15049 (non-QPM)	-0.009	-0.18	0.17	0.07	-0.03	0.31
81	L21 x CZL059 (non-QPM)	-0.002	0.42	-0.64	0.36	0.01	0.42
82	L21 x CML444 (non-QPM)	0.019	0.05	-0.05	-0.09	0.05	-0.09
83	L21 x CML395 (non-QPM)	-0.009	-0.31	0.54	-0.35	-0.03	-0.64
84	L22 x CZL15049 (non-QPM)	-0.010	0.18	-0.34	0.37	-0.08	0.72
85	L22 x CZL059 (non-QPM)	-0.007	0.44	-0.55	-0.07	0.02	0.85
86	L22 x CML444 (non-QPM)	0.006	-0.01	-0.25	-0.11	-0.04	0.88
87	L22 x CML395 (non-QPM)	0.010	-0.61	1.14	-0.20	0.11	-2.45
88	L23 x CZL15049 (QPM)	0.000	-0.35	0.01	0.18	-0.01	0.11
89	L23 x CZL059 (QPM)	0.002	0.67	0.35	-0.22	0.02	-1.16

90	L23 x CML444 (non-QPM)	-0.004	0.02	-0.36	-0.25	-0.02	0.95
91	L23 x CML395 (non-QPM)	0.001	-0.34	0.01	0.28	0.01	0.10
92	L24 x CZL15049 (QPM)	0.009	-0.16	-0.20	-0.44	0.06	0.18
93	L24 x CZL059 (QPM)	-0.001	-0.20	0.44	0.50	0.00	-0.74
94	L24 x CML444 (non-QPM)	-0.001	-0.22	0.07	-0.05	0.04	0.01
95	L24 x CML395 (non-QPM)	-0.008	0.57	-0.29	-0.02	-0.10	0.55
96	L25 x CZL15049 (QPM)	0.002	-0.54	-0.14	-0.01	0.01	0.43
97	L25 x CZL059 (QPM)	0.002	0.08	0.17	-0.55	-0.06	0.49
98	L25 x CML444 (non-QPM)	-0.009	0.26	-0.40	0.01	0.02	-0.03
99	L25 x CML395 (non-QPM)	0.005	0.18	0.39	0.54	0.02	-0.89
100	L26 x CZL15049 (QPM)	0.008	-0.07	0.03	0.33	0.15	-0.44
101	L26 x CZL059 (QPM)	-0.006	0.38	-0.13	0.38	-0.07	0.02
102	L26 x CML444 (non-QPM)	-0.007	-0.09	0.25	0.04	0.03	-0.73
103	L26 x CML395 (non-QPM)	0.004	-0.24	-0.14	-0.77	-0.11	1.15
104	L27 x CZL15049 (QPM)	0.002	-0.05	-0.04	-0.23	-0.12	0.27
105	L27 x CZL059 (QPM)	0.010	-0.05	-0.32	-0.11	0.07	0.24
106	L27 x CML444 (non-QPM)	-0.008	-0.37	0.82	0.30	0.02	-1.36
107	L27 x CML395 (non-QPM)	-0.005	0.46	-0.45	0.03	0.03	0.84
108	L28 x CZL15049 (non-QPM)	-0.002	0.33	0.03	0.07	0.11	-0.46
109	L28 x CZL059 (non-QPM)	-0.004	-0.70	0.29	0.66	-0.03	-1.22
110	L28 x CML444 (non-QPM)	0.000	0.94	-0.23	-0.62	-0.10	1.11
111	L28 x CML395 (non-QPM)	0.005	-0.58	-0.08	-0.13	0.02	0.57
112	L29 x CZL15049 (non-QPM)	0.000	0.37	-0.56	-0.41	-0.01	1.37
113	L29 x CZL059 (non-QPM)	-0.014	-0.41	0.20	0.02	-0.01	-0.39
114	L29 x CML444 (non-QPM)	-0.002	-0.08	0.21	-0.05	0.07	-0.28
115	L29 x CML395 (non-QPM)	0.015	0.11	0.16	0.42	-0.05	-0.70
116	L30 x CZL15049 (non-QPM)	-0.008	-0.28	-0.03	0.81	-0.08	0.07
117	L30 x CZL059 (non-QPM)	-0.011	0.15	-0.37	0.50	0.20	-0.63
118	L30 x CML444 (non-QPM)	0.004	0.21	0.41	-1.28	0.03	0.33
119	L30 x CML395 (non-QPM)	0.014	-0.10	0.00	-0.04	-0.15	0.23
120	L31 x CZL15049 (QPM)	0.013	-0.14	-0.33	-0.41	0.02	0.63
121	L31 x CZL059 (QPM)	0.006	-0.22	0.20	-0.13	0.06	-0.26
122	L31 x CML444 (non-QPM)	-0.004	-0.28	0.47	0.50	-0.10	-0.57
123	L31 x CML395 (non-QPM)	-0.016	0.63	-0.33	0.03	0.02	0.20
124	L32 x CZL15049 (non-QPM)	-0.010	-0.11	0.23	0.18	-0.11	-0.18
125	L32 x CML444 (non-QPM)	0.011	-0.02	0.06	0.19	0.01	-0.04
126	L32 x CML395 (non-QPM)	0.009	0.28	-0.53	-0.14	0.05	0.29
127	L35 x CZL15049 (non-QPM)	-0.008	-0.85	1.41	-0.44	-0.15	-0.94
128	L35 x CZL059 (non-QPM)	-0.010	0.25	0.22	0.42	-0.06	-0.84
129	L35 x CML444 (non-QPM)	0.006	-0.03	-0.40	-0.10	0.13	0.67
130	L35 x CML395 (non-QPM)	0.010	0.62	-1.21	0.11	0.08	1.11
SE		0.005	0.40	0.30	0.36	0.06	0.57

Appendix 18. GCA of 33 lines and four testers for biochemical traits for self-pollinated seed samples obtained from Potchefstroom during 2017/2018 and 2018/2019 cropping seasons

Line	Tryptophan	Moisture	Protein	Oil	Fibre	Starch
1	0.012	-0.38	-0.39	0.47	0.00	0.36
2	-0.002	-0.19	0.10	-0.05	-0.03	0.67
3	0.004	-0.11	-0.50	-0.02	0.06	0.44
4	0.002	0.24	0.11	-0.35	0.11	-0.45
5	-0.001	-0.28	0.46	-0.30	0.00	0.21
6	0.004	0.31	-0.53	0.10	-0.07	0.12
7	0.005	0.60	-0.69	-0.42	0.20	0.58
8	0.000	0.07	-0.08	0.27	0.07	-0.57
9	0.002	-0.21	0.37	0.31	-0.17	-0.13
10	-0.001	0.29	-0.12	0.53	0.11	-0.57
11	-0.005	0.03	0.35	0.68	-0.09	-0.81
12	0.013	-0.12	-0.32	0.47	0.00	-0.16
13	0.004	0.19	-0.68	-0.41	0.10	1.06
14	0.006	0.87	-0.61	-0.55	0.08	1.12
15	0.016	-0.30	0.54	-0.03	0.08	-1.91
16	0.002	0.30	-0.40	-0.28	0.02	1.06
17	0.008	0.83	0.06	0.26	-0.03	-0.90
18	0.002	0.30	-0.68	0.17	0.02	0.82
19	-0.012	0.00	0.16	-0.72	-0.06	0.38
20	-0.009	-0.69	0.33	-0.38	-0.12	0.64
21	-0.012	-0.18	0.19	0.37	0.00	0.02
22	-0.014	-0.21	0.43	-0.35	0.00	-0.75
23	0.005	0.56	0.00	0.50	0.11	-1.22
24	0.010	0.27	0.23	0.40	0.04	-1.16
25	0.003	0.43	-0.09	-0.22	-0.10	0.52
26	0.002	0.02	-0.84	0.06	0.08	1.22
27	0.001	-0.85	0.20	-0.41	-0.04	0.47
28	-0.011	-0.36	1.26	0.45	0.01	-2.02
29	-0.010	-0.65	0.23	-0.12	-0.12	1.03
30	-0.006	-0.21	-0.18	0.73	-0.07	0.34
31	0.007	-0.18	-0.23	-0.36	-0.16	0.74
32	-0.015	-0.65	1.00	-0.70	0.06	-0.56
35	-0.015	-0.07	0.66	-0.39	-0.10	-0.57
SE	0.003	0.41	0.24	0.22	0.05	0.44
Tester						
1	0.015	0.08	-0.29	0.37	0.15	-0.54
2	0.016	0.15	-0.27	-0.03	-0.04	0.16
3	-0.014	0.11	0.17	-0.32	-0.01	0.72
4	-0.016	-0.33	0.38	-0.02	-0.10	-0.34
SE	0.002	0.10	0.21	0.05	0.04	0.23

Appendix 19. SCA of 130 hybrids for biochemical traits for self-pollinated seed samples obtained from Potchefstroom during 2017/2018 and 2018/2019 cropping seasons

Entry	Pedigree	Tryptophan	Moisture	Protein	Oil	Fibre	Starch
1	L1 x CZL15049 (QPM)	-0.010	-0.47	-0.39	-0.49	-0.03	0.46
2	L1 x CZL059 (QPM)	0.005	0.28	0.59	0.17	0.07	-1.13
3	L1 x CML444 (non-QPM)	0.006	0.41	-0.14	0.31	-0.07	0.23
4	L1 x CML395 (non-QPM)	-0.002	-0.23	-0.05	0.01	0.04	0.43
5	L2 x CZL15049 (QPM)	0.006	-0.13	0.13	-0.07	0.07	-0.10
6	L2 x CZL059 (QPM)	0.006	0.37	-0.12	-0.23	0.03	0.52
7	L2 x CML444 (non-QPM)	-0.009	-0.68	0.08	0.40	-0.02	-0.33
8	L2 x CML395 (non-QPM)	-0.004	0.43	-0.07	-0.10	-0.08	-0.10
9	L3 x CZL15049 (QPM)	0.001	-0.47	0.09	0.31	-0.01	-0.32
10	L3 x CZL059 (QPM)	-0.002	-0.83	-0.36	-0.44	-0.02	1.33
11	L3 x CML444 (non-QPM)	-0.002	0.49	0.06	0.16	-0.05	0.23
12	L3 x CML395 (non-QPM)	0.002	0.80	0.23	-0.02	0.09	-1.26
13	L4 x CZL15049 (QPM)	0.006	1.24	-0.83	0.48	0.06	0.71
14	L4 x CZL059 (QPM)	0.004	-0.88	0.43	-0.65	0.09	-0.18
15	L4 x CML444 (non-QPM)	-0.009	0.21	-0.07	0.62	0.04	-0.68
16	L4 x CML395 (non-QPM)	-0.003	-0.57	0.49	-0.44	-0.19	0.14
17	L5 x CZL15049 (QPM)	0.007	-0.22	0.73	-0.51	-0.04	0.04
18	L5 x CZL059 (QPM)	0.007	0.33	-0.08	-0.20	0.04	0.38
19	L5 x CML444 (non-QPM)	-0.010	0.52	-0.68	0.29	-0.02	0.16
20	L5 x CML395 (non-QPM)	-0.004	-0.64	0.05	0.43	0.02	-0.59
21	L6 x CZL15049 (QPM)	0.012	-0.61	0.40	0.08	0.02	-0.62
22	L6 x CZL059 (QPM)	-0.002	0.64	-0.49	-0.59	-0.11	1.01
23	L6 x CML444 (non-QPM)	-0.009	-0.18	-0.14	0.92	0.08	-0.83
24	L6 x CML395 (non-QPM)	-0.002	0.14	0.26	-0.40	0.01	0.42
25	L7 x CZL15049 (QPM)	0.004	-0.06	0.17	0.11	0.11	-0.57
26	L7 x CZL059 (QPM)	0.009	-0.18	-0.30	0.02	-0.07	0.75
27	L7 x CML444 (non-QPM)	-0.012	0.73	0.27	0.19	0.11	-0.28
28	L7 x CML395 (non-QPM)	-0.001	-0.50	-0.12	-0.32	-0.15	0.10
29	L8 x CZL15049 (QPM)	0.009	-0.48	0.68	0.41	0.04	-1.55
30	L8 x CZL059 (QPM)	0.006	0.92	-0.41	0.00	-0.02	0.40
31	L8 x CML444 (non-QPM)	-0.012	-0.61	-0.04	-0.44	0.00	0.66
32	L8 x CML395 (non-QPM)	-0.004	0.17	-0.22	0.04	-0.02	0.48
33	L9 x CZL15049 (QPM)	0.003	0.40	0.07	-0.12	-0.01	0.26
34	L9 x CZL059 (QPM)	0.004	0.15	0.35	-0.13	-0.09	0.12
35	L9 x CML444 (non-QPM)	-0.002	-0.45	-0.10	0.37	0.00	-0.64
36	L9 x CML395 (non-QPM)	-0.005	-0.11	-0.31	-0.12	0.11	0.25
37	L10 x CZL15049 (QPM)	0.004	1.59	-0.60	-0.12	0.27	-0.46
38	L10 x CZL059 (QPM)	-0.010	-0.43	0.19	-0.17	-0.02	0.31
39	L10 x CML444 (non-QPM)	0.008	-0.99	0.33	-0.28	-0.25	0.32
40	L10 x CML395 (non-QPM)	-0.002	-0.18	0.09	0.57	0.00	-0.18
41	L11 x CZL15049 (QPM)	0.012	-0.49	0.03	-0.15	-0.10	0.49
42	L11 x CZL059 (QPM)	0.005	-0.44	0.75	0.05	-0.07	-0.81
43	L11 x CML444 (non-QPM)	-0.010	0.06	0.05	0.24	0.11	-0.23
44	L11 x CML395 (non-QPM)	-0.007	0.87	-0.82	-0.14	0.07	0.54

45	L12 x CZL15049 (QPM)	0.012	-0.34	-0.09	0.60	0.14	-0.85
46	L12 x CZL059 (QPM)	-0.003	-0.21	0.35	-0.25	-0.02	0.07
47	L12 x CML444 (non-QPM)	-0.008	-0.49	0.42	-0.36	-0.19	0.06
48	L12 x CML395 (non-QPM)	-0.002	1.03	-0.66	0.02	0.08	0.71
49	L13 x CZL15049 (QPM)	0.000	0.68	-0.42	0.34	0.21	-0.74
50	L13 x CZL059 (QPM)	-0.002	0.42	0.46	-0.35	0.02	-0.80
51	L13 x CML444 (non-QPM)	0.002	-0.65	0.05	0.13	-0.07	1.25
52	L13 x CML395 (non-QPM)	-0.001	-0.47	-0.08	-0.12	-0.15	0.28
53	L14 x CZL15049 (QPM)	0.001	-0.18	0.18	-0.21	0.01	0.26
54	L14 x CZL059 (QPM)	0.000	0.23	-0.17	0.03	0.01	0.12
55	L14 x CML444 (non-QPM)	0.010	0.31	0.27	0.09	0.05	-0.51
56	L14 x CML395 (non-QPM)	-0.012	-0.37	-0.26	0.09	-0.07	0.12
57	L15 x CZL15049 (QPM)	0.011	-0.27	-0.37	0.44	0.00	-0.26
58	L15 x CZL059 (QPM)	-0.009	0.31	-0.58	-0.43	0.01	1.38
59	L15 x CML444 (non-QPM)	-0.003	0.21	0.56	-0.20	-0.03	-0.39
60	L15 x CML395 (non-QPM)	0.000	-0.26	0.40	0.19	0.03	-0.73
61	L16 x CZL15049 (QPM)	0.001	0.29	-0.52	0.21	0.09	0.22
62	L16 x CZL059 (QPM)	0.001	-0.06	0.45	-0.06	-0.08	-0.50
63	L16 x CML444 (non-QPM)	0.003	-0.44	-0.05	0.03	-0.02	0.44
64	L16 x CML395 (non-QPM)	-0.006	0.20	0.14	-0.18	0.02	-0.17
65	L17 x CZL15049 (QPM)	-0.006	0.71	-0.03	-0.09	0.11	-0.49
66	L17 x CZL059 (QPM)	-0.001	-0.78	0.25	0.17	-0.17	-0.32
67	L17 x CML444 (non-QPM)	0.004	0.81	-0.55	-0.15	0.00	0.88
68	L17 x CML395 (non-QPM)	0.003	-0.75	0.34	0.07	0.07	-0.09
69	L18 x CZL15049 (QPM)	0.005	-0.22	-0.51	0.23	0.01	0.64
70	L18 x CZL059 (QPM)	0.010	0.69	-0.19	0.12	0.02	-0.48
71	L18 x CML444 (non-QPM)	-0.001	-0.08	-0.19	-0.35	0.03	0.35
72	L18 x CML395 (non-QPM)	-0.015	-0.40	0.90	0.01	-0.06	-0.53
73	L19 x CZL15049 (non-QPM)	-0.011	-0.05	0.44	-0.14	-0.07	0.23
74	L19 x CZL059 (non-QPM)	-0.005	-0.31	0.05	0.34	-0.04	-0.34
75	L19 x CML444 (non-QPM)	0.007	0.17	-0.44	-0.18	-0.01	0.30
76	L19 x CML395 (non-QPM)	0.008	0.18	-0.04	-0.03	0.11	-0.20
77	L20 x CZL15049 (non-QPM)	-0.005	-0.22	0.86	0.12	-0.03	-0.95
78	L20 x CML444 (non-QPM)	0.015	-0.08	-0.24	-0.92	-0.12	0.61
79	L20 x CML395 (non-QPM)	0.005	0.44	-0.88	0.78	0.11	0.49
80	L21 x CZL15049 (non-QPM)	-0.015	-0.85	0.21	-0.08	-0.07	0.59
81	L21 x CZL059 (non-QPM)	-0.009	0.41	-0.03	0.43	0.04	-0.06
82	L21 x CML444 (non-QPM)	0.011	0.52	-0.08	-0.33	0.10	-0.47
83	L21 x CML395 (non-QPM)	0.012	-0.08	-0.08	-0.01	-0.07	-0.07
84	L22 x CZL15049 (non-QPM)	-0.016	0.64	-0.17	-0.13	-0.07	-0.01
85	L22 x CZL059 (non-QPM)	-0.013	-0.31	-0.30	0.33	-0.06	0.43
86	L22 x CML444 (non-QPM)	0.014	0.43	-0.26	0.12	-0.04	0.40
87	L22 x CML395 (non-QPM)	0.014	-0.76	0.75	-0.33	0.17	-0.83
88	L23 x CZL15049 (QPM)	0.000	-0.58	0.36	-0.24	-0.10	-0.47
89	L23 x CZL059 (QPM)	0.001	-0.19	-0.41	0.16	-0.01	0.47
90	L23 x CML444 (non-QPM)	-0.012	0.21	-0.11	0.11	0.14	0.10
91	L23 x CML395 (non-QPM)	0.010	0.55	0.17	-0.03	-0.03	-0.12
92	L24 x CZL15049 (QPM)	-0.005	0.41	0.08	-0.52	-0.14	0.06

93	L24 x CZL059 (QPM)	-0.005	-0.08	-0.30	0.49	0.08	-0.52
94	L24 x CML444 (non-QPM)	0.014	-0.11	-0.14	-0.07	0.03	0.38
95	L24 x CML395 (non-QPM)	-0.005	-0.22	0.38	0.10	0.04	0.07
96	L25 x CZL15049 (QPM)	0.011	-0.05	-0.33	-0.54	-0.08	1.26
97	L25 x CZL059 (QPM)	0.004	0.16	0.53	0.07	0.10	-0.89
98	L25 x CML444 (non-QPM)	-0.019	0.26	0.47	-0.16	0.01	-0.90
99	L25 x CML395 (non-QPM)	0.004	-0.38	-0.66	0.63	-0.03	0.52
100	L26 x CZL15049 (QPM)	0.002	-0.70	-0.17	-0.73	-0.05	0.96
101	L26 x CZL059 (QPM)	0.010	0.56	0.05	-0.40	0.00	0.40
102	L26 x CML444 (non-QPM)	-0.006	0.30	0.00	0.40	0.10	-0.49
103	L26 x CML395 (non-QPM)	-0.007	-0.17	0.14	0.74	-0.05	-0.87
104	L27 x CZL15049 (QPM)	0.002	1.13	-0.54	0.66	0.14	-0.07
105	L27 x CZL059 (QPM)	0.004	-0.37	-0.38	0.05	-0.01	0.63
106	L27 x CML444 (non-QPM)	-0.010	-0.22	0.63	-0.49	-0.17	-0.88
107	L27 x CML395 (non-QPM)	0.003	-0.55	0.31	-0.21	0.04	0.31
108	L28 x CZL15049 (non-QPM)	-0.003	-0.29	-0.51	0.82	-0.21	0.64
109	L28 x CZL059 (non-QPM)	-0.001	-1.39	1.23	-0.23	0.02	-2.07
110	L28 x CML444 (non-QPM)	-0.008	0.97	-0.25	-0.23	0.31	0.12
111	L28 x CML395 (non-QPM)	0.010	0.70	-0.47	-0.36	-0.12	1.30
112	L29 x CZL15049 (non-QPM)	-0.003	-0.08	0.38	-0.65	-0.06	0.16
113	L29 x CZL059 (non-QPM)	-0.014	0.54	-0.32	1.26	0.14	-0.38
114	L29 x CML444 (non-QPM)	0.014	-0.62	-0.20	-0.24	-0.12	0.21
115	L29 x CML395 (non-QPM)	0.003	0.15	0.16	-0.37	0.04	-0.01
116	L30 x CZL15049 (non-QPM)	-0.011	0.33	0.19	0.01	-0.11	-0.55
117	L30 x CZL059 (non-QPM)	-0.012	-0.43	-0.24	-0.17	0.05	0.48
118	L30 x CML444 (non-QPM)	0.016	0.36	0.39	0.27	0.02	-0.54
119	L30 x CML395 (non-QPM)	0.006	-0.27	-0.32	-0.10	0.04	0.59
120	L31 x CZL15049 (QPM)	0.009	-0.76	0.51	0.04	-0.11	0.22
121	L31 x CZL059 (QPM)	0.002	0.44	-0.14	-0.47	0.00	0.18
122	L31 x CML444 (non-QPM)	0.003	-0.21	-0.32	0.21	0.03	0.11
123	L31 x CML395 (non-QPM)	-0.015	0.52	-0.03	0.22	0.07	-0.52
124	L32 x CZL15049 (non-QPM)	-0.012	0.52	-1.00	0.26	0.06	1.01
125	L32 x CML444 (non-QPM)	0.012	-0.75	0.25	-0.35	-0.06	0.37
126	L32 x CML395 (non-QPM)	0.014	0.37	0.49	0.06	-0.03	-1.23
127	L35 x CZL15049 (non-QPM)	-0.012	-0.09	0.61	-0.05	-0.02	-0.26
128	L35 x CZL059 (non-QPM)	-0.009	-0.59	0.13	0.29	0.01	-0.46
129	L35 x CML444 (non-QPM)	0.010	-0.04	-0.17	0.17	0.09	-0.03
130	L35 x CML395 (non-QPM)	0.010	0.70	-0.56	-0.41	-0.08	0.73
SE		0.006	0.53	0.34	0.34	0.07	0.64

Appendix 20. GCA of 33 lines and four testers for biochemical traits for self-pollinated seed samples obtained from two locations in Zimbabwe during cropping season

Line	Tryptophan	Moisture	Protein	Oil	Fibre	Starch
1	0.001	-1.14	-0.23	0.34	0.00	-0.30
2	0.017	1.23	0.45	-0.34	-0.03	-0.06
3	0.004	-0.45	-0.64	-0.23	0.06	0.56
4	0.006	0.88	-0.42	-0.14	0.11	0.07
5	-0.004	-1.00	0.03	-0.62	0.00	1.01
6	0.003	1.07	-0.43	0.04	-0.07	0.07
7	0.006	1.30	-0.73	-0.35	0.20	0.35
8	0.011	0.01	0.25	0.42	0.07	-0.90
9	0.006	0.10	0.98	0.56	-0.17	-0.91
10	0.009	1.63	-0.09	0.74	0.11	-0.91
11	0.013	-1.20	1.08	0.85	-0.09	-1.33
12	0.006	-1.00	-0.14	0.62	0.00	-0.34
13	0.007	0.51	-0.81	-0.17	0.10	0.31
14	0.009	0.70	-0.22	-0.12	0.08	-0.07
15	0.005	-1.19	-0.23	0.48	0.08	-0.50
16	0.004	-0.03	-0.65	-0.21	0.02	0.51
17	0.009	0.41	-0.05	0.27	-0.03	-0.33
18	0.002	0.58	-0.44	0.25	0.02	-0.33
19	-0.009	-0.30	-0.03	-0.66	-0.06	0.74
20	-0.012	0.56	0.91	-0.34	-0.12	0.10
21	-0.014	-2.19	0.25	-0.26	0.00	0.51
22	-0.017	1.00	0.19	-0.71	0.00	0.73
23	0.002	0.65	-0.14	0.47	0.11	-0.50
24	0.001	-0.15	-0.15	0.27	0.04	-0.04
25	0.000	-1.41	-0.34	-0.03	-0.10	0.36
26	0.005	0.26	-0.81	0.20	0.08	0.26
27	0.002	-0.66	0.03	-0.51	-0.04	0.49
28	-0.019	1.11	0.61	0.52	0.01	-0.66
29	-0.012	-1.02	0.34	-0.18	-0.12	0.26
30	-0.014	0.93	0.25	0.09	-0.07	-0.06
31	0.001	-0.72	-0.41	-0.21	-0.16	0.26
32	-0.015	-2.12	0.95	-0.99	0.06	1.03
35	-0.021	1.26	1.11	-0.42	-0.10	-0.11
SE	0.003	0.49	0.17	0.07	0.05	0.16
Tester						
1	0.009	1.15	-0.23	0.36	0.15	-0.50
2	0.013	-0.99	-1.02	0.20	-0.04	0.26
3	-0.009	0.16	0.36	-0.35	-0.01	0.20
4	-0.012	-0.37	0.84	-0.20	-0.10	0.06
SE	0.001	0.22	0.05	0.03	0.04	0.07

Appendix 21. SCA of 130 hybrids for biochemical traits for self-pollinated seed samples obtained from two locations in Zimbabwe during 2017/2018 and 2018/2019 cropping seasons

Entry	Pedigree	Tryptophan	Moisture	Protein	Oil	Fibre	Starch
1	L1 x CZL15049 (QPM)	0.011	0.90	-0.69	-0.09	-0.03	0.31
2	L1 x CZL059 (QPM)	-0.008	0.12	0.00	0.05	0.07	0.07
3	L1 x CML444 (non-QPM)	0.001	0.07	0.25	-0.14	-0.07	-0.07
4	L1 x CML395 (non-QPM)	-0.004	-1.03	0.49	0.17	0.04	-0.33
5	L2 x CZL15049 (QPM)	0.000	0.16	-0.30	-0.06	0.07	0.12
6	L2 x CZL059 (QPM)	0.016	1.53	-0.18	0.03	0.03	0.00
7	L2 x CML444 (non-QPM)	-0.010	-1.35	-0.24	-0.03	-0.02	0.24
8	L2 x CML395 (non-QPM)	-0.007	-0.27	0.78	0.05	-0.08	-0.37
9	L3 x CZL15049 (QPM)	0.008	1.57	-0.23	0.38	-0.01	-0.83
10	L3 x CZL059 (QPM)	-0.007	0.16	-0.34	0.09	-0.02	-0.19
11	L3 x CML444 (non-QPM)	-0.006	-2.19	0.80	-0.32	-0.05	0.70
12	L3 x CML395 (non-QPM)	0.004	0.51	-0.17	-0.16	0.09	0.31
13	L4 x CZL15049 (QPM)	0.006	1.02	-0.07	0.27	0.06	-0.26
14	L4 x CZL059 (QPM)	-0.005	-1.22	-0.56	0.06	0.09	0.35
15	L4 x CML444 (non-QPM)	-0.010	-0.25	0.21	-0.22	0.04	0.19
16	L4 x CML395 (non-QPM)	0.009	0.51	0.48	-0.12	-0.19	-0.30
17	L5 x CZL15049 (QPM)	0.004	-2.48	0.23	0.02	-0.04	0.25
18	L5 x CZL059 (QPM)	-0.001	0.18	0.07	-0.27	0.04	0.53
19	L5 x CML444 (non-QPM)	-0.005	1.48	0.06	-0.02	-0.02	-0.35
20	L5 x CML395 (non-QPM)	0.001	0.88	-0.29	0.26	0.02	-0.44
21	L6 x CZL15049 (QPM)	0.003	0.05	-0.07	0.11	0.02	-0.46
22	L6 x CZL059 (QPM)	0.001	-1.46	0.05	-0.43	-0.11	0.90
23	L6 x CML444 (non-QPM)	-0.005	1.64	0.49	0.19	0.08	-0.68
24	L6 x CML395 (non-QPM)	-0.001	-0.16	-0.41	0.12	0.01	0.23
25	L7 x CZL15049 (QPM)	-0.006	1.47	0.33	0.10	0.11	-0.44
26	L7 x CZL059 (QPM)	0.010	-1.84	-0.60	-0.29	-0.07	0.92
27	L7 x CML444 (non-QPM)	0.001	0.55	0.07	0.31	0.11	-0.37
28	L7 x CML395 (non-QPM)	-0.005	-0.12	0.26	-0.14	-0.15	-0.13
29	L8 x CZL15049 (QPM)	0.002	-0.72	0.10	0.03	0.04	0.08
30	L8 x CZL059 (QPM)	-0.004	-1.61	-0.31	0.01	-0.02	0.29
31	L8 x CML444 (non-QPM)	-0.002	0.74	0.44	-0.04	0.00	-0.39
32	L8 x CML395 (non-QPM)	0.003	1.64	-0.17	-0.01	-0.02	0.00
33	L9 x CZL15049 (QPM)	0.002	-0.43	0.00	-0.16	-0.01	0.42
34	L9 x CZL059 (QPM)	0.015	-1.19	0.79	0.10	-0.09	-0.62
35	L9 x CML444 (non-QPM)	-0.005	0.49	-0.49	0.15	0.00	-0.03
36	L9 x CML395 (non-QPM)	-0.013	1.19	-0.24	-0.10	0.11	0.21
37	L10 x CZL15049 (QPM)	0.016	1.49	0.17	1.06	0.27	-1.46
38	L10 x CZL059 (QPM)	0.000	-1.82	-0.09	-0.33	-0.02	0.57
39	L10 x CML444 (non-QPM)	-0.010	-1.25	-0.35	-0.31	-0.25	0.67
40	L10 x CML395 (non-QPM)	-0.007	1.63	0.33	-0.43	0.00	0.20
41	L11 x CZL15049 (QPM)	-0.008	-0.33	0.00	0.05	-0.10	0.11
42	L11 x CZL059 (QPM)	0.021	0.06	0.26	0.14	-0.07	-0.26
43	L11 x CML444 (non-QPM)	-0.008	1.65	-0.60	-0.07	0.11	0.18
44	L11 x CML395 (non-QPM)	-0.006	-1.32	0.40	-0.14	0.07	-0.05

45	L12 x CZL15049 (QPM)	0.009	-0.33	-0.58	-0.11	0.14	0.35
46	L12 x CZL059 (QPM)	0.002	-0.21	0.19	0.22	-0.02	-0.34
47	L12 x CML444 (non-QPM)	-0.003	0.99	0.20	-0.16	-0.19	0.15
48	L12 x CML395 (non-QPM)	-0.010	-0.39	0.25	0.04	0.08	-0.18
49	L13 x CZL15049 (QPM)	-0.004	1.68	-0.14	-0.28	0.21	-0.10
50	L13 x CZL059 (QPM)	0.000	0.77	-0.15	-0.27	0.02	0.21
51	L13 x CML444 (non-QPM)	-0.005	-1.71	0.80	0.53	-0.07	-0.30
52	L13 x CML395 (non-QPM)	0.007	-0.68	-0.46	0.01	-0.15	0.18
53	L14 x CZL15049 (QPM)	0.002	1.27	0.10	-0.03	0.01	0.00
54	L14 x CZL059 (QPM)	-0.002	-0.37	-0.13	-0.09	0.01	0.29
55	L14 x CML444 (non-QPM)	0.007	-1.17	-0.19	-0.07	0.05	0.10
56	L14 x CML395 (non-QPM)	-0.007	0.33	0.28	0.18	-0.07	-0.41
57	L15 x CZL15049 (QPM)	0.011	0.40	-0.54	0.02	0.00	0.06
58	L15 x CZL059 (QPM)	0.002	0.94	-0.22	-0.14	0.01	0.22
59	L15 x CML444 (non-QPM)	-0.001	-1.26	0.77	-0.07	-0.03	0.03
60	L15 x CML395 (non-QPM)	-0.012	-0.03	0.04	0.18	0.03	-0.33
61	L16 x CZL15049 (QPM)	0.006	-0.43	-0.12	0.04	0.09	-0.08
62	L16 x CZL059 (QPM)	0.004	0.91	0.12	-0.13	-0.08	0.01
63	L16 x CML444 (non-QPM)	-0.005	-0.94	0.22	0.44	-0.02	-0.38
64	L16 x CML395 (non-QPM)	-0.006	0.51	-0.16	-0.36	0.02	0.43
65	L17 x CZL15049 (QPM)	0.010	0.20	-0.82	0.21	0.11	0.06
66	L17 x CZL059 (QPM)	-0.008	-0.66	0.47	0.15	-0.17	-0.56
67	L17 x CML444 (non-QPM)	0.000	1.72	0.01	-0.44	0.00	0.51
68	L17 x CML395 (non-QPM)	-0.003	-1.21	0.41	0.07	0.07	-0.03
69	L18 x CZL15049 (QPM)	0.012	0.09	-1.18	-0.10	0.01	0.77
70	L18 x CZL059 (QPM)	-0.004	-0.82	0.86	0.16	0.02	-0.55
71	L18 x CML444 (non-QPM)	0.000	1.28	-0.65	-0.17	0.03	0.17
72	L18 x CML395 (non-QPM)	-0.009	-0.49	1.03	0.09	-0.06	-0.40
73	L19 x CZL15049 (non-QPM)	-0.001	-1.60	0.31	-0.16	-0.07	0.12
74	L19 x CZL059 (non-QPM)	-0.017	1.46	0.53	0.02	-0.04	-0.14
75	L19 x CML444 (non-QPM)	0.009	0.41	-0.25	-0.06	-0.01	0.27
76	L19 x CML395 (non-QPM)	0.009	-0.21	-0.53	0.19	0.11	-0.27
77	L20 x CZL15049 (non-QPM)	-0.016	-0.25	0.17	0.14	-0.03	-0.31
78	L20 x CML444 (non-QPM)	0.013	-1.26	-0.69	-0.08	-0.12	0.46
79	L20 x CML395 (non-QPM)	0.016	0.57	-0.44	0.12	0.11	0.10
80	L21 x CZL15049 (non-QPM)	-0.007	-2.69	1.38	0.22	-0.07	-0.73
81	L21 x CZL059 (non-QPM)	-0.021	1.65	0.04	0.20	0.04	-0.59
82	L21 x CML444 (non-QPM)	0.020	0.62	-0.54	0.10	0.10	0.15
83	L21 x CML395 (non-QPM)	0.007	0.48	-0.82	-0.53	-0.07	1.16
84	L22 x CZL15049 (non-QPM)	-0.012	2.37	0.41	-0.09	-0.07	-0.25
85	L22 x CZL059 (non-QPM)	-0.010	-0.77	0.08	0.10	-0.06	-0.21
86	L22 x CML444 (non-QPM)	0.004	0.23	-0.45	0.16	-0.04	-0.20
87	L22 x CML395 (non-QPM)	0.017	-1.77	0.02	-0.18	0.17	0.64
88	L23 x CZL15049 (QPM)	0.004	0.27	-0.13	-0.19	-0.10	0.26
89	L23 x CZL059 (QPM)	0.013	2.01	0.34	0.25	-0.01	-0.86
90	L23 x CML444 (non-QPM)	-0.008	-0.70	0.30	-0.11	0.14	-0.07
91	L23 x CML395 (non-QPM)	-0.010	-1.52	-0.45	0.04	-0.03	0.65
92	L24 x CZL15049 (QPM)	0.003	0.42	0.23	-0.07	-0.14	0.12

93	L24 x CZL059 (QPM)	-0.002	0.68	-0.35	-0.04	0.08	0.16
94	L24 x CML444 (non-QPM)	-0.002	-2.45	0.54	0.13	0.03	-0.23
95	L24 x CML395 (non-QPM)	0.000	1.41	-0.36	-0.04	0.04	-0.07
96	L25 x CZL15049 (QPM)	0.002	-0.27	-0.75	0.18	-0.08	0.12
97	L25 x CZL059 (QPM)	0.002	-1.63	0.26	-0.31	0.10	0.56
98	L25 x CML444 (non-QPM)	0.004	0.32	0.10	-0.04	0.01	-0.15
99	L25 x CML395 (non-QPM)	-0.008	1.64	0.45	0.16	-0.03	-0.54
100	L26 x CZL15049 (QPM)	-0.003	0.46	-0.59	-0.27	-0.05	0.40
101	L26 x CZL059 (QPM)	0.012	-0.40	-0.32	-0.44	0.00	0.86
102	L26 x CML444 (non-QPM)	0.006	0.80	0.90	0.41	0.10	-1.03
103	L26 x CML395 (non-QPM)	-0.016	-0.80	0.07	0.29	-0.05	-0.24
104	L27 x CZL15049 (QPM)	0.003	1.05	0.10	-0.08	0.14	-0.10
105	L27 x CZL059 (QPM)	0.001	0.02	-0.51	0.18	-0.01	-0.22
106	L27 x CML444 (non-QPM)	-0.003	-0.83	0.58	0.12	-0.17	-0.23
107	L27 x CML395 (non-QPM)	-0.002	-0.18	-0.10	-0.23	0.04	0.53
108	L28 x CZL15049 (non-QPM)	-0.009	1.81	0.87	-0.40	-0.21	-0.33
109	L28 x CZL059 (non-QPM)	-0.006	-0.17	0.24	0.04	0.02	-0.09
110	L28 x CML444 (non-QPM)	-0.002	-0.95	-0.92	0.13	0.31	0.45
111	L28 x CML395 (non-QPM)	0.016	-0.62	-0.12	0.21	-0.12	-0.04
112	L29 x CZL15049 (non-QPM)	-0.011	-2.66	0.59	-0.16	-0.06	0.42
113	L29 x CZL059 (non-QPM)	-0.012	1.73	0.48	0.15	0.14	-0.94
114	L29 x CML444 (non-QPM)	0.010	0.83	-0.45	-0.06	-0.12	0.27
115	L29 x CML395 (non-QPM)	0.012	0.16	-0.56	0.07	0.04	0.23
116	L30 x CZL15049 (non-QPM)	-0.002	-2.38	0.73	0.12	-0.11	-0.26
117	L30 x CZL059 (non-QPM)	-0.006	0.78	-0.23	-0.37	0.05	0.85
118	L30 x CML444 (non-QPM)	0.010	0.50	-0.66	0.02	0.02	-0.03
119	L30 x CML395 (non-QPM)	-0.003	1.16	0.23	0.22	0.04	-0.57
120	L31 x CZL15049 (QPM)	0.007	1.74	-0.59	-0.28	-0.11	0.68
121	L31 x CZL059 (QPM)	0.009	0.48	-0.07	0.03	0.00	0.16
122	L31 x CML444 (non-QPM)	-0.018	-0.22	0.30	0.02	0.03	-0.37
123	L31 x CML395 (non-QPM)	0.001	-1.94	0.42	0.22	0.07	-0.48
124	L32 x CZL15049 (non-QPM)	-0.017	-1.76	-0.12	-0.16	0.06	0.70
125	L32 x CML444 (non-QPM)	0.012	2.03	-0.66	0.15	-0.06	-0.30
126	L32 x CML395 (non-QPM)	0.017	-1.20	-0.19	0.20	-0.03	-0.16
127	L35 x CZL15049 (non-QPM)	-0.018	-1.71	0.72	0.07	-0.02	-0.01
128	L35 x CZL059 (non-QPM)	-0.016	-0.50	0.69	0.13	0.01	-0.50
129	L35 x CML444 (non-QPM)	0.018	0.55	-0.40	-0.10	0.09	0.34
130	L35 x CML395 (non-QPM)	0.015	1.73	-0.95	-0.12	-0.08	0.15
SE		0.006	0.76	0.22	0.13	0.07	0.24

Appendix 22. Heterosis of grain yield and agronomic traits of 130 hybrids across 13 environments during 2017/2018 and 2018/2019 cropping seasons

Entry	Hybrids	GY		ASI		PH		EH		EPP		ER		EA		Sum (GY and EPP)	Rank
		MID PH	BP H	MID PH	BP H	MID PH	BP H	MID PH	BP H	MID PH	BP H	MID PH	BP H	MID PH	BP H		
1	L1 x CZL15049 (QPM)	116.62	130.86	-52.77	-60.18	43.54	55.99	57.30	78.63	-13.92	9.52	127.71	102.78	-7.32	-9.86	243.08	29.77
2	L1 x CZL059 (QPM)	144.67	148.08	-10.40	-17.56	39.91	44.74	55.63	71.74	-14.24	-6.82	117.53	60.96	-7.66	-13.56	271.69	114.42
3	L1 x CML444 (non-QPM)	94.88	124.39	135.70	-265.79	44.11	48.48	55.47	60.16	-23.41	-7.89	183.66	109.89	-0.67	-7.61	187.97	-97.30
4	L1 x CML395 (non-QPM)	141.95	161.22	-34.61	-39.44	33.51	34.20	50.97	56.48	-10.16	12.96	269.47	194.09	-0.71	-8.56	305.97	-148.32
5	L2 x CZL15049 (QPM)	116.02	117.96	2.37	40.23	29.35	49.90	35.40	72.55	-15.98	7.73	206.00	211.32	-9.04	-11.53	225.73	-171.02
6	L2 x CZL059 (QPM)	122.74	131.81	-6.62	-20.43	27.66	30.88	36.23	36.87	-14.22	-6.15	248.80	185.27	0.90	-5.54	234.18	-195.25
7	L2 x CML444 (non-QPM)	95.16	111.95	80.04	-191.55	35.38	48.31	43.23	53.90	-14.93	3.08	399.99	308.93	-3.81	-10.53	195.27	-499.31
8	L2 x CML395 (non-QPM)	163.47	169.14	-85.92	-86.04	24.12	31.04	35.02	44.16	-1.57	24.71	267.07	227.47	-4.48	-12.03	355.75	-122.28
9	L3 x CZL15049 (QPM)	99.42	110.30	-31.23	-41.86	39.75	53.92	52.42	84.49	-10.66	-0.05	308.14	248.66	-9.27	-11.17	199.02	-337.34
10	L3 x CZL059 (QPM)	90.71	111.77	-29.15	-34.60	30.55	27.85	49.47	55.45	-14.56	-11.83	275.32	250.37	-3.72	-5.50	176.09	-340.38
11	L3 x CML444 (non-QPM)	92.37	96.03	324.50	-402.18	46.50	52.88	61.03	65.39	-6.60	-0.71	265.99	241.67	-8.44	-10.75	181.09	-307.38
12	L3 x CML395 (non-QPM)	156.08	166.64	-68.21	-70.66	45.73	46.78	70.44	73.99	-2.99	7.37	59.35	64.90	-6.42	-9.72	327.11	219.00
13	L4 x CZL15049 (QPM)	59.18	79.64	8.26	30.35	40.11	47.20	67.29	69.56	0.06	0.56	255.86	236.33	-3.38	-5.09	139.43	-344.29
14	L4 x CZL059 (QPM)	106.60	146.24	-26.25	-31.05	37.08	46.62	50.78	88.02	-14.05	0.13	108.93	61.60	-6.92	-8.94	238.92	84.25
15	L4 x CML444 (non-QPM)	98.02	107.10	131.25	-272.46	38.80	39.12	51.14	74.74	-24.20	-20.03	92.39	48.80	-7.80	-10.41	160.90	37.92
16	L4 x CML395 (non-QPM)	135.59	162.31	-27.61	-34.01	39.09	44.42	70.52	98.48	0.70	2.21	189.23	142.18	-8.96	-12.45	300.82	-9.18
17	L5 x CZL15049 (QPM)	95.19	98.97	-29.49	-33.74	41.52	49.70	71.71	76.23	-0.45	6.94	243.56	203.64	-13.38	-18.09	200.65	-215.08
18	L5 x CZL059 (QPM)	135.59	152.48	-20.44	-23.28	38.36	46.98	58.33	94.56	16.66	25.21	292.27	188.63	-11.32	-19.19	329.94	-120.45
19	L5 x CML444 (non-QPM)	101.40	112.32	120.98	-330.35	46.13	46.74	71.74	95.82	-12.35	-10.37	222.55	137.33	-15.20	-23.22	191.00	-130.46
20	L5 x CML395 (non-QPM)	146.07	147.76	-35.87	-46.61	38.51	42.86	71.39	96.75	8.53	15.38	108.29	64.73	-9.89	-19.18	317.74	173.79
21	L6 x CZL15049 (QPM)	146.04	180.39	-24.42	-33.00	45.04	50.74	60.55	62.67	-4.67	4.29	367.42	331.26	-5.79	-7.40	326.05	-359.44
22	L6 x CZL059 (QPM)	140.38	159.87	-52.31	-53.58	43.83	69.23	64.35	111.58	-6.08	-0.99	293.71	239.93	-10.87	-15.71	293.18	-213.88
23	L6 x CML444 (non-QPM)	171.71	235.97	178.80	-338.63	52.39	67.13	72.70	105.81	0.65	4.73	340.83	280.61	-6.74	-12.39	413.06	-189.25
24	L6 x CML395 (non-QPM)	169.61	211.51	-57.79	-62.94	45.67	65.98	67.63	101.15	0.97	9.31	290.61	270.40	-6.91	-13.42	391.40	-149.28
25	L7 x CZL15049 (QPM)	79.64	91.98	-49.41	-60.74	46.00	48.50	74.38	79.17	-24.64	-6.36	244.35	199.18	-4.76	-6.52	140.62	-291.63
26	L7 x CZL059 (QPM)	88.05	111.74	-28.64	-48.24	36.32	50.85	55.26	90.55	-27.45	-22.81	457.51	410.91	-5.57	-10.83	149.53	-702.49
27	L7 x CML444 (non-QPM)	98.14	99.36	-46.03	-244.52	45.22	50.29	68.70	92.12	-22.54	-8.94	491.98	442.50	-7.19	-12.93	166.02	-748.34
28	L7 x CML395 (non-QPM)	147.05	160.63	-64.41	-76.46	37.55	47.62	70.32	95.27	-14.22	5.35	359.33	353.21	-2.33	-9.29	298.81	-402.11
29	L8 x CZL15049 (QPM)	222.19	448.82	-77.40	-53.25	44.70	59.93	72.04	96.97	1.36	3.37	294.57	252.99	-16.95	-25.94	675.74	171.07
30	L8 x CZL059 (QPM)	213.37	399.26	-85.70	-90.06	44.96	47.61	65.68	81.39	5.71	19.80	218.97	183.63	-16.89	-28.40	638.14	280.83
31	L8 x CML444 (non-QPM)	222.04	507.24	1080.70	-170.04	49.94	57.00	76.42	80.39	-4.27	-1.54	270.67	229.60	-19.77	-31.29	723.48	274.27
32	L8 x CML395 (non-QPM)	236.11	482.49	-89.56	-91.93	42.19	43.68	63.65	68.36	19.68	20.84	423.76	413.35	-18.22	-30.58	759.11	-29.20
33	L9 x CZL15049 (QPM)	185.13	256.80	-38.11	-38.71	54.11	62.53	77.23	99.82	4.14	8.02	277.32	281.97	-16.77	-21.40	454.09	-67.03
34	L9 x CZL059 (QPM)	149.95	195.57	-24.38	-30.72	39.09	48.21	58.32	75.95	3.13	24.53	170.21	116.11	-9.08	-17.27	373.18	113.21
35	L9 x CML444 (non-QPM)	166.91	264.35	132.17	-383.33	52.49	52.68	65.94	72.09	-7.52	0.84	246.31	176.98	-14.27	-22.47	424.57	38.02

36	L9 x CML395 (non-QPM)	199.08	279.78	-55.17	-39.98	38.55	43.32	63.63	70.74	14.67	20.16	95.71	70.23	-10.33	-19.68	513.69	377.76
37	L10 x CZL15049 (QPM)	230.77	340.06	-29.08	-36.62	44.10	62.72	59.59	103.29	-7.66	-2.17	155.97	162.61	-16.90	-21.74	561.00	281.06
38	L10 x CZL059 (QPM)	188.65	262.08	-4.45	-6.15	33.89	34.09	50.58	51.23	-14.31	-6.73	284.80	216.73	-18.98	-26.46	429.70	-26.39
39	L10 x CML444 (non-QPM)	177.65	304.30	171.70	-339.47	45.75	55.76	60.51	72.40	-10.65	-11.44	112.73	75.10	-20.56	-28.34	459.85	320.92
40	L10 x CML395 (non-QPM)	214.92	325.41	-61.06	-66.08	34.56	38.69	56.53	67.07	0.67	5.56	227.89	194.64	-14.35	-23.48	546.56	161.86
41	L11 x CZL15049 (QPM)	217.69	222.30	-22.46	-30.14	43.47	67.31	56.62	107.77	-3.82	8.08	247.64	198.93	-13.32	-11.58	444.25	22.58
42	L11 x CZL059 (QPM)	133.40	141.54	-26.58	-27.23	35.49	39.69	51.19	57.04	-11.24	-8.77	274.14	246.75	-4.59	-6.50	254.93	-254.87
43	L11 x CML444 (non-QPM)	150.75	173.92	105.17	-286.04	52.41	67.98	68.24	87.30	-8.63	-2.46	210.80	188.05	-12.07	-14.43	313.58	-58.77
44	L11 x CML395 (non-QPM)	142.04	148.62	-31.18	-40.51	34.56	42.89	52.21	68.35	1.16	12.46	239.02	230.50	-5.23	-8.72	304.28	-151.29
45	L12 x CZL15049 (QPM)	128.12	198.11	-60.22	-67.04	44.04	52.92	66.19	78.13	16.09	32.26	330.04	271.71	-11.85	-14.77	374.58	-200.55
46	L12 x CZL059 (QPM)	151.96	210.65	-46.47	-58.87	43.94	52.36	62.88	90.70	1.94	36.78	198.86	175.41	-8.22	-14.56	401.32	49.83
47	L12 x CML444 (non-QPM)	131.84	231.29	9.06	-336.60	47.65	48.78	66.79	81.68	6.86	28.50	215.60	190.83	-10.67	-17.38	398.49	20.11
48	L12 x CML395 (non-QPM)	187.65	281.62	-30.03	-51.57	44.51	48.52	72.40	89.00	16.77	34.51	70.11	66.84	-5.24	-13.21	520.55	402.05
49	L13 x CZL15049 (QPM)	148.68	143.64	-34.21	-54.07	51.50	57.90	80.63	96.39	6.28	16.28	334.47	300.86	-7.79	-9.27	314.88	-303.39
50	L13 x CZL059 (QPM)	88.78	102.68	-5.61	44.46	36.25	46.93	50.07	73.06	-10.25	-5.39	230.75	185.57	1.79	-0.58	175.83	-241.70
51	L13 x CML444 (non-QPM)	139.06	151.58	516.63	-220.19	50.89	52.41	74.55	87.43	-5.19	-1.34	35.18	16.71	-14.09	-16.66	284.10	262.96
52	L13 x CML395 (non-QPM)	161.21	163.46	4.62	29.50	37.52	43.93	63.08	76.24	8.61	17.58	233.21	215.98	-0.91	-4.86	350.86	-92.56
53	L14 x CZL15049 (QPM)	136.30	137.13	-26.46	-35.34	29.87	42.00	59.01	80.37	-3.04	9.44	504.16	481.59	-4.00	-5.35	279.82	-696.58
54	L14 x CZL059 (QPM)	152.05	165.73	3.03	6.97	33.97	37.79	49.63	65.31	1.09	3.48	347.83	251.20	0.26	-4.91	322.35	-272.03
55	L14 x CML444 (non-QPM)	104.63	119.29	126.59	-288.19	43.86	49.10	62.07	67.14	-14.22	-8.04	241.19	167.57	-14.25	-19.21	201.66	-173.64
56	L14 x CML395 (non-QPM)	168.73	171.08	-46.42	-52.56	36.56	36.63	60.31	66.34	-14.25	-4.26	541.52	445.69	-4.81	-11.21	321.29	-649.90
57	L15 x CZL15049 (QPM)	178.26	334.01	-21.88	-37.54	36.46	56.57	51.53	84.08	-3.25	-0.38	357.01	289.38	-11.94	-19.75	508.64	-106.06
58	L15 x CZL059 (QPM)	213.49	358.53	-47.91	-54.84	34.93	37.09	48.93	54.39	-12.44	-1.81	204.43	185.04	-10.33	-21.12	557.77	199.75
59	L15 x CML444 (non-QPM)	214.54	441.05	375.39	-361.87	47.02	59.54	67.42	72.49	-8.67	-6.96	194.81	176.03	-20.72	-30.69	639.96	320.53
60	L15 x CML395 (non-QPM)	206.21	385.60	-44.16	-44.84	34.66	40.86	54.34	58.05	0.88	2.84	150.66	141.76	-19.06	-29.88	595.54	352.06
61	L16 x CZL15049 (QPM)	115.17	122.02	17.84	-854.20	48.89	52.99	62.43	86.64	18.66	22.78	239.15	208.35	-3.69	-4.90	278.63	-160.28
62	L16 x CZL059 (QPM)	71.11	74.09	29.54	-764.98	30.62	42.97	40.84	53.66	-10.38	-0.01	130.53	101.79	9.43	3.94	134.81	-110.88
63	L16 x CML444 (non-QPM)	61.11	79.21	-490.48	-1063.19	41.37	44.81	47.39	50.21	-8.52	-7.24	495.96	421.67	3.83	-2.03	124.56	-794.87
64	L16 x CML395 (non-QPM)	122.25	132.24	-46.52	-288.95	38.98	47.58	51.26	55.10	7.69	10.31	218.74	206.95	-2.79	-9.19	272.48	-141.23
65	L17 x CZL15049 (QPM)	153.84	166.09	-51.77	-58.12	45.04	52.56	65.49	86.38	-8.81	-3.85	312.84	242.95	-3.45	-7.95	307.28	-237.11
66	L17 x CZL059 (QPM)	74.29	74.63	-22.43	-37.89	30.13	39.02	46.39	62.87	-18.94	-11.34	122.46	130.99	15.06	14.06	118.64	-163.93
67	L17 x CML444 (non-QPM)	124.03	153.44	29.18	-343.03	47.09	47.27	69.23	75.68	-6.65	-6.23	166.68	176.90	-3.90	-4.07	264.58	-71.03
68	L17 x CML395 (non-QPM)	156.35	172.19	-49.32	-63.75	36.50	41.56	60.70	67.86	-3.05	1.19	298.57	273.22	1.97	1.06	326.68	-248.14
69	L18 x CZL15049 (QPM)	111.50	123.42	-63.88	114.82	41.75	61.84	59.12	105.52	5.66	20.30	221.28	143.12	-4.59	-11.03	260.87	-87.91
70	L18 x CZL059 (QPM)	-17.13	-24.73	153.03	1151.85	11.37	12.65	18.15	16.33	-39.60	-38.66	338.10	302.12	34.69	30.47	-120.12	-825.50
71	L18 x CML444 (non-QPM)	97.11	100.54	-625.66	453.32	41.22	52.52	57.55	71.31	-7.08	0.45	183.16	159.91	-5.43	-7.77	191.02	-138.85
72	L18 x CML395 (non-QPM)	129.18	139.02	-69.74	-82.50	26.10	31.31	35.28	46.15	-13.50	-2.58	260.80	202.62	0.40	-1.05	252.13	-210.64
73	L19 x CZL15049 (non-QPM)	157.55	245.17	-55.24	-61.81	39.28	42.11	61.83	62.17	11.49	13.20	164.45	140.63	-7.11	-7.41	427.41	136.85
74	L19 x CZL059 (non-QPM)	186.01	261.31	-31.70	-46.15	38.11	52.30	50.67	90.44	-11.62	4.16	188.59	116.97	-9.07	-12.85	439.86	156.22
75	L19 x CML444 (non-QPM)	150.40	267.45	42.34	-382.26	48.41	53.09	59.56	86.86	-4.26	2.09	99.35	49.88	-12.36	-16.56	415.68	295.37
76	L19 x CML395 (non-QPM)	156.47	249.05	-79.29	-85.37	39.51	49.22	67.55	97.57	1.81	4.41	99.81	61.98	-8.07	-13.35	411.74	271.37
77	L20 x CZL15049 (non-QPM)	181.41	368.26	-68.56	-68.86	45.28	53.06	74.57	85.49	-8.64	-8.18	371.12	303.66	-16.57	-23.13	532.85	-102.23

78	L20 x CML444 (non-QPM)	101.13	270.10	24.98	-261.00	52.34	52.39	81.07	99.00	-4.58	0.66	255.26	155.50	-16.72	-26.42	367.31	-0.31
79	L20 x CML395 (non-QPM)	256.15	502.84	-40.05	-52.83	41.56	46.58	68.74	86.66	13.14	14.83	308.89	215.01	-13.73	-24.49	786.96	301.28
80	L21 x CZL15049 (non-QPM)	130.31	152.00	-34.74	-44.83	42.34	53.32	52.62	82.49	-7.53	-1.12	211.00	204.64	-9.28	-16.20	273.66	-116.50
81	L21 x CZL059 (non-QPM)	143.01	152.67	-52.11	-55.79	35.03	40.89	58.99	67.15	-6.12	-12.47	358.68	264.48	-18.45	-27.34	277.09	-300.28
82	L21 x CML444 (non-QPM)	102.41	139.67	282.12	-372.02	41.74	44.81	58.58	61.15	-11.29	-9.69	257.44	184.03	-12.29	-22.32	221.10	-185.76
83	L21 x CML395 (non-QPM)	145.60	172.32	-26.87	-32.49	31.31	33.09	58.01	59.60	-6.61	-1.17	496.58	415.11	-11.76	-22.58	310.15	-567.20
84	L22 x CZL15049 (non-QPM)	183.09	215.56	270.70	-172.15	52.20	54.28	67.45	97.79	14.74	27.18	102.31	87.34	-11.18	-11.18	440.57	273.28
85	L22 x CZL059 (non-QPM)	178.91	195.21	576.06	-145.37	47.11	63.38	70.45	81.21	7.54	39.93	148.92	114.20	-13.19	-16.54	421.58	188.19
86	L22 x CML444 (non-QPM)	137.45	186.79	-140.47	-171.33	59.85	66.00	74.18	75.11	11.82	30.68	217.45	173.17	-18.88	-22.53	366.74	17.53
87	L22 x CML395 (non-QPM)	18.10	33.44	314.24	-147.93	18.95	28.11	32.26	32.34	4.95	17.59	407.53	379.48	16.14	9.80	74.08	-738.87
88	L23 x CZL15049 (QPM)	169.01	345.07	-36.27	-43.81	40.85	51.91	64.15	70.88	8.61	13.28	369.94	359.93	-9.97	-18.34	535.97	-165.59
89	L23 x CZL059 (QPM)	202.74	368.88	-35.81	-37.90	41.68	47.66	62.04	95.92	-0.14	21.33	230.32	171.14	-18.54	-28.67	592.81	238.56
90	L23 x CML444 (non-QPM)	184.99	421.32	119.73	-284.35	47.75	51.13	76.56	98.26	2.02	11.89	223.68	165.69	-15.06	-26.06	620.23	271.98
91	L23 x CML395 (non-QPM)	232.99	460.39	-28.64	-36.99	38.78	40.50	64.53	85.98	9.69	15.59	370.83	321.76	-6.63	-19.46	718.66	52.16
92	L24 x CZL15049 (QPM)	95.21	96.59	-11.67	58.44	52.87	61.33	79.31	87.95	-8.31	-1.50	305.69	283.78	3.39	1.39	181.99	-412.26
93	L24 x CZL059 (QPM)	120.65	133.48	-6.43	45.62	45.60	55.04	65.72	98.82	-2.60	4.54	256.64	176.04	2.37	0.32	256.07	-179.30
94	L24 x CML444 (non-QPM)	124.81	140.03	1307.45	-350.48	51.50	51.79	74.55	94.56	-2.28	-0.08	134.44	81.45	-1.97	-4.60	262.48	53.16
95	L24 x CML395 (non-QPM)	142.06	143.33	-38.87	-49.23	39.80	44.52	67.26	87.67	18.14	25.59	377.66	300.28	2.31	-1.45	329.12	-349.68
96	L25 x CZL15049 (QPM)	128.66	145.17	-13.65	349.39	46.58	56.43	74.06	97.73	-10.62	6.64	187.73	150.96	-6.52	-6.97	269.85	-55.35
97	L25 x CZL059 (QPM)	42.85	61.40	-26.75	217.98	24.30	30.89	47.88	63.14	-24.98	-23.00	157.18	184.40	4.81	1.24	56.28	-291.35
98	L25 x CML444 (non-QPM)	95.10	95.70	-536.70	267.22	45.31	47.15	65.62	70.56	-12.98	-1.61	15.16	5.10	-8.55	-12.26	176.20	176.75
99	L25 x CML395 (non-QPM)	149.25	163.81	-48.21	-69.39	34.68	37.72	53.52	59.08	2.98	21.48	257.75	260.98	1.55	-3.56	337.52	-179.20
100	L26 x CZL15049 (QPM)	180.21	274.17	-27.48	-36.41	38.80	46.26	58.54	68.93	-12.78	-8.46	176.10	144.75	-20.55	-27.68	433.14	160.52
101	L26 x CZL059 (QPM)	152.02	217.24	-1.06	-4.86	37.44	46.57	45.17	71.06	-16.73	-8.47	143.81	79.79	-20.69	-30.32	344.06	171.47
102	L26 x CML444 (non-QPM)	177.81	306.09	208.69	-353.76	50.73	50.80	68.42	84.57	-10.34	-10.34	164.00	94.68	-22.74	-32.52	463.22	259.80
103	L26 x CML395 (non-QPM)	192.99	297.26	-2.61	-13.54	32.93	37.62	52.44	68.14	3.37	7.38	144.30	93.70	-12.54	-24.31	501.01	299.86
104	L27 x CZL15049 (QPM)	94.82	96.21	-22.43	411.03	44.76	45.81	56.96	64.57	-3.61	4.50	182.92	123.29	-11.84	-20.31	191.92	-82.14
105	L27 x CZL059 (QPM)	111.82	120.85	-62.69	104.12	42.71	59.61	51.86	82.12	-11.39	-5.76	116.18	46.51	-12.31	-23.47	215.52	88.61
106	L27 x CML444 (non-QPM)	93.96	110.24	-565.77	475.36	49.20	55.96	64.04	82.79	-16.01	-13.36	106.71	40.08	-15.75	-26.91	174.82	70.69
107	L27 x CML395 (non-QPM)	114.50	118.72	-17.09	236.52	35.17	46.57	54.33	73.11	-0.97	6.24	286.13	177.70	-11.23	-23.68	238.49	-190.43
108	L28 x CZL15049 (non-QPM)	356.70	993.03	120.42	-207.06	35.25	63.51	43.22	122.22	19.47	28.29	477.90	1416.29	8.39	-14.09	1397.49	-491.00
109	L28 x CZL059 (non-QPM)	281.62	747.20	412.07	-256.06	34.68	43.44	39.68	65.56	12.18	40.87	376.44	229.51	5.64	-13.68	1081.88	483.97
110	L28 x CML444 (non-QPM)	240.91	813.64	-229.66	-280.20	41.46	61.37	47.66	89.02	-0.26	12.77	457.79	285.77	7.84	-11.40	1067.06	327.06
111	L28 x CML395 (non-QPM)	268.75	799.76	821.43	-170.20	25.69	38.00	34.19	70.54	7.22	16.36	246.28	126.92	11.67	-7.48	1092.09	714.70
112	L29 x CZL15049 (non-QPM)	74.88	101.67	-62.25	-50.84	39.34	40.61	48.67	55.75	-2.74	15.07	336.42	289.94	-6.16	-10.24	188.88	-421.08
113	L29 x CZL059 (non-QPM)	110.72	156.86	-40.82	-47.83	42.62	59.17	57.78	89.41	-15.41	-13.82	149.05	121.73	-4.17	-4.67	238.35	-23.59
114	L29 x CML444 (non-QPM)	69.79	81.22	330.01	-355.09	53.23	59.86	61.43	80.04	-16.58	-6.43	313.42	268.07	-9.49	-9.65	128.00	-434.35
115	L29 x CML395 (non-QPM)	97.52	124.67	-15.43	-18.05	37.67	48.98	57.42	76.74	-6.38	9.53	266.59	259.80	0.42	-0.82	225.34	-300.65
116	L30 x CZL15049 (non-QPM)	101.81	133.43	-27.66	-47.41	44.23	48.91	63.65	77.88	-11.22	5.48	312.52	218.64	-0.76	-4.75	229.50	-296.15
117	L30 x CZL059 (non-QPM)	86.66	128.26	-28.18	-44.12	33.64	45.54	47.12	69.72	-0.60	1.64	405.94	377.32	9.01	8.82	215.96	-585.13
118	L30 x CML444 (non-QPM)	68.83	80.70	682.06	-331.97	41.84	44.60	53.17	64.53	-16.47	-5.94	-39.60	-43.01	-4.84	-5.34	127.12	219.91
119	L30 x CML395 (non-QPM)	96.44	124.12	-61.69	-65.96	29.36	36.69	51.15	63.39	-6.14	10.27	305.36	248.39	5.16	3.50	224.69	-337.72

120	L31 x CZL15049 (QPM)	150.30	166.17	-39.03	-39.17	44.59	58.04	61.81	92.01	-13.90	0.59	151.87	124.48	-5.71	-7.23	303.16	39.75
121	L31 x CZL059 (QPM)	61.07	80.42	-60.04	-63.78	27.71	31.40	40.25	48.47	-10.80	-10.13	201.16	168.80	2.85	0.46	120.56	-252.71
122	L31 x CML444 (non-QPM)	110.45	112.76	-28.32	-190.51	43.60	48.77	61.08	62.61	-8.50	1.39	340.48	293.15	-15.34	-17.87	216.10	-384.32
123	L31 x CML395 (non-QPM)	137.46	149.30	-42.15	-54.25	29.23	29.26	50.46	50.98	-7.18	7.24	383.00	375.39	-7.30	-10.99	286.82	-453.28
124	L32 x CZL15049 (non-QPM)	124.64	248.60	-56.33	-59.10	46.00	44.68	60.38	69.87	14.28	27.52	289.60	266.50	-4.48	-10.75	415.04	-125.83
125	L32 x CML444 (non-QPM)	124.18	283.59	-33.68	-200.05	48.58	55.01	51.85	67.43	-1.14	16.34	168.88	107.24	-10.99	-20.32	422.97	178.16
126	L32 x CML395 (non-QPM)	147.62	290.69	-81.57	-86.08	39.00	50.42	53.60	70.46	10.37	24.50	263.22	202.92	-5.13	-15.86	473.18	28.03
127	L35 x CZL15049 (non-QPM)	147.64	211.86	-35.04	-49.79	35.57	53.59	43.19	80.42	9.85	15.22	73.04	63.54	-12.79	-16.98	384.57	277.76
128	L35 x CZL059 (non-QPM)	177.64	230.35	-63.54	-69.58	32.01	32.61	42.64	43.31	-13.57	5.68	290.83	230.29	-16.70	-23.60	400.10	-80.72
129	L35 x CML444 (non-QPM)	146.07	238.18	500.86	-374.97	38.15	48.11	45.53	54.83	-1.03	9.19	145.30	107.30	-14.76	-22.31	392.41	176.88
130	L35 x CML395 (non-QPM)	198.24	281.18	-100.45	-100.47	29.52	33.90	43.51	51.72	10.24	16.83	447.01	406.37	-11.68	-20.28	506.49	-314.93

NB: Summation (Sum) was made for both mid- and better parent heterosis for grain yield (GY) and ears per plant (EPP) while “Rank” was obtained by subtraction of mid- and better heterosis for ear rot (ER) and ear aspect (EA) from SUM

Appendix 23. Heterosis of biochemical traits for 130 hybrids across six environments during 2017/2018 and 2018/2019 cropping seasons

Entry	Pedigree	Trip		Protein		Oil		Starch		Fibre		Sum
		MID PH	BP H	MID PH	BP H	MID PH	BP H1	MID PH	BP H	MID PH	BP H	
1	L1 x CZL15049 (QPM)	-6.67	0.00	19.70	28.35	12.44	23.43	1.18	1.88	-7.00	-8.37	80.31
2	L1 x CZL059 (QPM)	6.70	8.11	27.19	35.40	11.68	20.18	1.88	2.60	-10.43	-14.41	113.74
3	L1 x CML444 (non-QPM)	-17.91	-10.30	17.68	41.76	17.26	17.59	3.35	3.51	-14.83	-18.74	72.94
4	L1 x CML395 (non-QPM)	-26.53	-21.32	35.60	51.50	15.05	15.60	1.18	2.70	-13.67	-16.76	73.78
5	L2 x CZL15049 (QPM)	-4.57	-2.47	13.43	28.79	9.46	32.03	0.81	0.87	-0.42	7.66	78.35
6	L2 x CZL059 (QPM)	12.13	15.85	2.41	17.17	4.46	23.32	3.37	3.45	-5.83	-1.53	82.17
7	L2 x CML444 (non-QPM)	-33.07	-23.12	6.19	7.89	9.48	19.05	3.38	3.87	-4.92	-8.75	-6.33
8	L2 x CML395 (non-QPM)	-41.02	-33.67	21.93	32.78	14.70	25.74	0.76	1.63	-10.46	-14.97	22.85
9	L3 x CZL15049 (QPM)	-11.79	-8.96	14.27	19.24	19.69	39.01	-0.86	-0.62	-4.53	-4.61	69.99
10	L3 x CZL059 (QPM)	-15.64	-7.84	2.84	8.08	4.03	18.32	2.64	2.87	-12.58	-15.18	15.30
11	L3 x CML444 (non-QPM)	-35.71	-21.52	13.50	21.04	19.85	25.85	2.10	2.89	-8.81	-11.66	28.00
12	L3 x CML395 (non-QPM)	-31.53	-18.24	15.53	15.97	17.51	24.38	-0.09	0.47	-11.14	-13.00	24.00
13	L4 x CZL15049 (QPM)	-11.29	-8.75	11.06	17.11	3.90	8.67	1.36	2.67	-0.77	-3.55	24.73
14	L4 x CZL059 (QPM)	-5.10	-2.58	7.32	13.98	-2.06	0.50	2.59	3.94	-3.17	-3.44	18.59
15	L4 x CML444 (non-QPM)	-34.00	-24.72	11.86	18.03	0.71	5.81	2.84	3.62	-2.63	-3.06	-15.85
16	L4 x CML395 (non-QPM)	-29.57	-21.32	29.22	31.03	-1.26	2.93	0.45	2.57	-13.81	-14.38	14.05
17	L5 x CZL15049 (QPM)	-3.04	10.61	15.65	28.33	7.63	33.55	0.89	1.79	-6.21	-10.44	95.41
18	L5 x CZL059 (QPM)	4.26	12.12	5.41	17.85	4.19	26.47	2.84	3.74	-6.58	-8.02	76.88
19	L5 x CML444 (non-QPM)	-39.27	-37.53	4.39	4.91	6.99	19.41	2.99	4.47	-5.00	-6.32	-33.64
20	L5 x CML395 (non-QPM)	-37.32	-36.75	18.52	26.24	12.34	26.44	-0.25	-0.16	-9.95	-12.16	9.06
21	L6 x CZL15049 (QPM)	-11.15	-7.77	2.89	16.18	0.45	1.09	2.55	4.86	-5.39	-9.85	9.10
22	L6 x CZL059 (QPM)	-7.76	1.37	2.35	16.45	-8.75	-7.62	4.25	6.62	-12.82	-14.35	6.91
23	L6 x CML444 (non-QPM)	-40.04	-26.32	0.48	1.58	7.06	17.09	3.97	5.74	-6.07	-7.57	-30.44
24	L6 x CML395 (non-QPM)	-35.82	-22.87	11.91	21.23	-3.68	4.48	3.17	6.36	-13.34	-15.63	-15.22
25	L7 x CZL15049 (QPM)	-10.32	-5.26	16.19	18.52	13.36	40.19	-0.08	-1.08	-1.76	-3.43	71.52
26	L7 x CZL059 (QPM)	9.24	9.27	13.66	15.14	4.48	26.41	1.19	2.21	-7.39	-11.70	81.60
27	L7 x CML444 (non-QPM)	-26.32	-18.31	18.55	35.19	15.95	29.02	0.32	1.90	-3.72	-8.34	56.30
28	L7 x CML395 (non-QPM)	-26.15	-19.78	30.79	38.76	10.29	23.75	-1.03	-0.80	-13.75	-17.02	55.83
29	L8 x CZL15049 (QPM)	-5.52	-3.04	15.98	35.52	34.03	76.93	2.61	7.98	-5.29	-6.12	164.49
30	L8 x CZL059 (QPM)	-3.01	5.32	1.81	19.91	32.48	70.95	5.41	10.95	-7.22	-10.82	143.83
31	L8 x CML444 (non-QPM)	-32.64	-18.31	4.76	9.26	22.80	45.16	6.62	11.58	-9.94	-13.57	49.22
32	L8 x CML395 (non-QPM)	-37.59	-25.95	10.32	23.53	39.45	66.29	3.83	10.18	-10.71	-13.39	90.06

33	L9 x CZL15049 (QPM)	-7.08	-3.80	9.13	28.11	10.87	16.38	2.63	4.85	-10.81	-14.19	61.10
34	L9 x CZL059 (QPM)	-7.07	-5.21	15.46	36.61	13.95	17.34	2.84	5.08	-19.34	-19.97	79.00
35	L9 x CML444 (non-QPM)	-34.95	-26.32	3.70	8.60	14.83	20.21	3.58	5.25	-13.95	-14.49	-5.10
36	L9 x CML395 (non-QPM)	-40.20	-33.67	22.31	37.57	9.83	14.08	1.26	4.30	-13.60	-15.07	15.48
37	L10 x CZL15049 (QPM)	-0.91	1.69	0.30	18.25	28.41	20.17	-0.43	1.66	10.96	20.59	69.14
38	L10 x CZL059 (QPM)	-10.28	-2.58	2.34	21.61	11.87	17.78	3.11	5.29	-3.23	-7.70	49.14
39	L10 x CML444 (non-QPM)	-31.32	-16.71	-0.65	4.46	4.92	7.43	4.75	6.37	-7.43	-11.57	-20.75
40	L10 x CML395 (non-QPM)	-44.09	-33.67	13.59	28.29	19.05	20.97	1.21	4.18	-5.47	-10.63	9.53
41	L11 x CZL15049 (QPM)	-3.49	2.67	10.34	31.30	6.64	12.03	3.69	7.91	-9.65	-12.32	71.08
42	L11 x CZL059 (QPM)	12.61	13.33	15.08	38.03	6.27	13.85	3.68	7.92	-14.58	-14.68	110.78
43	L11 x CML444 (non-QPM)	-34.51	-27.92	5.11	11.46	1.92	18.43	5.42	9.11	-8.16	-8.41	-10.99
44	L11 x CML395 (non-QPM)	-42.78	-38.29	17.02	33.35	4.03	19.85	3.01	8.10	-12.78	-13.50	4.28
45	L12 x CZL15049 (QPM)	12.10	18.42	13.38	15.59	10.48	13.66	1.88	3.60	1.26	5.42	89.11
46	L12 x CZL059 (QPM)	0.03	0.06	21.53	24.76	13.98	15.07	1.64	3.37	-8.10	-8.82	80.43
47	L12 x CML444 (non-QPM)	-32.10	-24.72	16.11	7.04	3.04	10.09	4.34	5.52	-13.94	-14.48	-10.68
48	L12 x CML395 (non-QPM)	-31.83	-25.95	21.79	24.13	19.97	27.16	1.42	3.97	-8.78	-10.33	40.66
49	L13 x CZL15049 (QPM)	-3.45	1.30	8.50	13.60	12.51	43.57	-0.16	0.35	6.04	13.14	76.22
50	L13 x CZL059 (QPM)	0.68	1.37	9.75	15.74	3.80	29.54	1.63	2.14	-2.06	-5.02	64.65
51	L13 x CML444 (non-QPM)	-29.72	-21.52	2.05	8.45	16.98	34.00	4.40	5.51	-2.79	0.17	20.16
52	L13 x CML395 (non-QPM)	-28.08	-21.32	11.25	12.04	13.61	31.25	1.10	1.38	-9.49	-13.02	21.23
53	L14 x CZL15049 (QPM)	-17.15	-15.85	16.89	17.88	-1.64	14.37	0.30	1.20	-2.20	-2.88	15.99
54	L14 x CZL059 (QPM)	-7.57	-3.89	13.06	14.80	7.47	22.38	1.01	1.91	-8.00	-10.20	49.17
55	L14 x CML444 (non-QPM)	-15.53	-2.30	14.84	26.95	13.33	19.13	0.89	2.36	-5.47	-7.88	59.67
56	L14 x CML395 (non-QPM)	-41.43	-33.67	25.02	28.82	3.31	9.47	-0.58	-0.48	-12.59	-13.90	-9.53
57	L15 x CZL15049 (QPM)	5.03	6.02	13.50	26.69	16.48	40.10	4.05	11.19	-4.64	-3.84	123.06
58	L15 x CZL059 (QPM)	-0.60	4.01	10.19	23.93	15.37	35.83	6.60	13.92	-6.76	-8.88	109.24
59	L15 x CML444 (non-QPM)	-24.36	-11.91	17.26	17.31	16.98	26.87	5.69	12.30	-7.80	-10.04	60.14
60	L15 x CML395 (non-QPM)	-22.88	-12.07	23.08	31.85	29.49	41.59	3.07	11.07	-8.70	-9.95	105.20
61	L16 x CZL15049 (QPM)	-3.41	0.00	15.37	18.18	7.26	23.49	0.12	0.84	2.39	7.98	61.85
62	L16 x CZL059 (QPM)	1.96	4.01	11.64	15.16	0.91	13.78	2.55	3.28	-7.02	-8.87	53.29
63	L16 x CML444 (non-QPM)	-26.47	-16.71	13.29	23.15	8.50	13.02	2.27	3.57	-6.72	-8.43	20.62
64	L16 x CML395 (non-QPM)	-42.99	-36.75	19.10	20.80	3.75	8.92	1.11	1.18	-9.38	-11.99	-24.88
65	L17 x CZL15049 (QPM)	-7.04	-1.86	6.58	25.41	12.19	18.66	-0.33	1.06	-2.50	-8.42	54.67
66	L17 x CZL059 (QPM)	-11.74	-1.26	2.31	21.33	16.71	21.08	1.47	2.90	-10.57	-13.44	52.80
67	L17 x CML444 (non-QPM)	-28.40	-10.30	-3.69	1.08	3.17	7.19	3.90	4.78	-5.16	-8.07	-22.28
68	L17 x CML395 (non-QPM)	-39.56	-25.95	14.95	29.58	10.14	13.55	0.49	2.71	-9.15	-12.86	5.91
69	L18 x CZL15049 (QPM)	-6.20	-5.41	2.33	2.76	5.94	9.42	2.14	2.35	-6.54	-9.86	13.33
70	L18 x CZL059 (QPM)	1.26	7.96	13.91	15.17	6.21	7.64	1.27	1.50	-8.12	-8.60	54.92

71	L18 x CML444 (non-QPM)	-32.63	-19.91	5.69	17.39	1.31	7.82	3.84	4.19	-7.42	-7.76	-12.30
72	L18 x CML395 (non-QPM)	-40.33	-30.58	32.69	37.33	3.10	8.85	0.34	1.35	-13.11	-14.37	12.75
73	L19 x CZL15049 (non-QPM)	-2.99	65.71	12.94	28.23	7.96	40.10	0.58	1.02	-9.70	-12.11	153.56
74	L19 x CZL059 (non-QPM)	-2.67	54.29	12.90	29.16	10.05	39.62	0.82	1.25	-10.26	-10.63	145.42
75	L19 x CML444 (non-QPM)	-11.73	22.86	2.66	4.31	0.51	16.94	3.03	4.04	-9.41	-9.93	42.61
76	L19 x CML395 (non-QPM)	-7.84	31.43	8.89	18.58	15.65	35.71	0.73	1.10	-10.01	-10.48	104.25
77	L20 x CZL15049 (non-QPM)	-23.70	27.78	22.36	42.57	19.14	52.14	1.15	2.68	-10.57	-15.05	144.12
78	L20 x CML444 (non-QPM)	17.85	61.11	7.59	11.91	-3.77	10.30	4.68	5.69	-13.46	-15.13	115.36
79	L20 x CML395 (non-QPM)	-20.65	11.11	15.30	28.74	21.05	39.95	2.44	4.83	-11.73	-14.35	102.77
80	L21 x CZL15049 (non-QPM)	-18.12	27.50	23.41	37.67	17.36	32.37	0.54	0.79	-5.59	-6.76	121.52
81	L21 x CZL059 (non-QPM)	-12.04	27.50	7.17	20.45	21.88	34.69	1.72	1.98	-8.66	-6.89	103.35
82	L21 x CML444 (non-QPM)	9.34	40.00	6.85	6.83	7.75	10.15	3.17	3.47	-5.69	-7.59	87.56
83	L21 x CML395 (non-QPM)	-25.59	-2.50	19.18	27.59	4.95	8.11	1.13	2.19	-14.17	-14.99	35.06
84	L22 x CZL15049 (non-QPM)	-33.64	0.00	5.02	24.75	12.66	40.08	1.22	1.71	-6.02	-9.22	51.80
85	L22 x CZL059 (non-QPM)	-22.01	9.52	-0.52	19.11	8.01	31.38	2.57	3.09	-10.00	-10.33	51.16
86	L22 x CML444 (non-QPM)	-23.40	-4.76	0.24	6.12	2.40	14.51	3.86	3.81	-10.41	-10.60	2.78
87	L22 x CML395 (non-QPM)	-23.24	-2.38	21.40	38.12	1.50	14.45	-0.17	1.12	-5.83	-7.05	50.80
88	L23 x CZL15049 (QPM)	-5.78	-3.70	16.00	24.63	19.90	35.78	0.85	3.16	-5.92	-7.61	90.83
89	L23 x CZL059 (QPM)	3.21	6.64	14.14	23.53	17.75	30.64	1.27	3.61	-6.36	-7.58	100.79
90	L23 x CML444 (non-QPM)	-37.25	-27.92	8.09	11.97	13.49	16.44	4.64	6.46	-2.35	-3.78	-4.09
91	L23 x CML395 (non-QPM)	-32.80	-24.41	19.29	23.17	24.08	28.30	1.60	4.77	-10.41	-10.75	44.01
92	L24 x CZL15049 (QPM)	-8.00	-7.77	9.44	25.65	15.71	45.30	0.69	1.80	-7.07	-9.82	82.81
93	L24 x CZL059 (QPM)	-11.78	-6.53	5.64	22.22	28.89	58.30	1.19	2.32	-5.94	-6.04	100.26
94	L24 x CML444 (non-QPM)	-26.75	-13.51	5.58	8.36	25.26	41.36	2.62	3.19	-5.82	-6.08	46.12
95	L24 x CML395 (non-QPM)	-41.26	-32.12	15.01	26.60	29.66	47.56	0.68	2.61	-9.81	-10.55	48.73
96	L25 x CZL15049 (QPM)	-8.65	-8.33	7.29	17.26	18.42	41.65	1.60	2.12	-4.92	2.41	71.36
97	L25 x CZL059 (QPM)	-4.97	0.06	13.34	24.79	5.96	24.07	2.25	2.79	-8.98	-12.49	68.28
98	L25 x CML444 (non-QPM)	-39.90	-29.52	6.64	8.69	15.36	24.48	2.90	2.93	-7.35	-10.78	-8.43
99	L25 x CML395 (non-QPM)	-36.84	-27.49	22.07	28.13	27.68	38.89	0.41	1.73	-12.86	-16.97	54.58
100	L26 x CZL15049 (QPM)	-8.96	-5.13	10.86	15.69	-0.59	6.36	2.87	3.59	-3.19	-4.89	24.69
101	L26 x CZL059 (QPM)	2.63	4.01	14.85	19.01	2.13	7.16	3.74	4.48	-9.21	-10.43	58.00
102	L26 x CML444 (non-QPM)	-31.64	-23.12	19.80	40.08	11.58	14.64	2.29	2.45	-3.66	-5.11	36.08
103	L26 x CML395 (non-QPM)	-42.59	-36.75	23.40	34.05	13.69	15.92	1.84	3.37	-12.72	-13.09	12.93
104	L27 x CZL15049 (QPM)	22.38	97.37	7.02	22.31	11.92	37.72	0.66	0.46	-2.39	-5.05	199.83
105	L27 x CZL059 (QPM)	35.14	102.63	-1.56	13.37	10.98	33.62	2.65	2.85	-10.88	-11.19	199.68
106	L27 x CML444 (non-QPM)	-14.37	13.16	10.67	13.11	6.53	17.99	1.67	0.92	-12.04	-12.49	49.68
107	L27 x CML395 (non-QPM)	-10.53	21.05	13.30	24.16	7.05	19.56	1.70	2.30	-11.29	-11.81	78.60
108	L28 x CZL15049 (non-QPM)	-6.33	60.00	15.00	40.01	8.56	11.24	-0.65	0.55	-13.13	-13.90	128.38

109	L28 x CZL059 (non-QPM)	2.74	62.86	14.61	40.65	9.29	14.15	-1.02	0.18	-11.55	-13.51	143.46
110	L28 x CML444 (non-QPM)	-30.21	-2.86	0.20	8.47	2.30	15.69	2.87	3.54	-4.44	-6.70	0.00
111	L28 x CML395 (non-QPM)	-9.84	28.57	12.31	30.85	1.88	14.26	1.21	3.25	-17.97	-19.04	82.49
112	L29 x CZL15049 (non-QPM)	-13.09	30.95	24.11	28.37	-4.40	14.12	1.24	-0.35	-10.11	-14.93	80.95
113	L29 x CZL059 (non-QPM)	-20.31	11.90	20.53	25.54	15.92	35.45	0.37	1.98	-8.19	-10.44	91.38
114	L29 x CML444 (non-QPM)	-19.57	0.00	14.95	23.71	4.49	12.53	2.00	4.21	-11.30	-13.34	42.32
115	L29 x CML395 (non-QPM)	-17.62	4.76	25.65	25.06	8.09	17.36	0.07	0.88	-13.89	-16.76	64.25
116	L30 x CZL15049 (non-QPM)	-13.09	30.95	16.77	26.98	19.12	22.53	-0.62	0.10	-9.55	-13.48	102.74
117	L30 x CZL059 (non-QPM)	-8.44	28.57	4.27	14.23	10.48	11.51	1.56	2.28	-6.64	-7.91	64.46
118	L30 x CML444 (non-QPM)	-9.99	11.90	8.38	10.99	2.34	9.36	1.88	3.18	-7.75	-8.86	38.04
119	L30 x CML395 (non-QPM)	-23.24	-2.38	19.63	24.96	13.38	20.20	-0.40	-0.33	-13.71	-15.67	51.82
120	L31 x CZL15049 (QPM)	23.35	66.00	15.53	18.50	11.36	58.73	3.26	3.95	-9.66	-13.38	200.68
121	L31 x CZL059 (QPM)	28.61	62.00	13.86	17.61	7.40	49.48	3.70	4.40	-13.11	-14.09	187.06
122	L31 x CML444 (non-QPM)	-19.95	-10.00	16.88	26.88	26.23	60.26	3.12	3.25	-11.41	-12.27	106.67
123	L31 x CML395 (non-QPM)	-37.29	-28.00	24.65	26.27	25.39	60.67	1.56	3.05	-12.35	-14.14	76.30
124	L32 x CZL15049 (non-QPM)	-32.06	2.38	13.97	28.63	7.06	31.45	2.22	2.56	-1.00	-4.98	56.22
125	L32 x CML444 (non-QPM)	-15.74	4.76	12.29	13.47	0.73	11.34	3.44	3.65	-7.47	-8.26	33.95
126	L32 x CML395 (non-QPM)	-19.49	2.38	23.15	33.34	7.85	20.20	0.47	1.62	-10.71	-12.43	69.52
127	L35 x CZL15049 (non-QPM)	-31.51	4.88	32.13	51.40	7.44	27.32	0.58	1.97	-11.19	-12.09	94.20
128	L35 x CZL059 (non-QPM)	-19.63	14.63	21.82	40.65	8.92	26.37	1.52	2.93	-14.83	-16.61	97.22
129	L35 x CML444 (non-QPM)	-12.99	9.76	7.78	10.42	9.67	17.33	3.72	4.57	-9.11	-11.15	50.26
130	L35 x CML395 (non-QPM)	-20.62	2.44	12.80	23.93	8.21	16.70	1.71	3.94	-19.49	-20.44	49.11

NB: Summation (Sum) was made for both mid- and better parent heterosis for tryptophan, protein, oil and starch