# Genetic variability and inheritance studies for low pH tolerance in tropical and sub-tropical maize germplasm

By

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## DECLARATION

I, Kesbell K.E. Kaonga, do hereby declare that the thesis hereby submitted for qualification for the degree Philosophiae Doctor in Agriculture at the University of the Free State represents my own original, independent work and that I have not previously submitted the same work for a qualification at another university/ faculty.

I further more cede copyright of the thesis in favour of the University of the Free State.

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Kesbell Kaswela Eston Kaonga Date

## DEDICATION

This work is specifically dedicated to our last born daughter Deliness Kaonga, who misssed parental care during the course of my study, secondly to my wife Judith Lwesha Kaonga, our son Arisai Kaonga, and our daughters Byenala and Clevereen Kaonga for their patience and hard times they may have gone through during my study period.

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## ABBREVIATIONS AND SYMBOLS

| | |
|---|---|
| AD | Days to anthesis |
| ADD | Agricultural Development Division |
| AEA | Average environmental axis |
| AECa | Average environment coordination abscissa |
| AECo | Average environment coordination ordination |
| Al | Aluminium |
| AMMI | Additive main effects and multiplicative interaction |
| ANOVA | Analysis of variance |
| ASI | Anthesis-silking interval |
| ATTC | Agricultural Technology Clearing Committee |
| B | Boron |
| BKA | Baka Research Station |
| BKE | Bembeke Research Site |
| BKT | Bembeke Turnoff Research Site |
| C | Carbon |
| Ca | Calcium |
| CIMMYT | International Maize and Wheat Improvement Center |
| Cl | Chlorine |
| CLA | Chitala Research Station |
| cm | Centimetre (s) |
| CML | CIMMYT maize line |
| CRD | Completely Randomised Design |
| Cu | Copper |
| CV | Coefficient of variation |
| CZE | Chitedze Research Station |
| DC | Double cross |
| DM | Downy mildew |
| DS | Days to silking |
| DT | Drought tolerant |
| DT2 | Distal transition zone |
| ExY | Environment by year/season interaction |

| | |
|---|---|
| EH | Ear height |
| EPP | Ears per plot |
| $F_1$ | First filial generation |
| FAO | Food and Agriculture Organisation of the United Nations |
| FAOSTAT | Food and Agriculture Organisation Statistics |
| Fe | Iron |
| FeHEDTA | Ferric hydroxethylethylenediaminetriacetate. |
| FEWSNET | Famine early warning system net work |
| FSRL | Final seminal root length |
| GxE | Genotype by environment interaction |
| GxExY | Genotype by environment by year interaction |
| GxY | Genotype by year interaction |
| G | Genotype |
| GA | Genetic advance |
| GCA | General combining ability |
| GCV | Genotypic coefficient of variation |
| GDP | Gross domestic product |
| GEI | Genotype by environment interaction |
| GGE | Genotype and genotype by environment interaction |
| GLS | Gray leaf spot |
| GT | Grain texture |
| GWS | Genome wide selection |
| GY | Grain yield |
| $h^2b$ | Broad sense heritability |
| H | Hydrogen |
| ha | Hectare (s) |
| IFPRI | International Food Policy Research Institute |
| IITA | International Institute of Tropical Agriculture |
| IPCA | Interaction principal component analysis |
| ISRL | Initial seminal root length |
| K | Potassium |
| $KAl(SO4)_2$ | Potassium aluminium sulphate |
| kg $ha^{-1}$ | Kilogram per hectare |

| | |
|---|---|
| L | Litre |
| LB | Leaf blight disease |
| LOX | Lipoxygenase |
| LSD | Least significant difference |
| LU | Lunyangwa Research Station |
| m | Metre (s) |
| masl | Metre (s) above sea level |
| Max | Maximum |
| Mg | Magnesium |
| Min | Minimum |
| Mn | Manganese |
| Mo | Molybdenum |
| MOA | Ministry of Agriculture |
| MRU | Meru Research Station |
| MSE | Mean square error |
| MSV | Maize streak virus |
| MT | Metric ton |
| MVAC | Malawi Vulnerability Assessment Committee |
| N | Nitrogen |
| NADH | Nicotinamideadehyde |
| NBOS | National Bureau of Statistics |
| NCSS | Number Cruncher Statistical System |
| Ni | Nickel |
| NSRL | Nett seminal root length |
| NUE | Nitrogen use efficiency |
| $O_2$ | Oxygen |
| OPV | Open-pollinated variety |
| P | Phosphorus |
| PAL | Phenylalanine ammonia lyase |
| PC | Principal component |
| PCA | Principal component analysis |
| PCV | Phenotypic coefficient of variation |
| PH | Plant height |

| | |
|---|---|
| *Pi* | Cultivar performance measure |
| POD | Peroxidase |
| QPM | Quality protein maize |
| QTL | Quantitative trait loci |
| r | Pearson correlation coefficient |
| $R^2$ | Coefficient of determination |
| $r_{cop}$ | Cophenetic correlation |
| RDP | Rural Development Programme |
| RE | Rotten ears |
| RFLP | Restriction fragment length polymorphism |
| RL | Root lodging |
| ROS | Reaction oxygen species |
| Rti | Root tolerance index |
| S | Sulphur |
| SCA | Specific combining ability |
| SE | Standard error |
| SH | Shelling percentage |
| SL | Stem lodging |
| SSA | Sub-Saharan Africa |
| SVD | Single value decomposition |
| SWT | 100 seed weight |
| TSA | Tsangano Research Site |
| TSS | Total sum of squares |
| UN | United Nations |
| UPGMA | Unweighted pair-group method with arithmetic averages |
| US | United States |
| VIG | Plant vigour |
| *Wi* | Wricke's ecovalence |
| WFP | World food programme |
| Y | Year |
| Zn | Zinc |
| Σ | Summation |
| $\sigma^2 e$ | Error variance |

| | |
|---|---|
| $\sigma^2 g$ | Genotypic variance |
| $\sigma^2 i$ | Stability variance |
| $\sigma^2 o$ | Environmental variance |
| $\sigma^2 p$ | Phenotypic variance |
| % | Percent |
| °C | Degrees Celsius |

# CHAPTER 1

## General introduction

### 1.1 Origin, importance and production constraints of maize

Maize (*Zea mays* L.) is an important crop and is favoured as well as indispensable food for over one billion people in Sub-Saharan Africa (SSA) and Latin America (Gupta *et al*., 2009). It is a cultivated sub-species of teosinte, a wild naturally found grass with its centre of origin the Mesoamerican region, now Mexico and Central America (Mangelsdorf, 1974). It was discovered by Columbus's men in Cuba in 1492 and later introduced to Europe and Africa by explorers in 1500 as reported by Gibson and Benson (2002). It is a very popular crop but the name "maize" is not English. The genus *Zea* was derived from an old Greek name for a food grass (Mangelsdorf, 1974), while the sub-species "*mays*" derived from Spanish: *maíz* after Taíno *mahiz* (Encyclopædia Britannica, 2010). It has a number of uses and in the tropics it is grown for direct consumption by man and animals as well as various industrial uses (Powell *et al.*, 2004).

Worldwide, reports indicate that maize is cultivated on approximately eight million hectares (ha) of low pH soils (Brewbaker, 1985; Pandey and Gardner, 1992) and yields can be reduced by up to 70% under these conditions (Welcker *et al.*, 2005). Reports also indicate that on these soils, aluminium (Al) or manganese (Mn) toxicity, calcium (Ca), magnesium (Mg), phosphorus (P) and molybdenum (Mo) deficiencies are the main causes of yield reduction (Aldrich *et al.*, 1973; Granados *et al.*, 1993). In Africa, acid soils in the tropical area are estimated to cover 29% of the continent (Eswaran *et al*., 1997). However, von Uexküll and Mutert (1995) reported that low pH soils are present all over the world with 41% in America, 26% in Asia, 17% in Africa, 10% in Europe and 6% in Australia and New Zealand. Acidity is a major constraint to maize production and other crops on tropical soils. This is because at low pH (pH<5) toxic $Al^{3+}$ ions are released into the soil solution, and hinder root growth thus affecting the development of the entire plant (Kochian, 1995; Kidd and Proctor, 2000). Al toxicity causes short, thick and under developed roots and

plants, thus reducing nutrient uptake and increases susceptibility to drought (Sasaki *et al.*, 1996).

### 1.2 Maize production in Malawi

It is commonly said that "maize is life" for countries in SSA and this is true for Malawi more than any other country. The National Bureau of Statistics (NBOS) of the Government of Malawi data for 2006/07 reported that maize represented about 69% of area covered by 16 major crops grown in the country. The FAOSTAT for 2011 estimated that maize represented about 44% of the total area covered by more than 40 crops in Malawi. Other essential crops include groundnut, tobacco, cassava, sweet potato, cotton, rice, soybean, sorghum and millet. Almost 75% of maize in Malawi is cultivated in pure stands while mixed stands represent about 25%. Cultivation is mostly by resource-challenged smallholder farmers (MOA, 1994).

Malawi's maize requirement is 2.4 million metric tons (MT) per year and in 2009 the country registered a 1.2 million MT surplus while in 2010 the country had a surplus of approximately 800 000 MT this slight reduction as compared to the previous year, probably because of drought in some districts in the southern region (FAOSTAT, 2011). In 2013 the country produced 3.6 MT representing a surplus of 1.2 MT (FAOSTAT, 2013). The country saw a record harvest in 2014 of just over 3.9 MT (GIEWS, 2015)

### 1.3 Maize agro-ecology in Malawi

Malawi covers an area of 118 000 $km^2$ which is relatively small, yet it is endowed with diverse agro-ecology areas (Figure 1.1). About 1.2 million ha are grown to maize which is widely cultivated across the 28 districts which are grouped into eight Agricultural Development Divisions or ADDs (Karonga, Mzuzu, Kasungu, Salima, Lilongwe, Machinga, Blantyre and Shire Valley) and three regions (northern, central and southern). Approximately 57% of all maize in Malawi is cultivated in the central region, followed by the southern region (24%) and northern region (19%) (Table 1.1 and Figure 1.2). Among

the ADDs, Karonga, Mzuzu, Kasungu, and Salima combined represent 80% of all area cultivated to maize in the country (MOA, 1994; MVAC, 2013).

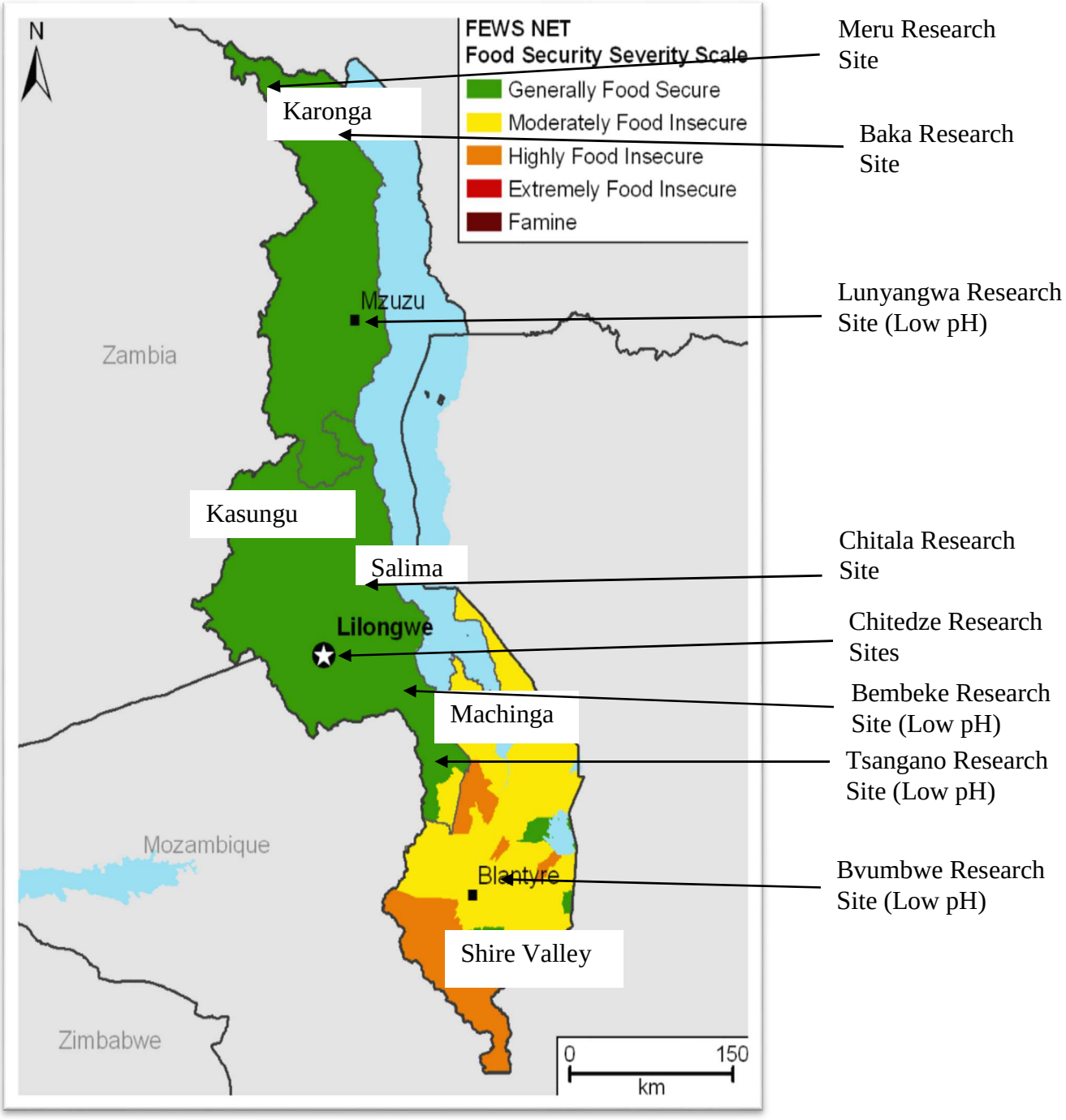


**Figure 1.1 Map of Malawi depicting eight agricultural development divisions and experimental sites at research stations**

**Table 1.1 Malawi mean maize hectarage and production comparisons for 2010 versus 2011 and 2011 versus 2012**

| | Area (ha) | | | Production (MT) | | | Area (ha) | | | Production (MT) | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **ADD** | **2009/10** | **2010/11** | **% change** | **2009/10** | **2010/11** | **% change** | **20010/11** | **2011/12** | **% change** | **20010/11** | **2011/12** | **% change** |
| Karonga | 45855 | 48960 | 6.8 | 116603 | 137578 | 18.0 | 48960 | 49996 | 2.1 | 137578 | 127381 | -7.4 |
| Mzuzu | 143569 | 151262 | 5.4 | 307758 | 357446 | 16.1 | 151262 | 156046 | 3.2 | 357446 | 344552 | -3.6 |
| Kasungu | 305909 | 308921 | 1.0 | 752808 | 804331 | 6.8 | 308921 | 323692 | 4.8 | 804331 | 814454 | 1.3 |
| Salima | 59287 | 60208 | 1.6 | 145859 | 157168 | 7.8 | 60208 | 56659 | -5.9 | 157168 | 124322 | -20.9 |
| Lilongwe | 341252 | 346453 | 1.5 | 714180 | 784013 | 9.8 | 346453 | 347140 | 0.2 | 784013 | 739271 | -5.7 |
| Machinga | 287509 | 287976 | 0.2 | 389779 | 382004 | -2.0 | 287976 | 276207 | -4.1 | 382004 | 296374 | -22.4 |
| Blantyre | 250026 | 254663 | 1.9 | 332359 | 542210 | 63.1 | 254663 | 256199 | 0.6 | 542210 | 438895 | -19.1 |
| Shire Valley | 42211 | 42106 | -0.2 | 42211 | 28594 | -32.3 | 42106 | 31890 | -24.3 | 28594 | 20743 | -27.5 |
| Total | 1475618 | 1500549 | 18.0 | 2801557 | 3193344 | 87.4 | 1500549 | 1497829 | -23.4 | 3193344 | 2905992 | -105.3 |

**Source: Ministry of Agriculture Crop Estimates for 2010, 2011, 2012**

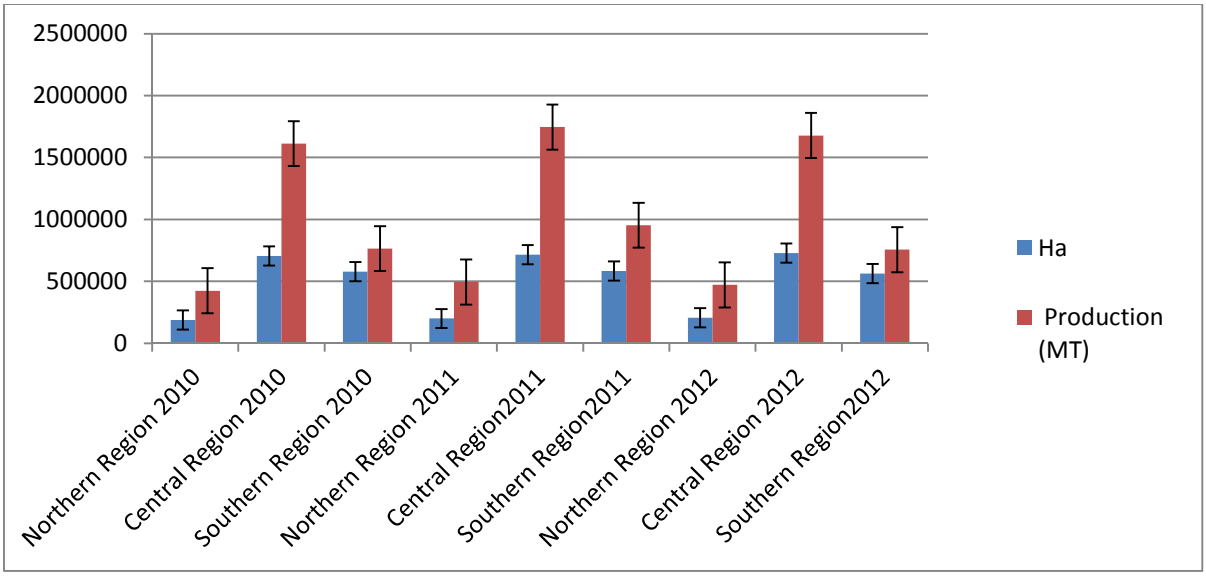


**Figure 1.2 Malawi mean maize hectarage and production per region from 2010 to 2012**

### 1.4 Abiotic constraints to maize production in Malawi

Soil acidity is prevalent in most parts of Malawi and a limiting factor in crop production. The increasing population is creating pressure on land and continuous mono-cropping and slashing and burning of crop residues during land clearing have exacerbated the problem. More acid soils are found in the high rainfall areas (>1000 mm per year) where there is moderate to high leaching, while the alkaline soils are found in low rainfall areas (< 500 mm per year). Regions with soil pH less than 5.5 have been identified in the country and according to the soils database prepared by the Soils Commodity Team, over 40% of the country has such soil. The largest hectarage of very acid soils are found in the following ADDs: Lilongwe, Mzuzu and Blantyre. Chilimba (1994) reported higher Al saturation percentages in some areas of Bembeke, Lunyangwa, Nkhatabay and Mulanje. The soil pH in the ADDs in the country is outlined in Table 1.2.

**Table 1.2 Percentage area covered by soil pH values below 5.6 in four agricultural development divisions**

| ADD | Soil pH | Area % coverage |
|---|---|---|
| Blantyre | 4.2 – 5.5 | 36 |
| Kasungu | 4.2 – 5.5 | 10 |
| Lilongwe | 4.7 – 5.5 | 65 |
| Mzuzu | 4.4 – 5.5 | 33 |

**Source: Chilimba and Saka 1998**

The well-known low pH soils are found in most parts of Bembeke, Kanyama and Mayani in Dedza; Namwera rural development programme (RDP) in Mangochi; Tsangano in Ntcheu; Mulanje RDP in Mulanje; Thyolo RDP in Thyolo; Nkhata Bay RDP in Mzuzu ADD (Lunyangwa, Ntchenechena, Mphompha, Uzumala, Mzuzu city, Mzimba central and South Mzimba) and Misuku Hills in Chitipa. High pH soils or alkaline/sodic soils are located in Shire Valley, along Lake Chilwa and Lake Malawi (Chilimba and Komwa, 2003). In such low pH soils, crop yields are limited and sometimes total crop losses occur. For instance, Munthali and Chilimba (2004) reported a yield reduction of more than 85% in low pH soils in Lunyangwa as compared to the potential yield of 8.5-10 ton $ha^{-1}$ for maize hybrids under normal fertility conditions.

The problem of low-soil pH can be solved by using soil amendments such as liming, although most farmers in developing countries cannot afford such amendments (Pandey *et al.*, 1994). A more sustainable solution would be to select Al tolerant maize genotypes for use in acid soils which, in the long run, is less expensive, sustainable and more environmentally friendly.

Other abiotic stresses are droughts and floods common in low-land areas of the country**.** Mazunda and Droppelmann (2012) reported that in a country of which its economic base is heavily dependent on agriculture, not only are the rural livelihoods affected due to the negative impacts on the agricultural sector, but non-farm and urban households are not spared either, given the strong relationship of production and prices between agriculture and the rest of the economy. According to the Malawi Vulnerability Assessment Committee (MVAC, 2010), 718 000 people were declared food insecure between March and June in eight districts in southern Malawi due to poor harvests as a result of prolonged

dry spells in the 2009/2010 season. The number of affected people is expected to increase to 1.1 million by October 2010 (FEWSNET, 2010). FEWSNET (2012) estimated that above one and a half million people would be in need of food relief between October 2012 and March 2013.

Flooding affected the country in early 2013 in such a way that the United Nations (UN) World Food Programme (WFP) in conjunction with the Government of Malawi were providing food relief to about 6 700 households which were flood victims (FEWSNET, 2013). Incidences of food shortages worsen and sharp price increases occur which reduce households' disposable incomes. It is mostly small-scale farmers and those residing in the flood-prone southern regions of the country that stay vulnerable (Selka, 2012). The economic losses as a result of climate related disasters are evident: Malawi loses 1.7% of its gross domestic product (GDP) on average every year due to the combined effects of droughts and floods. This is equivalent to approximately US$22 million in 2005 prices (Mazunda and Droppelmann, 2012).

### 1.5 Biotic constraints to maize production in Malawi

Economic importance maize diseases in Malawi include viral disease such as maize streak virus (MSV), fungal diseases such as leaf blight (LB) caused by *Exserohilum turcicum* (Leonard and Snugs) and gray leaf spot (GLS) caused by the pathogen *Cercospora zeae-maydis* (Tehon and Daniels) and downy mildew (DM) another fungal disease caused by the genus *Peronosclerospora*. GLS can cause yield losses of up to 60% (Ringer and Grybauskas, 1995). The most destructive disease world-wide is DM (Frederiksen and Renfro, 1977) and in Malawi two species are known to cause this disease, these are *P. philippinensis* and *P. sorghi*. Two pathotypes of *P. sorghi* have been reported, one capable of infecting both maize and sorghum and the other infecting only maize (Anaso *et al.*, 1987). The disease was first identified in maize in Mozambique (Plumb-Dhindsa and Mondjane, 1984). In Malawi its occurrence on sorghum was reported by Beck (1980) and its observation on maize was in the 2004/05 season in the Blantyre ADD where over 40 000 farm families were left food insecure especially in the Mulanje and Thyolo districts. Adenle and Cardwell (2000) reported that the tassel bracts may proliferate, resulting in a very bushy appearance, causes distortion and/or stunting of the maize plant. It frequently

occurs in areas of fields subject to flooding where the zoospores infect the growing point of the young maize plants.

Another biotic stress in maize production in Malawi is witch weed *Striga spp.* Its origin is not very clear (Holm *et al*., 1977) and it is believed to be indigenous to tropical and sub-tropical Africa and Asia. In Malawi the most important genera for cereals is *S. asiatica* locally known as *kaufiti* and is the most widely spread in the country as opposed to other witch weeds like *S. hemonthica* and *Alectra vogelli* for legumes. Kabambe *et al.* (2008) reported that yield losses depend on level of infestation, susceptibility of the maize genotype, soil fertility and crop management practices. *Striga* seeds are shed in large numbers (over 50 000 per plant) and remain viable for long time (up to 20 years) (Ramaiah *et al.*, 1983).

### 1.6 Malawi National Maize Breeding Programme

The Malawian National Maize Breeding Programme, with its main office at Chitedze Agricultural Research Station, was established with the aim of variety development and breeder seed production as well as seed distribution to growers. Major achievements have been reached in the development of new maize varieties and identification of improved varieties for tolerance to stresses obtained from other breeding institutions. To this effect nine maize hybrids were released in 2013, three of which are both drought and low nitrogen (N) tolerant (CIMMYT, 2013). For drought alone, the programme has released a total of five cultivars since 2009. These are Musungabanja (ZM309), Mwayi open-pollinated variety (OPV) ZM523, MH30, MH31 and MH32. In terms of dissemination, four newly released hybrids of 2013 were already selected for production by different seed companies. In terms of nutrition, two quality protein maize (QPM) varieties were released in 2008 and 2009, an OPV, Chitedze2QPM and a hybrid (MH29), respectively (Kaonga, 2009; Mviha *et al*., 2011). There are a good number of released hybrids from the programme which are tolerant to GLS, MSV as well as LB and are distributed by seed companies.

Despite all these achievements varieties for low pH tolerance are yet to be developed. Hence the objectives of this study were:

1. To evaluate maize genotypes of diverse genetic variability for tolerance to Al as a proxy for low pH tolerance.
2. To study maize genotypes of diverse genetic variability for tolerance to low pH soils by use of phenotypic and morphological traits.
3. To study the genotype by environment interaction (GxE) and stability of the tropical and sub-tropical maize genotypes.
4. To estimate combining ability among well adapted inbred lines and low pH lines from CIMMYT-Colombia.

## 1.7 References


Adenle, V.O. and K.F. Cardwell. 2000. Seed transmission of *Peronosclerospora sorghi*, causal agent of maize downy mildew in Nigeria. Plant Pathology 49: 628-635.

Aldrich, S.R. 1973. Plant analysis: Problems and opportunities. pp. 213-222. In: L.M. Walsh and J.D. Beaton (eds.) Soil testing and plant analysis. SSSA, Madison, WI.

Aldrich, S.R., W.O. Scott and E.R. Leng. 1975. Modern corn production. A & L Publication Champaign, IL.

Anaso, A.B., P.D. Tyagi, A.M. Emechebe and S.K. Manzo. 1987. Identity of a downy mildew in Nigeria Guinea savannah. Samaru Journal of Agricultural Research 5: 13-22.

Beck, B.D.A. 1980. Sorghum diseases in Malawi. In: R.J. Williams, R.A. Frederiksen, L.K. Mughogho (Eds.). Proceedings of the International Workshop on Sorghum Diseases, 11–5 December 1978, Hyderabad, India. Andra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics.

Brewbaker, J.L. 1985. The tropical environment for maize cultivation. In: A. Brandolini, F. Salamini (Eds.). Breeding strategies for maize production improvement in the tropics. Firenze: FAO; Instituto Agronomico per I'Oltremare.

Chilimba, A.D.C. 1994. Annual Report: Soil Fertility and Plant Nutrition Commodity Team, Department of Agricultural Research Services, Ministry of Agriculture, Lilongwe, Malawi.

Chilimba, A.D.C., S. Chigwenembe, B.W. Lungu and P.A. Sonjera. 2004. The effects of different organic fertilizers and their interactions with inorganic fertilizer on maize yield. In: Annual report of the Soils Fertility and Plant Nutrition Commodity Team, Ministry of Agriculture, Lilongwe, Malawi.

Chilimba, A.D.C. and M.M. Komwa. 2003. Soil fertility status in Lilongwe Agricultural Development Division. A Final Report. Chitedze Agricultural Research Station, Lilongwe, Malawi.

CIMMYT. 2013. Drought Tolerant Maize in Malawi: A Bright Spot for DTMA. DT Maize 2: 1-4.

Encyclopædia Britannica, 2010. The Teacher – Friendly guide to the evolution of maize. Encyclohttp://maize.teacherfriendlyguide.org/index.php/what-is-maize.

Eswaran, H., Reich, P., and Beigroth, F. 1997. Global distribution of soils with acidity. In A. C. Moniz et al. (Eds.), *Soil Plant Interactions at Low pH* (pp. 159-164). Brazilian Soil Science Society Vicosa.

FAO. 2001. Food balance sheets: A handbook. Rome. ftp://ftp.fao.org/ docrep/ fao /011 /x9892e/x9892e00.pdf

FAOSTAT. 2011. Food and Agriculture Organization Statistical Database: http// faostat. fao.org.

FAOSTAT. 2013. Statistical Database of the Food and Agriculture of the United Nations. http://www.fao.org

FEWSNET. 2007. Farming and Early Warning System Network. Summary of crop production estimates, Lilongwe, Malawi.

FEWSNET. 2010. Malawi Food Security Outlook Update. FEWSNET Malawi, Lilongwe.

FEWSNET. 2012. Malawi Food Security Outlook Update. FEWSNET Malawi, Lilongwe.

FEWSNET. 2013. Malawi Food Security Outlook Update. FEWSNET Malawi, Lilongwe

Frederiksen, R.A. and B.L. Renfro. 1977. Global status of maize downy mildew. Annual Review of Phytopathology 15: 249-275.

Gibson, L. and G. Benson. 2002. Origin, history and uses of corn (*Zea mays)*. Iowa State University. Department of Agronomy.

Giews (Global Information and early warning system on food and agriculture). 2015. Country Briefs Malawi. http://www.fao.org/giews/countrybrief/country.jsp

Granados, G., S. Pandey and H. Ceballos. 1993. Response to selection for tolerance to acid soils in a tropical maize population. Crop Science 33: 936–940.

Gupta, H.S., P.K. Aggarwal, V. Mahajan, G.S. Bisht, A. Kumar, P. Verma and A. Srivastava. 2009. Quality protein maize for nutritional security: Rapid development of short duration hybrids through molecular marker assisted breeding. Current Science 96: 230–237.

Holm, L.G., D.L. Plucknett, J.V. Pancho and J.P. Herberger. 1977. The world's worst weeds*:* Distribution and Biology. The University Press of Hawaii, Honolulu. pp 456–464

Kabambe, V.H., P. Ngwira and R.P. Ganunga. 2008. Integrated Management of Witch weed (*Striga asiatica*) in Malawi. Lilongwe, Malawi.

Kaonga, K.K.E. 2009. Release dossier for Chitedze 2 QPM and MH29 QPM presented to the Agricultural Technology Clearing Committee (ATCC). 17th February 2009. Lilongwe. Malawi.

Kochian, L.V. 1995. Cellular mechanisms of aluminium toxicity and resistance in plants. Annual Review of Plant Physiology and Plant Molecular Biology 46: 237-260.

Mangelsdorf, P.C. 1974. Corn: its origin, evolution and improvement. Harvard Univ. Press, Cambridge. pp. 3-10.

Mazunda, J and K. Droppelmann. 2012. Maize Consumption Estimation and Dietary Diversity Assessment Methods in Malawi. Lilongwe, Malawi. International Food Policy Research Institute (IFPRI) Series number: 11.

MOA (Malawi Government Ministry of Agriculture) 1994. Guide to Agricultural production in Malawi 1994. Extension Aids Branch. Ministry of Agriculture. Lilongwe.

Munthali, M.W. and A.D.C. Chilimba. 2004. Effects of composting materials and methods of composting on quality of compost and maize yields. In: 2004 Annual Report of Soils and Agricultural Engineering Commodity Group, Ministry of Agriculture, Chitedze Research Station, Lilongwe, Malawi. pp. 52.

MVAC (Malawi Vulnerable Assessment Committee). 2010. Food Security Monitoring report. Lilongwe, Malawi.

MVAC (Malawi Vulnerability Assessment Committee). 2013 National Food Security Forecast, April 2013 to March 2014. Bulletin No. 9/13 Volume 1.

Mviha, P.J.Z., A.P. Mtukuso, M.H.P. Banda and B.F. Chisama. 2011. A Catalogue of Agricultural Technologies released by the Ministry of Agriculture and Food Security 2004-2011. Department of Agricultural Research Services. Lilongwe, Malawi. pp.4-5.

Nordin, S. 2005. Low Input Food and Nutrition Security: growing and eating more using less. Malawi: World Food Programme.

Pandey, S., H. Ceballos, R. Magnavacca, A.F.C. Bahia-Filho and J. Duque-Vargas. 1994. Genetics of Tolerance to Soil Acidity in Tropical Maize. Crop Science 34: 1511–1514.

Pandey, S. and C.O. Gardener. 1992. Recurrent selection for population, variety, and hybrid improvement in maize. Advances in Agronomy 48: 1-87.

Plumb-Dhindsa, P. and A.M. Mondjane. 1984. Index of plant diseases and associated organisms of Mozambique. Tropical Pest Management 30: 407-429.

Powell, J.M.R., A. Pearson and P.H. Hiernaux. 2004. Review and Interpretation. Crop livestock interactions in the West Africa Dry lands. Agronomy Journal. 96: 469-483.

Kidd, P.S. and J. Proctor. 2000. Effect of Aluminium on the growth and mineral composition of *Betula pendula* Roth. Journal of Experimental Botany 51: 1057-1066.

Ramaiah, K.V.C., C. Parker, M.J.V. Rao and L.J. Musselman. 1983. Striga identification and control handbook. Information Bulletin No. 15, International Crops Institute for the Semi-Arid Tropics, Patancheru, A.P., India.

Ringer, C.E. and A.P. Grybauskas. 1995. Infection cycle components and disease progress of grey leaf spot on field cover. Plant Disease 79:24-28.

Sasaki, M., Y. Yamamoto and H. Matsumoto. 1996. Lignin deposition induced by aluminium in wheat (*Triticum aestivum*) roots. Physiologia Plantarum 96: 193–198.

Selka, P.C. 2012. Malawi: Resilience in the Face of Persistent drought. US Agency for international Development. http://www.usaid.gov/what-we-do/working-crises-and-conflict/building-resilience/malawi-2012

Von Uexküll, H.R. and E. Mutert. 1995. Global extent, development and economic impact of acid soils. In: R.A. Date, N.J. Grundon, G.E. Raymet and M.E. Probert (Eds.). Plant-Soil Interactions at Low pH: Principles and Management, Dordrecht, The Netherlands, Kluwer Academic, pp. 5-19.

Welcker, C., C.B. Andreau, C. De Leon, S.N. Parentoni, J. Bernal, J. Felicite, C. Zonkeng, F. Salazar, L. Narro, A. Charcosset and W.J. Horst. 2005. Heterosis and Combining Ability for Maize Adaptation to Tropical Acid Soils: Implications for Future Breeding Strategies. Crop Science 45: 2405-2413.

# CHAPTER 2

## Literature review

### 2.1 Importance of maize and consumption levels

Maize is the most significant cereal crop in the Gramineae family in eastern and southern Africa, representing over 29% of the total harvested area of annual food crops and 25% of total caloric intake and income (FAOSTAT, 2010). It is one of the most important food staples in SSA, providing nourishment to over 300 million resource-poor smallholders. Its cultivation spans the entire continent and it is the dominant cereal food crop in many countries accounting for 56% of the total harvested area of food crops and 30-70% of the total caloric consumption (FAOSTAT, 2007).

Consumption is high in Southern Africa; the per capita average is about 195 kg in South Africa, 181 kg in Malawi, 168 kg in Zambia and 153 kg in Zimbabwe (Hassan, 1998). According to Calba *et al.* (2001) it was estimated that for SSA to be food secure by 2050, food production should be multiplied by seven as compared to the 1995 level. This requires proper planning for increased agricultural productivity which is sustainable without or with minimal environmental degradation.

#### 2.1.1 Important abiotic factors affecting maize production

The major abiotic constraints to maize production includes drought, low N soils and low pH soils. With respect to low pH, maize is planted on approximately 8 million ha of acid soils all over the world (Brewbaker, 1985; Pandey and Gardner, 1992). Soil acidity is found to be a major yield-limiting factor for many crops and covers extensive areas of land in tropical, sub-tropical and temperate zones; with low pH occupying approximately 3.95 billion ha, about 30% of the ice free land of the world (von Uexküll and Mutert, 1995). The lower yield of crops grown in acid soil is basically due to combinations of low pH, toxicity of iron (Fe), Al and Mn as well as deficiencies of N, P, Mg and Ca. However, Al toxicity was found to be the main problem in maize production because of root growth inhibition, consequently reducing the water and nutrient uptake and its interference in different

physiological processes of crop development (Roy *et al.*, 1988). The key effect of low pH soil on the plant is a slow growing root system, accompanied by the establishment of surface roots. This negatively influences the use of soil nutrients and induces plants to be more susceptible to drought (Piñeros *et al.*, 2005; Hartwig *et al.*, 2007). Soil amelioration can be implemented by correcting the low pH soil status. However, the use of soil amendments such as liming, which is well known to increase soil pH, may have some adverse effects to the environment and have a temporary effect and are too expensive for resource challenged farmers in developing countries. The low pH change has been reported to occur only in a restricted top soil layer upon liming, while the sub-soil surface layers of the soil profile with toxic Al remain acidic (Custódio *et al*., 2002).

### 2.2 Concept of low pH, definition and origin

The concept of low pH first came about by a Danish chemist, Soren Peder Lauritz Sorensen in 1909. Soil pH is a measure of the acidity or basicity in soils and pH is defined as the negative logarithm of hydrogen ions ($H^+$ or, more precisely, $H_3O^+$ aq) in a solution. According to Brady (1990) the pH scale ranges from 0 to 14, with 7 being neutral. According to this notion, a pH below 7 denotes acidity and above 7 denotes alkalinity. Soil pH is considered a significant variable in soils as it dictates many chemical processes that take place. It significantly affects plant nutrient availability by determining the chemical forms of the nutrient. The optimum pH range for most plant species is between 5.5 and 7.0 however, some plants have adapted to thrive at pH values beyond this range.

Acid soils have a low pH because of the parent materials from which they derived or originated from through weathering and have low basic cation (Ca, Mg, K and Na) content because these elements have been reduced from the soil by leaching or via harvested crops (Granados *et al.,* 1993). Generally acid soils have low pH and contain toxic levels of Al and Mn also are deficient in Ca, Mg, P, K, and Mo (Duque-Vargas *et al.*, 1994) and occurring mainly in the form of stable Al silicate complexes, which is non-toxic to plants (Ma and Ryan, 2010). When Al solubilises and forms octahedral hexahydrate $[Al(H_2O)_6]^{3+}$ also known as $Al^{3+,}$ it becomes toxic to plants even at micro-molar concentration (Kochian *et al.,* 2005).

Globally, 30% of all land area is reported to be comprised of low pH soils and 50% of the world's cultivated lands are potentially acidic; thus Al toxicity is considered as one of the most significant limitations to crop production (Piñeros *et al*., 2005). In Brazil, more than 500 million ha are reported to have acid soils, especially those covered by Savannah (Cerrado biome) vegetation (Vitorello *et al*., 2005). The soils of these areas have high acidity (average pH 4.6), a high concentration of Al and Mn, and deficiencies of $Ca^{2+}$, $Mg^{2+}$ as well as P. These limitations, if not corrected, can lead to remarkable reduction in crop productivity. Development of genotypes tolerant to low-soil pH has gained importance in recent years. There is great variability in low-soil pH tolerance between species and even between genotypes within species (Huang *et al.,* 2009). The mechanisms of tolerance to Al can be summarised into two classes: (i) those that eliminate absorbed Al or prevent/reduce its uptake by the roots (Al exclusion) and (ii) detoxification mechanisms, which usually act by Al complexation, followed by the transfer and storage of these complexes in vacuoles (internal tolerance) (Hartwig *et al.,* 2007).

According to Kochian *et al*. (2005), the main site of Al accumulation and toxicity is the root meristem, primarily the distal part of the transition zone. The rapid root growth inhibition after exposure signifies that the Al instantly terminates cell enlargement and elongation before interfering with cell division (Kochian *et al.,* 2005). After an adequate exposure of the root system to Al, its toxicity is manifested through a set of symptoms expressed in its continuous and increasing effect on the morphology and physiology of the roots, which involves decrease in the following: biomass; the number and length of the roots, often coupled with an increase in the mean radius and root volume; and the uptake of water and mineral nutrients, resulting in severe losses of root elongation and the subsequent productivity.

### 2.2.1 Research findings on aluminium toxicity effects

Studies showed that the binding of Al to cell wall components changes the cation exchange capacity (Panda *et al.,* 2009). Ma *et al*. (2004) reported that visco-elasticity and other properties of the cell wall are affected, resulting in alterations that interfere with growth. Al can cause decline in the elasticity of the cell wall and stimulate the synthesis and accumulation of lignin (Peixoto *et al.,* 2007) through the activation of a peroxidase (POD)

linked to the cell wall, which is involved in the improvement of hydroxyproline-rich glycoprotein binding to phenolic acids. The enzymes activated by Al are comprised of nicotinamideadehyde (NADH) oxidase, phenylalanine ammonia lyase (PAL), and lipoxygenase (LOX). NADH oxidases are responsible for the synthesis of hydrogen peroxide, which is significant for rapid polymer binding catalysed by the cell wall POD. PAL is the key enzyme in the biosynthesis of phenylopropanoids and LOX is responsible for the peroxidation of membrane polyunsaturated fatty acids resulting in the formation of hydroperoxides. These compounds are reported to be highly reactive and quickly degraded into compounds that, by the octadecanoic pathway results in the production of jasmonic acid, which functions in the lignin synthesis signalling pathway (Xue *et al.,* 2008).

Kochian *et al*. (2004a; 2004b) indicated that Al can disrupt the cytoskeletal dynamics, interacting with microtubules and actin filaments. Al can also interfere with signal transduction, particularly in the $Ca^{2+}$ signalling pathway (Rengel and Zhang, 2003). According to Sivaguru *et al.* (2000) and Jones *et al.* (2006) Al can increase callus synthesis, blocking the plasmodesmata and preventing cell wall loosening, thus limiting the expansion of cells. The plasma membrane has a negatively charged surface, making it a sensitive target for Al toxicity. Al strongly binds to phospholipids, which leads to alterations of the lipid composition (Peixoto *et al.,* 2001), decreases membrane fluidity and increases the folding of density of lipids (Chen *et al.,* 1991a; 1991b). Al can also inhibit the $H^+$- ATPase in the plasma membrane, which deters the development of and maintenance of the $H^+$ gradient (Ahn *et al.,* 2001). Therefore Al interferes with transportation of secondary ions, indirectly causing changes of ion homeostasis in root cells. Al also rapidly and effectively inhibits the influx of $Ca^{2+}$ into cells by modulating the activity of transporters which causes alterations in the membrane potential (Kochian *et al*., 2005). It has strong affinity for phosphate groups that makes the $Al^{3+}$ bind to DNA, negatively affecting its template activity and chromatin structures (Silva *et al.,* 2000) and this alters the cell division process (Barceló and Poschenrieder, 2002; Kochian *et al*., 2005).

### 2.3 Mechanisms for low pH tolerance

It is important to note that plants have developed various mechanisms to overcome the effects of toxic Al in the soil. These mechanisms can be divided into two groups (i)

symplastic mechanisms comprising of immobilisation or neutralisation of Al within the cell and (ii) exclusion or apoplastic mechanisms that deter the Al from penetrating into the cell, by its immobilisation or neutralisation in the rhizosphere (Kochian, 1995; Samac and Tesfaye, 2003). In the symplastic mechanism, Al within the cell is reported to react with several entities such that it can form complexes with organic acids (Foy, 1988; Taylor, 1988), with proteins or other compounds (Suhayda and Haug, 1995). Internal Al is kept inactive in the cytoplasm or in the vacuoles; this is an advantage because it prevents its negative effects in many cellular processes. However, the intracellular mechanisms of tolerance are not well understood, since both tolerant and sensitive plants have an accumulation of Al when grown in soil conditions of high availability of this element. Different forms of Al can be transported into vacuoles, where it is stored without causing further damage to the cell. The exclusion mechanisms of Al are well studied (Samac and Tesfaye, 2003; Kochian *et al*., 2004a; 2004b) and validated on the basis of genetic, physiological and molecular evidence. In these mechanisms, chelating compounds are reported to be released by the roots forming non-toxic compounds with Al, avoiding the entry of this element into cells.

In a number of crop species, the exudation of organic acids by root apices is a major means of Al tolerance as reported in maize (Piñeros *et al.*, 2002), wheat (Sasaki *et al*., 2004), and sorghum (Magalhaes *et al*., 2007). On the other hand, organic acids, especially citrate and malate, are reported to form stable complexes with the $Al^{3+}$ in the rhizosphere, reducing the toxic effects in the root system (Kochian *et al*., 2004a; 2004b).

### 2.3.1 Genes and inheritance for tolerance to aluminium toxicity

Genes play a significant role in Al tolerance. The first gene identified for Al tolerance isolated in plants was the *ALMTI* gene in wheat which is a malate transporter which is activated by Al (Sasaki *et al*., 2004). Genes *SbMATE* (Magalhaes *et al*., 2007) and *HvMATE* (Furukawa *et al*., 2007) were isolated from sorghum and barley respectively and function as a citrate transporters, also induced by Al. About two years later, advances in research led to the identification of homologous genes of the *ALMT* and *MATE* multigene families which were isolated from several other plant species. In addition, a transcription factor of the zinc finger type called *STOPI*, is related to Al tolerance in Arabidopsis, which

functions in regulating the expression of *AtMATE* and *AtALMT* genes (Liu *et al.,* 2009). Recently, *Nramp aluminium transporter 1 (Nrat1),* expressed in the plasma membrane and in the tonoplast, was identified to be associated with Al tolerance in rice (Xia *et al.,* 2010) and this suggested a possibility of involvement with the flux of Al and its mobilisation to the cell vacuole.

It is important to note that the genetic control of Al tolerance in crops varies from an inheritance controlled by one or two genes, as observed in wheat, to a quantitative inheritance, where genes with smaller effects act as modifiers, such as in maize (Cançado *et al.,* 2005; Ferreira *et al.,* 2006;). In wheat, tolerance to Al appears to be controlled by one or two major genes, with the main gene located on chromosome 4D (Aniol and Gustafson, 1984; Lagos *et al.,* 1991). Delhaize *et al*. (1993) associated the Alt1 locus with a large proportion of the variability in tolerance among wheat cultivars. Subsequently, the *ALMT1* gene which encodes a malate transporter activated by Al, was cloned by Sasaki *et al.* (2004) and would be the gene underlying the Alt1 locus.

Minella and Sorrells (1992) reported that simple inheritance of Al tolerance was observed in barley and identified a gene (*Alp*) which had a major effect in Al tolerance (Minella and Sorrells, 1992; 1997). They concluded that the variations in Al tolerance among barley cultivars were controlled by different alleles at this locus; however, other genes with smaller effects may have an influence on this trait. The *Alp* gene was mapped to chromosome 4H (Tang *et al*., 2000).

### 2.3.2 Genetic variability in various crops for aluminium tolerance

Different crop species exhibit different behaviours in soils with high Al saturation (Parentoni *et al*., 2001). Variations exist within crop species and tribes. For instance rye is considered to be the most Al tolerant species of the Triticale tribe (Miftahudin and Gustafson, 2002) and genes with larger effects on Al tolerance were identified to be located on chromosomes 6RS (*Alt*), 3RL (*Alt*2) and 4RL (*Alt*3).

Parentoni *et al.* (2001) reported some species considered to be extremely tolerant to Al: some of the tropical forage grass species (Gamba, Signal, Jaragua and Capitata grass),

cassava and cowpea. Crops such as rice, coffee, potato, rubber, palm oil, rye and oat are considered to be highly tolerant to Al. However, sweet potato, maize, cabbage, wheat, millet, pea, eggplant, soybean, elephant grass, barley, onions, beet, pumpkin, sorghum and shrubs like leucaena present low to medium tolerance to Al. Carrots, spinach, celery, cotton, common bean and alfalfa are among the species which are extremely sensitive to Al. A large degree of interspecific variability of Al tolerance was reported in several crop species (Parentoni *et al*., 2001; Samac and Tesfaye, 2003). Also Caniato *et al.* (2007) indicated a wide morphological variability for Al tolerance in a group of 13 sorghum lines, ranging from highly sensitive (20% relative root growth) to highly tolerant (>100% relative root growth), when measured in nutrient solution containing 60 µM of Al activity.

Al tolerance in maize is reported to be of complex inheritance, since progenies derived from crosses between tolerant and sensitive lines show continuous frequency distributions under Al stress (Magnavaca *et al.*, 1987; Sawasaki and Furlani, 1987). Magnavaca *et al.* (1987) reported a predominance of additive effects in the genetic variation linked with Al tolerance in maize. However, Moon *et al.* (1997) identified a gene with partial dominance (*ALM1*) responsible for tolerance to Al toxicity in this species with the favourable allele identified in a line derived from a somaclonal variant of the cateto race (Cat-100-6). Subsequently, Sibov *et al.* (1999) mapped two quantitative trait loci (QTLs), called ALM1 and ALM2 on chromosome 6 and 10, respectively, which are involved in the genetic control of Al tolerance in maize. Ninamango-Cárdenas *et al*. (2003) also mapped five Al tolerance QTLs on maize chromosomes 2, 6 and 8, explaining about 60% of the phenotypic variation of the trait. Of the two QTLs (ALM1 and ALM2), only the one on chromosome 6 was consistent between the two genetic mapping studies in maize, being equivalent to ALM1. Recently, Maron *et al.* (2009) characterised a member of the MATE family in maize, Zm MATE1, co-localised with the major Al tolerance QTL in the same region as chromosome 6. According to the author this candidate gene encodes a protein located in the plasma membrane that activates the citrate release in the root apex.

Al tolerance in rice appears to be quantitatively inherited (Khatiwada *et al.*, 1996; Wu *et al.*, 1997). This observation was confirmed by mapping studies in crosses between different crop species of the genus (Wu *et al.*, 2000; Nguyen *et al.*, 2002). The evaluation of diallel crosses in soybean revealed that additive effects are predominant in Al tolerance (Spehar,

1995; Spehar and Galwey, 1996). Bianchi-Hall *et al.* (2000) reported more than five QTLs with minor effects, and concluded that the control of Al tolerance in this species is quantitative. The diallel crossing in alfalfa, a crop highly Al sensitive, also concluded that non-additive effects were more important than the additive effects in the control of Al tolerance (Campbell *et al.*, 1994).

### 2.4 Types of mechanisms for aluminium tolerance

Plants have developed different means to overcome Al stress either by precluding $Al^{3+}$ from entering the root (extrusion mechanisms) or by being able to deactivate or neutralise toxic $Al^{3+}$ absorbed by the root system which is a true tolerance mechanisms. So far the only well documented mechanism of Al resistance is the exclusion of Al from the root tip based on exudation of organic acids, which chelate $Al^{3+}$ creating stable, non-toxic complexes (Kochian *et al.,* 2004a; 2004b).

The root apex was identified as the main site of Al-induced root growth inhibition (Bennet and Breen, 1991; Ryan *et al*., 1993). The most frequently measured effect of Al toxicity is the inhibition of root growth, but it is important to bear in mind that a number of physiological and biochemical processes in the plant cell have been affected before growth inhibition occurs (Rengel, 1996). Many enzymes have been found to be up-regulated upon exposure to Al and these include PODs (Ezaki *et al*., 1996, Hamel *et al.,* 1998). In transgenic Arabidopsis, expression of a POD gene was identified to confer a degree of resistance to Al (Ezaki *et al*., 2000). PODs were identified to have an important function in plant metabolism and physiology, and are considered to play a role in the responses of plants to infection and abiotic stress stimuli (Gaspar *et al.*, 1985). Many plant defence responses involving PODs have been identified and these include lignification (Walter, 1992), cross-linking or bonding of cell wall compounds (Bradley *et al*., 1992), suberisation or impregnation of cell walls and wound healing (Sherf *et al.,* 1993). The gene encoding the Arabidopsis blue copper binding protein induces Al resistance in yeast cells (Ezaki *et al.*, 2000).

### 2.4.1 Physiological mechanisms of aluminium tolerance

Hartwig *et al.* (2007) reported that Al detoxification can be accomplished by its complexation in the symplast with different organic compounds and/or by compartmentalisation of Al or its complexes in vacuoles. In this case Al would change little or nothing in plant metabolism, enabling growth and development even after Al input into the symplast. This tolerance mechanism is associated with endemic species of regions with acidic soils, where the ability to address Al toxicity is a prerequisite for survival. There are a few crop species that accumulate high concentrations of Al in their shoots without suffering from toxicity (Ryan *et al.*, 2001; Jansen *et al*., 2002).

According to Kochian *et al.* (2004b) the main tolerance mechanisms that promote Al exclusion or prevent its absorption by the roots include Al immobilisation in the cell wall, Al selective permeability in the plasma membrane, pH increases in the rhizosphere or the root apoplast and release of organic acids such as citrate, oxalate and malate, and phenolic compounds by the roots. The production and release of organic acids is perhaps the major mechanism of Al tolerance. Evidence that supports this statement was discussed and concluded by Kochian *et al.* (2004b) and they include:

i) A strong correlation exists between Al tolerance and exudation of organic acids in many crop species.

ii) The addition of organic acids in the nutrient medium reduces Al toxicity.

iii) Al/organic acid complexes (di and tri-carboxylic) do not cross the membrane and are not significantly absorbed by the roots.

iv) The exudation of organic acids activated by Al occurs at the root apex, the location of the primary effect of Al toxicity.

v) The activation of the exudation mechanism is triggered specifically by $Al^{3+}$.

vi) In the plasma membrane there are anionic channels activated by Al that facilitate the efflux of organic acids.

Ma *et al.* (2001) also reported the identification of two temporal patterns of organic acid exudation as follows:

i) The plants are characterised by having an almost immediate response to the release of organic acids by the roots when exposed to Al. The authors suggested that the process

appears to involve the activation of pre-existing proteins, as found in wheat, tobacco and barley.

ii) An existence of a lag-phase between Al exposure and organic acids release was found and this process is assumed to involve the stimulation of gene expression (Ma *et al*., 2001; Magalhaes *et al*., 2007).

It is also indicated that genotypes with more robust antioxidant systems are usually more tolerant to excess Al, but the mechanism by which Al exacerbates the formation of reaction oxygen species (ROS) is still not fully understood (Darko *et al*., 2004).

### 2.4.2 Genetic mechanism for aluminium tolerance

A study using QTL mapping reported five distinct genomic regions which are significant for Al tolerance in maize (Ninamango-Cárdenas *et al.,* 2003). Consequently, maize has been the subject of breeding programmes seeking to increase Al tolerance or understand the basis for it. The use of nutrient solution experiments by various authors showed that the trait is quantitatively inherited with a prevalence of additive genetic effects (Lopes *et al.*, 1987; Sawasaki and Furlani, 1987). Prioli (1987) suggested that due to its high heritability the trait is expected to be controlled by a small number of genes.

Miranda *et al.* (1984) found that the inheritance of two dominant genes is responsible for tolerance to Al toxicity. Rhue *et al.* (1978) and, Garcia and Silva (1979) also found that tolerance to Al toxicity is determined by one dominant locus for sensitivity. In another study using restriction fragment length polymorphism (RFLP) Sibov *et al.* (1999) also identified indicators that were involved with the two loci (or two groups) located on chromosome 6 and 10. Brondani and Paiva (1996) associated Al tolerance with a gene or block of genes located on chromosome 2 while Torres *et al.* (1997) associated chromosome 8 to Al tolerance. Ninamango-Cárdenas *et al.* (2003) also identified five genomic regions presumably linked to maize Al tolerance, suggesting that this trait is quantitatively inherited and controlled by a few genes. Their study identified four QTLs for Al tolerance in maize located on chromosome 2, 6 and 8. Boni *et al.* (2009) suggested that different results on inheritance of Al tolerance could be a function of the germplasm used because there is a possibility that the genotypic constitution of genetic material can generate a differentiated

and apparently inconsistent phenotypic expression. The authors recommended more efforts on the inheritance mechanisms of Al tolerance in maize because the results reported in the literature are considered to be inconsistent and inconclusive.

## 2.5 Use of modern tools in breeding for low pH tolerance: QTLs, marker assisted selection and transgenic's

In maize, Al tolerance is seemingly a quantitative trait and Guimarães *et al.* (2012) recommended the use of a combination of strategies for QTL introgression, complemented by early phenotyping of lines to increase the chances of success in generating tolerant materials. The existence of a QTL with a major effect co-localised with genes homologous to the $ALT_{SB}$ gene was reported (Sibov *et al*., 1999; Ninamango-Cárdenas *et al*., 2003). Maron *et al*. (2009) recommended that other genomic regions should be monitored on the basis of early phenotypic selection or genome-wide selection (GWS). Parentoni *et al.* (2003) reported a high correlation between performance *per se* in maize inbred lines and its general combining ability (GCA) evaluated in diallel crosses in a study of phenotypic selection in nutrient solution. In another study, three cycles of marker-assisted backcrossing in maize were sufficient to recover approximately 99% of the recurrent genome (Morris *et al*., 2003).

Molecular markers for assisted introgression are also available for sorghum and were described by Magalhaes *et al.* (2007). Oliveira *et al.* (2010) also reported that markers distributed in the sorghum genome, are available and are being used for introgression of superior alleles of the $ALT_{SB}$ gene in elite lines from Brazil and Niger. In barley, transgenic plants that overexpress the *ALMT1* gene were created. Wheat genes that showed a high increase in the rate of malate release, lead to an increased tolerance to Al (Delhaize *et al*., 2004). Magalhaes *et al.* (2007) also demonstrated that *Arabidopsis* plants transformed with the $ALT_{SB}$ genes showed higher Al tolerance and citrate exudation than non-transgenic plants. These results showed that the overexpression of these heterologous genes confers increased tolerance to Al and suggest an additional strategy for crops which have limited genetic variability for this trait.

Significant advances in the knowledge of the physiological and molecular basis for Al tolerance were obtained through the cloning of genes of major effects, such as *AMLT1* in wheat (Sasaki *et al*., 2004) and $ALT_{SB}$ in sorghum (Magalhaes *et al*., 2007), which are involved in the Al exclusion mechanism. Guimarães *et al.* (2012) indicated that newly identified genes and QTL have provided important support for a broader understanding of other mechanisms involved in Al tolerance in plants and the availability of cultivars with higher levels of Al tolerance would increase in time and efficiency with the broad integration of molecular and physiological knowledge into breeding programmes.

## 2.6 Diallel evaluation

The Danish animal breeder, Schmidt first coined the diallel crossing concept in 1919 (Pirchiner, 1979), it was later introduced into plant breeding. According to Sughrone and Hallauer (1997) "diallel" refers to making all possible crosses among a group of genotypes. The genotypes could for example, be individuals, clones or homozygous lines. According to Griffing (1956) and, Mather and Jinks (1977) the diallel mating design enable the determination of a magnitude of additive and non-additive components of heritable variation. It is the most popular technique used by plant breeders to get information of value on inbred lines of different parents and to assess the gene action in various traits (Pickett, 1993).

Griffing (1956) came up with a range of diallel analytical procedures. This has permitted plant breeders to come up with the right selection strategies and compare heterotic patterns at an early stage of hybrid production (Gouis, 2002). The four methods used are i) parents, ii) $F_1$ and reciprocal crosses iii) parents and $F_1$, and iv) only the $F_1$. Depending on the decision by the plant breeder, the linear analysis model can be for either fixed or random effects. When the genotypes are highly selected and inbred, a fixed model for analysis is commonly engaged for applied breeding programmes (Agrobase, 2010). In this case when testing for combining ability the sampling error becomes the residual and consequently variance components and standard errors can be estimated. When estimating additive and dominance variances, the following is assumed: absence of epistasis, absence of reciprocal differences, normal diploid segregation, absence of linkage and multiple alleles, homozygous parents, independent gene distribution, and zero inbreeding coefficients

(Griffing, 1956). However, it has been noted that these assumptions are rarely observed in practice (Baker, 1978) and since diallel cross analysis guides the selection of parents with additive and non-additive effects for specific traits, it enables the plant breeders to select parents to be used in hybridisation or population breeding programmes (Murtaza *et al.*, 2005).

## 2.7 Combining ability analysis

Griffing (1956) outlined a general procedure for diallel analysis which permits non-allelic interaction. This technique partitions the average measured performance of a cross into major components apart from the general mean ($\mu$) and environment variance ($\sigma^2e$) by use of the analysis of variance (ANOVA).

### 2.7.1 General combining ability analysis

GCA is used to denote the parents/line/hybrid's mean performance/contribution in a cross combination (Sprague and Tatum, 1942). Falconer and Mackay (1996) defined it as the average performance of the parental inbred line in all single crosses, when expressed as a deviation from the average of all crosses. Additive and additive epistatic variances are the primary components of GCA (Matzinger, 1963). Additive, additive x higher order interactions of additive genetic variance have been responsible for the differences in important variation in GCA (Baker, 1978).

### 2.7.2 Specific combining ability analysis

Specific combining ability (SCA) refers to those cases in which cross combinations perform relatively better or worse than would be anticipated on the basis of the mean performance of the parental inbred lines (Sprague and Tatum, 1942). It is thus the deviation to a greater or lesser extent from the sum of the GCA of the two parents. SCA is due to non-additive gene action (Falconer and Mackay, 1996). In other words, variations or differences in SCA are considered to be attributable to non-additive genetic variance (Baker, 1978).

### 2.7.3 Importance of combining ability analysis

GCA and SCA effects are significant in identification of parents and crosses which are responsible for the expression of a particular type of gene action (Meredith, 1984). It is important to note that both GCA and SCA are effective genetic parameters used in deciding the next stage of the breeding programme (Dabholkar, 1992). Multiple crossing or composite breeding programmes are facilitated through selection of parents based on GCA for development of synthetics and choice of suitable $F_1$, especially where one intends to use appropriate selection techniques like recurrent selection, mass selection and reciprocal selection (Dabholkar, 1992).

### 2.7.4 Research findings on combining ability studies in maize

Gowda (2013) carried out a study to investigate the GCA effects of parental inbred lines and SCA effects of single-cross hybrids for yield and yield related traits and explore their use in the generation of hybrids. A total of 170 $F_1$ were developed and tested by crossing 34 parental inbred lines with five testers. The SCA: GCA ratio of variances revealed that there were prevalence of non-additive gene action in the expression of all the traits under investigation. Six inbred lines were identified with good GCA for yield and yield related traits.

El-Badawy (2013) carried out a study involving a half diallel cross with seven inbred lines of maize under two different N levels for six quantitative characters. Results indicated that mean squares for all traits were significant for GCA and SCA. Ratios of GCA:SCA indicated that the additive and additive x additive types of gene action were responsible for the expressions for days to 50% anthesis, number of kernel rows per ear and shelling percentage in both N levels and combined analysis. Significant interaction mean squares between N levels and GCA and SCA were detected for most traits. The results suggested that the crosses may be of great importance in breeding programmes either towards development of maize hybrids or synthetic varieties.

Kurawa (2012) conducted genetic analysis studies of progenies from diallel crosses among eight varieties of different maturity groups of maize and observed significant differences

for GCA and SCA, indicating presence of additive as well as non-additive gene action. In both environments, the GCA mean squares were highly significant and higher than the SCA mean squares for all traits with a few exceptions. The study revealed significant GCA x environment interaction, indicating different parental varieties behaved differently under different environments, hence there was need to select different parental varieties for hybrid production for a specific environment. Significant SCA x environment interaction indicated hybrid performance varied with respect to environments. A suggestion was made to have specific hybrids produced for specific environments.

Vivek *et al.* (2009), in a combining ability study of parental inbred lines for grain yield and resistance to seven diseases, observed significant differences for both GCA and SCA effects for most diseases. Correlations between GCA effects for disease scores were generally non-significant, suggesting the possibility of pyramiding genes for disease resistance in the parental inbred lines. Matthews *et al.* (2008), in a study of a diallel cross among the nine lines observed that both SCA and GCA were significant sources of variation in the inheritance for resistance to ear damage. GCA was also a significant source of variation in the inheritance for resistance to larval growth. GCA effects for reduced larval weight were significant for two lines.

## 2.8 Heritability estimation

Heritability was defined as the proportion of variance due to heritable differences and genotypic variance to the total phenotypic variance (Meredith, 1984). The higher the proportionate value, the more transmissible is the character. On the other hand, the lower the ratio or proportionate value, the higher the influence of the environment on the phenotypic expression of the character. Thus it defines the proportion of the total variance that is due to the mean effects of genes.

Heritability can be defined in two senses:

i) Broad sense heritability which is total genetic variance (Meredith, 1984). While Dudley and Moll (1969) defined it as the ratio of total genetic variance to phenotypic variance which expresses the degree to which individuals' phenotypes are determined by their genotype.

ii) Narrow sense heritability which is the ratio of additive genetic variance to phenotypic variance (Dudley and Moll, 1969) and expresses the extent to which phenotypes are determined by the genes transmitted from parents.

### 2.8.1 Importance of narrow sense heritability

Inbreeding is important mostly when developing inbred lines through selfing and selection, and is needed when heterosis or vigour is desired. To avoid mating related individuals (inbreeding), narrow sense heritability is employed in estimating the degree of relatedness or resemblance between parents and progenies (Meredith, 1984; Chaudhary, 1991). Narrow sense heritability estimates the degree of correspondence between breeding values and phenotypic values and expresses the level of genetic variance in the population, which is mainly responsible for altering the genetic make-up of the population through selection (Falconer, 1989; Dabholkar, 1992).

Narrow sense heritability ($h^2$) can be written as: $h^2 = V_A / V_P$

$h^2 = V_A / (V_P = V_A + V_D + V_I + V_E)$

$V_P = V_A + V_D + V_I + V_E$

Where: $V_A$ denotes additive variance, $V_D$ denotes dominance variance, $V_I$ denotes interaction variance, and $V_E$ denotes environmental variance (Falconer, 1989).

It is important to note that heritability is valid not only of the trait under investigation, but also of a population being sampled and the environmental conditions to which individuals have been exposed to (Falconer, 1989; Dabhokar, 1992). Populations which are genetically more uniform are anticipated to express lower heritability than genetically diverse populations, since environmental variances constitute part of the phenotypic variance, which influences the degree of heritability.

### 2.8.2 Research findings on heritability studies in maize

In a study to investigate broad sense heritability and correlations between the traits and total grain yield, Aminu and Izge (2012) reported heritability estimates for number of stands per plot, anthesis-silking interval, plant height, weight of cobs and grain yield of above 60% within a range of 60.61-67.44%, while days to 50% anthesis, days to 50% silking, ear height and de-husked cobs, recorded heritability estimates of below 60% i.e.

47.91%, 50.03%, 58.45% and 55.06% respectively. Higher and relatively moderate broad sense heritability of the traits suggested that variations were transmissible and had the potential for generating high yielding varieties via selection of promising plants in succeeding generations.

The correlation analysis which indicates associations or some relationships indicated that anthesis-silking interval (r = 0.88), number of cobs per plant (r = 0.55 and r = 0.32), number of cobs per plot (r = 0.83), weight of cobs (r = 0.8 and r = 0.86), de-husked cobs (r = 0.95, r = 0.49 and r = 0.87) and 100-seed weight (r = 0.46 and r = 0.32) exhibited positive and significant genotypic (g), phenotypic (p) and environmental (e) correlation with grain yield. The authors, Aminu and Izge (2012) concluded that heritability as well as correlations were good methods for improving yield and selecting genotypes tolerant to drought.

In another study to investigate genetic variation, heritability and genetic advance of grain yield and its component traits Bello *et al.* (2012) reported that the effect of interaction of genotype and genotype by year were significant for ear weight and grain yield, while the effect of year was highly significant for all the traits. Additive gene effects contributed to high levels of phenotypic and genotypic coefficients of variation as well as high heritability accompanied with high genetic advance recorded for grain yield, number of grains per ear, ear weight, as well as plant and ear heights. This indicated that effective selection is possible for improving these traits.

## 2.9 Heterosis

Heterosis is essential in crop improvement and is considered to be the phenomena of enhanced hybrid performance (Hartl and Clark, 1989). Falconer (1989) defined heterosis as the difference between the crossbred and parental inbred lines or simply the superiority over inbred lines. It is often expressed in two ways: Where interest is primarily in the $F_1$ performance *per se*, it is expressed as the $F_1$ minus the highest performing parent, expressed as a percentage of that parent used and is referred to as "high parent heterosis" (Meredith, 1984). Secondly, as the $F_1$ minus mid-parent expressed as a percentage of the mid-parent, this was also referred to as "mid-parent heterosis" (Meredith, 1984; Lamkey and Edwards, 1999). For heterosis to occur there should be heterozygosity as a fundamental precondition

(Flintham *et al.,* 1997). Other geneticists believe that dominance and epistasis are the essential genetic foundation of heterosis such that loci with no dominance do not cause heterosis. The degree of heterosis following a cross between two particular parental inbred lines or populations is dependent on the square of the difference of rate of gene occurrence or frequency between populations such that heterosis in the $F_1$ is $HF_1= \sum dy^2$, where "d" denotes the deviation of the heterozygote from the homozygote mid-parent, while "y" denotes gene frequency (Coors, 1999).

### 2.9.1 Research findings on heterosis studies in maize

Salazar *et al.* (1997) conducted a study to investigate eight segregating populations and their 56 reciprocal crosses, in five acidic-soil locations in order to establish relative importance of nuclear and cytoplasmic factors for yield, days to silking, ear height, ears per plant, and ear rot. Average and specific heterosis represented 65 and 31% of the total sum of squares for heterosis for yield. Population heterosis effects for yield were not significant, suggesting the effects would be of little importance in selecting parental inbred lines for developing superior hybrids. Specific heterosis effects were negative and significantly different for yield and ears per plant only for one cross, suggesting that non-additive gene effects were at play in determining yield of specific cross combinations. According to the author, the unavailability of reciprocal differences for all characters suggested that nuclear genes were responsible for tolerance to soil acidity.

## 2.10 Correlations

When a change in one variable is associated with change in another variable it is referred to as correlation (Falconer, 1989). The measure of association between two traits is referred to as a correlation coefficient. Correlations are either positive or negative; positive when an increase in one variable leads to an increase in another or when it is negative, an increase in one variable will lead to a decrease in another (Falconer, 1989). Associated traits are considered to be significant for three reasons: (i) gene action leading into association through the pleiotropic action of genes whereby one gene affects more than one phenotypic

trait (ii) linked to alterations brought in by selection and (iii) linked with natural selection (Falconer and Mackay, 1996).

Two types of correlations are considered to be important in plant breeding (Meredith, 1984):

i) Correlation via phenotype which is considered to be the association between two traits that is visible and determined from measurements of the same traits in a number of individuals in a given population. Phenotypic values are estimated by genotypic values and environmental deviations. This type of correlation is composed of correlation due to environmental agents and non-additive gene action (Falconer, 1989; Dabholkar, 1992). In cases where two traits have high heritability, association due to environmental agents will be insignificant (Falconer, 1989).

ii) Genetic correlation is considered to be the correlation of breeding values which is a result of additive gene action (Falconer and Mackay, 1996). Genetic association between two or more traits may result from one gene affecting many traits (pleiotropic effects) or gene linkage that governs inheritance of two or more traits (Falconer, 1989). This depicts the degree to which the two measurements are associated genetically.

### 2.10.1 Research findings on correlation in maize

Bulent (1996) conducted a study to investigate the associations among several agronomic characteristics in parental inbred lines, hybrids and between parental inbred lines and their offspring of maize in short season areas. Phenotypic correlations of each measured trait between as well as among hybrids and inbred lines were not the same. The highest correlation coefficient ($r = 0.78$) was recorded between days to 50% anthesis and grain yield. The trend showed that the better yielding inbred lines did not necessarily give rise to better yielding offspring. Given that days to 50% pollen shed plays a significant role in two main traits (yield and moisture stress tolerance) for hybrids, suggested that an effort to achieve most favourable anthesis dates during inbred line development could be an important criterion to predict short season hybrid performance.

Alake *et al.* (2008) conducted a study to determine genetic variation and correlation in yield and yield associated traits of tropical maize. There was close similarity between the

genotypic correlation coefficient and phenotypic correlation coefficient for all characters, indicating that selection for these traits would be successful. Heritability estimates were high for all the traits investigated except for days to 50% flowering. Traits investigated showed significant association in the positive direction with grain yield except for days to flowering and silking which showed significant negative genotypic association with grain yield. Principal component analysis (PCA) showed that some characters contributed significantly to variations found in the maize genotypes evaluated and these included seedling emergence, kernel weight, grain yield, number of kernels per row, number of kernel rows per ear and days to anthesis. Also some traits like number kernel rows per ear, grain yield per plant, ear length and number of kernels per row showed high heritability coupled with high genetic advance and could be considered as criteria when selecting maize for grain yield.

## 2.11 Stability analysis

### 2.11.1 Stability definition and its concept

Yield stability of a genotype refers to the situation whereby a particular genotype is capable of evading fluctuations in yield over a range of environmental conditions (Heinrich *et al*., 1983). Related to stability is wide adaptability which refers to a situation whereby a genotype exhibits good performance over a wide geographical region under changeable climatic environmental conditions. Adaptability or stability of a cultivar usually relates to three biological mechanisms. These are: physiological, morphological and phenological. Individual genotypes may react to brief fluctuations in an environment in two different ways. Genotypes that are capable of buffering against environmental changes and develop a replica of phenotype over a range of environments are known to possess a 'biological or static' stability. This is usually not beneficial in crop breeding, since it will not show improved vigour or heterosis under improved growing conditions. On the other hand 'agronomic or dynamic' stability allows a predictable response to environments and stability with respect to the agronomic concept, and has no deviation from this response to environments (Becker and Leon, 1988). With respect to quantitative characters, the many genotypes usually respond similarly to desirable or unfavourable environmental conditions. According to Baker (1988) genotype by environment interactions (GEI) could be classified into two types:

i) Qualitative interactions. This is sometimes called crossover interactions and it is here that the direction of true treatment differences varies.
ii) Quantitative interactions. This is sometimes called non-crossover interactions and the real treatment differences vary in the degree, but not in direction (ranking of genotypes does not change from one environment to another).

The crossover or qualitative interaction is significant in agricultural production in comparison to non-crossover or quantitative interactions (Baker, 1988; Crossa, 1990). With respect to quantitative characters, the majority of genotypes respond in a similar manner to desirable or undesirable environmental conditions. If a crossover (qualitative) type of GEI (one that leads to genotype rank changes) is present, selection of genotypes based on mean yield by use of combination of stability and yield would likely be lower than for those genotypes selected based on yield alone (Kang *et al.*, 1991). This could also be clarified by investigating the outcome to growers when investigators commit a Type I error i.e. rejecting the null hypothesis when it is true and Type II error i.e. accepting the null hypothesis when it is false, when selection was based on yield alone and when it was based on both yield and stability.

### 2.11.2 Phenotypic stability analysis techniques

Phenotype is considered to be an organism's actual visible properties, such as morphology, development, and behaviour. Several procedures for assessing phenotypic stability have been proposed by various authors. However, Lin *et al*. (1986) studied the statistical relationship between nine stability statistics and identified and classified three concepts of stability into the following types:
I) Type I: a stable genotype is identified with a small variance across all environments. This type of stability is significant when the test locations considered are not very diverse and is identical to the statistical concept of stability as described by Becker and Leon (1988).
II) Type II: a stable genotype has a reaction to the environment similar to the mean reaction of all genotypes in the experiment. Type II stability is identical to the dynamic concept described by Becker and Leon (1988).

III) Type III: the residual mean square from the regression model on the environmental index is a small value i.e. a smaller deviation from the regression. Type III stability is dynamic and the method of Eberhart and Russel (1966) is employed for its estimation.

#### 2.11.2.1 Cultivar performance technique for estimating cultivar stability

Cultivar performance measure (*Pi*) is another technique proposed by Lin and Bins (1988). Whereby *P* denotes a genotype while *i* is the mean squares of the distance between genotype one and the genotype with the maximum performance. A small *Pi* value indicates a small difference between the genotype with maximum yield and the best performing genotype. A pairwise GEI mean square between the maximum and each genotype can be estimated as indicated by Crossa (1990).

#### 2.11.2.2 Wricke's ecovalence technique for estimating cultivar stability

Ecovalence is another technique of Wricke (1962) who proposed the procedure for measuring stability by employing each genotype's contribution to the GEI sum of squares as a stability measure. Ecovalence (*Wi*) was the name given to this concept or statistic. Genotypes associated with *Wi* values that are low or close to zero tend to have smaller deviations from the mean across environments and are more stable and possess a high ecovalence i.e. low value of *Wi* = high ecovalence. Becker and Leon (1988) demonstrated ecovalence by plotting yield numerical values of genotypes in several environments against the respective environmental means.

#### 2.11.2.3 Shukla's stability variance parameter for estimating cultivar stability

Stability variance technique is another statistic procedure developed by Shukla (1972). The technique is dependent on the residuals from the additive model. The variance of a cultivar is defined as the variance of the cultivar across locations. For the purpose of ranking, stability variance ($\sigma^2 i$) is equivalent to ecovalence (*Wi*) (Wricke, 1962). Shukla's (1972) stability variance ($\sigma^2 i$) is also equivalent to Type II stability (Lin *et al*., 1986). According to Shukla (1972) there was an indication that genotypes could not be described if there was

a small proportion of GEI due to heterogeneity among regression coefficients. In addition, there is absence of independence between means of sites and performance as well as between intercepts and slopes. Instead he suggested the use of the GEI sums of squares which is partitioned into variance components corresponding to each of the genotypes. The identification of a stable genotype according to Shukla (1972) is as follows: stability variance ($\sigma^2 i$) must be equal to the environmental variance ($\sigma^2 e$), for a variety to be classified as stable thus $\sigma^2 = 0$. A relatively large value of $\sigma^2 i$ implies greater instability of genotype *i* since the stability variance is the difference between two sums of squares, the value can be negative, but negative estimates of variances are rare in variance components computations and are assumed as *v* equivalent to zero in most cases.

#### 2.11.2.4 Regression coefficient and deviation mean squares

Yield is considered as the most important trait for variety selection. To this effect the most widely used criteria for selecting high yield and stable performance is average yield performance, site mean yield regression response and deviations from regression (Eberhart and Russel, 1966; Freeman, 1973). The first estimated parameter is the slope *bi* from the regression of the yields of genotype I on an environmental index (Finlay and Wilkinson, 1963). Where *b* is equal or close to 1.0, it implies that a genotype responds to changeable environmental conditions in a similar manner as the sample mean. Finlay and Wilkinson (1963) proposed that regression coefficient approaching zero imply stable performance. The joint linear regression has been employed as a technique for analysing and interpreting the non-additive GEI of two way-classification data.

Finlay and Wilkinson (1963) proposed that regression coefficient close to 1.0 imply average stability. When that is accompanied with high mean yield, varieties have good general adaptation. Conversely, when accompanied with low mean yield, genotypes have poor adaptation to all test environments. Regression values increasing above 1.0 describe genotypes with increasing sensitivity to environmental change, for example below average stability and specifically adapted to high yielding environments. Regression coefficients decreasing below 1.0 provide a measure of greater buffering ability to changeable environmental conditions (above average stability) and therefore specifically adapted to

low yielding environmental conditions. Stability analysis provides a method to establish the reaction of a genotype to changeable environmental conditions.

### 2.11.3 Multivariate techniques for stability analysis

Multivariate approaches are employed in stability analysis in order to obtain additional information on multivariate reaction to environments by genotypes. These analyses are suited for computing two-way matrices of genotypes and environments (Crossa, 1990). According to Becker and Leon (1988) multivariate analysis has three major objectives: i) to remove noise from data patterns, ii) to summarise the data and iii) to show the structure in the data.

Genotypes with similar reaction can be clustered, hypothesised and later evaluated and data can be easily summarised and analysed. The aim of the several multivariate analysis techniques is to allocate test varieties into qualitatively homogeneous stability subsets (Becker and Leon, 1988). Within subsets, no significant GEI occurs, while differences among subsets are due to GEI. However, there are some setbacks in multivariate analysis techniques which include: i) many dissimilarity techniques and clustering strategies exist and selecting between them can consequently depict different cluster groups and ii) non-existent structure could find its way into the data.

#### 2.11.3.1 Additive main effects and multiplicative interaction analysis technique

This model is observed to constitute ANOVA for genotypes and environment main effects with PCA of the GEI into one model with additive and multiplicative parameters. It has been considered important in getting insight of complicated GEI (Kang, 1996). Results are plotted in a very enlightening biplot that depicts both major and interaction effects for both test varieties and test locations. The additive main effects and multiplicative interaction (AMMI) model is employed to split estimated interaction components and adjust mean yield for the interaction. This model partitions data into pattern rich models and eliminates noise-rich residual to increase efficiency. The main advantage for using AMMI is that it gives information for a large component of variability in its first few components with

successive readings indicating decreasing percentage pattern and decreasing percentage of noise (Purchase, 1997).

The model AMMI is important in gaining insight of complicated interactions, gaining efficiency, improving selection efficiency and increasing experimental efficiency (Gauch, 1990). It has become an important statistical tool in identification of morphological and physiological characters associated with tolerance to stress and reveals the relative significance of several environmental factors or stresses (Gauch, 1993). The other merit of this model is that it can be employed in modelling and gaining insight about interactions. According to Crossa (1990) the AMMI model is particularly useful in organising patterns and associations for genotypes and environments. The analysis procedure is that in the first ANOVA the total variation is partitioned into three orthogonal sources, test varieties as genotypes, test locations as environments and GEI. As a guide, Ramagosa and Fox (1993), reported that in most yield trials the proportion of sum of squares due to variations among environments ranges from 80-90% and that the variation due to GEI are often larger than the genotypic differences. The other uniqueness of AMMI analysis is that the interaction principal component analysis (IPCA) sum of squares alone is often larger than that for genotype. Generally as genotypes and environments become more diverse, GEI tends to increase and may reach 40-60% of the total variation. Usually the environmental main effect, which contributes up to 90% of the total variation, is not much relevant, especially in selection techniques.

The AMMI technique produces graphs (biplots) which focus on the data structure relevant to selection, in other words on the genotype and GEI sources (Ramagosa and Fox, 1993). PCA partitions GEI into various orthogonal axes. There is some controversy on the number of axes included in the AMMI model and how judgements and indications of genetic stability can be made if too many axes are considered. Gauch and Zobel (1996) pointed out that generally AMMI 1 and AMMI 2 models with IPCA 1 and IPCA 2 respectively, are often chosen and that the graphical outlay of axes, either as IPCA 1 or IPCA 2 against main effects, or IPCA 1 against IPCA 2, is not an issue and it gives adequate information. With AMMI 3 and higher models, IPCA 3 and higher axes are mostly dominated by noise, have little or no predictive value and no biological explanation and can thus be ignored. Another major importance of the AMMI model is that it gives a cost-effective means for obtaining

efficiency in research experiments and maximising benefits on investments (Gauch and Zobel, 1996). Gains in efficiency of yield estimations have been observed to be equivalent to subsequent additional number of replication by a factor of two to five (Crossa and Cornelius, 1993).

## 2.12 References


Agrobase, 2010. Agronomix Software Inc., 71 Waterloo str, Winnipeg, Manitoba, R3NOS4, Canada.

Ahn, S.J., M. Sivaguru, H. Osawa, G.C. Chung and H. Matsumoto. 2001. Aluminium inhibits the $H^+$-ATPase activity by permanently altering the PM surface potentials in squash roots. Plant Physiology 126: 1381–1390.

Alake, C.O, D.K. Ojo, O.A. Oduwaye and M.A. Adekoya. 2008. Genetic Variability and Correlation Studies in Yield and Yield Related Characters of Tropical Maize (*Zea mays* L.) Journal of Agricultural Sciences, Environment and Technology 8:14-27.

Aminu, D. and A.U. Izge. 2012. Heritability and Correlation Estimates in Maize (*Zea mays* L.) Under Drought Conditions in Northern Guinea and Sudan Savannas of Nigeria. World Journal of Agricultural Sciences 8: 598-602.

Aniol, A. and J.P. Gustafson. 1984. Chromosome location of genes controlling aluminium tolerance in wheat, rye and triticale. Canadian Journal of Genetics and Cytology 26: 701-705.

Baker, R.J. 1978. Issues in Diallel Analysis. Crop Science 18: 533-536.

Baker, R.J. 1988. Tests for crossover genotype x environment interactions. Canadian Journal of Plant Science 68: 405-410.

Barceló, J. and C. Poschenrieder. 2002. Fast root growth responses, root exudates, and internal detoxification as clues to the mechanisms of aluminium toxicity and resistance: a review. Environmental and Experimental Botany 48: 75-92.

Becker, H.C. and J. Leon. 1988. Stability analysis in plant breeding. Plant Breeding 101: 1-23.

Bello, O.B., S.A. Ige, M.A. Azeez, M.S. Afolabi, S.Y. Abdulmaliq and J. Mahamood. 2012. Heritability and Genetic Advance for Grain Yield and its Component Characters in Maize (*Zea mays* L.). International Journal of Plant Research 2: 138-145.

Bennet, R.R. and C.M. Breen. 1991. The aluminium signal: new dimensions to mechanisms of aluminium tolerance. In: Wright, R. J., Baligar, V. C. and Murrmann, R.P. (Eds.) Plant-Soil Interactions at Low pH. Dordrecht, Kluwer, pp.703-716.

Bianchi-Hall, C.M., T.E. Carter, M.A. Bailey, M.A.R. Mian, T.W. Rufty, D.A. Ashley, H.R. Boerma, C. Arellano, R.S. Hussey and W.A. Parrott. 2000. Aluminium Tolerance Associated with Quantitative Trait Loci Derived from Soybean PI 416937 in Hydroponics. Crop Science 40: 538-545.

Boni, T.A., A.J. Prioli, S.M.A.P. Prioli, L.C. Lucio and R. de Mello. 2009. Inheritance of aluminium tolerance in maize. Crop Breeding and Applied Biotechnology 9: 147-153.

Bradley, D.J., P. Kjellbom and C.J. Lamb. 1992. Elicitor and wound induced oxidative cross linking of proline-rich plant cell wall protein: A novel, rapid defence response. Cell 70: 21-30.

Brady, N.C. 1990. The Nature and Properties of Soils. Macmillan Publishing Company, New York, NY.

Brewbaker, J.L. 1985. The tropical environment for maize cultivation. In: A. Brandolini, F. Salamini (Eds.). Breeding strategies for maize production improvement in the tropics. Firenze: FAO; Instituto Agronomico per I'Oltremare.

Brondani, C. and E. Paiva. 1996 ''RFLP'' analysis of aluminium tolerance in chromosome 2 in maize. Pesquisa Agropecuária Brasileira 31: 575-579.

Bulent, S., 1996. Phenotypic correlations between maize inbreds and their single cross hybrids in short season areas. Euphytica 89: 291-296.

Calba, C.H., W.J. Horst and C. Zonkeng. 2001. Maize grain yield correlated responses to change in acid soil characteristics after 3 years of soil amendments'. 7th Eastern and Southern Africa Regional Maize conference. 11th- 15th Feb. pp. 222 -227.

Campbell, T.A., P.R. Jackson and Z.L. Xia. 1994. Effect of aluminium stress on alfalfa root proteins. Journal of Plant Nutrition 17: 461-471.

Cançado, G.M.A., V.E.D. Rosa-Junior, J.H. Fernandez, L.G. Maron, R.A. Jorge and M. Menossi. 2005. Glutathione. S-transferase and aluminium toxicity in maize. Functional Plant Biology 32: 1045-1055.

Caniato, F.F., C.T. Guimaraes, R.E. Schaffert, V.M.C. Alves, L.V. Kochian, A. Borem, P.E. Klein and J.V. Magalhaes. 2007. Genetic diversity for aluminium tolerance in sorghum. Theoretical and Applied Genetics 114: 863-876.

Chaudhary, R.C. 1991. Introduction to plant breeding. Oxford and IB Publishing Co. PVT. LD. New Delhi-Bombay.

Chen, J., E. Sucoff and E.J. Stadelman. 1991a. Aluminium and Temperature alteration of cell membrane permeability of *Quercus rubra*. Plant Physiology 96: 644-649.

Chen, Z.F., Z.W. Zhang, Z.Y. Li and Y.F. Wang, 1991b. Study on the correlation between the earliness of Upland cotton and its yield and fibre quality. China Cottons 5: 16-17.

Crossa J. 1990. Statistical analysis of multilocation trials. Advances in Agronomy 44: 55-85.

Coors, J.G. 1999. Selection methodology and heterosis. In: Coors J. and Pandy S. (Ed.) Genetics and exploitation of heterosis in crops. American Society of Agronomy and Crop Science Society. Madison, pp.225-245.

Crossa, J. and P.L. Cornelius, 1993. Recent development multiplicative models for cultivar trials. In: D.R. Buxton, R. Shibles, R.A. Fortberg, B.L. Blad, K.H. Asay, G.M. Paulsen and R.F. Wilson (Eds.) International Crop Science. Crop Science Society of America, Madson, WI, pp. 571-577.

Custódio, C.C., D.C. Bomfim, S.M. Saturnino and N.B. Machado Neto. 2002. Estresse por alumínio e por acidez em cultivaresde soja. Scientia Agricola 59: 145-153.

Dabholkar, A.R., 1992. Elements of Biometrical Genetics. Concept Publ. Camp., New Delhi, India.

Darko, E., H. Ambrus, E. Stefanovits-Banyai, J. Fodor, F. Bakos and B. Barnanas. 2004. Aluminium toxicity, Al tolerance and oxidative stress in Al-sensitive wheat genotype and in Al-tolerant lines developed by in vitro microscopore selection. Plant Science 166: 583-591.

Delhaize E., C.D. Craig Beaton, R.J. Bennet, V.C. Jagadish and P.I. Randall. 1993. Aluminium tolerance in wheat (*Triticum aestivum).* Plant Physiology 103: 685-693.

Delhaize, E., P.R. Ryan, D.M. Hebb, Y. Yamamoto, T. Sasaki and H. Matsumoto. 2004. Engineering high level aluminium tolerance in barley with the ALMT1 gene. Proceedings of the National Academy of Sciences of the USA 101: 15249-15254.

Dudley, J.W. and R.H. Moll. 1969. Interpretation and use of estimates of heritability and genetic variance in plant breeding. Crop Science 9: 257-262.

Duque-Vargas, J., S. Pandey, G. Granador, G., Ceballos H. and E. Knapp. 1994. Inheritance of tolerance to soil acidity in tropical maize. Crop Science 34: 50-54.

Eberhart, S.A. and W.A. Russel. 1966. Stability parameters for comparing varieties. Crop Science 6: 36-40.

El-Badawy, M.E.M. 2013. Heterosis and Combining Ability in Maize using Diallel Crosses among Seven New Inbred Lines. Asian Journal of Crop Science 5: 1-13.

Ezaki, B., R.C. Gardner, Y. Ezaki and H. Matsumoto. 2000. Expression of aluminium-induced genes in transgenic Arabidopsis plants can ameliorate aluminium stress and/or oxidative stress. Plant Physiology 122: 657-666.

Ezaki, B., S. Tsugita and H. Matsumoto. 1996. Expression of a moderately anionic peroxidase is induced by aluminium treatment in tobacco cells: possible involvement of peroxidase isoenzymes in aluminium ion stress. Physiologia Plantarum 96: 21-28.

Falconer, D.S. 1989. Introduction to Quantitative Genetics, 3rd Ed. Longmans Green/John Wiley & Sons, Harlow, Essex, UK/New York.

Falconer, D.S. and T.F.C. Mackay. 1996. Introduction to Quantitative Genetics, 4th Ed. Longmans Green, Harlow, Essex, UK.

FAOSTAT. 2007. Food and Agriculture Organization Statistical Database. FAO.

FAOSTAT. 2010. Food and Agriculture Organization Statistical Database: http// faostat.fao.org.

Ferreira, R.P., A. Moreira and J.B. Rassini. 2006. Toxidez de aluminio em culturas anuais. Sao Carlos: Embrapa Pecuaria Sudeste. (Embrapa Pecuaria Sudeste. Documentos 63). pp. 35.

Finlay, K.W. and G.N. Wilkinson. 1963. The analysis of adaptation in plant breeding programme. Australian Journal of Agricultural Research 14: 742-754.

Flintham, J.E., W.J. Angus and M.D. Gale. 1997**.** Heterosis, over dominance for grain yield, and alpha-amylase activity in $F_1$-hybrids between near isogenic *Rhl* dwarf and tall wheats. Journal Agriculture Science 129: 371-378.

Foy, C.D. 1988. Plant adaptation to acid aluminium-toxic soils. Communications in Soil Science and Plant Analysis 19: 959-987.

Freeman, G.H. 1973. Statistical methods for the analysis of genotype x environment interactions. Heredity 31: 339-354.

Furukawa, J., N. Yamaji, H. Wang, N. Mitani, Y. Murata, K. Sato, M. Katsuhara, K. Takeda and J.F. Ma. 2007. An aluminium-activated citrate transporter in barley. Plant and Cell Physiology 48:1081-1091.

Garcia Júnior, O. and W.J. Silva. 1979. Análise genética da tolerância ao alumínio em milho. Ciênc. Cult. 31**:** 585.

Gaspar, T.H., C. Penel and H.A. Greppin. 1985. A two-step control of basic and acidic peroxidases and its significance for growth and development. Physiologia Plantarum 64: 418-423.

Gauch, H.G. 1990. Using interaction to improve yield estimates. In: M.S. Kang (Ed.) Genotypes x environment interaction and plant breeding. Department of Agronomy. Louisiana State University, Batonrouge, Louisiana, pp. 141-150.

Gauch, H.G. 1993. Prediction, parsimony and noise. American Scientist 81:468-478.

Gauch, H.G and R.W. Zobel. 1996. AMMI analysis of yield trials. In: M.S. Kang and H.G. Gauch (Eds.) Genotype by environment interaction. CRC Press, Boca Raton, New York, pp. 85 -122.

Gouis, J. 2002. Genetic Improvement of Nutrient Use Efficiency in Wheat, In: The Molecular and Physiological Basis of Nutrient Use Efficiency in Crops (eds. M. J. Hawkesford and P. Barraclough), Wiley-Blackwell, Oxford, UK.

Gowda, R., 2013. Combining Ability Studies in Maize (*Zea mays* L.). Molecular Plant Breeding 3: 116-127.

Granados, G., S. Pandey and H. Ceballos. 1993. Response to selection for tolerance to acid soils in a tropical maize population. Crop Science 33: 936-940.

Griffing, B. 1956. Concept of General and Specific Combining Ability in relation diallel crossing systems. Australian Journal of Biological Sciences 9: 463-493.

Guimarães, J.T.F., M.C.L. Cohen, L.C.R. Pessenda, M.C. França, C.B. Smith and A.C.R. Nogueira. 2012. Mid- and late-Holocene sedimentary process and palaeovegetation changes near the mouth of the Amazon River. The Holocene 22: 359-370.

Hamel, F., C. Breton and M. Houde. 1998. Isolation and characterization of wheat aluminium-regulated genes: possible involvement of aluminium as a pathogenesis response elicitor. Planta 205:531-538.

Hartl, D.L. and A.G. Clark, 1989. Principles of population genetics (2nd Ed.). Snauer Associates, Inc. Publishers, Sunderland.

Hartwig, I., A.C. Oliveira, F.I.F. Carvalho, I. Bertan, J.A.G. Silva, D.A.M. Schnidt, I.P. Valerio, L.C. Maia, D.A.R. Fonseca and C.E.S. Reis. 2007. Mecanismos associados à tolerância ao alumínio em plantas. Semina: Ciências Agrárias 28: 219-228.

Hassan, R.M. 1998. Maize Technology Development and Transfer: A GIS Application for Research Planning in Kenya. CAB International.

Heinrich, G.M., C.A. Francis and J.D. Eastin. 1983. Stability of grain sorghum yield components across diverse environments. Crop Science 23**:** 209-212.

Huang, C.F., N. Yamaji, N. Mitani, M. Yano and Y. Nagamura. 2009. A bacterial-type ABC transporter is involved in aluminium tolerance in rice. Plant Cell 21: 655-667.

Jansen, S., M.R. Broadley, W. Robbrecht and E. Smets. 2002. Aluminium hyper-accumulation in angiosperms: a review of its phylogenetic significance. The Botanical Review 68: 235-269.

Jones, D.L., E.B. Blancaflor, L.V. Kochian and S. Gilroy. 2006. Spatial coordination of aluminium uptake, production of reactive oxygen species, callus production and wall rigidification in maize roots. Plant, Cell and Environment 29: 1309-1318.

Kang, M.S. 1996. Using genotype by environment interaction for crop cultivar development. Advances in Agronomy 62: 199-252.

Kang, M.S., D.P. Gorman and H.N. Pham. 1991. Application of stability statistic to international maize yield trials. Theoretical and Applied Genetics 81: 162-165.

Khatiwada, S.P., D. Senadhira, A.L. Carpena, R.S. Zeigler and P.G. Fernandez. 1996. Variability and genetics of tolerance for aluminium toxicity in rice (*Oryza sativa* L.) Theoretical and Applied Genetics 93: 738-744.

Kochian, L.V. 1995. Cellular mechanisms of aluminium toxicity and resistance in plants. Annual Review of Plant Physiology and Plant Molecular Biology 46: 237–260.

Kochian, L.V., M.A. Peneros, and O.A. Hoekenga. 2005. The physiology, genetics and molecular biology of plant aluminium resistance and toxicity. Pant Soil 274: 75-195.

Kochian, L.V., O.A. Hoekenga and M.A. Pineros. 2004a. How do crop plants tolerate acid soils? Mechanisms of aluminium tolerance and phosphorous efficiency. Annual Review of Plant Biology 55: 459-493.

Kochian, L.V., M.A. Peneros and O.A. Hoekenga. 2004b. The physiology, genetics and molecular biology of plant aluminium resistance and toxicity. Plant and Soil 274: 175-195.

Kurawa, I.A. 2012. Genetic analysis of progenies from diallel crosses among eight varieties of different maturity groups of maize. Ahmadu Bello University, Zaria Nigeria.

Lagos, M.B., M.I.M. Fernandes, C.E.O. Camargo, L.C. Federizzi and F.I.T. Carvalho. 1991. Genetics and monosomic analysis of aluminium tolerance in wheat (*Triticum aestivum* L.). Brazilian Journal of Genetics 14: 1011-1020.

Lamkey, J.R. and J.W. Edwards. 1999. Quantitative genetics of heterosis. In: J.G. Coors and S. Pandey (Eds.). The Genetics and Exploitation of Heterosis American Society of Agronomy and Crop Science, USA, pp. 31-48.

Lin, C.S. and M.R. Binns. 1988. A superiority measure of cultivar performance for cultivar x location data. Canadian Journal Plant Science 68: 193-198.

Lin, C.S., M.R. Binns and L.P. Lefkovitch. 1986. Stability analysis: Where do we stand? Crop Science 26: 894-900.

Liu, J., J.V. Magalhaes, J. Shaff and L.V. Kochian. 2009. Aluminium-activated citrate and malate transporters from the MATE and ALMT families function independently to confer Arabidopsis aluminium tolerance. The Plant Journal 57: 389-399.

Liu Yong-jian, I., Duan Chuan, Tian Meng-liang, Hu Er-liang and Huang Yu-bi1. 2010. Yield Stability of Maize Hybrids Evaluated in Maize Regional Trials in Southwestern China Using Nonparametric Methods. Agricultural Sciences in China. 9: 1413-1422.

Lopes, MA, R. Magnavaca A.F.C. Bahia Filho and E.E.G. Gama. 1987. Avaliação de populações de milho e seus cruzamentos para tolerância a toxidez de alumínio em solução nutritiva. Pesq Agropec Bras 22:257-263.

Ma, J.F. and P.R. Ryan. 2010. Understanding how plants cope with acid soils. Functional Plant Biology 37: 3-6.

Ma, J.F., P.R. Ryan and E. Delhaize. 2001. Aluminium tolerance in plants and the complexing role of organic acids. Trends in Plant Science 6: 273-278.

Ma, J.F., S. Nagao, K. Sato, H. Ito, J. Furukawa and K. Takeda. 2004. Molecular mapping of a gene responsible for Al-activated secretion of citrate in barley. Journal of Experimental Botany 55: 1335-1341.

Magalhaes, J.V., J. Liu, C.T. Guimaraes, U.G.P. Lana, V.M.C. Alves, Y.H. Wang, , R.E. Schaffert, O.A. Hoekenga, M.A. Pineros and J.E. Shaff. 2007. A gene in the multidrug and toxic compound extrusion (MATE) family confers aluminium tolerance in sorghum. Nature Genetics 39: 1156-1161.

Magnavaca, R., R.C.O. Gardner and R.B. Clark. 1987. Inheritance of aluminium tolerance in maize. In: Galbelman, H.W. and B.C. Loughman (Eds.) Genetic aspects of plant mineral nutrition. Martinus Nijhoff, Dordrecht, pp. 201-211.

Maron, L.G., M.A. Pineros, C.T. Guimaraes, J.V. Magalhaes, J.K. Pleiman, C. Mao, J. Shaff, S.N.J. Belicuas and L.V. Kochian. 2009. Two functionally distinct members of the MATE (multi-drug and toxic compound extrusion) family of transporters potentially underlying two major aluminium tolerance QTLs in maize. The Plant Journal 61: 728-740.

Mather, K. and J.I. Jinks, 1977. Introduction to Biometrical Genetics. Chapman and Hall, London, UK.

Matthews, G.A., W. P. Williams and C. A. Daves. 2008. Diallel Analysis of Corn Earworm (Lepidoptera: Noctuidae) Resistance in Maize. Journal of Agricultural and Urban Entomology 24: 59-66.

Matzinger, D.F. 1963. Experimental estimates of genetic parameters and their applications in self-fertilizing plants. In: W.D. Hanson and H.F. Robinson (Eds.), Statistical genetics and plant breeding no. 982. NAS-NRC.

Meredith, W.R. Jr. 1984. Quantitative Inheritance. In: R.J. Kohel and C.F. Lewis (Eds.) Madison, WI. pp 131-150

Miftahudin, S.G.J. and J.P. Gustafson. 2002. AFLP markers tightly linked to the aluminium-tolerance gene Alt3 in rye (*Secale cereale* L.). Theoretical and Applied Genetics 104: 626-631.

Minella, E. and M.E. Sorrells. 1992. Aluminium tolerance in barley: Genetic relationships among genotypes of diverse origin. Crop Science 32: 593-598.

Minella, E. and M.E. Sorrells. 1997. Inheritance and chromosome location of *Alp*: a gene controlling aluminium tolerance in 'Dayton' barley. Plant Breeding 116: 465-469.

Miranda L.T., P.R. Furlani, L.E.C. Miranda and E. Sawazaki. 1984. Genetics of environmental resistance and super genes: Latente aluminium tolerance. The Maize Genetics Cooperation Newsletter 58: 46-48.

Moon, D.H., L.M.M. Ottoboni, A.P. Souza, S.T. Sibov, M., P. Gaspar and P. Arruda. 1997. Somaclonal-variation-induced aluminium-sensitive mutant from an aluminium-inbred maize tolerant line. Plant Cell Reports 16: 686-691.

Morris, M.D., J.M. Ribaut and M. Khairallah. 2003. Money matters (II): Costs of maize inbred line conversion schemes at CIMMYT using conventional and marker-assisted selection. Molecular Breeding 11: 235-247.

Murtaza, N., M. Kitaoka and G.M. Ali. 2005. Genetic differentiation of cotton cultivars by polyacrylamide gel electrophoresis. Journal Central Europe Agriculture 6: 69-76.

Nguyen, V.T., S. Nguyen, B.D.S. Sarkarung, C. Martinez, A.H. Paterson and H.T. Nguyen. 2002. Mapping of genes controlling aluminium tolerance in rice: Comparison of different genetic backgrounds. Molecular Genetics 267: 772-780.

Ninamango-Cárdenas, F.E., C.T. Guimarães, P.R. Martins, S.N. Parentoni, N.P. Carneiro, M.A. Lopez, J.R. Moro and E. Paiva. 2003. Mapping QTLs for aluminium tolerance in maize. Euphytica 130: 223-232.

Oliveira, B.C.F.S., P.M.A. Moura, B.H. Macie, C.T. Guimaraes, F.F. Canaito, R.E. Schaffert, S.C Jr. Fonseca, S.N. Jardim-Belicuas and J.V. Magalhaes. 2010. Utilizacao de marcadores moleculares na selecao assistidac para tolerancia ao aluminio em sorgo. Sete lagos: (Embrapa Milho e sorgo. Circular Tecnica, 155 p7)

Panda, S.K., F. Baluska and H. Matsumoto. 2009. Aluminium stress signalling in plants. Plant signalling and behaviour 4: 592-597.

Pandey, S. and C.O. Gardner. 1992. Recurrent selection for population, variety and hybrid improvement in tropical maize. Advances in Agronomy 48: 1-87.

Parentoni, S.N., V.M.S. Alves, A.C. Oliveira, J. Magalhaes, A.M. Coelho, E. Schaffert, C.T. Guimaraes, E.E.G. Gama, C.L. Godoy, M.X. Santos, P.E.O. Guimaraes, C.A.P. Pacheo, W.P. Meirelles, P.H.E. Ribeiro, G.V.E. Pita and A.F.C. Bahia Filho. 2003. Genetics of aluminium tolerance in maize evaluated in nutrient solution with and without control experiments. In: International symposium of plant breeding, Mexico, 2003. Book of abstracts. Mexico: CIMMYT.

Parentoni, S.N., V.M.S. Alves, S.K. Milah, G.M.A. Cançado and A.F.C. Bahia Filho. 2001. Melhoramento para toerancia ao aluminio como fator de adapatacao a solos acidos. In: Nass L et al (Eds.) Recursos geneticos e melhoramento. Randonopolis, Fundacao MT, pp. 783-852.

Peixoto, C.J., R.C. Alves and L.C. Cameron. 2007. Glutamine and carbohydrate supplements reduce ammonemia increase during endurance field exercise. Universidade Federal do Estado do Rio de Janeiro, Brazil.

Peixoto, P.H.P., J. Cambraia, R. Sant'anna, P.R. Mosquim and M.A. Moreira. 2001. Aluminum effects on fatty acid composition and lipid peroxidation of a purified plasma membrane fraction of root apices of two sorghum cultivars. Journal of Plant Nutrition 24: 1061-1070.

Pickett, A.A. 1993. Hybrid Wheat – Results and Problems. Journal of Agricultural Science 12: 294-294.

Piñeros, M.A., J.E. Shaff, H.S. Manslank, V.M. Carvalho Alves and L.V. Kochian. 2005. Aluminum Resistance in Maize Cannot Be Solely Explained by Root Organic Acid Exudation. A Comparative Physiological Study. Plant Physiology 137: 231-241.

Piñeros, M.A., J.V. Magalhaes, V.M. Carvalho Alves and L.V. Kochian. 2002. The physiology and biophysics of an aluminium tolerance mechanism bases on root exudation in maize. Plant Physiology 129:1194-1206.

Pirchner, F. 1979. Populationsgenetik in der Tierzucht. 2. Aufl-, Paul Parey, Hamburg and Berlin, German.

Prioli, A.J. 1987. Análise genética da tolerância à toxidez ao alumínio em milho (*Zea mays* L.). Campinas, (Doctoral Thesis in Plant Genetics) – Universidade Estadual de Campinas.

Purchase, J.L. 1997. Parametric analysis to describe G x E interaction and yield stability in winter wheat. PhD Thesis. Department of Agronomy, Faculty of Agriculture, University of Orange Free State, Bloemfontein, South Africa. pp 4-83.

Ramagosa, I. and P.N. Fox, 1993. Genotype x environmental interaction and adaptation. In: M.D. Hayward, N.O. Bosemark and I. Ramagosa (Eds.) Plant Breeding: Principles and Prospects. Chapman and Hall, London, pp. 373-390.

Rengel, Z. 1996. Uptake of aluminium by plant cells. New Phytologist 134: 389-406.

Rengel, Z. and W.H. Zhang. 2003. Role of dynamics of intracellular calcium in aluminium-toxicity syndrome. New Phytologist 159: 295-314.

Rhue, R.D., C.O. Grogan, E.W. Stockmeyer and H.L. Everett. 1978. Genetic control of aluminium tolerance in corn. Crop Science 18: 1063-1067.

Roy, A.K., A. Sharma and G. Taludker. 1988. Some aspects of aluminium toxicity in plants. Botanical Review 54: 145-147.

Ryan, P.R., E. Delhaize and D.L. Jones. 2001. Function and mechanism of organic anion exudation from plant roots. Annual Review of Plant Physiology and Plant Molecular Biology 52: 527–560.

Ryan, P.R., J.M. DiTomaso and L.V. Kochian. 1993. Aluminium toxicity in roots: an investigation of spatial sensitivity and the role of the root cap. Journal of Experimental Botany 44: 437-446.

Salazar, F. S., S. Pandey, L. Narro, J. C. Perez, H. Ceballos, S.N. Parentoni and A.F.C. Bahia-Filho. 1997. Diallel Analysis of Acid-Soil Tolerant and Intolerant Tropical Maize Populations. Crop Science 37: 1457-1462.

Samac, D.A. and M. Tesfaye. 2003. Plant improvement for tolerance to aluminium in acid soils - review. Plant Cell, Tissue and Organ Culture 75: 189-207.

Sasaki, T., Y. Yamamoto, B. Ezaki, M. Katsuhara, S.J. Ahn, P.R. Ryan, E. Delhaize and H. Matsumoto. 2004. A wheat gene encoding aluminium – activated malate transporter. The Plant Journal 37: 645-653.

Sawasaki, E. and P.R. Furlani.1987. Genetica da tolerancia ao aluminio em milho cateto. Bragantia 46: 269-278.

Sherf, B.A., A.M. Bajar and P.E. Kolattudkudy. 1993. Abolition of an inducible highly anionic peroxidase activity in transgenic tomato. Plant Physiology 101: 201-208.

Shukla, A.G.K. 1972. Some statistical aspects of partitioning genotype-environment components of variability. Heredity 29: 237-245.

Sibov, S.T., M. Gaspar, M.J. Silva, L.M.M. Ottoboni, P. Arruda and A.P. Souza. 1999. Two genes control aluminium tolerance in maize: genetic and molecular mapping analyses. Genome 42: 475-482.

Silva, I., T. Smyth, D. Moxley, T. Carter, N. Alen and T. Rufty. 2000. Aluminium accumulation at nuclei of cells in the root tips. Fluorescence detection using lumogallion and confocal laser scanning microscopy. Plant Physiology. 123: 543-552.

Sivaguru, M., T. Fujiwara, J. Amaj, F. Baluka, Z. Yang, H. Osawa, T. Maeda, T., Mori, D. Volkmann and H. Matsumoto. 2000. Aluminum-induced 1®3-b-D-glucan inhibits cell-to-cell trafficking of molecules through plasmo-desmata. A new mechanism of aluminium toxicity in plants. Plant Physiology. 124:991-1005.

Spehar C.R. 1995. Diallel analysis for mineral element absorption in tropical adapted soybeans [*Glycine max* (L.) Merrill]. Theoretical and Applied Genetics. 90:707–713

Spehar C.R. and N.W. Galwey. 1996. Diallel analysis for aluminium tolerance in tropical soybeans [Glycine max (L.) Merrill]. Theoretical and Applied Genetics 92:267–272.

Sprague, G.F. and L.A. Tatum. 1942. General Versus Specific Combining Ability in a single cross of corn. Journal of American Society of Agronomy 34: 923-932.

Sughrone, J.R. and A.R. Hallauer. 1997. Analysis of the diallel mating design for maize inbred lines. Crop Science 37: 400-405.

Suhayda, C.G. and A. Haug. 1995. Citrate chelation as a potential mechanism against aluminium toxicity in cells: The role of calmodulin. Canadian Journal of Biochemistry Cell Biology 63: 1167-1175.

Tang, Y., M.E. Sorrells, L.Y. Kochian and D.G. Garvin. 2000. Identification of RFLP markers linked to the barley aluminium tolerance gene *Alp*. Crop Science 40: 778-782.

Taylor, G.J. 1988. The Physiology of Aluminium Tolerance in higher plants. Communications in Soil Science and Plant Analysis 19: 1179-1194.

Torres, G.A, S.N. Parentoni, M.A. Lopes and E. Paiva. 1997. A search for RFLP markers to identify genes for aluminium tolerance in maize. Brazilian Journal of Genetics 20: 459-465.

Vitorello, V.A., F.R. Capaldi and V.A. Stefanuto. 2005. Recent advances in aluminium toxicity and resistance in higher plants. Brazilian Journal of Plant Physiology 17: 129-143.

Vivek, B.S., O. Odongo., J. Njuguna, J. Imanywoha, G. Bigirwa, A. Diallo and K. Pixley. 2009. Diallel analysis of grain yield and resistance to seven diseases of 12 African maize (*Zea mays* L.*)* inbred lines. Euphytica 172: 329-340.

Von Uexküll, H.R. and E. Mutert. 1995. Global extent, development and economic impact of acid soils. In: R.A. Date, N.J. Grundon, G.E. Raymet and M.E. Probert (Eds.) Plant-Soil Interactions at Low pH: Principles and Management, . Dordrecht, The Netherlands, Kluwer Academic, pp. 5-19.

Walter, M.H. 1992. Regulation of lignification in defence. In: T. Boller, F. Meins, Eds, Genes involved in Plant Defence. Springer Verlag, New York, pp 327-352.

Wricke, G. 1962. Über eine method zur erffassung der okologischen Strubreite in feldversuchen. Z.Pflanzenzüchtg.47: 92-96.

Wu, P., B. Zhao, J. Yan, A. Luo, Y. Wu and D. Senadihra. 1997. Genetic control of seedling tolerance aluminium toxicity in rice. Euphytica 97: 289-293.

Wu, P., C.Y. Liao, B. Hu, K.K. Yi, W.Z. Jin, J.J. Ni and C. He. 2000. QTLs and epistasis for aluminium tolerance in rice at different seedling stages. Theoretical and Applied Genetics 100: 1295-1303.

Xia, J.X., N. Yamaji, T. Kasai and J.F. Ma. 2010. Plasma membrane-localized transporter for aluminium in rice. Proceedings of the National Academy of Sciences of the USA 107: 18381–18385.

Xue, Y.J., Tao, I. and Z.M. Yang. 2008. Aluminium induced cell wall peroxidase activity and lignin synthesis are differentially regulated by jasmonate and nitric oxide. Journal of Agricultural and Food Chemistry 56: 9676-9684.

# CHAPTER 3

## A hydroponic nutrient solution experiment for testing low pH tolerance in tropical and sub-tropical maize genotypes

### 3.1 Abstract

Low pH soil is a major constraint to maize production by resource-poor farmers due to toxic levels of $Al^{3+}$ and P fixation. Selecting tolerant maize genotypes under low pH soil in the field is confounded by associated external factors like diseases. In this study, 70 maize genotypes were evaluated in a hydroponic nutrient solution experiment at Chitedze Research Station in a glasshouse. The objective was to identify tolerant genotypes to the presence of $KAl(SO_4)_2$ in a nutrient solution as a proxy to low pH soil conditions. A completely randomised design (CRD) with four replicates was used. Significant differences ($p<0.05$) were observed for initial seminal root length (ISRL), final seminal root length (FSRL), root tolerance index (Rti) and net seminal root length (NSRL). In terms of FSRL the genotype sum of squares contributed 91.1% of variation and this was supported by a heritability value of 92%. The environmental influence contribution was low (7.6%). The NSRL, which represented the effective root growth or elongation during the experimental period varied significantly ($p<0.05$) among the maize genotypes tested. The sum of squares for genotypes contributed 58.3% to the total variation. The heritability was 74% implying that the phenotypic differences among the maize genotypes in terms of NSRL were due to genetic differences. In terms of NSRL, genotypes IWD C3 SYN F2-B, VPO52, and LPHpop4 were considered tolerant, and DT-YSTR SYNTHETIC-B, TZE-W POP DTC2 STR-B, TZE-YDT STR C4-B, LPHpop3, LPHpop13 and LPHpop14 were sensitive to Al toxicity. The tolerant genotypes identified in this study will be used in the National Maize Breeding Programme as source populations to develop new low pH tolerant parental inbred lines.

### 3.2 Introduction

Acid soils generally have low pH, contain toxic levels of Al and Mn and are deficient in Ca, Mg, P, potassium (K), and Mo. These characteristics are known to limit the fertility of

acid soils (Duque-Vargas *et al.*, 1994). Al is a major soil constituent and its toxicity is observed in most acid soils where the pH levels are below 5.5. Low pH is a major constraint to production of maize and other crops on tropical soils. Al toxicity is reported to inhibit the growth of crop plants on approximately 40% of the earth's potentially arable soils (Manyowa *et al*., 1988). At low pH (pH<5) toxic $Al^{3+}$ ions are released into the soil, and hinder root growth, this greatly affects the development of the entire plant (Kochian, 1995; Kidd and Proctor, 2000). Al toxicity causes short, thick and under developed roots and plants. This significantly reduces nutrient uptake and increases susceptibility to drought (Sasaki *et al.,* 1996). More than eight million ha of acid soils are planted to maize in the tropics (Pandey *et al.,* 1994) and soil acidity reduces yield by about 10% of the maize produced in the developing countries (Borrero *et al.,* 1995).

Soil acidity is becoming common in most parts of Malawi and is limiting crop production. Continuous cultivation and burning of crop residues during land preparation has contributed to the problem. More acid soils occur in the high rainfall areas (>1000 mm per year) with moderate to high leaching, whereas the alkaline soils occur in low rainfall areas (< 500 mm per year). The bulk of very acid soils are located in Lilongwe, Mzuzu and Blantyre ADDs. Chilimba (1994) reported higher Al saturation percentages in Nkhatabay, Mulanje, Bembeke and Lunyangwa. The soils database prepared by the Soils Commodity Team indicated that over 40% of the country has soil pH less than 5.5 (Munthali, 2007).

Considerable genetic tolerance to soil acidity is expressed in maize (Piñeros and Kochian, 2001). In addition, extensive genetic variability with respect to Al tolerance exists in plants both at inter and intraspecific levels (Ishikawa and Wagatsuma, 1998). In maize, the majority of commercial genotypes are sensitive to Al toxicity, such that breeding for more adapted cultivars seems to be the best strategy to improve farming of this crop in regions with acid soils.

### 3.2.1 Hydroponic nutrient solution

Trejo-Téllez and Gómez-Merino (2012) defined a nutrient solution for hydroponic systems as an aqueous solution containing mainly inorganic ions from soluble salts of essential elements for higher plants. A hydroponic system of cultivation refers to growing plants in

water containing dissolved nutrients (therefore without soil). Currently 17 elements are considered essential for most plants, these are carbon (C), hydrogen (H), oxygen ($O_2$), sulphur (S), copper (Cu), zinc (Zn), boron (B), chlorine (Cl), nickel (Ni), N, K, P, Ca, Mg, Fe, Mn, and Mo (Salisbury and Ross, 1992). With the exception of C and $O_2$, which are supplied from the atmosphere, the essential elements are obtained from the growth medium.

### 3.2.2 Justification for use of hydroponic nutrient solution experiment

Conventional breeding methods take time and are influenced by environmental conditions and sometimes the expression of genes is masked by epistatic interactions, whereby the expression of a particular gene depends on another gene. Testing of maize for Al tolerance can be effectively done in the field if the environment (such as diseases and weather) can be manipulated and this could be expensive and time consuming considering the number of genotypes that need to be evaluated. Reports indicate that there are three efficient and less time consuming methods used: screening in nutrient solutions (Magnavaca *et al.,* 1987; Cançado *et al.,* 1999), potted soils (Ahlrichs *et al.,* 1990) and root staining with haematoxylin (Ruiz-Torres *et al.,* 1992). Among these three methods, nutrient solution screening seems to be attractive since it is less expensive and provides adequate Al stress, thereby allowing preliminary screening of a large number of genotypes in a small area and consequently reduces the number of promising genotypes to be analysed in the field (Magnavaca *et al*., 1987). In addition the results obtained with the solution culture screening method correlate positively with those obtained using field screening (Gomez-Urea *et al.,* 1996) showing that this method could be representative of what happens in the field. The effect of Al tolerance in nutrient solution culture could be quantified in terms of root length measurements. Early symptoms of Al toxicity occur in the root for obvious reasons as roots are in direct contact with toxic $Al^{3+}$ ions. Sensitive genotypes tend to accumulate higher amounts of Al in their root tissues (Carver *et al.,* 1988).

Al solution tests improve efficiency in selection for tolerance because there is effective control of environmental variations, which is difficult to achieve under field conditions. In the present study, $KAl(SO_4)_2$ was used as a proxy to low pH soil conditions and the nutrient composition was according to Magnavaca *et al.* (1987). The cost of liming low pH soils

and applying adequate P to a maize crop is beyond the reach of most small-scale farmers. Maize breeding for low pH tolerance could offer a solution. However, conventional breeding methods take time and are influenced by environmental conditions. A more suitable solution would be to select Al tolerant maize genotypes for use in acid soils which, in the long run, is less expensive, sustainable and more environmentally friendly. The Al solution test improves efficiency of selection for tolerance because there is effective control of environmental variations, which is difficult to achieve under field conditions. The objective of this study was to identify maize genotypes that are tolerant to low pH or Al toxicity.

## 3.3 Materials and methods

### 3.3.1 Experimental materials

Two hundred and ninety OPV maize genotypes were sourced in October 2010 from CIMMYT-Zimbabwe and CIMMYT-Colombia (267 and 23 genotypes, respectively). The genotypes which had adequate seed for both hydroponic and field trials were selected. Further selections were carried out based on grain texture (a preferred trait in Malawi) and important genetic variation based on their pedigrees which have pre-characterised attributes. This included QPM, maize tolerance to: drought, DM, MSV, striga as well as yellow and orange genotypes. Finally, a total of 70 OPVs including those released and commonly grown in Malawi were used in the hydroponic nutrient solution experiment to determine their response to Al toxicity in a hydroponic nutrient solution experiment (Table 3.1).

**Table 3.1 Description of the tropical and sub-tropical maize genotypes used in the study**

| | Pedigree | Origin | Pre-characterised traits |
|---|---|---|---|
| 1 | 99TZEFY-STR QPM CO-B | IITA | QPM, STR, yellow |
| 2 | DT-WSTR SYNTHETIC-B | IITA | DT, STR, white |
| 3 | DT-YSTR SYNTHETIC-B | IITA | DT, STR, yellow |
| 4 | EVDT-Y2000 STR QPM CO-B | IITA | DT, STR, yellow QPM |
| 5 | EVD-W 99 STR QPM CO-B | IITA | QPM, STR, white |
| 6 | IAR-FLINT-Q-B | IITA | Flint |
| 7 | IWD C3 SYN F2-B | IITA | White colour |
| 8 | LOW N POOL C3-B | IITA | Low N |
| 9 | MULTICOB EARLY DT –B | IITA | DT, multiple cobbing |
| 10 | OBA SUPER1(9021-18(IITA))-B | IITA | QPM |
| 11 | OBATANPA/IWDC2SYNF2/IWDC2SY | IITA | QPM |
| 12 | OBATANPA/IWDC2SYNF2/IWDC2SYNF2-B | IITA | QPM |
| 13 | OBATANPA/TZLCOMP4C3F2/TZLC | IITA | QPM |
| 14 | OBATANPA/TZLCOMP4C3F2/TZLCOMP4C3F2-B | IITA | QPM |
| 15 | POP66 SR/DMR-LSRY/DMR-LSRY | IITA | MSV, DM |
| 16 | POP66 SR/TZUTSR-WSGY/T | IITA | MSV, DM, white |
| 17 | SYN DTE STR-Y-B | IITA | DT, MSV, yellow |
| 18 | SYN DTE STY-W-B | IITA | DT, MSV, white |
| 19 | TZE COPM3 DTV C2 F2-B | IITA | DT |
| 20 | TZE E-WPOP X LD(SET2)-B | IITA | White |
| 21 | TZE-W POP DTC2 STR-B | IITA | DT, MSV, STR |
| 22 | TZE-WDT STR QPM-CO-B | IITA | DT, MSV,QPM, STR |
| 23 | TZE-YDT STR C4-B | IITA | MSV, DT, STR |
| 24 | TZE-YPOP DTC2 STR-B | IITA | DT, yellow, MSV, STR |
| 25 | VPO0721 | CMMYT Zimbabwe | GLS, LB, MSV |
| 26 | VPO5148 | CMMYT Zimbabwe | GLS, LB, MSV |
| 27 | VPO5173 | CMMYT Zimbabwe | GLS, LB, MSV |
| 28 | VPO5179 | CMMYT Zimbabwe | GLS, LB, MSV |
| 29 | VPO5187 | CMMYT Zimbabwe | GLS, LB, MSV |
| 30 | VPO52 | CMMYT Zimbabwe | GLS, LB, MSV |
| 31 | VPO627 | CMMYT Zimbabwe | GLS, LB, MSV |
| 32 | VPO630 | CMMYT Zimbabwe | GLS, LB, MSV |
| 33 | VPO710 | CMMYT Zimbabwe | GLS, LB, MSV |
| 34 | VPO712 | CMMYT Zimbabwe | GLS, LB, MSV |
| 35 | VPO716 | CMMYT Zimbabwe | GLS, LB, MSV |
| 36 | VPO717 | CMMYT Zimbabwe | GLS, LB, MSV |

| | | | |
|---|---|---|---|
| 37 | VPO738 | CMMYT Zimbabwe | GLS, LB, MSV |
| 38 | VPO739 | CMMYT Zimbabwe | GLS, LB, MSV |
| 39 | VPO741 | CMMYT Zimbabwe | GLS, LB, MSV |
| 40 | VPO743 | CMMYT Zimbabwe | GLS, LB, MSV |
| 41 | VPO744 | CMMYT Zimbabwe | GLS, LB, MSV |
| 42 | VPO76 | CMMYT Zimbabwe | GLS, LB, MSV |
| 43 | VPO86 | CMMYT Zimbabwe | GLS, LB, MSV |
| 44 | VPO96 | CMMYT Zimbabwe | GLS, LB, MSV |
| 45 | VPO97 | CMMYT Zimbabwe | GLS, LB, MSV |
| 46 | LPHpop4 = Cimcali 05B ROYA1 | CMMYT Colombia | low pH |
| 47 | LPHpop3 = Cerrito98SCMV2B(SA7)-#-B | CMMYT Colombia | low pH |
| 48 | LPHpop6 = Cimcali03HCG1A | CMMYT Colombia | low pH |
| 49 | LPHpop8 = GLSI01HG"A" | CMMYT Colombia | low pH |
| 50 | LPHpop9 = Granada 01Phaeo1AS2 | CMMYT Colombia | low pH |
| 51 | LPHpop10 = GRANADA01PHAE1AS1COGSCMV | CMMYT Colombia | low pH |
| 52 | LPHpop11 = ICAV-305 | CMMYT Colombia | low pH |
| 53 | LPHpop13 = PSA3 | CMMYT Colombia | low pH |
| 54 | LPHpop14 = S03TLYQAB05 | CMMYT Colombia | low pH |
| 55 | LPHpop15 = S03TLYQAB05 | CMMYT Colombia | low pH |
| 56 | LPHpop16 = VILLAVICENCIO01PHAEOIACLA | CMMYT Colombia | low pH |
| 57 | LPHpop17 = Villavicencio03Asp1C(LET-EARLY) | CMMYT Colombia | low pH |
| 58 | LPHpop18 = Menegua03Gloeo1C(S3) | CMMYT Colombia | low pH |
| 59 | LPHpop19 = Villavicencio03Phaeo1A | CMMYT Colombia | low pH |
| 60 | LPHpop20 = MENEGUA01PHAEO | CMMYT Colombia | low pH |
| 61 | LPHpop21 = Caicedonia00Phaeo1A | CMMYT Colombia | low pH |
| 62 | LPHpop23 = POB SIKUANI | CMMYT Colombia | low pH |
| 63 | LPHpop1 = Cap. Miranda 99Bact1F-1 | CMMYT Colombia | low pH |
| 64 | LPHpop2 = Cerrito98Achap2B-#-B | CMMYT Colombia | low pH |
| 65 | LPHpop7 = Cimcali99BSCMVSA7Ac-#-B | CMMYT Colombia | low pH |
| 66 | LPHpop12 = menegua01cog1c(pob cog) | CMMYT Colombia | low pH |
| 67 | ZM309 (Msungabanja) | Malawi | DT, GLS MSV, LB |
| 68 | ZM523 (Mwayi OPV) | Malawi | DT, GLS MSV, LB |
| 69 | ZM623 | Malawi | GT, LB, MSV |
| 70 | ZM721 | Malawi | GT, LB, MSV |

**QPM = Quality protein maize, DT = drought, MSV = Maize Streak Virus, LB = Leaf Blight, GLS = Gray leaf spot, STR = Striga, SR = Streak, TZ = Tropical Zea, TZE = Tropical Zea Early, TZL = Tropical Zea Late, IWD = Intermediate White Dent, IAR = Institute of Agriculture Research, COMP = composite, VPO = Populations from Dr. Viveki's stock ID, CIMMYT-Zimbabwe, LPHpop = Low pH populations (a code to designate long pedigrees for populations) from CIMMYT-Colombia, and ZM = Popular OPVs released in Malawi, breeding stock originated from CIMMYT-Zimbabwe**

### 3.3.2 Experimental procedure and design

The study was carried out during the off season in October 2011 at the Chitedze Research Station. Hundred seeds were randomly counted out per genotype and these were washed with distilled water. The seeds were then sterilized in 1% sodium hypochlorite solution for 5 minutes and rinsed twice with distilled water. These seeds were germinated in groups of 20 between paper-sheets moistened with distilled water for 7 days, incubated at 27$^{o}$C for the first 3 days to allow good germination. After the 7 days roots and shoots were visible and ready for measurement (Figure 3.1A). The ISRL was measured from a random sample of 10 seedlings per genotype from the 20 seedlings per paper sheet. After measurements of the ISRL, all 20 seedlings were transplanted into plastic containers (Figure 3.1B). Four of the containers per genotype which represented replications were placed in a glasshouse and seeds were grown for 7 days in 5 L aerated nutrient solution containing 6 ppm of Al in the form of $KAl(SO_4)_2$ (Magnavaca, 1982). The remaining container per genotype was used as a control in which only the nutrient solution was used i.e. no $KAl(SO_4)_2$. After 7 days from sowing the seedlings were transplanted on plastic gauze with a fine mesh so that only the roots of the seedlings were immersed in the nutrient solution. The procedure was to open the plastic gauze with a tweezer and insert the roots until they are in contact with the solution.


A: Germination in moistened paper after 7 days

B: 7 days after transplanting in $KAl(SO_4)_2$

**Figure 3.1 Germination of maize genotypes in news prints paper and appearance 7 days after transplanting**

### 3.3.3 Nutrient solution preparation

The composition of nutrient solutions used for growth of maize genotypes was as described by Magnavaca (1987) (µmol element $l^{-1}$): 10 900 $NO_3$-N; 3500 Ca; 2300 K; 1300 $NH_4$-N; 850 Mg; 590 S; 590 Cl; 25 B; 9.1 Mn; 2.29 Zn; 0.88 Mo; 0.63 Cu; 77 Fe as ferric hydroxethylethylene diamine triacetate (FeHEDTA). Al was added to the nutrient solution as $KAl(SO_4)_2$ and P as $KH_2PO_4$. The pH was checked and adjusted to 4.0 using 0.1 M HCl.

### 3.3.4 Data collection, measurements and calculations of derived data

After 7 days, FSRL was measured in centimetres from a random sample of 10 seedlings per genotype per replication. The measurements were averaged and the mean ISRL and FSRL were used to calculate the relative seminal root length (RSRL) as derived data using the following equations:

i) $$RSRL = \frac{FSRL - ISRL}{ISRL}$$

ii) $$RTi = \frac{RSRL\ (Al^{+}\ \text{treated plants})}{RSRL\ (Al^{+}\ \text{control plants})}$$

iii) $$\%\ \text{Response} = \frac{RSRL\ (Al^{+}\ \text{treated plants})}{RSRL\ (Al^{+}\ \text{control plants})} \times 100$$

iv) $$NSRL = \frac{FSRL}{ISRL}$$

### 3.3.5 Statistical analysis

#### 3.3.5.1 Analysis of variance

The data was subjected to ANOVA using Agrobase (2010). ANOVAs for each measured parameter and derived data was carried out. A graph for NSRL with standard errors was plotted in Excel.

## 3.4 Results

### 3.4.1 Observed symptoms of aluminium toxicity

The presence of Al in the nutrient solution caused a delay in the vegetative growth of some maize genotypes with reduced development of new leaves and decreased development of shoots. Al toxicity symptoms were evident after 3 days from transplanting, such as lateral root shortening, darkening and stunting. The maize genotypes DT-YSTR SYNTHETIC-B, TZE-W POP DTC2 STR-B, TZE-YDT STR C4-B, LPHpop3, LPHpop13, and LPHpop14 were sensitive to Al with a minimum NSRL of 0.6 cm each. Purple colour and interveinal leaf chlorosis was observed in shoots of Al-stressed maize plants in the susceptible genotypes after 7 days from transplanting (Figure 3.2).

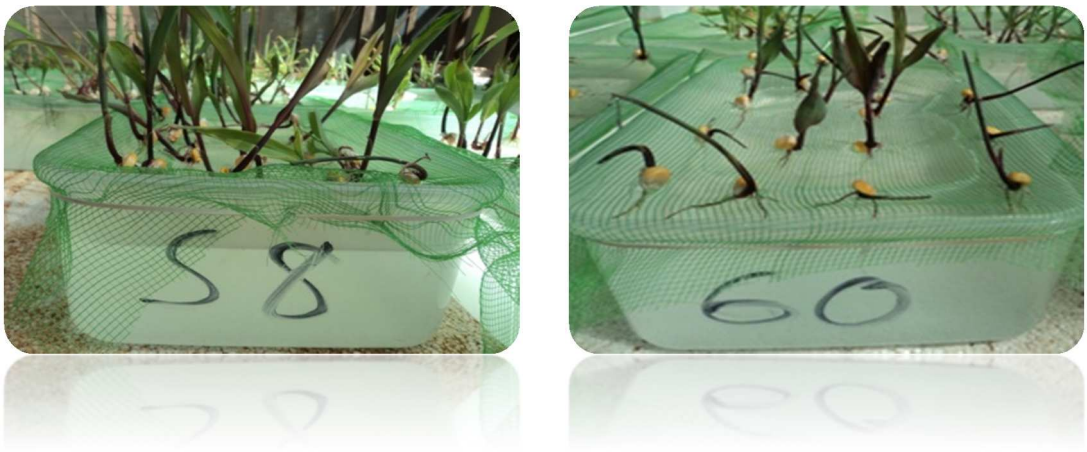


**Figure 3.2 Partial view of purple colouration and shortened roots observed in susceptible genotypes**

In some susceptible genotypes purple-green colour (depicting P deficiency) and chlorosis were observed. On the other hand the maize genotypes IWD C3 SYN F2-B (3.0 cm), VPO52 (3.5 cm) and LPHpop4 (3.0 cm), did not present severe symptoms of Al toxicity in their shoots (Figure 3.3).


**Figure 3.3 Partial view of new roots emerged from tolerant genotypes 7 days after transplanting**

### 3.4.2 Analysis of variance

Significant differences ($p<0.05$) were observed for FSRL, RTi and NSRL (Table 3.2). In terms of FSRL the results indicated that the contribution of genotype estimated using sum of squares was high (91.1%) and this was supported by a high heritability value of 96.0% (Table 3.2). The environmental influence was low (7.6%). The repeatability, which is derived from the coefficient of determination ($R^2$) was high (92.0%). This meant that the phenotypic differences between the genotypes in the trial were due to genotypic differences, hence little of the phenotypic differences were due to environmental effects. Genotypes VPO76, TZE-WDT STR QPM-CO-B, EVD-W 99 STR QPM CO-B, SYN DTE STY-W-B and LPHpop10 had long root lengths, values of 10.0, 9.4, 8.5, 8.5 and 8.1 cm respectively, while LPHpop7 and DT-YSTR SYNTHETIC-B had the shortest root length, values of 1.5 and 1.7 cm, respectively (Table 3.2; Appendix1).

RTi results indicated that the influence of the genetic component estimated using sum of squares (53.2%) was moderate and this was supported by a moderate heritability value of 56.0% (Table 3.2). Entries SYN DTE STY-W-B, LPHpop10, VPO717, VPO76 and

EVDT-Y2000 STR QPM CO-B had high root tolerance index values of 1.1, 1.0, 1.0, 0.9 and 0.8, respectively (Appendix 1). With respect to percent response as described in Section 3.3.5, results indicated that the influence of the genetic component estimated using sum of squares (54.3%) was moderate and this was supported by moderate heritability value of 58.0% (Table 3.2). Entries SYN DTE STY-W-B, LPHpop10, VPO717, VPO76 and EVDT-Y2000 STR QPM CO-B had a high percent response of 5.4, 4.0, 0.5, -9.0 and -15.7% respectively (Table 3.2; Appendix 1). Compared to the control plants, entry SYN DTE STY-W-B had the highest percent response and Rti of 5.4 and 1.1 respectively.

NSRL results indicated that the influence of the genetic component estimated using sum of squares (59.0%) was moderately high and this was supported by high heritability value of 74.0%. Entries VPO52, IWD C3 SYN F2-B, LPHpop4, ZM309, had the highest NSRL of 3.5, 3.0, 3.0, and 2.5 respectively (Table 3.2). NSRL which represented the effective root growth or elongation during the experimental period varied significantly ($P<0.05$) among the maize genotypes tested. The sum of squares for genotypes contributed 58.3% to the total variation. The heritability value from the ANOVA was 74% (Table 3.2) implying that the phenotypic differences among the maize genotypes in terms of NSRL were due to genetic differences. On average, the roots grew 1.3 cm in Al nutrient solution and the maximum was 3.5 cm. In the control, the roots grew 5.6 cm on average with a maximum of 11.5 cm. Thus there was a clear effect of Al toxicity on the maize genotypes (Appendix 1). VPO52 (3.5 cm) had the highest NSRL (Figure 3.4) followed by IWDC3SYNF2-B and LPHpop4 with 3.0 cm each.

No significant correlation was observed between NSRL and FSRL and Zero Al (control) treatments, as well as for percentage response versus Rti. The rest were all significantly ($P<0.01$) and positively correlated except NSRL vs ISRL which were significantly ($P<0.01$) and negatively correlated (Table 3.4).

**Table 3.2 Root length measurements and derived data before and 7 days after transplanting the glasshouse hydroponic experiment**

| | G | Pedigree | ISRL (cm) | FSRL (cm) | Zero Al (cm) | Rti | % response | RSRL Trtd (cm) | RSRL Zero Al (cm) | NSRL (cm) | Rank |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Top 10 | 30 | VPO52 | 1.37 | 3.45 | 4.37 | 0.79 | -21.13 | 2.47 | 3.30 | 3.47 | 1 |
| genotypes | 7 | IWD C3 SYN F2-B | 1.40 | 3.46 | 5.07 | 0.68 | -32.09 | 2.02 | 3.20 | 3.02 | 2 |
| | 46 | LPHpop 4 | 1.43 | 4.01 | 5.70 | 0.72 | -27.84 | 1.99 | 3.31 | 2.99 | 3 |
| | 67 | ZM309 | 0.78 | 1.84 | 3.40 | 0.61 | -38.53 | 1.50 | 3.82 | 2.50 | 4 |
| | 18 | SYN DTE STY-W-B | 3.43 | 8.49 | 8.20 | 1.05 | 5.37 | 1.49 | 1.39 | 2.49 | 5 |
| | 20 | TZE E-WPOP X LD(SET2)-B | 1.27 | 2.73 | 3.70 | 0.74 | -26.37 | 1.21 | 1.97 | 2.21 | 6 |
| | 1 | 99TZEFY-STR QPM CO-B | 2.85 | 4.99 | 6.73 | 0.74 | -25.87 | 1.19 | 2.03 | 2.19 | 7 |
| | 58 | LPHpop 18 | 1.37 | 2.36 | 3.97 | 0.62 | -38.38 | 1.10 | 2.74 | 2.10 | 8 |
| | 11 | OBATANPA/IWDC2SYNF2/IWDC2SY | 1.40 | 2.89 | 3.97 | 0.72 | -27.79 | 1.06 | 1.83 | 2.06 | 9 |
| | 37 | VPO738 | 1.87 | 3.48 | 4.17 | 0.84 | -16.62 | 1.03 | 1.43 | 2.03 | 10 |
| Bottom 10 | 68 | ZM523 | 3.27 | 2.45 | 4.53 | 0.54 | -46.28 | -0.25 | 0.41 | 0.75 | 61 |
| genotypes | 14 | OBATANPA/TZLCOMP4C3F2/TZLCOMP4C3F2-B | 3.83 | 2.56 | 4.77 | 0.56 | -43.75 | -0.26 | 0.36 | 0.74 | 62 |
| | 12 | OBATANPA/IWDC2SYNF2/IWDC2SYNF2-B | 3.93 | 2.81 | 4.47 | 0.64 | -36.22 | -0.27 | 0.19 | 0.73 | 63 |
| | 8 | LOW N POOL C3-B | 6.13 | 4.29 | 6.13 | 0.71 | -29.39 | -0.28 | 0.06 | 0.72 | 64 |
| | 54 | LPHpop 14 | 6.23 | 4.05 | 6.43 | 0.65 | -35.51 | -0.36 | 0.03 | 0.64 | 65 |
| | 23 | TZE-YDT STR C4-B | 5.23 | 3.21 | 4.67 | 0.80 | -20.35 | -0.38 | -0.07 | 0.62 | 66 |
| | 3 | DT-YSTR SYNTHETIC-B | 2.87 | 1.67 | 4.27 | 0.41 | -59.28 | -0.39 | 0.26 | 0.61 | 67 |
| | 21 | TZE-W POP DTC2 STR-B | 4.47 | 2.72 | 5.60 | 0.49 | -50.96 | -0.39 | 0.50 | 0.61 | 67 |
| | 47 | LPHpop 3 | 5.73 | 3.36 | 6.07 | 0.57 | -42.74 | -0.41 | 0.09 | 0.59 | 69 |
| | 53 | LPHpop 13 | 4.33 | 2.31 | 4.37 | 0.53 | -46.80 | -0.44 | 0.06 | 0.56 | 70 |
| | | **Mean** | **3.73** | **4.08** | **5.64** | **0.71** | **-29.09** | **0.32** | **0.89** | **1.32** | |
| | | **LSD** | **0.95** | **1.20** | **1.87** | **0.22** | **22.01** | **0.88** | **1.27** | **0.88** | |
| | | **Prob** | **0.001** | **0.00** | **0.001** | **0.00** | **0.001** | **0.001** | **0.001** | **0.00** | |
| | | **CV (%)** | **15.8** | **18.3** | **20.5** | **19** | **46.9** | **171.5** | **88.3** | **42** | |
| | | **Min** | **0.78** | **1.47** | **2.67** | **0.41** | **-59.28** | **-0.44** | **-0.07** | **0.56** | |
| | | **Max** | **10.10** | **9.99** | **11.50** | **1.05** | **5.37** | **2.47** | **3.82** | **3.47** | |
| | | **R-Squared** | **0.96** | **0.92** | **0.85** | **0.53** | **0.54** | **-** | **-** | **0.69** | |
| | | **Heritability** | **0.98** | **0.96** | **0.91** | **0.56** | **0.58** | **-** | **-** | **0.74** | |
| | | **MSE** | **0.35** | **0.56** | **1.34** | **0.02** | **185.90** | **0.30** | **0.61** | **0.30** | |

**LSD = Least significant difference, CV = coefficient of variation, Min = minimum, Max = maximum, MSE = Mean square error, G = genotype, ISRL = initial seminal root length; FSRL = final seminal root length; Zero Al = Zero Aluminium or control; RTi = root tolerance index; RSRLTRTD = relative seminal root length treated with aluminium; RSRLzero Al = relative seminal root length with zero aluminium; NSRL = net seminal root length.**

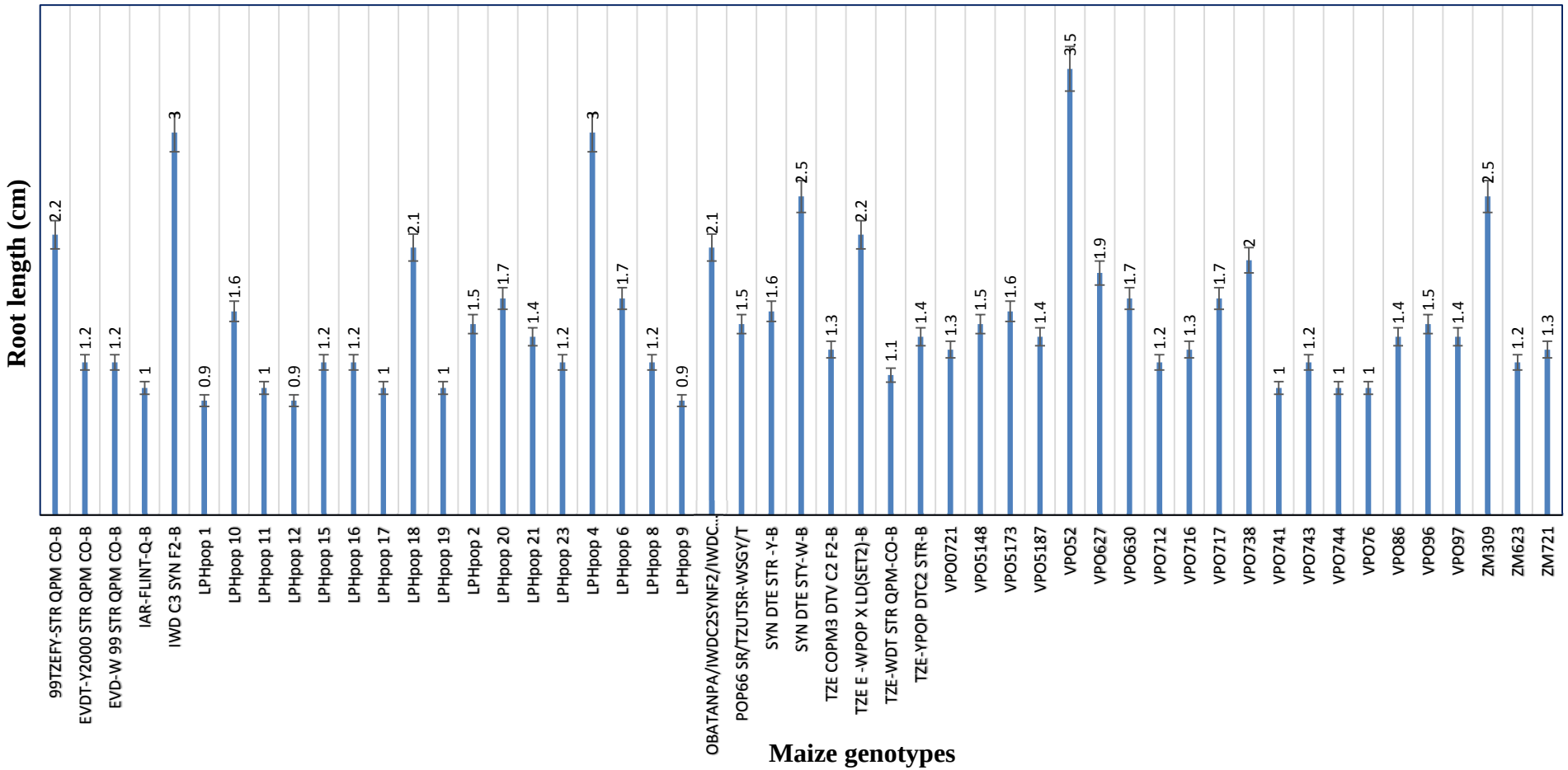


**Figure 3.4 Graph of nett seminal root length for genotypes**

**Table 3.3 Genetic and phenotypic variances and heritability estimates from ANOVA for the measured and derived data**

| | Variable | Genetic variance | Phenotypic variance | Broad-sense heritability | R-Squared | CV (%) | P for entry |
|---|---|---|---|---|---|---|---|
| 1 | ISRL | 4.78 | 5.18 | 0.90 | 0.95 | 17.2 | *** |
| 2 | FSRL | 4.28 | 4.80 | 0.89 | 0.92 | 18.3 | *** |
| 3 | NSRL | 0.27 | 0.57 | 0.47 | 0.69 | 41.5 | *** |
| 4 | Rti | 0.0086 | 0.027 | 0.32 | 0.54 | 19.2 | *** |
| 5 | % Response | 85.68 | 271.595 | 0.32 | 0.54 | 46.9 | *** |
| 6 | Al Control | 4.40 | 5.78 | 0.76 | 0.85 | 20.6 | *** |

**CV = coefficient of variation, ISRL= Initial seminal root length; FSRL = Final seminal Root length; NSRL = Net seminal root length; RTi = Root tolerance index; Al Control = Aluminium control, *** P for entry from ANOVA**

**Table 3.4 Pearson's coefficient of correlation among the measured and derived data**

| Variable | ISRL | FSRL | Zero Al(control) | Rti | % response |
|---|---|---|---|---|---|
| FSRL | 0.72** | | | | |
| Zero Al(control) | O.76** | 0.91** | | | |
| Rti | 0.22** | 0.56** | 0.19** | | |
| %Response | 0.22** | 0.56 | 0.19** | 1.00 | |
| NSRL | -0.49** | 0.08 | -0.03 | 0.27** | 0.27** |

****P≤0.01; ISRL = initial seminal root length; FSRL = final seminal root length; NSRL = net seminal root length; RTi = root tolerance index; Al control = aluminium control**

### 3.5 Discussion

The results indicated that after 7 days from transplanting into the hydroponic nutrient solution, there was a general reduction in root growth of all the tested genotypes at low pH of 4.0 and $KAl(SO_4)_2$. The change in colour from green to purple in susceptible genotypes could be attributed to low P stress as it is fixed under low pH conditions. Purple discolouration is among the key symptoms for P stress in maize plants. Al toxicity is reported to be responsible for significant changes in biochemical and structural patterns of plant cells reflecting on reduction of cell multiplication (Minocha *et al*., 1992) and cell growth altering auxin action in cell wall (Ma *et al*., 1999). The root is the plant organ most affected by Al toxicity and more specifically, its tip is considered to be the main site for Al toxicity (Archambault *et al*., 1997). As a result, root elongation is considered to be the most sensitive parameter in a short period of time and thus may represent the whole plant reaction to Al. Noble *et al.* (1988) demonstrated that it was possible to observe damage within 24 hr caused by Al in roots of soybean plants directly proportional to Al concentration in the nutrient solution.

In susceptible genotypes the common symptom is poor plant growth as a result of root injury (Meda and Furlani, 2005; Juan-Ping *et al*., 2006). This is because root development plays a major role in a plant's response to water and nutrient availability. Poorly developed roots negatively affect exploration of bulk soil reducing nutrient and water uptake (Okiyo *et al*., 2010). The observation of Al toxicity symptoms, like root darkening and root-tip stunting in this hydroponic experiment could be related to the rapid entry of Al into the root cells. In the susceptible genotypes the roots were thick and shortened and this is in agreement with Blancaflor *et al.* (1998) and Horst *et al.* (1999). They reported that the root morphological alterations like shrinking and tip curling, observed in roots of some of the plant materials, could be attributed to alterations in the root's cytoskeleton. The authors also demonstrated that changes in the organisation and stability of microtubules and microfilaments in root cells of maize were correlated to Al toxicity, besides the rapid inhibition of root elongation. Braccini *et al.* (2000) also reported that in the presence of Al, root elongation of coffee genotypes were more affected than root dry matter.

In the present study, root elongation was the best parameter to make comparisons among maize genotypes with respect to Al tolerance. It also appeared to be a cheaper and better technique compared to other methods reported like root staining with haematoxylin (Ruiz-Torres *et al.*, 1992). According to Concado et al (1999) root apices are excised and photographed both stereoscopic and light microscopes after staining with 0.2% haematoxylin (Merck) and to observe the presence of haematoxylin – Al complexes in internal tissues you need to carryout transversal sectioning of the apices. This suggest more labour costs and time for this method considering the large number of genotypes evaluated in breeding programmes. The root is the first plant organ to be affected as it is directly in contact with the toxic $Al^{3+}$ ions. The shoot can be difficult to measure as it may require processing dry weight and fresh weight biomass using destructive sampling. Reports also indicate that shoots do not provide a true picture on Al tolerance (Mascarenhas *et al*, 1984; Bernai and Clark, 1998). Bernai and Clark (1998) observed that differences in dry matter production in sorghum genotypes were not as significant as root elongation, the latter being the best discriminative parameter. Root elongation has been considered the most sensitive characteristic to quantify Al tolerance due to the fact that the elongation zone is the site where Al toxicity is primarily detected (Blancaflor *et al.,* 1998). The most sensitive site for Al action in the root is the distal transition zone (DTZ) (Kollmeier *et al.,* 2000). These authors showed that application of Al solution exclusively in the DTZ inhibited root elongation in a similar pattern to whole-root application. The differential tolerance to Al by the genotypes tested could be related to Al exclusion mechanisms (Silva *et al*., 2000; 2002) and/or symplast tolerance (Watanabe *et al.,* 2001). Other research findings indicated that exclusion mechanisms are based on the reduction of $Al^{3+}$ activity in root tips, like the exudation of low molecular weight organic compounds, which may form stable complexes with Al, reducing its toxicity to roots, such as citrate (Miyasaka *et al.,* 1991), malate (Delhaize *et al.,* 1993), polypeptides (Basu *et al.,* 1994) and flavonoids (Kidd *et al.,* 2001). More than one type of organic acid may be released by Al stressed roots (Larsen *et al.,* 1998; Ma *et al.,* 2000).

### 3.6 Conclusions and recommendations

It was possible to demonstrate that nutrient solution is a practical and efficient tool for evaluating maize genotypes for low pH tolerance. Root elongation appears to be the best

parameter to compare for Al tolerance among genotypes. In this experiment genotypes IWD C3 SYN F2-B, VPO52 and LPHpop4 were considered highly tolerant, SYN DTE STY-W-B, ZM309 were considered tolerant and 99TZEFY-STR QPM CO-B and OBATANPA/IWDC2SYNF2/IWDC2SY moderately tolerant and DT-YSTR SYNTHETIC-B, TZE-W POP DTC2 STR-B, TZE-YDT STR C4-B, LPHpop3, LPHpop13, and LPHpop14 were sensitive to Al toxicity. Conventional breeding methods will continue to be used until Al-tolerant genes from various plants and/or microbes are isolated and transgenic plants with significantly increased Al tolerance are produced. The highly tolerant genotypes identified in this study namely IWD C3 SYN F2-B, VPO52 and LPHpop4 will be used in the National Maize Breeding Programme in Malawi as source populations to develop new low pH tolerant parental inbred lines using the pedigree method.

### 3.7 References


Agrobase. 2010. Agronomix Generation II Software, Inc. 71 Waterloo St. Winnipeg, Manitoba, R3N054, Canada.

Ahlrichs J.L., M.C., Karr, V.C. Baliggar and R.J. Wright. 1990. Rapid bioassay of aluminium toxicity in soil. Plant and Soil 122: 279-285.

Archambault, D. J., G. Zhang and G. Taylor. 1997. Spatial variation in the kinetics of Aluminium (Al) uptake in roots of wheat (*Triticum aestivum* L.) exhibiting differential resistance to Al. Evidence for metabolism-dependent exclusion of Al. Journal of Plant Physiology 151: 668-674.

Basu, U., A.G. Good and G.J. Taylor. 2001. Transgenic *Brassica napus* manganese superoxide dismutase cDNA are resistant to aluminium. Plant, Cell and Environment 24: 1269-1278.

Basu, U., A. Basu and G. J. Taylor. 1994. Differential exudation of polypeptides by roots of aluminium resistant and aluminium-sensitive cultivars of *Triticum aestivum* L. in response to aluminium stress. Plant Physiology 106: 151-158.

Bernai, J.H. and R.B. Clark.1998. Growth traits among sorghum genotypes in response to aluminium. Journal of Pant Nutrition 21: 297-305.

Blancaflor, E. B., D. L. Jones and S. Gilroy. 1998. Alterations in cytoskeleton accompany aluminium induced growth inhibition and morphological changes in primary roots. Plant Physiology 118: 159-172.

Borrero, J.C., S. Pandey, H. Ceballos, R. Magnavaca and A.F.C. Bahia-Filho. 1995. Genetic variances for tolerance to soil acidity in a tropical maize production. Maydica 40: 283-288.

Braccini, M. C. L., H. E. P. Martinez, A. L. Braccini and S. M. Mendonça. 2000 Avaliação do pH da rizosfera de genótipos de café em resposta à toxidez de alumínio no solo. Bragantia 59: 83-88.

Cançado, G.M.A., L.L. Loguercia, P.R. Martins, S.N. Prentoni, E. Paiva, A. Borem, M.A. Lopes.1999. Heamatoxylin staining as a phenotypic index for Al tolerance selection in tropical maize (*Z. mays* L.). Theoretical and Applied Genetics 99: 747-754.

Carver, B.F., W.P. Inskeep, N.P. Wilson and R.L. Westman. 1988. Seedling tolerance to Aluminium toxicity in hard red winter wheat germplasm. Crop Science 28: 463-467.

Chilimba, A.D.C. 1994. Annual Report: Soil Fertility and Plant Nutrition Commodity Team, Department of Agricultural Research Services, Ministry of Agriculture, Lilongwe, Malawi.

Delhaize, E., P. R. Ryan and P. J. Randall. 1993. Aluminum tolerance in wheat (*Triticum aestivum* L.).II. Aluminum-stimulated excretion of malic acid from root apices. Plant Physiology 103: 695-702.

Duque-Vargas, J., S. Pandey, G. Granador, H. Ceballos and E. Knapp. 1994. Inheritance of tolerance to soil acidity in tropical maize. Crop Science 34: 50-54.

Gomez-Urea, R., C. Hernan, P. Shiraji, F.C. Antonio, F. Bahia and A.L. Lous. 1996. A greenhouse screening technique for acid tolerance in maize. Agronomy Journal 88: 806-812.

Horst, W.J., N. Schmohl, M. Kollmeier, F. Baluska, and M. Sivaguru. 1999. Does aluminium affect root growth of maize through interaction with the cell wall-plasma membrane cytoskeleton continuum? Plant and Soil 215: 163-174.

Ishikawa, S. and T. Wagatsuma. 1998. Plasma membrane permeability of root tip cells following temporary exposure to Al ions is a rapid measure of aluminium tolerance among plant species. Plant Cell Physiology 39: 516-525.

Juan-Ping, W., H. Raman, G.M.N. Zhang and M.X. Zhuo. 2006. $Al^{3+}$ tolerance in barley (*Hordeum vulgare* L) Physiological mechanisms, genetics and screening methods. Journal of Zhejing University 7: 769-787.

Kidd, P.S. and J. Proctor. 2000. Effect of Aluminium on the growth and mineral composition of *Betula pendula* Roth. Journal of Experimental Botany 51: 1057-1066.

Kidd, P.S., M. Llugany, C. Poschenrieder, B. Gunse and J. Barcelo. 2001. The role of root exudates in aluminium resistance and silicon–induced amelioration of aluminium toxicity in three varieties of maize (*Zea mays* L.). Journal of Experimental Botany 52: 1339-1352.

Kochian, L.V. 1995. Cellular mechanisms of Aluminum toxicity and resistance in plants. Annual Review of Plant Physiology and Plant Molecular Biology 46: 237–260.

Kollmeier, M., H.H. Felle and W.J. Horst. 2000. Genotypical differences in aluminium resistance of maize are expressed in the distal part of the transition zone. Is reduced basipetal auxin flow involved in inhibition of root elongation by aluminium? Plant Physiology 122: 954-956.

Larsen, P. B., J. Degenhardt, C.Y. Tai, L.M. Stenzler, S. H. Howell and L.V. Kochian. 1998. Aluminum resistant Arabidopsis mutants that exhibit altered patterns of aluminium accumulation and organic acid release from roots. Plant Physiology 117: 9-18.

Ma, J. F., R. Yamamoto, D. Nevins, J. H. Matsumoto and P. H. Brown, 1999. Al binding in the epidermis cell wall inhibits cell elongation of okra hypocotyl. Plant Cell Physiology 40: 549-556.

Ma, J. F., S. Taketa and Z. M. Yang. 2000. Aluminum tolerance genes on the short arm of chromosome 3R are linked to organic acid release in triticale. Plant Physiology 122: 687-694.

Magnavaca, R., R.C.O. Gardner and R.B. Clark. 1987. Inheritance of aluminium tolerance in maize. In: Galbelman H.W. and B.C. Loughman (Eds.) Genetic aspects of plant mineral nutrition. Martinus Nijhoff, Dordrecht, pp. 201-211.

Magnavaca, R. 1982. Genetic variability and the inheritance of aluminium tolerance in maize (*Zea mays* L.). Lincoln, University of Nebraska. PhD thesis.

Manyowa, N.M., T.E. Miller and B.P. Foster. 1988. Alien species as sources for Aluminium tolerance genes for wheat *Triticum aestivum*. Proceedings of the 7th International Wheat Genetics Symposium pp. 851-857.

Mascarenhas, H. A. A., Camargo, C. E.O. and Falivene, S. M. P. 1984. Efeito do alumínio sobre o crescimento de raízes, peso seco da parte aérea e raízes de diferentes cultivares de soja. *Bragantia*, 43, 191-200.

Meda, AR. and P.R. Furlani. 2005. Tolerance to Al3+ toxicity by tropical Leguminous plants as cover crops. Brazilian Archives of Biology and Technology. 48: 28-32.

Minocha, R., S.C. Minocha, S.L. Long and W.C. Shortle. 1992. Effects of aluminium on DNA synthesis, cellular polyamines, polyamine biosynthetic enzymes and inorganic ions in cell suspension cultures of a woody plant, *Catharanthus roseus*. Plant Physiology 85: 417-424.

Miyasaka, S.C., J.G. Buta, R.K. Howell and C.D. Foy. 1991. Mechanisms of aluminium tolerance in snap beans. Root exudation of citric acid. Plant Physiology 96: 737-743

Munthali, M.W. 2007. Integrated Soil Fertility Management Technologies: A Counteract to Existing Milestone in Obtaining Achievable Economical Crop Yields in Cultivated Lands of Poor Smallholder Farmers in Malawi. In: Advances in intergrated soil Fertility Management in Sub-Saharan Africa: Challenges and opportunities, pp. 531-536.

Noble, A.D., M.V. Fey and M.E. Sumner. 1988. Calcium-aluminium balance and the growth of soybean roots in nutrient solutions. Soil Science Society of America Journal: 52: 1651-1656.

Okiyo, T., S. Gudu, O. Kiplagat and J. Owuoche, 2010. Combining drought and aluminium toxicity tolerance to improve sorghum productivity African Crop Science Journal 18: 147-154.

Pandey, S., H. Ceballos, R. Magnavaca, A.F.C. Bahia, J. Duque-Vargas and L.E. Vinasco. 1994. Genetics of tolerance to soil acidity in tropical maize. Crop Science 34: 1511-1514.

Piñeros M.A. and L.V. Kochian. 2001. A patch-clamp study on the physiology of Al toxicity and Al tolerance in maize. Identification and characterization of Al 3+ - induced anion channels. Plant Physiology 125: 292 – 305.

Ruiz-Torres, N.A., B.F. Carver and R.L. Westman. 1992. Agronomic Performance in acid soils of wheat lines selected for haematoxylin staining pattern. Crop Science 32: 104-107.

Salisbury, F.B. and C.W. Ross. 1992. Plant Physiology. Wadsworth Publishing Company, ISBN 0-534-1562-0 California, USA.

Sasaki, M., Y. Yamamoto and H. Matsumoto. 1996. Lignin deposition induced by aluminium in wheat (*Triticum aestivum*) roots. Physiologia Plantarum 96: 193–198.

Silva, I.R., T.J. Smyth, D.F. Moxley, T.E. Carter, N.S. Allen and T.W. Rufty. 2000. Aluminum accumulation at nuclei of cells in the root tip. Fluorescence detection using lumogallion and confocal laser scanning microscopy. Plant Physiology 12: 543-552.

Silva, I.R., T.J. Smyth, N F. Barros and R.F. Novais. 2002. Physiological aspects of aluminium toxicity and tolerance in plants. In: Alvarez, V. H., Schaefer, C. E. G. R., Barros, N. F., Mello, J. W. V. and Costa, L. M. (Eds.) Tópicos em ciência do solo. Viçosa: Sociedade Brasileira de Ciência do solo. 2: 277-335.

Trejo-Téllez L.I. and F.C. Gomez-Merino. 2012. Nutrient Solutions for Hydroponic systems, Hydroponics - A Standard Methodology for Plant Biological Researches. Colegio de Postgraduados, Montecillo, State of Mexico. Mexico.

Watanabe, T., M. Osaki and T. Tadano. 2001. Al uptake kinetics in roots of *Melastoma malabathricum* L. - an Al accumulator plant. Plant and Soil 231: 283-291.

# CHAPTER 4

## Phenotypic evaluation for tolerance to low pH in tropical and sub-tropical maize germplasm

### 4.1 Abstract

Low-soil pH is one of the major abiotic factors contributing to low yields in Malawi. In this study 45 maize genotypes were evaluated using a (0, 1) alpha lattice design with three replications, using optimal and low pH sites for two consecutive seasons. The objective was to evaluate genetically diverse maize genotypes for tolerance to low pH soils by using phenotypic traits. A mean reduction in grain yield and yield components (100 seed weight, plant vigour etc.) of 69.9% was recorded under low pH conditions. Genotypes LPHpop16, LPHpop3, VPO739, VPO5173 and LOW N POOL C3-B performed relatively better under low pH conditions. Comparison between the glasshouse hydroponic trial and low pH field trial, indicated that among the top 10 yielding genotypes, SYN DTE –STY-W-B performed well and ranked first in terms of root tolerance index (RTi) with a net seminal root length (NSRL) of 2.5 cm followed by VPO717 with RTi of 1.0 cm and NSRL of 1.7 cm. Phenotypic traits associated with grain yield, such as plant vigour, 100 seed weight, shelling percentage, number of ears per plant, ear height and plant height can be used alongside grain yield when selecting germplasm for tolerance to low pH stress. Clustering of the genotypes based on morphological data across low pH environments showed that genotypes had similar chances of being grouped in any of four clusters. The five top yielding genotypes across low pH and optimal environments were comprised of two genotypes from CIMMYT-Colombia and three from CIMMYT-Zimbabwe. Under low pH conditions the top five yielding genotypes consisted of four from CIMMYT-Zimbabwe and one from CIMMYT-Colombia. Selection for low pH tolerance could be effectively carried out *in situ*.

### 4.2 Introduction

Malawi is located to the south east of Africa and is a land locked country, extending from 9°45’ to 17°5’ south of the equator and is about 900 km in length from north to south and

varying in width from 80 to 160 km. Its population is estimated at about 14 million people and is increasing with an average growth rate estimated at 3.3% per year (Saka *et al.*, 2004). Malawi is endowed with many natural resources. Its main resource base is agriculture, which plays a key role in the country's economy. The agriculture sector remains the engine of economic growth in Malawi as it contributes over 40% to GDP of which over 70% is generated by the smallholder sector; 90% of export earnings, provides employment to over 85% of the country's population and is a source of income for over 60% of the rural poor (Kumwenda and Kachule, 2003).

Maize is the most important staple food in Malawi such that in certain districts other foods like rice, sweet potato and cassava are considered as snacks and households will look for resources to buy maize. Approximately 70% of the cultivated area of the customary land is planted to maize each year. About 1.2 million ha of land in the country are planted to maize, producing an average grain yield of 1.1 MT $ha^{-1}$ (MOA, 2003; 2005) against a potential of 6 MT $ha^{-1}$ and 8 MT $ha^{-1}$ for OPVs and hybrid maize, respectively (Zambezi *et al.*, 1993). There clearly exists a yield gap between potential yields achievable and what the smallholder farmers are currently producing. The challenge for the country to attain sustainable maize productivity growth is to reduce the existing yield gap.

The introduction of targeted input subsidy in 2007 improved national yield performance, but still at household level some yield gaps exist against potential yields achievable due to inadequate availability of stress tolerant varieties for some ecologies. FAOSTAT (2013) reported that performance of maize in Malawi remained nearly static through the mid-2000s but it seems to have picked up in recent years. Farmers are being encouraged to combine proper use of subsidised fertiliser and compost manure to improve the maize yields. Unfortunately the quality of compost manure is compromised by the organic materials used due to poverty levels. Reducing the yield gap at household level and obtaining potential yields achievable requires combined efforts. These include breeding for stress tolerance in maize and use of effective agronomic practices, bearing in mind that the country's population is increasing while land is static.

Malawi upland soils are highly weathered and low in pH and available P. About 40% of the country's soils are oxisols and ultisols (US taxonomy), which are low in pH and P

(Munthali, 2007). Apart from low pH, low N soils are also a big problem in highly populated areas. Crop rotation with fallow is rarely practiced. Most farmers are practicing mono-cropping and in some places it is associated with removal of crop residues after harvest which could be depleting soil nutrients and organic matter. This has led to low-soil fertility, especially in the mid-altitude ecology [600-1300 metre above sea level (masl)] of the country.

### 4.3 Materials and methods

#### 4.3.1 Description of sites

The study was conducted at Research station sites from 2011 to 2013. The sites included four low pH sites and five optimal sites. In 2013 the genotypes were also evaluated at a managed low N site. The sites were Tsangano Experimental Research Station (1524 masl, 1071 mm annual rainfall, sandy clay loam soil, annual maximum (max) temperature of 22.9$^{o}$C). Bembeke Research Station - a low pH site (1524 masl, 1053 mm annual rainfall, sandy clay loam soil, 23.4$^{o}$C annual max temperature). Bvumbwe Research Station - a low pH site (1174 to 1228 masl, 1219 mm annual rainfall 25.2$^{o}$C annual max temperature), Lunyangwa Research Station - a low pH site (1342 masl, 1270 mm annual rainfall, 32$^{o}$C annual max temperatures). Baka Research Station, low-land (786 masl, 800 mm annual rainfall, sandy loam soil, 28.4$^{o}$C annual max temperatures). Chitedze Research Station - low N managed site (1219 masl, 954 mm annual rainfall, sandy clay loam, 26.2$^{o}$C annual max temperature). Chitala Research Station, low-land (610 masl, 800 mm annual rainfall, 28.3$^{o}$C max annual temperature).

#### 4.3.2 Experimental materials

A total of 202 genotypes were obtained from CIMMYT-Colombia and CIMMYT-Zimbabwe. These were used in preliminary screening in four sets of field trials in the 2010/11 season to come up with a workable set of genotypes (results not shown). In the 2011/12 and 2012/13 seasons a total of 45 genotypes were planted at 10 sites. Data from Bvumbwe sites for 2011/12 and 2012/13 was not included in the combined analyses due to gaps in the trial for 2011/12 as a result of cut worm and wire worm damage. The managed

low N site data for 2011/12 at Chitedze was also not included due to vandalism before harvest but the results for the 2012/13 site were reported separately. The genotypes were selected from the list provided in Chapter 3 (Table 3.1).

### 4.3.3 Experimental design

The experimental design used was a (0, 1) alpha lattice with three replications. Plot sizes were: two rows of 5.1 m per plot with 17 planting stations per row. Two seeds were planted per station and thinned to one while leaving two at both ends of the row. The phenotypic and agronomic traits measured in the study are listed in Table 4.1.

### 4.3.4 Salient management activities

#### 4.3.4.1 Fertilizer application

The Malawi government recommended rate of 92 kg N and 60 kg $P_2O_5$ was applied as split application as follows: 131 g of 23:21:0 + 4S was applied per row or 8 g per station if using the dollop method as basal dressing. This was applied within 14 days after emergence. This was followed by an application of 54 g of urea per row or 3 g per station if using the dollop method. This top dressing fertilizer was applied 21 days from planting as recommended (MOA, 1994).

### 4.3.5 Soil characterisation for low pH sites

#### 4.3.5.1 Soil sampling and laboratory analysis

Soil samples were collected from four low pH sites in 2010 using the grid sampling method at 15 cm depth as top soil and at 30 cm as sub-soil. Five samples of the same depth were thoroughly mixed to form a composite sample from which three sub-samples were prepared for analyses. The samples were analysed at the Soils and Agriculture Engineering Laboratory at Chitedze Research Station. Parameters analysed included pH, % organic carbon, % organic matter, % N, P, K, Ca, Mg and Al.

**Table 4.1 List of phenotypic and agronomic traits and measuring procedure**

| No | Abbreviation | Trait | Units | Trait description |
|---|---|---|---|---|
| 1 | AD | Days to anthesis | Days | The number of days from planting to 50% pollen shedding |
| 2 | DS | Days to silking | Days | The number of days from planting to 50% silking |
| 3 | PH | Plant height | cm | Measured from the ground surface to the flag leaf using a calibrated stick |
| 4 | EH | Ear height | cm | Measured from the ground surface to the node bearing the main ear |
| 5 | EPP | Ears per plot | Number | Number of cobs harvested per plot divided by number of plants per plot |
| 6 | SL | Stem lodging | Number | Number of plants with stalks broken below the ear per plot |
| 7 | RL | Root lodging | Number | Number of plants fallen with exposed roots per plot |
| 8 | SWT | 100 seed weight | g | Weight of 100 seeds per plot |
| 9 | SH | Shelling percentage | % | The ratio of grain weight to cob weight expressed as a percentage |
| 10 | GT | Grain texture | Score (1-5) | A scale of 1-5 was used where 1 = very flint (no depression at the top of the kernel), 3 = intermediate, 5 = very dent (the kernel has a depression) |
| 11 | GY | Grain yield | Kg/ha | Total grain yield from all the ears of each plot with moisture level adjusted to 12.5% and converted to kg/ha |
| 12 | GLS | Gray leaf spot | Score (1-5) | Scored using a scale of 1-5, where 1= no disease symptoms, 2 = presence of the disease, 3 = moderate infection, 4 = heavily infested, 5 = severe infection |
| 13 | LB | Leaf blight disease | Score (1-5) | Scored using a scale of 1-5, where 1= no disease symptoms, 2 = presence of the disease, 3 = moderate infection, 4 = heavily infested, 5 = severe infection |
| 14 | MSV | Maize streak virus disease | Score (1-5) | Scored using a scale of 1-5, where 1= no disease symptoms, 2 = presence of the disease, 3 = moderate infection, 4 = heavily infested, 5 = severe infection |
| 15 | Rust | Rust disease | Score (1-5) | Scored using a scale of 1-5, where 1= no disease symptoms, 2 = presence of the disease, 3 = moderate infection, 4 = heavily infested, 5 = severe infection |
| 16 | VIG | Plant vigour | Score (1,3,5) | Scored using a scale, where 1= healthy, vigorous plant, upright; 3 = moderate, 5 = weak, slender or thin plants |
| 17 | ASI | Anthesis-silking interval | Days | The difference between days from planting to 50% pollen shedding (AD) and days to 50% silking (DS) i.e. ASI = DS-AD |

## 4.4 Data analyses

The collected data and derived data were analysed using GenStat 16th Edition (2013), and Agrobase (2010). Dendrogram construction was carried out in the Number Cruncher Statistical System (NCSS) (Hintze, 2007) using unweighted pair group method with arithmetic mean (UPGMA). Morphological data were used and construction was based on Euclidean distance and standard deviation as scale type. The genotypic and phenotypic variances were computed from expected mean squares of ANOVA using the formula according to Hallauer and Miranda (1988) as follows:

Phenotypic variance denoted as $\sigma^2_p$

$\sigma^2_p = \sigma^2_e + \sigma^2_g$

Where: $\sigma^2_e =$ error variance and $\sigma^2_g =$ genotypic variance

Genotypic variance is denoted as $\sigma^2_g$

$\sigma^2_g = (MSg - MSe)/r$

Where: MSg = Mean square of genotypes, MSe = mean square error, and r = number of replicates in the experiment.

Genotypic coefficient of variation (GCV)

$GCV = (\sqrt{\sigma^2 g} / X)\ 100$

Where, $\sigma^2_{g=}$ genotypic variance and X = mean of the measured trait

Phenotypic coefficient of variation (PCV)

$PCV = (\sqrt{\sigma^2}_p / X)\ 100$

Where: $\sigma^2_p$ = Phenotypic variance, X = mean of the trait.

Broad sense heritability was computed using the following equation:

$H^2_B = \sigma^2_g / \sigma^2_p$

Where $H^2_B$ is the broad sense heritability, $\sigma^2_{g =}$ genotypic variance and $\sigma^2_p$ = phenotypic variance.

Genetic advance is denoted as GA.

$GA = k\ \sigma_p\ H^2$

Where: k = the standardised selection differential at 5% selection (2.063), $\sigma_p$ = phenotypic standard deviation of the character and $H^2$ heritability estimate

The across sites correlation coefficients (r) between the means for grain yield and other agronomic traits were computed in Agrobase (2010). The PCA was carried out using both GenStat Version 16 for latent loadings (Eigen vectors) and Agrobase (2010) for Eigenvalues and percent cumulative variation to give an insight of the explained variation in the genotypes and traits measured.

### 4.5 Results

All results were reported at a significance level of $P \leq 0.05$ unless otherwise indicated.

#### 4.5.1 Soil analytical results

The pH of the soils and soil nutrients for the sites are presented in Table 4.2. Lunyangwa had highly acidic soils (pH 4.50 sub-soil and pH 4.69 top soils). Tsangano and Bembeke had acidic soils at pH 5.35 and 5.38, 5.13 and 5.01 for top soil and sub-soil, respectively. Bvumbwe was classified as having moderately acidic soils at pH 5.67 and 5.66 top soil and sub-soil, respectively. The classification was based on Soil Test Interpretation Guide (Horneck *et al.*, 2011) as well as according to Mehlich (1984).

At classification of < 0.88 low, 0.88-2.35 medium and 2.35 high (Mehlich III - Mehlich, 1984) all the test sites had medium to low organic carbon. With respect to organic matter (% OM), at classification of 1.5 low, 1.5-4.0 medium and > 4.0 high all the sites had medium to low OM. In terms of percent N at classification of 0.08 very low 0.08-0.12 low, 0.12-0.2 medium, 0.20-0.30, it was only Bembeke site which was medium in sub-soil (0.16). The rest of the sites were low N. Tsangano had low P in top soil, medium in sub-soil, Bvumbwe had very high P and Lunyangwa had medium in top soil and low in sub-soil. Bembeke had low P in both sections of the soil profile at classification of P

(8 µg $g^{-1}$ very low, 9-18 µg $g^{-1}$ low, 19-25 µg $g^{-1}$ medium (adequate range) > 34 µg $g^{-1}$ very high) (Mehlich III - Mehlich, 1984).

**Table 4.2 Soil characterization for the low pH sites**

| Low pH site | Depth (cm) | pH | %OC | %OM | %N | P (µg $g^{-1}$) | Ca (µg $g^{-1}$) | Mg (µg $g^{-1}$) | Al% |
|---|---|---|---|---|---|---|---|---|---|
| Tsangano | 0-15 | 5.35 | 1.23 | 2.13 | 0.11 | 16.75 | 2.02 | 0.37 | 0.40 |
| | 15-30 | 5.38 | 1.97 | 3.40 | 0.10 | 19.27 | 2.18 | 0.37 | 1.33 |
| Bvumbwe | 0-15 | 5.67 | 1.37 | 2.36 | 0.12 | 64.58 | 3.38 | 0.95 | 0.60 |
| | 15-30 | 5.66 | 1.16 | 1.99 | 0.10 | 62.51 | 2.81 | 0.74 | 0.33 |
| Lunyangwa | 0-15 | 4.69 | 1.50 | 2.59 | 0.13 | 24.30 | 1.15 | 0.21 | 0.87 |
| | 15-30 | 4.51 | 1.05 | 1.81 | 0.09 | 10.46 | 0.58 | 0.11 | 0.60 |
| Bembeke | 0-15 | 5.13 | 1.82 | 3.14 | 0.16 | 16.30 | 2.05 | 0.42 | 0.60 |
| | 15-30 | 5.01 | 1.33 | 2.28 | 0.11 | 13.64 | 1.32 | 0.25 | 0.80 |

**OC = organic carbon; OM = organic matter; N = nitrogen; P = phosphorus; Ca = calcium; Mg = magnesium; Al = aluminium**

### 4.5.2 Combined ANOVA for grain yield and agronomic traits at four low pH environments across two seasons 2011/12 and 2012/3

Mean squares from the combined ANOVA across four sites and two seasons are given for the top 10 and bottom 10 maize genotypes in terms of grain yield and agronomic traits (Table 4.3). Results for all entries under low pH soil environments are presented in Appendix 7. Genotype mean squares were significant for days to anthesis, anthesis-silking interval, days to 50% silking, plant and ear height, number of ears per plant, LB disease, husk cover, GLS disease, grain texture, 100 seed weight and plant vigour. Location mean squares were significant for all the measured and derived traits. Season mean squares were significant for all characteristics except for ear height, husk cover, and stem lodging. The GEI (Table 4.3 - GxE) was significant for anthesis date, days to 50% silking, ear height, husk cover, grain texture, rotten ears, 100 seed weight, and plant vigour. Interaction of genotype by season (GxY) mean squares were significant for days to anthesis, days to 50% silking, plant height, number of ears per plant, LB disease, GLS disease, MSV disease, rust disease, grain texture, rotten ears and 100 seed weight.

The interaction of environment by season (ExY) was not significant for husk cover, plant height and rotten ears but was significant for the rest of the traits. Interaction of genotype by environment by season (GxExY) was significant for anthesis date, anthesis-silking interval, days to 50% silking, LB disease and root lodging.

### 4.5.3 Estimated contributions to total sum of squares across four low pH soil environments for the 2011/12 and 2012/13 seasons

Contribution to total sum of squares for genotype was the highest for husk cover (14.5%) and grain texture (8.4%, Table 4.4). Contribution due to environment was high for plant vigour (47.1%), grain yield (63.4%), ear height (41.7%) and days to 50% silking (40.6%). The contribution of season was high for rust disease (18.1%). GxE contribution was significant for grain texture (23.5%) and ear rots (27.4%). The interaction of genotype by season (GxY) sum of squares made the highest contribution to gray leaf spot and MSV (8.8%) and husk cover variation (7.9%). The interaction of ExY made the highest contribution to 100 seed weight (22.8%), root lodging (19.4%) and ear height (14.1%). The interaction of GxExY made the highest contribution to shelling percentage (11.8%) and anthesis date (11.2%) (Table 4.4).

### 4.5.4. Estimated percent reduction for grain yield and other salient phenotypic traits at four low pH soil environments versus four optimal environments across 2011/12 and 2012/13 seasons

The reduction in traits was estimated as the difference between the trait's trial mean for optimal and low pH and subtracted from 100% expressed as a percentage of the optimal i.e. Reduction % = $(X_{optimal} - X_{lowph})/ X_{optimal} * 100\%$ . The results are presented in Table 4.5. The combined mean reduction was 69.9%. The highest reduction was recorded for shelling percentage (87.5%) followed by number of ears per plant (78.0%) and then by plant height (76.6%).

**Table 4.3 Mean squares for combined ANOVA for grain yield and agronomic traits at four low pH environments across 2011/12 and 2012/13 seasons**

| Source | Genotypes | Environment | Year | GxE | GxY | ExY | GxExY | MSE |
|---|---|---|---|---|---|---|---|---|
| Df | 44 | 3 | 1 | 132 | 44 | 3 | 132 | 714 |
| GY | 4.04E+05 | 310600000** | 65600000** | 4.11E+05 | 5.01E+05 | 6821000** | 4.59E+05 | 3.99E+05 |
| AD | 60.55** | 5708.84** | 9122.61** | 35.8** | 49.45** | 1501.4** | 50.84** | 18.05 |
| ASI | 5.62** | 922.76** | 28.34** | 3.83 | 3.67 | 207.43** | 4.52** | 3.2 |
| DS | 62.99*** | 9903.85** | 8172.76** | 33.67** | 53.27** | 2245.89** | 45.59** | 18.3 |
| EH | 292.1* | 59649.2** | 164.8 | 310.1** | 219.5 | 30332.6** | 131.2 | 185.6 |
| EPP | 0.33* | 8.71** | 35.07** | 0.19 | 0.36* | 7.81** | 0.24 | 0.22 |
| LB | 0.88* | 36.22** | 48.87** | 0.71 | 1.2** | 42.24** | 0.81* | 0.59 |
| HC | 4.99** | 36.2** | 0.08 | 3.58** | 2.73 | 1.64 | 2.72 | 2.02 |
| GLS | 2.47* | 20.29** | 20.14** | 1.94 | 3.09** | 38.11** | 1.67 | 1.59 |
| GT | 1.75** | 64.85** | 47.70** | 1.65** | 0.85* | 3.25** | 0.48 | 0.49 |
| MSV | 0.17 | 17.84** | 20.01** | 0.14 | 0.41** | 6.63** | 0.28 | 0.2 |
| PH | 16886** | 230489** | 274015** | 7926 | 15505* | 17503 | 11701 | 10306 |
| RE | 1.36 | 13.14** | 45.22** | 2.61** | 2.12* | 1.53 | 2.63 | 1.43 |
| RL | 3.28 | 268.03** | 325.41** | 3.02 | 3.77 | 342.43** | 3.65* | 2.73 |
| Rust | 0.4 | 53.38** | 80.96** | 0.36 | 0.59** | 25.82** | 0.36 | 0.32 |
| SL | 3.06 | 48.77** | 1.63 | 2.73 | 2.55 | 135.27** | 2.89 | 2.5 |
| SWT | 60.58** | 2419.84** | 1117.69** | 29.63** | 42.7** | 3397.1** | 31.84 | 20.97 |
| SH | 139.2 | 12739** | 1131* | 188.4 | 148.2 | 908** | 209.6 | 176.6 |
| VIG | 1.81** | 184.46** | 9.42** | 0.92** | 0.75 | 49.95** | 0.66 | 0.56 |

*****P≤0.001; **P≤0.01; *P≤0.05; G = genotype, E = environment, Y = year, MSE = mean square error, Df = degree of freedom, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH= ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number**

**Table 4.4 Estimated percentage contributions to total sum of squares for traits at four low pH environments combined for 2011/12 and 2012/13 seasons**

| Variation | GY | AD | ASI | DS | EH | EPP | LB | GLS | GT | HC | MSV | PH | RE | RL | Rust | SL | SWT | SH | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotype | 1.2 | 4.5 | 3.4 | 3.8 | 3.0 | 5.1 | 5.2 | 7.0 | 8.4 | 14.5 | 3.8 | 6.8 | 4.8 | 2.7 | 3.9 | 4.7 | 6.0 | 2.6 | 6.8 |
| Environment | 63.4 | 28.6 | 38.3 | 40.6 | 41.7 | 9.1 | 9.6 | 2.6 | 21.4 | 4.8 | 17.6 | 6.4 | 3.1 | 15.2 | 23.8 | 5.1 | 16.2 | 16.4 | 47.1 |
| Year | 4.5 | 15.3 | 0.4 | 11.2 | 0.0 | 12.2 | 6.5 | 1.3 | 5.2 | 0.0 | 9.9 | 2.5 | 3.6 | 6.1 | 18.1 | 0.1 | 2.5 | 0.5 | 0.8 |
| GxE | 3.7 | 7.9 | 7.0 | 6.1 | 9.5 | 8.7 | 8.3 | 11.1 | 23.5 | 20.8 | 6.2 | 9.6 | 27.4 | 7.5 | 7.1 | 12.6 | 8.7 | 10.6 | 10.4 |
| GxY | 1.5 | 3.6 | 2.2 | 3.2 | 2.3 | 5.5 | 7.2 | 8.8 | 4.1 | 7.9 | 8.8 | 6.3 | 7.4 | 3.1 | 5.9 | 3.9 | 4.2 | 2.8 | 2.8 |
| ExY | 1.4 | 7.5 | 8.6 | 9.2 | 14.1 | 5.4 | 11.2 | 4.9 | 0.7 | 0.0 | 3.3 | 0.3 | 1.2 | 19.4 | 5.8 | 9.5 | 22.7 | 1.2 | 4.3 |
| GxExY | 4.1 | 11.2 | 8.3 | 8.2 | 2.7 | 7.2 | 9.4 | 9.5 | 4.7 | 0.3 | 6.0 | 9.5 | 1.6 | 9.1 | 3.5 | 8.9 | 9.1 | 11.8 | 2.5 |
| Residual | 19.4 | 21.4 | 31.6 | 17.7 | 26.6 | 46.7 | 41.8 | 54.8 | 31.7 | 47.6 | 44.0 | 58.3 | 50.9 | 36.8 | 31.6 | 54.7 | 29.7 | 53.7 | 25.5 |
| Rep | 0.8 | 0.0 | 0.2 | 0.0 | 0.0 | 0.3 | 0.8 | 0.6 | 0.2 | 4.2 | 0.5 | 0.3 | 0.0 | 0.1 | 0.3 | 0.4 | 1.0 | 0.4 | 0.1 |
| **CV (%)** | **42.4** | **5.1** | **67.1** | **5.0** | **28.1** | **54.2** | **35.2** | **82.9** | **58.9** | **27.8** | **36.5** | **77.0** | **102.5** | **92.1** | **44.6** | **127.6** | **20.3** | **19.2** | **27.4** |
| **Min** | **0.8** | **0.0** | **0.2** | **0.0** | **0.0** | **0.3** | **0.8** | **0.6** | **0.2** | **0.0** | **0.5** | **0.3** | **0.0** | **0.1** | **0.3** | **0.1** | **1.0** | **0.4** | **0.1** |
| **Max** | **63.4** | **28.6** | **38.3** | **40.6** | **41.7** | **46.7** | **41.8** | **54.7** | **31.7** | **47.6** | **44.0** | **58.3** | **50.9** | **36.8** | **31.6** | **54.7** | **29.7** | **53.7** | **47.1** |

**G = Genotype, E = environment, Y = year, CV = coefficient of variation, Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH= ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), HC = husk cover, MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number**

**Table 4.5 Estimated reduction of grain yield and other salient traits under low pH versus optimal conditions across the 2011/12 and 2012/13 seasons**

| Trait | Optimal | Low pH | % Reduction |
|---|---|---|---|
| GY | 3372.9 | 1490.3 | 44.2 |
| EH | 77.6 | 46.8 | 60.3 |
| EPP | 1.1 | 0.9 | 78.0 |
| PH | 172.3 | 131.9 | 76.6 |
| SWT | 29.9 | 22.6 | 75.5 |
| SH | 79.2 | 69.3 | 87.5 |
| VIG | 4.0 | 2.7 | 67.5 |
| **Mean** | | | **69.9** |

**GY = grain yield (kg ha$^{-1}$), EH = ear height (cm), EPP = ears per plant (#), PH = plant height (cm), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number**

### 4.5.5 Genotypic and phenotypic variance components, genetic advance and broad sense heritability estimates across four low pH soil environments combined for 2011/12 and 2012/13 seasons

The results in Table 4.6 indicated that phenotypic variances were higher than genotypic variances. Grain texture (0.56), days to 50% silking (0.55), anthesis date (0.54) and plant vigour (0.53) had relatively high broad sense heritability estimates. The genetic coefficients of variations were lower than phenotypic coefficients of variation except for plant height. The expected genetic advance was highest for plant height followed by ear height and these were followed by anthesis date and 100 seed weight. Grain yield had the lowest expected genetic advance with high phenotypic coefficient of variation (Table 4.7).

**Table 4.6 Genotypic variances, phenotypic variances and heritability estimates at low pH sites across two seasons 2011/12 and 2012/13**

| Trait | $\sigma^2_g$ | $\sigma^2_p$ | $H^2b$ | $H^2b$ % |
|---|---|---|---|---|
| GY | 2.300 | 401.400 | 0.006 | 0.623 |
| AD | 21.250 | 39.300 | 0.541 | 54.071 |
| ASI | 1.200 | 4.400 | 0.273 | 27.273 |
| DS | 22.345 | 40.645 | 0.550 | 54.976 |
| EH | 53.250 | 238.850 | 0.223 | 22.294 |
| EPP | 0.055 | 0.275 | 0.200 | 20.000 |
| LB | 0.145 | 0.735 | 0.197 | 19.728 |
| HC | 0.450 | 2.050 | 0.220 | 21.951 |
| GLS | 0.630 | 1.120 | 0.563 | 56.250 |
| GT | 1.485 | 3.505 | 0.424 | 42.368 |
| MSV | 0.015 | 0.185 | 0.081 | 8.108 |
| PH | 3290.000 | 13596.000 | 0.242 | 24.198 |
| RE | 0.035 | 1.395 | 0.025 | 2.509 |
| RL | 0.540 | 2.740 | 0.197 | 19.708 |
| Rust | 0.040 | 0.360 | 0.111 | 11.111 |
| SL | 0.280 | 2.780 | 0.101 | 10.072 |
| SWT | 19.815 | 40.785 | 0.486 | 48.584 |
| SH | 18.700 | 157.900 | 0.118 | 11.843 |
| VIG | 0.620 | 1.180 | 0.525 | 52.542 |
| **Min** | **0.015** | **0.185** | **0.081** | **0.623** |
| **Max** | **3290.000** | **13596.000** | **0.563** | **56.250** |

**Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH= ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number**

**Table 4.7 Genotypic coefficient of variation, phenotypic coefficient of variation and expected genetic advance at low pH sites across two seasons 2011/12 and 2012/13**

| Trait | GCV% | PCV% | GA | GA (% of mean) |
|---|---|---|---|---|
| GY | 12.4 | 164.1 | 0.5 | 32.7 |
| AD | 5.1 | 6.9 | 2.6 | 3.2 |
| ASI | 6.7 | 12.9 | 1.1 | 41.0 |
| DS | 5.1 | 6.9 | 2.7 | 3.1 |
| EH | 10.7 | 22.6 | 2.7 | 5.7 |
| EPP | 2.6 | 5.6 | 0.5 | 54.8 |
| LB | 2.6 | 5.8 | 0.6 | 26.9 |
| HC | 9.3 | 14.3 | 1.3 | 74.6 |
| GLS | 4.5 | 9.7 | 0.8 | 37.4 |
| GT | 5.0 | 6.7 | 1.1 | 43.7 |
| MSV | 1.0 | 4.2 | 0.2 | 19.8 |
| PH | 49.9 | 101.5 | 7.6 | 5.8 |
| RE | 1.8 | 11.2 | 0.2 | 21.3 |
| RL | 3.9 | 12.9 | 0.6 | 31.9 |
| Rust | 1.8 | 5.3 | 0.4 | 29.4 |
| SL | 4.8 | 15.0 | 0.6 | 47.7 |
| SWT | 9.4 | 13.4 | 2.5 | 11.2 |
| SH | 5.2 | 16.8 | 1.7 | 2.4 |
| VIG | 4.8 | 6.6 | 1.1 | 39.7 |
| **Min** | **1.0** | **4.2** | **0.2** | **2.4** |
| **Max** | **49.9** | **164.1** | **7.6** | **74.6** |

**GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, GA = genetic advance, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH= ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number, Min = minimum, Max = maximum.**

### 4.5.6 Mean performance for grain yield and other traits across four low pH soil environments combined for 2011/12 and 2012/13 seasons

The grain yield trial mean was 1490 kg ha$^{-1}$ (Table 4.8) and the top five performing genotypes were G24 (LPHpop16) G30 (LPHpop3) G22 (VPO739), G15 (VPO5173) and G27 (LOW N POOL C3-B). The latest maturing genotype was G35 (86 AD = 172 days

**Table 4.8 Mean performance for grain yield and other agronomic traits across four low pH environments combined for 2011/12 and 2012/13 seasons**

| | Entry | GY | AD | ASI | DS | EH | EPP | LB | HC | GLS | GT | MSV | PH | RE | RL | Rust | SL | SWT | SH% | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Top 10 genotypes | G24 | 1792 | 79.7 | 3.0 | 83.0 | 51.2 | 0.8 | 2.4 | 1.6 | 2.3 | 2.4 | 1.1 | 134 | 1.4 | 2.3 | 1.5 | 1.2 | 24 | 73 | 2.7 |
| | G30 | 1765 | 82.5 | 2.9 | 85.4 | 44.0 | 0.9 | 1.9 | 2.4 | 2.1 | 2.3 | 1.3 | 119 | 1.1 | 2.0 | 1.3 | 0.6 | 24 | 74 | 2.1 |
| | G22 | 1753 | 81.6 | 2.5 | 84.8 | 48.2 | 0.9 | 2.2 | 2.1 | 2.1 | 2.4 | 1.2 | 126 | 1.2 | 1.7 | 1.2 | 1.1 | 23 | 70 | 2.7 |
| | G15 | 1746 | 82.5 | 3.5 | 86.0 | 48.6 | 0.9 | 2.3 | 1.7 | 2.4 | 2.7 | 1.1 | 132 | 1.2 | 2.2 | 1.5 | 1.4 | 22 | 70 | 2.8 |
| | G27 | 1701 | 84.7 | 2.0 | 86.7 | 49.8 | 0.9 | 2.1 | 1.0 | 1.9 | 2.8 | 1.2 | 129 | 1.2 | 1.3 | 1.1 | 1.7 | 27 | 69 | 2.4 |
| | G6 | 1655 | 82.0 | 2.0 | 83.1 | 44.4 | 0.9 | 2.4 | 1.3 | 2.7 | 2.8 | 1.2 | 129 | 1.6 | 1.4 | 1.2 | 0.7 | 22 | 68 | 2.7 |
| | G16 | 1650 | 80.8 | 3.1 | 82.9 | 38.9 | 0.8 | 1.9 | 1.9 | 2.1 | 2.6 | 1.3 | 116 | 1.0 | 1.3 | 1.4 | 1.6 | 24 | 71 | 2.7 |
| | G21 | 1602 | 83.8 | 2.8 | 86.6 | 42.6 | 0.9 | 2.3 | 1.7 | 2.0 | 2.9 | 1.1 | 126 | 1.0 | 1.8 | 1.4 | 1.0 | 22 | 71 | 2.6 |
| | G34 | 1599 | 81.6 | 3.0 | 84.0 | 44.7 | 0.8 | 2.0 | 1.1 | 1.8 | 1.8 | 1.3 | 123 | 0.9 | 1.7 | 1.3 | 1.1 | 22 | 70 | 2.7 |
| | G26 | 1575 | 84.5 | 3.2 | 87.7 | 47.5 | 0.8 | 2.6 | 2.2 | 2.1 | 1.9 | 1.3 | 125 | 1.2 | 1.3 | 1.2 | 0.9 | 23 | 68 | 2.7 |
| Bottom 10 genotypes | G25 | 1401 | 84.5 | 2.7 | 86.4 | 50.8 | 0.9 | 2.2 | 1.5 | 1.9 | 2.5 | 1.2 | 141 | 1.1 | 1.5 | 1.3 | 1.1 | 23 | 69 | 2.5 |
| | G35 | 1396 | 86.3 | 3.0 | 89.3 | 45.2 | 0.8 | 2.1 | 2.3 | 2.3 | 3.2 | 1.1 | 126 | 1.4 | 2.0 | 1.2 | 1.1 | 26 | 69 | 2.8 |
| | G33 | 1385 | 83.0 | 3.0 | 86.5 | 46.6 | 0.8 | 2.0 | 1.2 | 2.1 | 2.5 | 1.2 | 127 | 1.0 | 2.4 | 1.3 | 1.3 | 22 | 70 | 2.5 |
| | G41 | 1376 | 80.3 | 2.8 | 83.5 | 40.6 | 0.8 | 2.0 | 1.9 | 3.7 | 2.6 | 1.3 | 118 | 1.0 | 1.8 | 1.2 | 1.0 | 21 | 67 | 2.8 |
| | G4 | 1372 | 83.5 | 3.4 | 87.3 | 48.6 | 0.8 | 2.3 | 2.2 | 2.2 | 2.7 | 1.1 | 127 | 1.7 | 1.8 | 1.4 | 0.9 | 23 | 68 | 2.4 |
| | G14 | 1362 | 83.6 | 2.7 | 86.3 | 46.5 | 0.8 | 2.2 | 2.5 | 2.3 | 2.3 | 1.2 | 148 | 0.9 | 2.0 | 1.0 | 1.3 | 22 | 68 | 2.7 |
| | G44 | 1359 | 83.9 | 2.4 | 86.7 | 48.1 | 0.9 | 2.1 | 1.2 | 2.1 | 2.4 | 1.3 | 135 | 0.9 | 1.8 | 1.4 | 1.0 | 23 | 67 | 3.3 |
| | G10 | 1314 | 84.6 | 2.8 | 87.5 | 46.2 | 1.0 | 2.3 | 1.4 | 2.1 | 2.9 | 1.3 | 123 | 0.9 | 2.3 | 1.4 | 1.3 | 19 | 68 | 2.5 |
| | G2 | 1282 | 82.4 | 2.3 | 84.8 | 48.2 | 0.8 | 2.4 | 1.6 | 1.8 | 2.4 | 1.2 | 127 | 0.9 | 2.5 | 1.4 | 1.7 | 22 | 65 | 3.0 |
| | G31 | 1195 | 80.3 | 2.6 | 82.9 | 45.4 | 0.9 | 2.0 | 2.3 | 2.1 | 2.6 | 1.3 | 123 | 1.3 | 2.2 | 1.3 | 0.9 | 22 | 64 | 3.1 |
| | **Mean** | **1490.6** | **83.1** | **2.7** | **85.8** | **46.8** | **0.9** | **2.2** | **1.7** | **2.1** | **2.5** | **1.2** | **131.9** | **1.2** | **1.8** | **1.3** | **1.2** | **22.6** | **69.3** | **2.7** |
| | **LSD** | **358** | **2.4** | **1** | **2.4** | **7.7** | **0.3** | **0.4** | **0.8** | **0.7** | **0.4** | **0.3** | **58** | **0.7** | **0.9** | **0.3** | **0.9** | **3** | **8** | **0.4** |
| | **CV (%)** | **42.4** | **5.1** | **67** | **5** | **28** | **54** | **35** | **83** | **59** | **28** | **37** | **77** | **103** | **92.1** | **44.6** | **127.6** | **20.3** | **19** | **27.4** |
| | **SE** | **631** | **4.2** | **1.8** | **4.3** | **13.6** | **0.5** | **0.8** | **1.4** | **1.3** | **0.7** | **0.5** | **101.5** | **1.2** | **1.7** | **0.6** | **1.6** | **4.6** | **13** | **0.8** |
| | **Min** | **1195.0** | **79.7** | **1.6** | **82.9** | **38.0** | **0.7** | **1.8** | **0.8** | **1.6** | **1.8** | **1.1** | **116.0** | **0.8** | **1.2** | **1.0** | **0.6** | **19.0** | **64.0** | **2.1** |
| | **Max** | **1792.0** | **86.3** | **3.5** | **89.3** | **53.9** | **1.0** | **2.7** | **2.6** | **3.7** | **3.2** | **1.5** | **148** | **1.7** | **2.7** | **1.5** | **2.2** | **27.0** | **75.0** | **3.3** |

**LSD = Least significant difference, CV = coefficient of variation, SE = Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH= ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number**

physiological maturity period) and the earliest of the group was G24 (80 AD = 160 days physiological maturity period). Maturity period for any maize genotype is twice the number of days to flowering. The genotype most susceptible to gray leaf spot disease was G 41. The shortest genotype as a result of low pH effect was G 16 (116 cm). Genotype G27 recorded the highest 100 seed weight (27 g) followed by G35 (26 g). The best shelling percentage was recorded for G30 (74%). The genotype with the best plant vigour was G30 followed by G27 and G4 (Table 4.8).

### 4.5.7 Pearson's correlation coefficients between grain yield and agronomic traits across four low pH soil environments combined for 2011/12 and 2012/13 seasons

Grain yield was positively and highly significantly correlated with anthesis date (r = 0.12), anthesis-silking interval (r = 0.35), days to silking (r = 0.21), number of ears per plant (r = 0.17) and shelling percentage (r = 0.19). Days to anthesis were significantly correlated with most traits excluding stem lodging and it was negatively correlated with plant and ear height as well as root lodging. Anthesis-silking interval also correlated with traits like: days to silking, shelling percentage and ears per plant. Days to silking correlated negatively with plant and ear height (-0.20 and -0.40) as well as with root lodging (-0.10). Correlation for plant height was positively with ear height, husk cover and 100 seed weight, 0.40, 0.10 and 0.2, respectively. Ear height correlated with traits like, root lodging, 100 seed weight, ears per plant, shelling percentage, vigor and diseases such as leaf blight and rust. Number of ears per plant furthermore correlates with among others, grain texture, 100 seed weight and vigor (Table 4.9).

### 4.5.8 Principal component analysis results, eigenvalues and eigenvectors for the traits across four low pH soil environments combined for 2011/12 and 2012/13 seasons

Results indicated that eight principal components were generated (Table 4.10) which accounted for 100% variability present in the maize genotypes evaluated. The first five PC had eigenvalues higher than 1 and their cumulative percentages accounted for 71.1% of the total variation present among the genotypes.

**Table 4.9 Pearson's correlation coefficients for grain yield and agronomic traits across four low pH environments for two seasons**

| | GY | AD | ASI | DS | PH | EH | RL | SL | HC | RE | GT | LB | GLS | Rust | MSV | SWT | VIG | SH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **AD** | 0.12** | | | | | | | | | | | | | | | | | |
| **ASI** | 0.35** | 0.30** | | | | | | | | | | | | | | | | |
| **DS** | 0.12** | 0.90** | 0.30** | | | | | | | | | | | | | | | |
| **PH** | -0.02 | -0.10** | -0.02 | -0.20** | | | | | | | | | | | | | | |
| **EH** | -0.03 | -0.30** | -0.01 | -0.40** | 0.40** | | | | | | | | | | | | | |
| **RL** | 0.02 | -0.10** | 0.03 | -0.10** | 0.07 | 0.34** | | | | | | | | | | | | |
| **SL** | 0.03 | 0.04 | 0.01 | 0.03 | -0.03 | -0.01 | 0.04 | | | | | | | | | | | |
| **HC** | -0.02 | 0.10** | -0.01 | 0.04 | 0.10** | 0.08 | -0.20** | 0.02 | | | | | | | | | | |
| **RE** | -0.06 | 0.20** | -0.03 | 0.20** | -0.03 | -0.20** | -0.20** | 0.10** | 0.30** | | | | | | | | | |
| **GT** | 0.03 | 0.09** | 0.02 | 0.12** | 0.01 | -0.02 | 0.00 | -0.04 | -0.10** | 0.04 | | | | | | | | |
| **LB** | 0.01 | 0.12** | 0.02 | 0.09** | 0.06 | 0.09** | 0.12** | 0.17** | 0.08 | 0.22** | 0.30** | | | | | | | |
| **GLS** | -0.02 | 0.14** | 0.00 | 0.14** | 0.04 | 0.03 | 0.13** | 0.03 | 0.00 | 0.16** | 0.30** | 0.50** | | | | | | |
| **Rust** | -0.08 | 0.08* | -0.01 | 0.01 | 0.16 | 0.11** | -0.08 | 0.15** | 0.30** | 0.34** | 0.30** | 0.60** | 0.40** | | | | | |
| **MSV** | -0.02 | 0.08* | -0.01 | 0.02 | 0.06 | 0.04 | -0.03 | 0.20** | 0.13** | 0.29** | 0.30** | 0.70** | 0.40** | 0.60** | | | | |
| **SWT** | 0.05 | 0.06* | 0.04 | 0.05 | 0.20** | 0.40** | 0.38** | 0.05 | -0.03 | 0.01 | -0.03 | 0.20** | 0.20** | 0.04 | 0.00 | | | |
| **VIG** | 0.03 | 0.13** | 0.02 | 0.16** | 0.01 | 0.09** | 0.29** | 0.12** | -0.07 | 0.14** | 0.10** | 0.30** | 0.20** | 0.20** | 0.10 | 0.40** | | |
| **SH** | 0.19** | 0.27** | 0.30** | 0.24** | 0.05 | 0.09** | 0.07 | 0.05 | 0.05 | 0.06 | 0.10** | 0.10** | 0.10** | 0.10 | 0.10 | 0.20** | 0.10** | |
| **EPP** | 0.17** | 0.67** | 0.30** | 0.65** | 0.07 | 0.12** | 0.07 | 0.05 | 0.05 | 0.06 | 0.10** | 0.10** | 0.10** | 0.10** | 0.10** | 0.20** | 0.10** | 0.40* |

****P≤0.01, * P≤0.05, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), PH = plant height (cm), EH= ear height (cm), RL = root lodging (#), SL= stem lodging (#), HC = husk cover, RE = rotten ears (#), GT = grain texture (1-5), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), Rust = rust disease (1-5), MSV = maize streak virus disease (1-5), SWT = 100 seed weight (g), VIG = vigour (1-5), SH = shelling percentage, EPP = ears per plant (#), (#) = number.**

**Table 4.10 Eigenvalues, percentages and cumulative percentages for the measured and derived data across four low pH soil environments combined for 2011/12 and 2012/13 seasons**

| Principal component | Eigenvalues | As percentages | Cumulative percentages |
|---|---|---|---|
| 1 | 2.2 | 18.5 | 18.5 |
| 2 | 1.8 | 15.7 | 34.2 |
| 3 | 1.5 | 13.1 | 47.4 |
| 4 | 1.5 | 12.5 | 59.8 |
| 5 | 1.3 | 11.3 | 71.1 |
| 6 | 1.2 | 10.0 | 81.1 |
| 7 | 1.1 | 9.7 | 90.8 |
| 8 | 1.1 | 9.2 | 100.0 |

### 4.5.9 Clustering of maize genotypes evaluated at four low pH soil environments combined across 2011/12 and 2012/13 seasons

The dendrogram was constructed using the UPGMA cluster analysis method. Forty five maize genotypes were clustered based on means for grain yield. At cut off point 1.0, three main clusters were observed (Figure 4.1) with a high cophenetic correlation of $r_{cop} = 0.82$. Thirteen genotypes from CIMMYT-Zimbabwe were grouped in cluster two with only two from CIMMYT-Colombia. The top performing genotypes were grouped in cluster three which comprised of 24 genotypes from both Colombia and Zimbabwe. Cluster one was comprised of six genotypes which were also from both CIMMYT research centres.

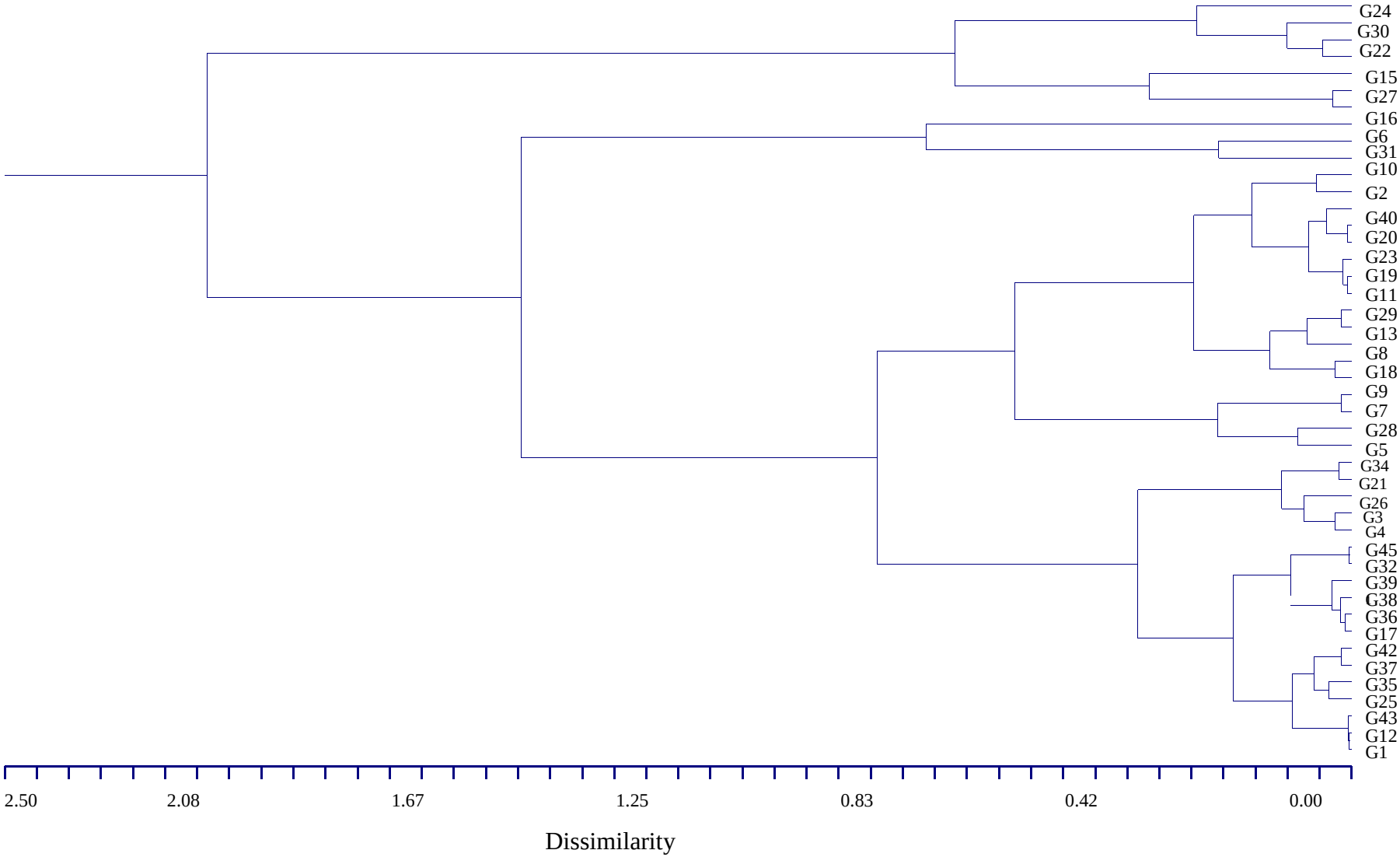


**Figure 4.1 Dendrogram based on Euclidean distance and UPGMA clustering using morphological data for genotypes at four low pH environments combined for 2011/12 and 2012/13 seasons**

### 4.5.10 Performance of maize genotypes across four optimal soil environments combined for 2011/12 and 2012/13 seasons

Mean squares from the combined ANOVA across four sites and across two years presented are for the top10 and bottom 10 maize genotypes in terms of grain yield (Table 4.11). Results for all entries under optimal environments are presented in Appendix 7. Significant differences due to genotypes were observed for 16 measured traits except for anthesis-silking interval, husk cover and root lodging. Environment mean squares were significant for all traits except for 100 seed weight. Season mean squares were significant for all traits excluding MSV and 100 seed weight. G x E mean squares were significant for most traits except for grain yield, anthesis-silking interval, number of ears per plant, leaf blight and gray leaf spot disease as well as shelling percentage. G x Y interaction mean squares were not significant for anthesis-silking interval, maize streak virus, rotten ears and rust disease. The interaction of E x Y mean squares was significant for traits except for diseases: leaf blight, MSV and rust, and the following traits: husk cover, stem and root lodging, rotten ears, plant vigour and 100 seed weight. The interaction G x E x Y was only significant for grain yield, anthesis date, days to 50% silking, gray leaf spot, grain texture and plant vigour (Table 4.11).

### 4.5.11. Estimated contributions to total sum of squares across four optimal environments combined for 2011/12 and 2012/13 seasons

Contribution due to genotype was the highest for 100 seed weight (14.1%), MSV (13.4%) and stem lodging (12.0%) (Table 4.12). Contribution due to environment was high for anthesis date (67.0%), plant vigour (53.7%), Rust (48.1%), ear height (48.2%). The contribution due to the effect of season was high for root lodging (24.1%), rust disease (18.5%) and rotten ears (16.5%). G x E contribution to variation was high for MSV (19.1%), husk cover (21.1%) and stem lodging (12.5%). The interaction of genotype by season sum of squares made the highest contribution to stem lodging (22.8%), root lodging (14.2%) and 100 seed weight (65.7%). The interaction of E x Y made the highest contribution to gray leaf spot (12.5%) anthesis date (14.1%) and days to 50% silking

**Table 4.11 Mean squares for combined ANOVA for grain yield and agronomic traits at four optimal environments for 2011/12 and 2012/13 seasons**

| Source | Genotypes | Environment | Year | GxE | GxY | ExY | GxExY | MSE |
|---|---|---|---|---|---|---|---|---|
| Df | 44 | 7 | 1 | 307 | 44 | 6 | 264 | 1334 |
| GY | 5753000*** | 1.1E+08** | 4E+07** | 1.33E+06 | 4978000** | 21230000** | 1597000** | 1.15E+06 |
| AD | 117.10** | 22428.24** | 3497.57** | 22.12** | 48.65** | 7204.79** | 18.78** | 8.70 |
| ASI | 3.30 | 442.03** | 437.178** | 5.00 | 6.20 | 207.96** | 5.30 | 4.90 |
| DS | 111.87** | 20256.23** | 6094.80** | 20.60** | 49.30** | 6081.36** | 20.66** | 9.30 |
| EH | 690.00** | 77831** | 3466.30** | 270.1** | 457.30** | 8028.30** | 236.10 | 199.10 |
| EPP | 0.07** | 0.40** | 1.22** | 0.03 | 0.0812** | 0.65** | 0.03 | 0.03 |
| LB | 0.80** | 79.38** | 50.09** | 0.32 | 1.01** | 6.44 | 43.10 | 0.27 |
| HC | 2.70 | 326.10** | 9.44* | 4.55** | 4.10** | 4.40 | 23.10 | 2.10 |
| GLS | 0.93** | 41.80** | 1.85* | 0.30 | 0.96** | 63.96** | 0.55* | 0.34 |
| GT | 2.40** | 55.50** | 45.90** | 1.10* | 1.60** | 8.67** | 1.03* | 0.80 |
| MSV | 0.60** | 35.28** | 0.00 | 0.40** | 0.00 | 5.41 | 32.10 | 0.20 |
| PH | 1277.50** | 101791.30** | 29780.1** | 557.8* | 933.30** | 21985.9** | 490.80 | 432.80 |
| RE | 1.18** | 85.10** | 80.96** | 0.67** | 0.30 | 5.20 | 22.10 | 0.40 |
| RL | 4.20 | 1571.03** | 2323.97** | 10.51** | 31.02** | 6.41 | 42.10 | 4.30 |
| Rust | 0.80** | 118.80** | 137.14** | 0.45** | 0.20 | 3.40 | 21.10 | 0.30 |
| SL | 3.94** | 128.45** | 8.80** | 2.05** | 7.48** | 2.40 | 29.20 | 1.30 |
| SWT | 80.30** | 145.60 | 50.80 | 29.20** | 89.86** | 2157.90 | 30.30 | 25.40 |
| SH | 241.80** | 3012.40** | 2294.20** | 119.90 | 174.20** | 1538.10** | 100.60 | 108.00 |
| VIG | 0.70** | 138.75** | 6.65** | 0.53** | 1.45** | 0.60 | 0.53** | 0.30 |

****P≤0.01; *P≤0.05; G = genotype, E = environment, Y = year, MSE = mean square error, Df = degree of freedom, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH= ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number**

**Table 4.12 Estimated percent contributions to total sum of squares at four optimal environments across 2011/12 and 2012/13 seasons**

| Source | GY | AD | ASI | DS | EH | EPP | LB | GLS | GT | HC | MSV | PH | RE | RL | Rust | SL | SWT | SH | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotypes | 11.9 | 5.0 | 2.2 | 5.1 | 6.3 | 7.5 | 6.6 | 7.8 | 9.3 | 4.3 | 13.4 | 6.5 | 10.6 | 1.9 | 4.8 | 12.0 | 14.1 | 7.6 | 4.0 |
| Environments | 15.6 | 65.7 | 19.5 | 63.0 | 48.2 | 3.1 | 44.6 | 24.2 | 14.7 | 34.6 | 38.5 | 35.2 | 34.7 | 32.6 | 48.1 | 17.8 | 1.2 | 6.4 | 53.7 |
| Year | 1.8 | 3.4 | 6.4 | 6.3 | 0.7 | 3.1 | 9.4 | 0.4 | 4.0 | 0.3 | 0.0 | 3.4 | 16.5 | 24.1 | 18.5 | 0.6 | 0.2 | 1.6 | 0.9 |
| GxE | 8.3 | 2.8 | 9.7 | 2.8 | 7.3 | 10.9 | 7.9 | 9.8 | 12.4 | 21.1 | 19.1 | 8.4 | 12.1 | 9.6 | 7.9 | 12.5 | 10.2 | 11.3 | 9.0 |
| GxY | 10.3 | 2.1 | 4.0 | 2.3 | 4.2 | 9.2 | 8.3 | 8.1 | 6.3 | 6.4 | 0.9 | 4.7 | 2.8 | 14.2 | 1.5 | 22.8 | 15.7 | 5.5 | 8.2 |
| ExY | 3.0 | 14.1 | 6.1 | 12.6 | 3.3 | 5.0 | 0.0 | 12.3 | 1.5 | 0.0 | 0.0 | 5.1 | 0.1 | 1.0 | 1.8 | 0.1 | 8.6 | 3.3 | 0.1 |
| GxExY | 9.9 | 1.6 | 6.8 | 1.9 | 4.3 | 9.3 | 0.7 | 4.7 | 8.0 | 1.0 | 0.0 | 5.0 | 0.0 | 0.3 | 0.2 | 0.5 | 5.3 | 9.4 | 3.0 |
| Rep | 0.6 | 0.0 | 0.2 | 0.0 | 0.0 | 0.7 | 0.3 | 0.5 | 0.1 | 0.0 | 0.1 | 0.6 | 0.3 | 0.2 | 1.0 | 0.5 | 0.4 | 0.0 | 0.1 |
| Residual | 38.7 | 5.3 | 45.1 | 6.0 | 25.7 | 51.3 | 22.2 | 32.2 | 43.7 | 32.4 | 28.0 | 31.1 | 22.9 | 16.1 | 16.2 | 33.1 | 44.4 | 54.9 | 21.1 |
| **CV (%)** | **31.8** | **4.6** | **194.2** | **4.6** | **18.2** | **15.2** | **27.1** | **103.1** | **36.0** | **103** | **35.9** | **12.1** | **80.3** | **301.5** | **31.3** | **169.4** | **16.8** | **13.1** | **27.3** |
| **Min** | **0.6** | **0.0** | **0.2** | **0.0** | **0.0** | **0.7** | **0.0** | **0.4** | **0.1** | **0.0** | **0.0** | **0.6** | **0.0** | **0.2** | **0.2** | **0.1** | **0.2** | **0.0** | **0.1** |
| **Max** | **38.7** | **65.7** | **45.1** | **63.0** | **48.2** | **51.3** | **44.6** | **32.2** | **43.7** | **34.6** | **38.5** | **35.2** | **34.7** | **32.6** | **48.1** | **33.1** | **44.4** | **54.9** | **53.7** |

**G = genotype, E = environment, Y = year, CV = coefficient of variation, Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), HC = husk cover, MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging#, SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number**

(12.6%). The interaction of G x E x Y made the highest contribution to grain yield (9.9%), shelling percentage (9.4%) and number of ears per pant (9.3%)

### 4.5.12 Genotypic and phenotypic variance components, genetic advance and broad sense heritability estimates across four optimal environments combined for 2011/12 and 2012/13 seasons

The results in Table 4.13 indicated that phenotypic variances were higher than genotypic variances. Anthesis date (0.86), days to 50% silking (0.85) and grain yield (0.67) had relatively high broad sense heritability estimates. Root lodging had the lowest heritability estimate (0.02). The genetic coefficient of variation was lower than phenotypic coefficient of variation. The expected genetic advance (GA) was the highest for grain yield (68.9) followed by plant height (29.5) and ear height (22.5). It was low for number of ears per plant (0.2) and root lodging (0.4) (Table 4.14).

**Table 4.13 Genotypic ($\sigma^2_g$) and phenotypic ($\sigma^2_p$) variances and broad sense ($H^2b$) heritability estimates at four optimal environments across 2011/12 and 2012/13 seasons**

| Trait | $\sigma^2_g$ | $\sigma^2_p$ | $H^2b$ | $H^2b$ % |
|---|---|---|---|---|
| GY | 230.20 | 345.00 | 0.67 | 66.71 |
| AD | 54.19 | 62.90 | 0.86 | 86.14 |
| ASI | 0.77 | 4.11 | 0.19 | 18.82 |
| DS | 51.29 | 60.58 | 0.85 | 84.67 |
| EH | 245.45 | 444.60 | 0.55 | 55.21 |
| EPP | 0.02 | 0.05 | 0.41 | 40.70 |
| LB | 0.27 | 0.53 | 0.50 | 49.98 |
| HC | 0.34 | 2.40 | 0.14 | 13.98 |
| GLS | 0.29 | 0.64 | 0.46 | 46.20 |
| GT | 0.79 | 1.61 | 0.50 | 49.51 |
| MSV | 0.20 | 0.40 | 0.52 | 51.63 |
| PH | 422.40 | 855.20 | 0.49 | 49.39 |
| RE | 0.38 | 0.80 | 0.48 | 47.68 |
| RL | 0.08 | 4.24 | 0.02 | 1.97 |
| Rust | 0.26 | 0.54 | 0.49 | 49.05 |
| SL | 1.30 | 2.64 | 0.49 | 49.44 |
| SWT | 27.47 | 52.80 | 0.52 | 52.00 |
| SH | 66.90 | 174.90 | 0.38 | 38.25 |
| VIG | 0.20 | 0.50 | 0.39 | 39.28 |

**$\sigma^2_g$ = genotypic variance, $\sigma^2_p$ = phenotypic variance, $H^2b$ = broad sense heritability, $H^2b$ % = broad sense heritability as percentage, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number.**

**Table 4.14 Genotypic coefficient of variation, phenotypic coefficient of variation and expected genetic advance at optimal combined for 2011/12 and 2012/13 seasons**

| Trait | GCV% | PCV% | GA | GA % of mean |
|---|---|---|---|---|
| GY | 8.3 | 10.1 | 68.9 | 2.4 |
| AD | 9.2 | 9.9 | 10.6 | 21.8 |
| ASI | 8.2 | 19.0 | 1.3 | 69.2 |
| DS | 8.8 | 9.6 | 10.3 | 20.5 |
| EH | 17.8 | 23.9 | 22.5 | 31.0 |
| EPP | 1.3 | 2.1 | 0.2 | 16.6 |
| LB | 3.7 | 5.3 | 0.7 | 39.5 |
| HC | 4.9 | 13.1 | 0.8 | 32.1 |
| GLS | 4.3 | 6.3 | 0.8 | 46.8 |
| GT | 6.5 | 9.2 | 1.3 | 68.4 |
| MSV | 4.1 | 5.7 | 0.6 | 55.0 |
| PH | 15.7 | 22.3 | 29.5 | 17.3 |
| RE | 6.9 | 10.0 | 0.9 | 109.2 |
| RL | 3.5 | 24.8 | 0.4 | 12.1 |
| Rust | 4.0 | 5.7 | 0.7 | 44.4 |
| SL | 13.8 | 19.7 | 1.6 | 243.0 |
| SWT | 9.6 | 13.3 | 7.5 | 26.1 |
| SH | 9.2 | 14.9 | 11.7 | 13.2 |
| VIG | 3.1 | 5.0 | 0.6 | 28.4 |

**GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, GA = genetic advance, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis, ASI = anthesis-silking interval (days), DS = days to silking (days), EH= ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number.**

### 4.5.13 Mean performance for grain yield and other traits across four optimal environments combined for 2011/12 and 2012/13 seasons

The grain yield trial mean was 3.3 t ha$^{-1}$ and the top seven performing genotypes were G20 (4.5 t ha$^{-1}$), G33 (4.0 t ha$^{-1}$), G8 (4.0 t ha$^{-1}$), G27 (4.0 t ha$^{-1}$), G5 (3.9 t ha$^{-1}$), G31 (3.8 t ha$^{-1}$) and G10 (3.8 t ha$^{-1}$) (Table 4.15). The lowest yielding were G40 (2.3 t ha$^{-1}$) and G2 (2.3 t ha$^{-1}$). The earliest maturing genotype was G24 (59 AD i.e. 118 days maturity period) and the shortest genotype was G2 (156 cm). The tallest genotype was G5 (189 cm). The best shelling percentage was recorded for G20 (83%) while G2 had the lowest shelling percentage. The genotype with the best plant vigour was G20 (1.5). High 100 seed weight was recorded for G40 (33.2 g).

**Table 4.15 Mean performance for grain yield across four optimal environments combined for 2011/12 and 2012/13 seasons**

| | Entry | GY | AD | ASI | DS | EH | EPP | LB | HC | GLS | GT | MSV | PH | RE | RL | Rust | SL | SWT | SH | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Top ten genotypes | G20 | 4489 | 65.0 | 1.0 | 66.7 | 81 | 1.1 | 1.9 | 1.3 | 1.5 | 1.8 | 1.2 | 173 | 1.1 | 1.4 | 1.3 | 0.4 | 32.0 | 83.0 | 1.5 |
| | G33 | 4003 | 61.3 | 1.2 | 63.4 | 75 | 1.2 | 1.8 | 1.5 | 1.4 | 1.9 | 1.6 | 168 | 0.7 | 1.0 | 1.7 | 0.9 | 29.5 | 82.1 | 1.9 |
| | G8 | 3965 | 65.9 | 1.1 | 67.6 | 85 | 1.2 | 1.9 | 1.6 | 1.9 | 1.7 | 1.2 | 182 | 0.7 | 1.4 | 2.0 | 1.2 | 30.1 | 80.9 | 1.9 |
| | G27 | 3965 | 66.4 | 1.4 | 68.4 | 82 | 1.2 | 1.9 | 1.6 | 1.7 | 2.1 | 1.2 | 179 | 0.8 | 0.3 | 1.6 | -0.1 | 30.7 | 79.8 | 1.9 |
| | G5 | 3921 | 68.3 | 1.0 | 70.0 | 87 | 1.1 | 1.9 | 1.9 | 1.5 | 1.9 | 1.1 | 189 | 0.7 | 0.8 | 1.4 | 1.0 | 32.1 | 79.6 | 1.9 |
| | G39 | 3902 | 64.1 | 0.6 | 65.6 | 70 | 1.1 | 2.0 | 1.2 | 1.5 | 1.9 | 1.1 | 161 | 0.9 | 0.6 | 1.8 | 0.8 | 31.4 | 79.3 | 2.1 |
| | G31 | 3820 | 64.8 | 1.0 | 66.6 | 82 | 1.1 | 2.2 | 1.3 | 1.8 | 1.8 | 1.2 | 176 | 0.8 | 0.3 | 1.7 | 1.0 | 27.6 | 80.4 | 2.0 |
| | G10 | 3817 | 67.7 | 2.0 | 70.2 | 86 | 1.1 | 2.0 | 0.9 | 1.9 | 2.0 | 1.2 | 183 | 0.8 | 0.6 | 1.7 | 0.2 | 31.1 | 81.8 | 2.0 |
| | G36 | 3757 | 62.9 | 1.1 | 64.9 | 83 | 1.1 | 1.9 | 1.3 | 1.6 | 2.0 | 1.3 | 179 | 0.8 | 0.8 | 1.9 | 0.7 | 28.6 | 79.5 | 2.0 |
| | G43 | 3750 | 61.9 | 0.9 | 63.8 | 69 | 1.1 | 2.0 | 1.3 | 1.6 | 1.9 | 1.2 | 162 | 0.9 | 0.2 | 1.7 | 1.7 | 31.0 | 77.4 | 1.9 |
| Bottom ten genotypes | G3 | 3014 | 64.1 | 0.8 | 65.7 | 75 | 1.2 | 1.4 | 1.3 | 1.7 | 1.6 | 1.3 | 163 | 0.7 | 0.5 | 1.5 | 1.0 | 30.1 | 76.4 | 2.0 |
| | G42 | 2996 | 63.2 | 1.0 | 64.9 | 71 | 1.0 | 1.8 | 0.9 | 1.6 | 1.7 | 1.2 | 168 | 0.5 | 1.6 | 1.7 | 0.5 | 31.3 | 78.7 | 2.2 |
| | G24 | 2983 | 59.1 | 1.3 | 61.1 | 72 | 1.1 | 2.2 | 1.8 | 1.3 | 2.0 | 1.1 | 167 | 0.7 | 0.7 | 1.7 | 0.8 | 29.1 | 75.9 | 2.2 |
| | G16 | 2901 | 63.2 | 0.8 | 64.9 | 80 | 1.0 | 1.8 | 2.1 | 1.8 | 1.8 | 1.1 | 173 | 0.8 | 0.5 | 1.8 | 0.6 | 32.3 | 77.7 | 2.0 |
| | G7 | 2663 | 65.6 | 1.4 | 67.6 | 78 | 1.1 | 1.9 | 0.9 | 1.4 | 2.0 | 1.3 | 171 | 0.8 | 0.7 | 1.5 | 0.6 | 30.9 | 80.0 | 2.0 |
| | G37 | 2594 | 65.3 | 1.3 | 67.2 | 66 | 1.1 | 1.7 | 1.0 | 1.5 | 2.1 | 1.2 | 162 | 0.6 | 0.2 | 1.9 | 0.9 | 30.4 | 74.1 | 2.0 |
| | G11 | 2517 | 67.8 | 1.0 | 69.4 | 76 | 1.1 | 2.0 | 1.3 | 1.8 | 1.8 | 1.4 | 169 | 0.7 | 0.6 | 1.6 | 0.5 | 26.7 | 77.5 | 2.1 |
| | G38 | 2413 | 69.0 | 1.1 | 70.3 | 78 | 1.0 | 1.9 | 1.0 | 1.4 | 1.9 | 1.4 | 175 | 0.5 | 0.8 | 1.4 | 0.8 | 30.5 | 72.8 | 2.0 |
| | G2 | 2326 | 62.1 | 1.2 | 64.5 | 69 | 1.0 | 2.0 | 1.3 | 1.9 | 1.8 | 1.3 | 156 | 1.0 | 0.5 | 1.5 | 1.5 | 29.3 | 67.4 | 2.1 |
| | G40 | 2295 | 66.5 | 1.1 | 68.0 | 73 | 1.1 | 1.9 | 1.2 | 1.4 | 1.9 | 1.2 | 169 | 0.8 | 0.6 | 1.4 | 0.5 | 33.2 | 77.8 | 2.0 |
| | **Mean** | **3304** | **64.7** | **1.1** | **66.5** | **76.9** | **1.1** | **1.9** | **1.3** | **1.6** | **1.9** | **1.3** | **171.3** | **0.8** | **0.7** | **1.6** | **0.8** | **30.4** | **78.1** | **2.0** |
| | **LSD** | **608** | **1.7** | **1.3** | **1.7** | **8** | **0.1** | **0.3** | **0.8** | **0.3** | **0.5** | **0.3** | **12** | **0.4** | **1.2** | **0.3** | **0.7** | **2.9** | **5.9** | **0.3** |
| | **CV %)** | **31.8** | **4.6** | **194** | **4.6** | **18.2** | **15.2** | **27.1** | **103** | **36** | **40** | **35.9** | **12.1** | **80.3** | **302** | **31.3** | **169** | **16.8** | **13.1** | **27.3** |
| | **Min** | **2295** | **59.1** | **0.6** | **61.1** | **66.0** | **1.0** | **1.4** | **0.9** | **1.3** | **1.5** | **1.0** | **156.0** | **0.5** | **0.1** | **1.3** | **0.0** | **25.9** | **67.4** | **1.5** |
| | **Max** | **4489** | **69.0** | **2.9** | **70.3** | **89.0** | **1.2** | **2.4** | **2.6** | **2.1** | **2.7** | **1.7** | **189.0** | **1.5** | **1.8** | **2.1** | **1.8** | **33.7** | **86.5** | **2.5** |

**LSD = Least significant difference, CV = coefficient of variation, Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number.**

### 4.5.14 Pearson's correlation coefficients between grain yield and other agronomic traits across optimal environments combined for 2011/12 and 2012/13 seasons

Days to anthesis were positively and significantly correlated with all traits apart from anthesis-silking interval (Table 4.16). Grain yield was positively and significantly correlated with days to anthesis days (r = 0.16), days to silking (r = 0.16), plant and ear height (r = 0.16 and r = 0.14, respectively) as well as with number of ears per plant (r = 0.80) and shelling percentage (r = 0.91). Negative correlations among other traits were recorded for example anthesis-silking interval was negatively correlated with root lodging (r = -0.10), husk cover (r = -0.18), leaf blight (r = -0.20) and gray leaf spot (r = -0.10) disease as well as with plant vigor (r = -0.33). Anthesis-silking interval also correlated positively with traits such as days to silking (r = 0.19), plant and ear height (r = 0.27 and 0.25, respectively), MSV (r = 0.09) and 100 seed weight (r = 0.18). Days to silking correlated significantly with all traits except for plant vigor. Ear rots were positively and significantly correlated with stem lodging (r = 0.30), husk cover (r = 0.20), grain texture (r = 0.20), leaf blight (r = 0.50), gray leaf spot (r = 0.40), rust (r = 0.30), MSV (r = 0.60), 100 seed weight (r = 0.30) and plant vigor (r = 0.30). Plant (r = -0.33), and ear height (r = -0.40), were negatively correlated with plant vigour. This implies that tall plants (higher values) were associated with good vigour as lower scores of plant vigour (below 3 in the scale of 1-5) indicates good plant vigour and higher scores indicate poor vigour and short plants. Shelling percentage furthermore correlated positively and significantly with number of ears per plant (r = 0.90), plant height (r = 0.17) and ear height (r = 0.20) (Table 4.16).

**Table 4.16 Pearson's correlation coefficients for grain yield and agronomic traits across all optimal environments for two seasons 2011/12 and 2012/13**

| | GY | AD | ASI | DS | PH | EH | RL | SL | HC | RE | GT | LB | GLS | Rust | MSV | SWT | VIG | SH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AD | 0.16** | | | | | | | | | | | | | | | | | |
| ASI | 0.04 | 0.09 | | | | | | | | | | | | | | | | |
| DS | 0.16** | 1.00** | 0.19** | | | | | | | | | | | | | | | |
| PH | 0.16** | 0.76** | 0.27** | 0.80** | | | | | | | | | | | | | | |
| EH | 0.14** | 0.60** | 0.25** | 0.60** | 0.93** | | | | | | | | | | | | | |
| RL | 0.03 | 0.25** | -0.10** | 0.20** | -0.04 | -0.10 | | | | | | | | | | | | |
| SL | 0.03 | 0.31** | -0.08 | 0.30** | 0.00 | -0.04 | 0.40** | | | | | | | | | | | |
| HC | 0.04 | 0.29** | -0.18** | 0.30** | 0.10** | 0.02 | 0.20** | 0.20** | | | | | | | | | | |
| RE | 0.03 | 0.39** | -0.03 | 0.40** | 0.06 | -0.10 | 0.06 | 0.30** | 0.20* | | | | | | | | | |
| GT | 0.08 | 0.12** | -0.06 | 0.10** | -0.20** | -0.20 | 0.10** | 0.10** | 0.10** | 0.20** | | | | | | | | |
| LB | 0.07 | 0.60** | -0.20** | 0.60** | 0.20** | 0.10 | 0.40** | 0.40** | 0.50* | 0.50** | 0.30** | | | | | | | |
| GLS | 0.08 | 0.60** | -0.10** | 0.60** | 0.30** | 0.20** | 0.20** | 0.30** | 0.40* | 0.40** | 0.30** | 0.70** | | | | | | |
| Rust | 0.07 | 0.46** | -0.06 | 0.50** | 0.32** | 0.18 | -0.20 | 0.03 | 0.30* | 0.30** | 0.30** | 0.50** | 0.60** | | | | | |
| MSV | 0.05 | 0.45** | 0.09** | 0.50** | 0.25** | 0.18 | -0.04 | 0.20** | 0.00 | 0.60** | 0.30** | 0.50** | 0.40** | 0.40** | | | | |
| SWT | 0.08 | 0.58** | 0.18** | 0.60** | 0.36** | 0.30** | 0.20** | 0.30** | 0.00 | 0.30** | 0.40** | 0.50** | 0.50** | 0.30** | 0.60** | | | |
| VIG | 0.04 | 0.12** | -0.33** | 0.09 | -0.33** | -0.40* | 0.40** | 0.40** | 0.30* | 0.40** | 0.30** | 0.70** | 0.50** | 0.20** | 0.30** | 0.20** | | |
| SH | 0.91** | 0.18** | 0.04 | 0.20** | 0.17** | 0.20** | 0.03 | 0.03 | 0.00 | 0.03 | 0.10** | 0.08 | 0.10** | 0.08 | 0.06 | 0.10** | 0.10** | |
| EPP | 0.80** | 0.16** | 0.04 | 0.20** | 0.16** | 0.10** | 0.03 | 0.03 | 0.00 | 0.03 | 0.10** | 0.07 | 0.08 | 0.07 | 0.05 | 0.08 | 0.08 | 0.90** |

****P≤0.01; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), PH = plant height (cm), EH = ear height (cm), RL = root lodging (#), SL = stem lodging (#), HC = husk cover, RE = rotten ears (#), GT = grain texture (1-5), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), Rust = rust disease (1-5), MSV = maize streak virus disease (1-5), SWT = 100 seed weight (g), VIG = vigour (1-5), SH = shelling percentage, EPP = ears per plant (#), # = number.**

### 4.5.15 Principal component analysis results, eigenvalues and eigenvectors for the traits across four optimal environments combined for 2011/12 and 2012/13 seasons

PCA generated 16 principal components (Table 4.17) which accounted for 100% of variability present in the maize genotypes evaluated. The first eight PCs had eigenvalues within a range of 1.0 – 7.1. Their cumulative percentages accounted for 85.9% of the total variation present among the genotypes.

**Table 4.17 Eigenvalues and eigenvectors for the traits across four optimal environments combined for 2011/12 and 2012/13 seasons**

| PC | Eigenvalues | As percentages | Cumulative percentages |
|---|---|---|---|
| 1 | 7.16 | 39.75 | 39.75 |
| 2 | 1.62 | 8.98 | 48.74 |
| 3 | 1.43 | 7.97 | 56.70 |
| 4 | 1.30 | 7.22 | 63.93 |
| 5 | 1.00 | 5.56 | 69.48 |
| 6 | 0.96 | 5.31 | 74.79 |
| 7 | 1.00 | 5.56 | 80.35 |
| 8 | 1.00 | 5.56 | 85.91 |
| 9 | 0.62 | 3.45 | 89.36 |
| 10 | 0.48 | 2.65 | 92.01 |
| 11 | 0.43 | 2.40 | 94.41 |
| 12 | 0.36 | 2.00 | 96.41 |
| 13 | 0.29 | 1.60 | 98.01 |
| 14 | 0.18 | 0.99 | 99.00 |
| 15 | 0.17 | 0.92 | 99.92 |
| 16 | 0.01 | 0.08 | 100.00 |

### 4.5.16 Clustering of the maize genotypes evaluated at four optimal environments combined for the 2011/12 and 2012/13 seasons

Forty five maize genotypes were clustered based on their means for grain yield. At cut off point 1.0, three main clusters were observed (Figure 4.2) with a high cophenetic correlation of $r_{cop} = 0.82$. Thirteen genotypes from CIMMYT-Zimbabwe were grouped in cluster II with only two from CIMMYT-Colombia. The top performing genotypes were grouped in cluster III which comprised of 24 genotypes from both Colombia and Zimbabwe. Cluster I was comprised of six genotypes which were also from both research centers.

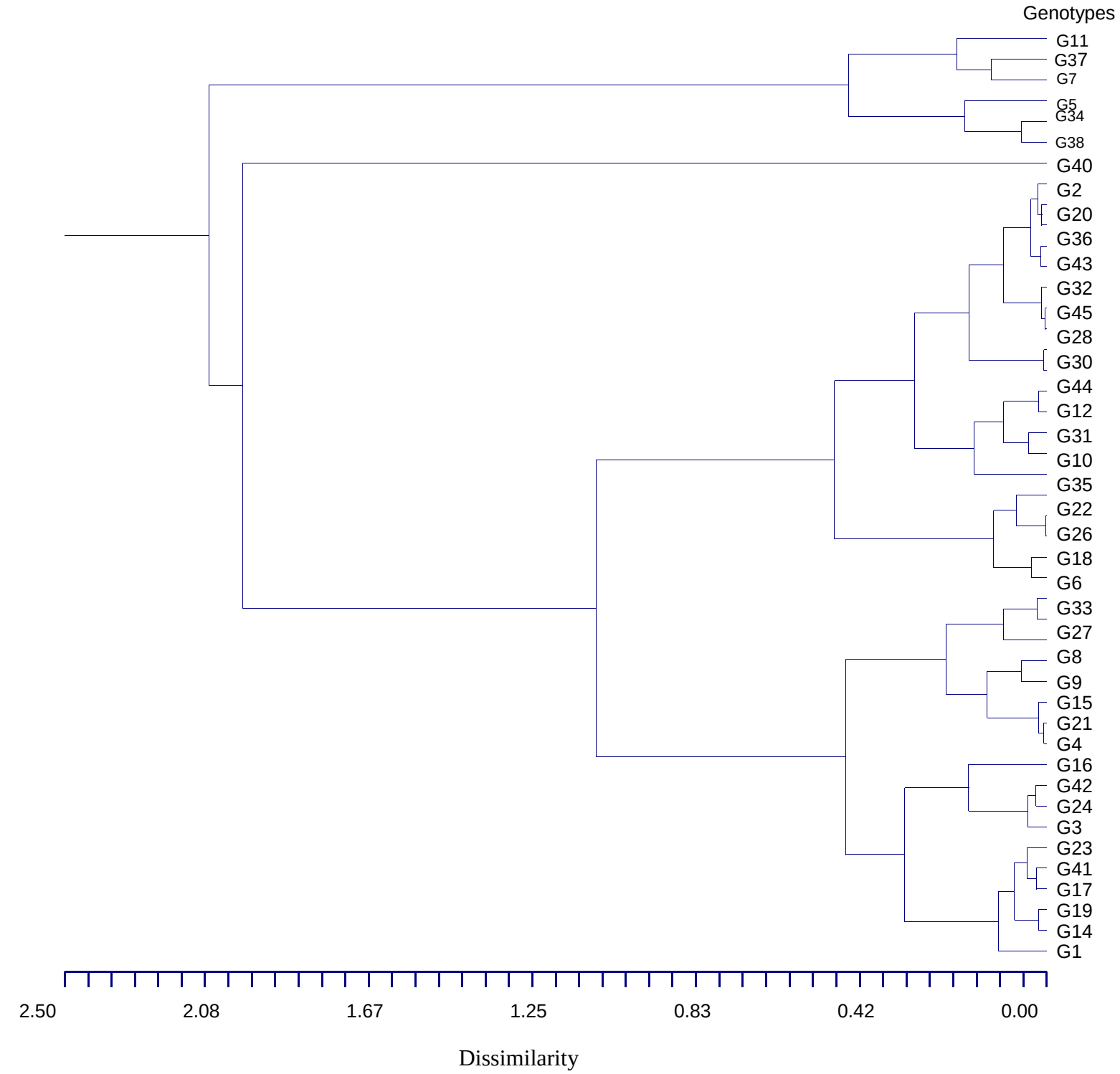


**Figure 4.2 Dendrogram based on Euclidean distance and UPGMA clustering using morphological data for genotypes at four optimal environments combined for 2011/12 and 2012/13 seasons**

### 4.5.17 Combined ANOVA for grain yield and agronomic traits for all environments, optimal and low pH for two seasons 2011/12 and 2012/13

Mean squares from the combined ANOVA across all environments and two seasons are given in Table 4.18. Genotype mean squares were highly significant ($P \leq 0.01$) for grain yield, days to anthesis, days to 50 % silking, ear height, leaf blight disease, husk cover, grain texture, maize streak virus, rust disease, root lodging, 100 seed weight, shelling percentage and plant vigour and significantly ($P \leq 0.05$) with number of ears per plant. Environment mean squares were highly significant for all the traits measured. Season mean squares were highly significant for days to anthesis, anthesis-silking interval, days to 50 % silking, number of ears per plant, plant height, rotten ears and all the diseases, 100 seed weight as well as shelling percentage. GxE was highly significant for grain yield, anthesis date, days to 50% silking, number of ears per plant, husk cover, grain texture, rotten ears, 100 seed weight, and plant vigour as well as MSV and rust. Interaction of GxY was not significant for anthesis-silking interval, number of ears per plant and stem lodging. ExY mean squares were significant for most traits but not for husk cover and rotten ears. Interaction of GxExY was highly significant for grain yield, anthesis date, days to 50% silking, grain texture, root and stem lodging, leaf blight disease and 100 seed weight as well as plant vigor.

### 4.5.18 Estimated contributions to total sum of squares across all environments for two seasons 2011/12 and 2012/13

Contribution to total sum of squares for genotype was the highest for 100 seed weight (4.88%) and MSV (4.85%, Table 4.19). Contribution due to environment was highest for days to 50% silking (80.45%) and for season the highest was rust disease (17.0%). GxE contribution was significant for husk cover (26.3%). The interaction of GxY made the highest contribution to gray leaf spot (5.7%). The interaction of ExY made the highest contribution to root lodging (21.9%) and the interaction of GxExY made the highest contribution to shelling percentage (11.03%) (Table 4.19).

**Table 4.18 Mean squares for combined ANOVA for grain yield and agronomic traits for all environments, optimal and low pH for two seasons 2011/12 and 2012/13**

| **Source** | Genotypes | Environment | Year | GxE | GxY | ExY | GxExY | MSE |
|---|---|---|---|---|---|---|---|---|
| Df | 44 | 7 | 1 | 307 | 44 | 6 | 264 | 1334 |
| GY | 3E+06** | 4.5E+08** | 1.81E+06 | 1E+06** | 3E+06** | 3E+07** | 1E+06** | 764200 |
| AD | 129.46** | 41689.99** | 1709.56** | 32.2** | 59.5** | 4870.22** | 37.4** | 13.54 |
| ASI | 4.99 | 712.359** | 285.673** | 4.24 | 3.73 | 191.02** | 4.865* | 3.99 |
| DS | 114.3** | 45472.23** | 666.96** | 33.53** | 59.48** | 5184.86** | 36.23** | 13.87 |
| EH | 518.4** | 132261.7** | 1176.5* | 340.3* | 458.9** | 15750.1** | 182.2 | 191.3 |
| EPP | 0.16* | 9.09** | 20.16** | 0.12** | 0.15 | 4.58** | 0.13 | 0.12 |
| LB | 0.88** | 83.57** | 12.37** | 0.51 | 1.14** | 42.15** | 0.83** | 0.44 |
| HC | 4.12** | 192.39** | 4.14 | 4.43** | 3.16* | 0.20 | 2.55 | 2.04 |
| GLS | 1.02 | 55.86** | 9.04** | 1.21* | 2.86** | 37.23** | 1.20* | 0.99 |
| GT | 1.52** | 55.77** | 0.01 | 1.51** | 1.52** | 18.64** | 0.78** | 0.65 |
| MSV | 0.41** | 16.45** | 20.68** | 0.28** | 0.41** | 5.35** | 0.19 | 0.20 |
| PH | 5820 | 261853** | 61886** | 5203 | 8806** | 52208** | 6018 | 5349 |
| RE | 1.20 | 97.71** | 14.17** | 2.02** | 2.32** | 4.31 | 3. 40 | 1.00 |
| RL | 6.33** | 395.1** | 9.30 | 3.94* | 8.66** | 595.95** | 5.71** | 3.17 |
| Rust | 0.83** | 89.76** | 213.61** | 0.42** | 0.56** | 21.43** | 0.27 | 0.30 |
| SL | 3.14* | 89.014** | 5.55 | 2.07 | 2.85 | 91.38** | 2.897** | 2.09 |
| SWT | 108.32** | 5805.43** | 740.77** | 34.33** | 56.64** | 2610.86** | 36.15** | 22.66 |
| SH% | 213.40** | 14288.60** | 3331.90** | 154.30 | 205.40* | 1050.30** | 152.30 | 142.20 |
| VIG | 1.72** | 190.8** | 0.24 | 0.72** | 1.23** | 19.75** | 0.59** | 0.43 |

****P≤0.01; *P≤0.05; G = Genotype, E = environment, Y = year, MSE = mean square error, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to 50% silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus diseases (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL = stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage (%), VIG = vigour (1-5), # = number**

**Table 4.19 Relative percent contribution to total sum of squares across two years at eight environments (optimal and low pH)**

| Source | GY | AD | ASI | DS | EH | EPP | LB | GLS | GT | HC | MSV | PH | RE | RL | Rust | SL | SWT | SH | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotypes | 2.55 | 1.54 | 1.49 | 1.27 | 1.59 | 2.06 | 2.73 | 2.02 | 3.29 | 4.10 | 4.85 | 2.07 | 2.52 | 2.56 | 2.90 | 3.40 | 4.88 | 2.21 | 3.31 |
| Environment | 57.80 | 79.10 | 33.79 | 80.35 | 64.70 | 18.13 | 35.52 | 15.12 | 19.25 | 26.11 | 22.31 | 14.81 | 27.90 | 21.81 | 42.71 | 13.14 | 35.66 | 23.59 | 58.56 |
| Year | 0.03 | 0.46 | 1.94 | 0.17 | 0.08 | 5.74 | 0.88 | 0.41 | 0.00 | 0.09 | 5.61 | 0.50 | 0.67 | 0.09 | 16.94 | 0.14 | 0.76 | 0.79 | 0.01 |
| GxE | 6.73 | 2.68 | 8.84 | 2.60 | 7.30 | 10.26 | 9.49 | 14.39 | 22.74 | 26.32 | 16.57 | 12.90 | 25.38 | 9.56 | 8.83 | 13.46 | 9.28 | 11.21 | 9.73 |
| GxY | 2.38 | 0.71 | 1.11 | 0.66 | 1.41 | 1.87 | 3.54 | 5.68 | 3.30 | 3.14 | 4.89 | 3.13 | 4.85 | 3.50 | 1.96 | 3.08 | 2.55 | 2.13 | 2.35 |
| ExY | 3.38 | 7.92 | 7.77 | 7.85 | 5.50 | 7.83 | 8.96 | 6.72 | 4.60 | 0.00 | 2.90 | 2.11 | 1.57 | 21.93 | 3.40 | 6.75 | 13.37 | 1.73 | 2.60 |
| GxExY | 7.24 | 2.68 | 8.70 | 2.41 | 2.80 | 9.70 | 7.74 | 9.49 | 8.46 | 2.54 | 4.46 | 10.70 | 1.31 | 9.24 | 1.91 | 9.41 | 7.99 | 11.03 | 3.42 |
| Rep | 0.17 | 0.00 | 0.00 | 0.00 | 0.00 | 0.20 | 0.30 | 0.40 | 0.00 | 0.70 | 0.30 | 0.10 | 0.10 | 0.10 | 0.60 | 0.10 | 0.50 | 011 | 0.00 |
| Residual | 19.9 | 4.90 | 36.34 | 4.67 | 16.61 | 44.18 | 30.87 | 45.77 | 38.35 | 37.02 | 38.13 | 53.67 | 35.73 | 31.25 | 20.79 | 50.54 | 24.96 | 47.8 | 19.99 |
| CV (%) | 36.00 | 5.00 | 103.10 | 4.90 | 22.20 | 35.1o | 34.90 | 94.00 | 54.80 | 34.40 | 36.50 | 48.90 | 101.00 | 106.00 | 36.40 | 142.80 | 18.40 | 11.90 | 27.50 |
| Min | 0.03 | 0.004 | 0.03 | 0.009 | 0.003 | 0.22 | 0.28 | 0.41 | 0.00 | 0.005 | 0.28 | 0.12 | 0.07 | 0.05 | 0.56 | 0.09 | 0.54 | 0.11 | 0.01 |
| Max | 57.80 | 79.10 | 36.30 | 80.40 | 64.70 | 44.20 | 35.50 | 45.80 | 38.30 | 37.00 | 38.10 | 53.70 | 35.70 | 31.30 | 42.70 | 50.50 | 35.70 | 47.80 | 58.60 |

**G = Genotype, E = environment, Y = year, CV = coefficient of variation, Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), HC = husk cover, MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL = stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number.**

### 4.5.19 Genotypic and phenotypic variance components, broad sense heritability and genetic advance estimates across the combined environments for both 2011/12 and 2012/13 seasons

The results in Table 4.20 indicated that phenotypic variances were higher than genotypic variances. Grain texture (0.6), days to 50% silking (0.5), anthesis date (0.5) and plant vigour (0.5) had relatively high broad sense heritability estimates. The genetic coefficients of variations were lower than phenotypic coefficients of variation (Table 4.21). The expected genetic advance was highest for plant height followed by grain texture. Shelling percentage had the lowest genetic advance value with a high phenotypic coefficient of variation.

**Table 4.20 Genotypic variances, phenotypic variances and heritability estimates across optimal and low pH environments for 2011/12 and 2012/13 seasons**

| Trait | $\sigma^2_g$ | $\sigma^2_p$ | $H^2b$ | $H^2b$ % |
|---|---|---|---|---|
| GY | 2500.00 | 401500.000 | 0.006 | 0.623 |
| AD | 21.250 | 39.300 | 0.541 | 54.071 |
| ASI | 1.200 | 4.400 | 0.273 | 27.273 |
| DS | 22.345 | 40.645 | 0.550 | 54.976 |
| EH | 53.250 | 238.850 | 0.223 | 22.294 |
| EPP | 0.055 | 0.275 | 0.200 | 20.000 |
| LB | 0.145 | 0.735 | 0.197 | 19.728 |
| GLS | 0.450 | 2.050 | 0.220 | 21.951 |
| GT | 0.630 | 1.120 | 0.563 | 56.250 |
| HC | 1.485 | 3.505 | 0.424 | 42.368 |
| MSV | 0.015 | 0.185 | 0.081 | 8.108 |
| PH | 3290.00 | 13596.000 | 0.242 | 24.198 |
| RE | 0.035 | 1.395 | 0.025 | 2.509 |
| RL | 0.540 | 2.740 | 0.197 | 19.708 |
| Rust | 0.040 | 0.360 | 0.111 | 11.111 |
| SL | 0.280 | 2.780 | 0.101 | 10.072 |
| SWT | 19.815 | 40.785 | 0.486 | 48.584 |
| SH | 18.700 | 157.900 | 0.118 | 11.843 |
| VIG | 0.620 | 1.180 | 0.525 | 52.542 |

**$\sigma^2_g$ = genotypic variance, $\sigma^2_p$ = phenotypic variance, $H^2b$ = broad sense heritability, $H^2b$ % = broad sense heritability as percentage, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH= ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), HC = husk cover, MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL= stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number.**

**Table 4.21 Genotypic coefficient of variation, phenotypic coefficient of variation and genetic advance across all eight environments for two years**

| Trait | GCV% | PCV% | GA | GA (% of mean) |
|---|---|---|---|---|
| GY | 10.1 | 128.5 | 0.3 | 10.6 |
| AD | 5.4 | 7.3 | 2.1 | 2.9 |
| ASI | 7.9 | 15.1 | 1.2 | 63.6 |
| DS | 5.4 | 7.3 | 2.1 | 2.8 |
| EH | 9.2 | 19.6 | 1.1 | 1.7 |
| EPP | 2.4 | 5.3 | 0.7 | 70.8 |
| LB | 2.8 | 6.2 | 0.7 | 36.8 |
| GLS | 5.0 | 10.6 | 0.9 | 49.6 |
| GT | 5.2 | 6.9 | 2.2 | 92.6 |
| MSV | 1.1 | 3.9 | 0.1 | 9.0 |
| PH | 46.9 | 95.4 | 1.7 | 108.0 |
| RE | 1.9 | 11.7 | 0.1 | 5.6 |
| RL | 5.7 | 12.8 | 0.5 | 31.2 |
| Rust | 1.6 | 4.9 | 0.2 | 11.9 |
| SL | 5.3 | 16.6 | 0.3 | 26.5 |
| SWT | 8.8 | 12.6 | 2.5 | 9.8 |
| SH | 5.0 | 14.6 | 0.9 | 1.2 |
| VIG | 5.1 | 7.0 | 2.0 | 85.2 |

**GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, GA = genetic advance, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL = stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number.**

### 4.5.20 Mean performance for grain yield and other traits across all environments for 2011/12 and 2012/13 seasons

The grain yield trial mean was 2.4 t ha$^{-1}$ (Table 4.22) and the top performing genotype was G20. None of the top ten genotypes were prolific with a mean number of ears per plant of 1. The genotype most susceptible to gray leaf spot disease was again G 41. The tallest genotype was G7 (213 cm), although it ranked with the bottom ten genotypes. Genotype G27 recorded the highest 100 seed weight (27 g) followed by G35 (26 g). In terms of shelling percentage, genotype G30 (74%) recorded the highest.

**Table 4.22 Mean performance combined across two years and across optimal and low pH environments for 2011/12 and 2012/13 seasons**

| | Entry | GY | AD | ASI | DS | EH | EPP | LB | HC | GLS | GT | MSV | PH | RE | RL | Rust | SL | SWT | SH | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Top 10 | G20 | 2977 | 74.4 | 1.8 | 76.7 | 63.8 | 1.0 | 1.7 | 1.5 | 1.9 | 2.3 | 1.2 | 146 | 1.0 | 1.6 | 1.3 | 0.9 | 27.5 | 77.3 | 1.9 |
| Genotypes | G27 | 2850 | 75.3 | 1.8 | 77.3 | 67.1 | 1.0 | 1.7 | 1.3 | 1.7 | 2.6 | 1.2 | 153 | 1.0 | 1.2 | 1.4 | 1.1 | 29.3 | 74.2 | 2.1 |
| | G8 | 2727 | 74.3 | 1.8 | 76.4 | 65.6 | 1.0 | 2.0 | 1.4 | 2.0 | 2.2 | 1.2 | 153 | 0.8 | 1.6 | 1.6 | 1.4 | 26.3 | 73.0 | 2.2 |
| | G33 | 2725 | 72.1 | 2.1 | 74.9 | 60.9 | 1.0 | 1.7 | 1.3 | 1.7 | 2.4 | 1.3 | 145 | 0.8 | 1.9 | 1.5 | 1.2 | 24.8 | 76.0 | 2.2 |
| | G5 | 2719 | 76.7 | 1.5 | 78.5 | 65.4 | 1.0 | 1.9 | 2.0 | 1.7 | 2.3 | 1.1 | 156 | 1.0 | 1.3 | 1.4 | 1.2 | 27.6 | 75.4 | 2.0 |
| | G30 | 2704 | 73.6 | 2.0 | 76.0 | 63.5 | 1.0 | 1.8 | 1.8 | 1.9 | 2.2 | 1.3 | 147 | 1.0 | 1.6 | 1.5 | 0.6 | 27.2 | 76.3 | 2.1 |
| | G39 | 2680 | 72.8 | 2.0 | 75.4 | 59.9 | 1.0 | 1.9 | 1.2 | 1.8 | 2.3 | 1.2 | 145 | 1.1 | 2.4 | 1.5 | 1.2 | 26.7 | 73.6 | 2.5 |
| | G45 | 2678 | 74.8 | 1.9 | 77.1 | 67.4 | 0.9 | 1.7 | 1.5 | 1.6 | 2.8 | 1.4 | 157 | 0.9 | 1.2 | 1.5 | 0.8 | 28.7 | 72.5 | 2.1 |
| | G22 | 2663 | 71.8 | 2.0 | 74.3 | 62.3 | 1.0 | 1.9 | 1.6 | 1.7 | 2.3 | 1.3 | 146 | 1.0 | 1.8 | 1.5 | 1.0 | 26.1 | 75.1 | 2.6 |
| | G28 | 2635 | 72.9 | 1.7 | 75.0 | 62.1 | 1.0 | 2.0 | 1.4 | 1.9 | 2.7 | 1.2 | 147 | 0.8 | 1.8 | 1.6 | 0.9 | 25.2 | 75.0 | 2.3 |
| Bottom 10 | G16 | 2275 | 71.9 | 2.0 | 73.9 | 60.0 | 0.9 | 1.7 | 2.0 | 1.9 | 2.3 | 1.2 | 143 | 0.9 | 1.2 | 1.6 | 1.2 | 27.8 | 74.2 | 2.3 |
| Genotypes | G41 | 2264 | 69.8 | 1.7 | 72.1 | 54.4 | 0.9 | 1.7 | 1.5 | 2.1 | 2.1 | 1.1 | 137 | 0.9 | 1.4 | 1.6 | 0.8 | 23.9 | 75.1 | 2.5 |
| | G1 | 2259 | 74.9 | 3.1 | 77.1 | 63.9 | 0.9 | 2.0 | 1.2 | 1.9 | 2.1 | 1.2 | 151 | 1.1 | 1.6 | 1.5 | 1.0 | 26.6 | 72.2 | 2.5 |
| | G42 | 2185 | 72.7 | 1.9 | 75.1 | 63.7 | 0.9 | 2.0 | 1.3 | 1.6 | 2.1 | 1.2 | 152 | 1.1 | 1.8 | 1.5 | 0.9 | 26.0 | 73.3 | 2.7 |
| | G7 | 2095 | 72.8 | 2.3 | 75.1 | 61.7 | 0.9 | 1.9 | 1.0 | 1.6 | 2.6 | 1.3 | 213 | 1.1 | 1.4 | 1.3 | 0.8 | 26.7 | 76.3 | 2.4 |
| | G11 | 2009 | 74.7 | 1.6 | 76.6 | 56.2 | 0.9 | 2.0 | 1.4 | 2.0 | 2.3 | 1.3 | 140 | 0.8 | 1.5 | 1.5 | 1.2 | 22.4 | 74.6 | 2.4 |
| | G37 | 2001 | 73.6 | 1.7 | 75.9 | 56.3 | 0.9 | 1.7 | 1.7 | 1.7 | 2.6 | 1.2 | 142 | 0.9 | 1.1 | 1.7 | 1.1 | 24.6 | 72.3 | 2.3 |
| | G40 | 1884 | 75.2 | 1.8 | 77.2 | 60.8 | 0.9 | 1.8 | 1.5 | 1.6 | 2.3 | 1.2 | 149 | 0.9 | 1.7 | 1.4 | 0.7 | 26.5 | 73.2 | 2.2 |
| | G38 | 1883 | 77.1 | 1.3 | 78.5 | 62.8 | 0.9 | 1.8 | 1.3 | 1.7 | 2.3 | 1.4 | 147 | 1.1 | 1.0 | 1.3 | 0.9 | 25.8 | 71.1 | 2.3 |
| | G2 | 1804 | 71.8 | 1.7 | 74.3 | 57.6 | 0.9 | 2.1 | 1.4 | 1.9 | 2.1 | 1.2 | 137 | 0.9 | 2.4 | 1.4 | 1.5 | 24.8 | 66.4 | 2.6 |
| | **Mean** | **2401** | **73.7** | **1.9** | **75.9** | **61.8** | **1.0** | **1.9** | **1.5** | **1.8** | **2.3** | **1.2** | **150** | **1.0** | **1.6** | **1.5** | **1.0** | **26.2** | **73.8** | **2.3** |
| | **LSD** | **506** | **2.4** | **1.01** | **2.4** | **3.9** | **0.3** | **0.44** | **0.8** | **0.7** | **0.56** | **0.36** | **58** | **0.68** | **0.94** | **0.32** | **0.9** | **2.6** | **7.5** | **0.4** |
| | **CV** | **36** | **5** | **103** | **4.9** | **22.2** | **35** | **34.9** | **94** | **55** | **34.4** | **36.5** | **49** | **101** | **106** | **36.4** | **143** | **18** | **11.9** | **28** |
| | **Min** | **1804** | **69.8** | **1.3** | **72.1** | **54.4** | **0.9** | **1.7** | **1.0** | **1.6** | **2.1** | **1.1** | **137** | **0.8** | **1.0** | **1.3** | **0.6** | **22.4** | **66.4** | **1.9** |
| | **Max** | **2977** | **77.1** | **3.1** | **78.5** | **67.4** | **1.0** | **2.1** | **2.0** | **2.1** | **2.8** | **1.4** | **213** | **1.1** | **2.4** | **1.7** | **1.5** | **29.3** | **77.3** | **2.7** |

**LSD = Least significant difference, CV = coefficient of variation, Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL = stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number.**

**Table 4.23 Pearson's correlation coefficients for grain yield and agronomic traits across optimal and low pH environments for 2011/12 and 2012/13 seasons**

| | GY | AD | ASI | DS | PH | EH | RL | SL | HC | RE | GT | LB | GLS | RUST | MSV | SWT | VIG | SH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AD | 0.12** | | | | | | | | | | | | | | | | | |
| ASI | 0.23** | 0.09** | | | | | | | | | | | | | | | | |
| DS | 0.12** | 0.99** | 0.09** | | | | | | | | | | | | | | | |
| PH | 0.05 | 0.14** | -0.01 | 0.11** | | | | | | | | | | | | | | |
| EH | 0.06** | 0.02 | 0.01 | 0.01 | 0.62** | | | | | | | | | | | | | |
| RL | 0.03 | 0.20** | 0.01 | 0.20** | -0.01 | 0.02 | | | | | | | | | | | | |
| SL | 0.03 | 0.25** | 0.01 | 0.24** | -0.01 | -0.1** | 0.21** | | | | | | | | | | | |
| HC | 0.01 | 0.18** | 0.00 | 0.15** | 0.11** | 0.05 | 0.03 | 0.09** | | | | | | | | | | |
| RE | -0.02 | 0.35** | -0.03 | 0.34** | -0.06** | -0.2** | -0.02 | 0.19** | 0.20** | | | | | | | | | |
| GT | 0.06 | 0.09 | 0.01 | 0.09 | -0.06 | -0.14 | 0.05 | 0.03 | -0.02 | 0.10 | | | | | | | | |
| LB | 0.04 | 0.40** | 0.01 | 0.40** | 0.06 | -0.01 | 0.28** | 0.29** | 0.25** | 0.34** | 0.3** | | | | | | | |
| GLS | 0.03 | 0.38** | 0.00 | 0.37** | 0.08** | 0.00 | 0.18** | 0.14** | 0.15** | 0.26** | 0.27** | 0.58** | | | | | | |
| RUST | 0.01 | 0.22** | 0.00 | 0.20** | 0.23** | 0.18** | -0.2** | 0.07** | 0.30** | 0.27** | 0.28** | 0.51** | 0.45** | | | | | |
| MSV | 0.02 | 0.35** | -0.02 | 0.33** | 0.08** | 0.03 | 0.00 | 0.22** | 0.08** | 0.41** | 0.26** | 0.58** | 0.39** | 0.48** | | | | |
| SWT | 0.07** | 0.45** | 0.02 | 0.44** | 0.21** | 0.25** | 0.30** | 0.18** | -0.01 | 0.16** | 0.25** | 0.32** | 0.30** | 0.17** | 0.4** | | | |
| VIG | 0.04 | 0.20** | 0.01 | 0.19** | -0.1** | -0.2** | 0.38** | 0.24** | 0.12** | 0.25** | 0.22** | 0.48** | 0.34** | 0.17** | 0.18** | 0.3** | | |
| SH | 0.55** | 0.15** | 0.19** | 0.15** | 0.09** | 0.11** | 0.05 | 0.04 | 0.05 | 0.04 | 0.12** | 0.09** | 0.08** | 0.08** | 0.07** | 0.12** | 0.09** | |
| EPP | 0.46** | 0.24** | 0.19** | 0.24** | 0.10** | 0.10** | 0.05 | 0.04 | 0.05 | 0.04 | 0.13** | 0.09** | 0.08** | 0.08** | 0.07** | 0.12** | 0.10** | 0.6** |

****P≤0.01; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), PH = plant height (cm), EH= ear height (cm), RL = root lodging (#), SL= stem lodging (#), HC = husk cover, RE = rotten ears (#), GT = grain texture (1-5), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), Rust = rust disease (1-5), MSV = maize streak virus disease (1-5), SWT = 100 seed weight (g), VIG = vigour (1-5), SH = shelling percentage, EPP = ears per plant (#), # = number.**

### 4.5.21 Pearson's correlation coefficients between grain yield and other agronomic traits across optimal and low pH environments combined for 2011/12 and 2012/13 seasons

Grain yield was positively and significantly correlated with number of ears per plant (r = 0.46), anthesis date (r = 0.12), anthesis-silking interval (r = 0.23), day to 50% silking (r = 0.12), ear height (r = 0.06), 100 seed weight (r = 0.07) and shelling percentage (r = 0.55) (Table 4.23). Correlation among other traits indicated that shelling percentage was positively and significantly correlated with anthesis date (r = 0.15), anthesis-silking interval (r = 0.19), days to 50% silking (r = 0.15) and number of ears per plant (r = 0.06) as well as plant height and ear height (r = 0.09 and 0.11). Ear rots were positively and significantly correlated with traits such as days to anthesis (r = 0.35), day to 50% silking (r = 0.34), stem lodging (r = 0.19), husk cover (r = 0.20), leaf blight (r = 0.34), gray leaf spot (r = 0.26), rust (r = 0.27), MSV (r = 0.41). Ear height (r =-0.2) was negatively correlated with plant vigour and seed size (100 seed weight) was positively correlated with grain texture (r = 0.25) and plant vigour (r = 0.3).

### 4.5.22 Principal component analysis results, eigenvalues and eigenvectors for the traits across all environments combined for 2011/12 and 2012/13 seasons

Results indicated that eight principal components were generated across all environments and these accounted for 100% variability present in the maize genotypes evaluated (Table 4.24). The first five PC had higher Eigenvalues and their cumulative percentages accounted for 71.1% of the total variation present among the genotypes.

**Table 4.24 Eigenvalues, percentages and cumulative percentages for the measured and derived data across four low pH soil environments combined for 2011/12 and 2012/13 seasons**

| PC | Eigenvalues | As percentages | Cumulative percentages |
|---|---|---|---|
| 1 | 2.2 | 18.5 | 18.5 |
| 2 | 1.8 | 15.7 | 34.2 |
| 3 | 1.5 | 13.1 | 47.4 |
| 4 | 1.5 | 12.5 | 59.8 |
| 5 | 1.3 | 11.3 | 71.1 |
| 6 | 1.2 | 10.0 | 81.1 |
| 7 | 1.1 | 9.7 | 90.8 |
| 8 | 1.1 | 9.2 | 100.0 |

**Table 4.25 Phenotypic and genotypic variances for grain yield and other traits at four optimal environments**

| Trait | $\sigma^2_g$ | $\sigma^2_p$ | $H^2b$ |
|---|---|---|---|
| AD | 2.26 | 4.34 | 0.52 |
| DS | 2.19 | 4.34 | 0.51 |
| EPP | 3E-04 | 0.001 | 0.27 |
| GY | 669.20 | 2E+05 | 0.01 |

**$\sigma^2g$ = genetic advance, $\sigma^2p$ = phenotypic variance, $H^2b$ =broad sense heritability, AD = days to anthesis, DS = days to silking (days), EPP = ears per plant (#), GY = grain yield (kg ha$^{-1}$), # = number.**

### 4.5.23 Clustering of the maize genotypes evaluated at four low pH and four optimal environments combined for the 2011/12 and 2012/13 seasons

The dendrogram was constructed using the UPGMA cluster analysis method based on morpho-agronomic data across optimal and low pH environment Figure 4.3. Cluster two genotypes comprised of well adapted released OPVs G44 (ZM523) and G43 (ZM309) alongside some four of the top ten based on mean grain yield across optimal and low pH environment (Table 4.22) G30, G33, G8 and G5. Though Cluster three was larger than cluster one, the two did not show any clear pattern of clustering. Both groups of genotypes from CIMMYT-Colombia and CIMMYT-Zimbabwe had equal chances to be grouped in the two clusters.

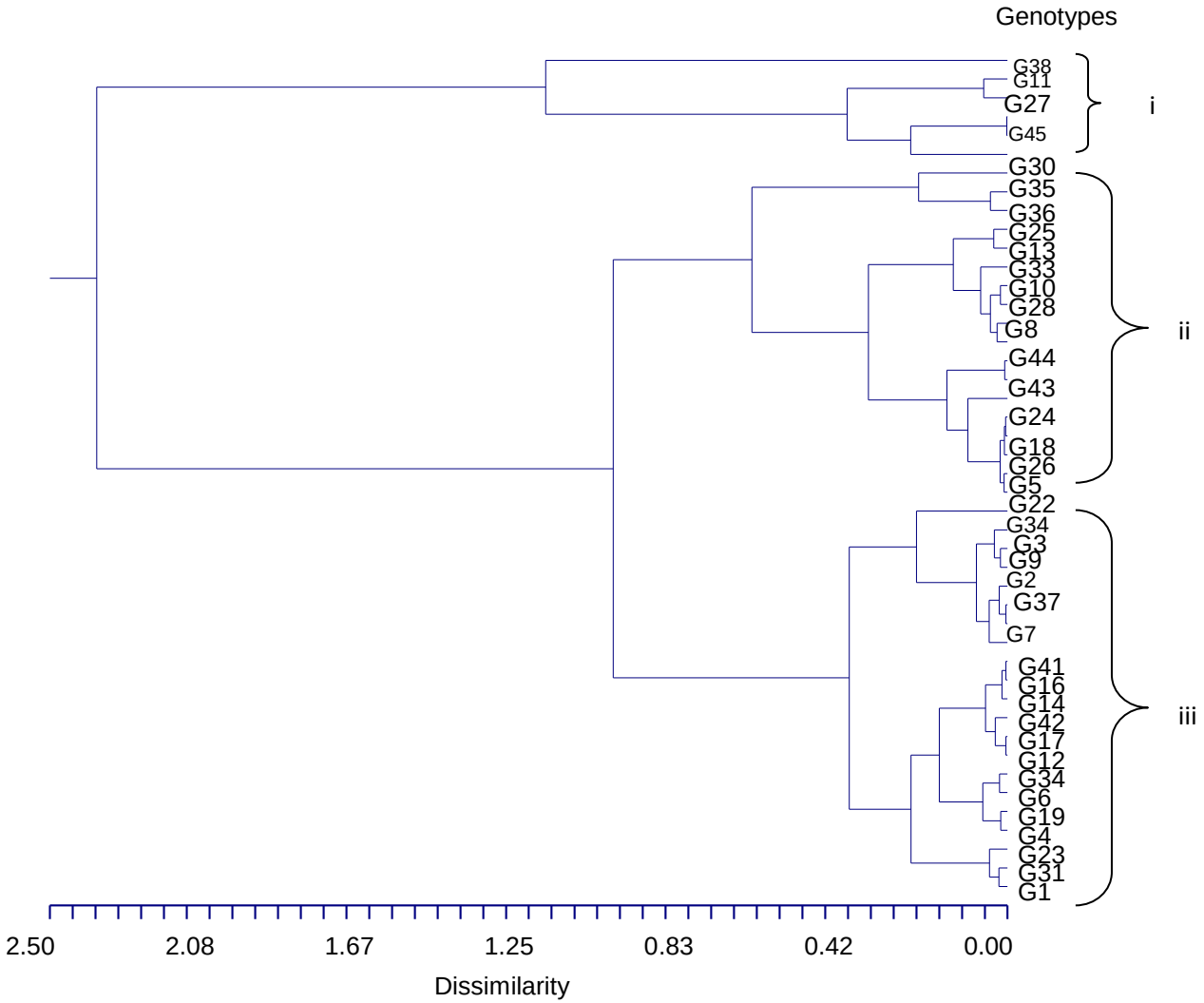


**Figure 4.3 Dendrogram based on Euclidean distance and UPGMA clustering using morphological data for genotypes at four low pH and four optimal environments combined for 2011/12 and 2012/13 seasons**

## 4.6 Discussion

Low pH soil is one of the most constraining edaphic factors contributing to low crop production. Even liming is known to be inefficient as it is restricted to the top soil layer while the sub-soil surface layers with toxic Al remain acid (Custódio *et al.*, 2002). In the present study, soil analysis from the 30 cm soil profile indicated that the sites had different soil pH levels. Lunyangwa low pH site had the most acidic soils as compared to Tsangano and Bembeke low pH sites. Bvumbwe was classified as having moderately acidic soils based on the Soil Test Interpretation Guide (Horneck *et al.*, 2011). In terms of inherent soil fertility with due considerations to resource poor farmers, all the sites had a low N concentration in the top soil. The across site analysis for low pH sites, optimal sites and combined across environments and seasons indicated highly significant effects for most of the traits (Tables 4.3, 4.11 and 4.18). This was an indication that genetic variability existed and suggested the possibility of selection and further improvement. The across sites ANOVA for low pH environments revealed that sites were significantly different and this confirmed soil analysis results. Similarly the ANOVA for optimal sites were also significantly different owing to the fact that Chitedze and Meru were in the mid-altitude ecology while Baka and Chitala were in the low-land ecology. Seasons were also significantly different for a number of traits, suggesting that selection from one season's data may not be reliable but across season data could provide reliable information about the genotypes. Partitioning of variation into four sources of interactions followed the same trend such that the effects of GxE, GxY, ExY, and GxExY were also significant for a number of traits.

Different sources of variation made different contributions to total variation with respect to various traits (Tables 4.4, 4.12 and 4.29). On average, environments made the highest contribution to total variation in all tested environments. Viana *et al.* (2009) indicated that spatial heterogeneity in experimental areas is a common fact and is related to the processes of soil genesis.

In general, the effects of low pH soil contributed to reduction in grain yields and yield components under low pH (Tables 4.5 and 4.7). The combined mean reduction was 69.9% and this is consistent with other findings (Welcker *et al*., 2005). Plant height reduction, reduced number of ears per plant and shelling percentage reduction under low pH soil conditions could be due to the indirect effect of the impaired nutrient uptake by maize plants as a result of inhibition of root development. This confirms results of Duque-Varga *et al.* (1994) who found that root inhibition leads to low water and nutrient uptake and low maize yields. The mean grain yield in combined analysis for low pH sites was 1.5 t $ha^{-1}$ (Table 4.8). This is just slightly above the average maize yields for the country (1.3 t $ha^{-1}$) (MOA, 1994). The mean grain yield trial in the combined ANOVA for optimal conditions was 3.3 t $ha^{-1}$ (Table 4.15) and for the combined environments was 2.4 t $ha^{-1}$ (Table 4.22). Comparison of the glasshouse hydroponic trial and field trial results indicated that of the top 10 yielding genotypes, SYN DTE-STY-W-B performed well and ranked first in terms of RTi with a NSRL of 2.5 cm and this was followed by VPO717 with RTi (1.0) and NSRL (1.7 cm). These results also confirm that the best performer in the field may not be the most tolerant to low pH stress because low pH is considered a complex stress which is associated with diseases and other stresses.

The partitioning of variance into its components allows plant breeders to estimate the relative importance of the various determinants of the phenotype, in particular the role of heredity versus environment (Duvick, 1986; Volenec *et al*., 2002). In the present study (Tables 4.6, 4.13 and 4.20), the obtained phenotypic variances ($\delta^2p$) were higher than genotypic variances ($\delta^2g$) at all the environments with low pH sites recording relatively lower values for both variance components.

According to Dabholkar (1992) heritability of a character is classified as low (5-10%), medium (10-30%) and high (30-60%). In the present study, results for low pH environments combined across seasons recorded high heritability values for anthesis date, days to 50% silking, husk cover, grain texture, 100 seed weight and plant vigour. At optimal environments 18 traits had high heritability values. Only root lodging (1.97%) had low value while anthesis-silking interval (18.82) and husk cover (13.98%) had medium heritability values. The results for

optimal environments were consistent with what was reported by Aminu and Izge (2012) and Bello *et al.* (2012).

Genetic advance shows the degree of gain that can be obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection (Bello *et al.*, 2012). Results for the optimal environment (Table 4.14) indicated higher genetic advance potential for grain yield and plant height and this was consistent with what was reported by Vashistha *et al.* (2013).

Phenotypic correlation is the association between two characters that can be directly observed, or can be determined from measurements of two characters in a number of individuals of the population (Falconer and Mackay, 1996). In the present study, correlation analysis was performed to check if grain yield was associated with some yield and yield components under low pH stress, optimal and across environments (Table 4.9; Table 4.17; Table 4.23). Significant and positive correlation between grain yield with both number of ears per plant and shelling percentage was observed in all combined analyses. In the present study low values of significant correlation coefficients were recorded for certain traits as was expected due to the large dataset used, but only values of 0.2 and larger were discussed in order to emphasize the most important correlations. In this study low pH stress contributed to lower values of significant correlation coefficients due to the stress effect at phenotypic level. Positive and significant correlation was observed for 100 seed weight under low pH environment only and not in the combined environment (Table 4.23). The results were consistent with other reports (Alvi *et al.*, 2003, Sofi and Rather, 2007; Sumathi and Muralidharen, 2010).

Anthesis date was positively and significantly correlated with grain yield at low pH and optimal environments except when combined across both environments. This was probably due to differences in ecology for the low-land optimal conditions. Low altitudes are associated with high temperatures and short seasons such that late maturing genotypes tend to perform poorly because they don’t have adequate time to accumulate adequate carbohydrates.

Under low pH conditions, higher number of days to anthesis date were recorded as compared to optimal environments (mean AD value of 83 for low pH versus 65 for optimal). The AD results suggest that selection for low pH should be done under low pH conditions because what could be classified as early under low pH may not be tolerant to other stresses like fungal diseases due to prolonged humid conditions and longer seasons in low pH environments. Reports from other researchers (Brun and Dudley, 1989; Byrne *et al*., 1995; Bänziger *et al*., 1997) indicated that selection under stress is more effective in maize, than indirect selection under optimal conditions.

Negative correlation was observed for grain yield and ear height across low pH and combined low pH and optimal environments and this was consistent with other reports (Srećkov *et al*., 2010). Yield was also negatively correlated with plant vigour due to the fact that a higher score in this study for vigour refers to poor vigour hence the reverse should be true that grain yield was positively correlated with plant vigour. The two are measured in different direction such that a score of one is the best for plant vigour in the scale of 1-5 while for grain yield the highest yielding genotype should record the highest number of weight units. It implies that an increase in plant vigour is associated with an increase in yield and a decrease in vigour is associated with decrease in yield. Stem lodging was also positively and significantly correlated with grain yield which was probably due to the indirect effect of low pH on the stalks of maize plants. According to Kochian *et al*. (2005) Al rapidly and effectively inhibits the influx of $Ca^{2+}$ into cells by modulating the activity of transporters and by changing the membrane potential. Stalks of maize plants under low pH are likely to be weak due to low levels of Ca which causes low rigidity of cell walls and may not be able to support the weight of maize ears; hence higher yields were associated or correlated with stem lodging under low pH soil environments.

Clustering of maize genotypes based on morphological data across low pH environments showed that maize genotypes had similar chances of being grouped in any of the four clusters. The top five genotypes in terms of mean grain yield performance were comprised of two from CIMMYT-Colombia and three from CIMMYT-Zimbabwe. On the other hand when the genotypes were clustered using across optimal and low pH environment morphological data, the well adapted released OPVs G44 (ZM523) and G43 (ZM309) alongside some four of the top ten based on mean grain yield across optimal and low pH environment G30, G33, G8 and

G5. This suggested that the four entries and the rest in this cluster are likely to be adapted to Malawi like the released ZM523 and ZM309. The two were the first drought tolerant OPVs to be released in the country.

### 4.7 Conclusions and recommendations

Low pH soil is one of the abiotic factors contributing to low yields in Malawi. In this study it contributed to reduction in grain yields and yield components for the maize genotypes which were evaluated. The mean reduction in yield and yield components of 69.9% due to impaired nutrient uptake confirmed the various reports on the effect of low pH stress on yield of maize. In this study, genotypes LPHpop16, LPHpop3, VPO739, VPO5173 and Low N Pool C3-B had relatively better performance under low pH soil conditions. It is interesting to note that among the top 10 genotypes it was SYN DTE –STY-W-B that ranked first in terms of RTi with a NSRL of 2.5 cm in the glasshouse hydroponic experiment and this was followed by VPO717 with RTi (1.0) and NSRL (1.7 cm). These OPVs will be crossed to disease tolerant lines to generate source populations for inbred lines extraction for use in breeding programme for low pH tolerance.

Phenotypic traits associated with grain yield, such as plant vigour, 100 seed weight, shelling percentage, number of ears per plant, ear height and plant height can be used alongside grain yield when selecting germplasm for tolerance to low pH stress. Traits associated with reproduction such as anthesis date and days to 50% silking tend to be influenced by lower temperatures under low pH environments such that early maturing genotypes mature late and selection may not be effective when done across optimal and low pH environments. In other words these results suggested that selection for low pH tolerance could be effectively carried out *in situ* and not indirectly under optimal environments. There is need to establish the cut off point for significant correlation coefficients under stress as the relationship is affected at phenotypic level as opposed to optimal environment.

## 4.8 References


Agrobase. 2010. Agronomix, Generation II. Agronomix software, Inc. 71 Waterloo St. Winnipeg, Manitoba, R3N054, Canada.

Alvi, M.B., M. Rafique, M.S. Tariq, A. Hussain, T. Mahmood and M. Sarwar. 2003. Character association and path coefficient analysis of grain yield and yield components maize (*Zea mays* L.). Pakistan Journal of Biological Sciences 6: 136-138.

Aminu, D. and A.U. Izge., 2012. Heritability and Correlation Estimates in Maize (*Zea mays* L.) Under Drought Conditions in Northern Guinea and Sudan Savannas of Nigeria. World Journal of Agricultural Sciences 8: 598-602.

Bänziger, M., F.J. Betran and H.R. Lafitte.1997. Efficiency of high nitrogen selection environments for improving maize for low-nitrogen target environments. Crop Science 37: 1103–1109.

Bello, O.B., S.A. Ige, M.A. Azeez, M.S. Afolabi, S.Y. Abdulmaliq and J. Mahamood. 2012. Heritability and Genetic Advance for Grain Yield and its Component Characters in Maize (*Zea Mays* L.). International Journal of Plant Research 2: 138-145

Brun, E.L. and J.W. Dudley. 1989. Nitrogen response in the USA and Argentina of corn populations with different proportion of flint and dent germplasm. Crop Science 29: 565-569.

Byrne, P.F., J. Bolaños, G.O. Edmeades and D.L. Eaton. 1995. Gains from selection under drought versus multilocation testing in related tropical maize populations. Crop Science 35: 63-69.

Custódio, C.C., D.C. Bomfim, S.M. Saturnino and N.B. Machado Neto. 2002. Estresse por alumínio e por acidez em cultivares de soja. Scientia Agricola 59: 145-153.

Dabholkar, A.R. 1992. Elements of Biometrical Genetics. Concept Publ. Camp., New Delhi, India.

Duque-Vargas, J., S. Pandey, G. Granados, H. Ceballos and E.R. Knapp. 1994. Inheritance of tolerance to soil acidity in tropical maize. Crop Science 34: 50-54.

Duvick, D.N. 1986. Plant breeding: Past achievements and expectations for the future. Economic Botany 40: 289-297.

Falconer, D.S. and T.F.C. Mackay. 1996. Introduction to Quantitative Genetics (4thedn) Longman Group Limited. England.

FAOSTAT. 2013. Statistical Database of the Food and Agriculture of the United Nations.http://www.fao.org

GenStat. 2013. Introduction to GenStat for Windows. 16.1th edition. VSN International, Hemel Hempstead, Hertfordshire HPI. IES, UK.

Hallauer, A.R. and F.J.B. Miranda. 1988 Quantitative Genetics in Maize Breeding. Iowa State Univ. Press, Ames.

Hintze, J.L. 2007. Number Cruncher Statistical System (NCSS). Kaysville Utah. USA.

Horneck, D.A., D.M. Sulivan, J.S. Owen and J.M. Hart., 2011. Soil Test Interpretation Guide. Oregon State University Extension Service.

Kochian, L.V., M.A. Piñeros and O.A. Hoekenga. 2005. The physiology, genetics and molecular biology of plant aluminium resistance and toxicity. Plant and Soil 274: 175-195

Kumwenda, I. and R. Kachule. 2003. Report on Stakeholders' Meeting on Farmer Organisations in Malawi. Kalikuti Hotel, Lilongwe, 18th -19th June 2003.

Mehlich, A. 1984. Mehlich III soil test extractant: a modification of the Mehlich II extractant. Communications in Soil Science and Plant Analysis 15: 1409-1416.

MOA- Ministry of Agriculture. 1994. Guide to Agriculture Production. Ministry of Agriculture, Lilongwe. Malawi

MOA - Ministry of Agriculture. 2003. National Fertilizer Strategy, Lilongwe. Malawi.

MOA- Ministry of Agriculture, 2005. Crop Estimates for 2004/5. Lilongwe. Malawi.

Munthali, M.W. 2007. Integrated Soil Fertility Management Technologies: A Counteract to Existing Milestone in Obtaining Achievable Economical Crop Yields in Cultivated Lands of Poor Smallholder Farmers in Malawi. In: Advances in intergrated soil Fertility Management in Sub-Saharan Africa: Challenges and opportunities, pp. 531-536.

Sofi, P. and A. G. Rather. 2007: Studies on genetic variability, correlation and path analysis in maize (*Zea mays* L.). Genetic Cooperation Newsletter. 81: 26-27

Srećkov, Z., J. Boćanski, A. Nastasić, I. Đalović and M. Vukosavljev. 2010. Correlation and path coefficient analysis of morphological traits of maize (*Zea mays* L.). Research Journal of Agricultural Science 42: 292-296.

Sumathi, P. and V. Muralidharan. 2010. Analysis of genetic variability, association and path analysis in the hybrids of sesame (*Sesamum indicum* L). Tropical Agricultural Research and Extension 3: 63-67

Sumathi, P., Nirmalakumari and K. Mohanraj. 2005. Genetic variability and traits interrelationship studies in industrially utilized oil rich CYMMIT lines of maize (*Zea mays* L). Madras Agric. J. 92: 612-617.

Vashistha, A., N. N. Dixit, S. K. Sharma and S. Marker. 2013. Studies on heritability and genetic advance estimates in maize genotypes. Bioscience Discovery 4: 165-168.

Viana, J.M.S., V.R. Faria and A.C. Silva. 2009. Bias in the prediction of genetic gain due to mass and half-sib selection in random mating populations. Genetics and Molecular Biology 32: 497-506.

Volenec, J.J., S.M. Cunningham, D.M. Haagenson, W.K. Berg, B.C. Joern and D.W. Wiersma. 2002. Physiological genetics of alfalfa improvement: Past failures, future prospects. Field Crops Research 75: 97-110.

Welcker, C., C. The, B. Andreau, C. De Leon, S. N. Parentoni, J. Bernal, J. Felicite, C. Zonkeng, F. Salazar, L. Narro, A. Charcosset and W. J. Horst. 2005. Heterosis and Combining Ability for Maize Adaptation to Tropical Acid Soils: Implications for Future Breeding Strategies. Crop Science 45: 2405-2413.

Zambezi, B.T., J.D.T. Kumwenda and R.B. Jones. 1993. Closing the maize yield gap in Malawi. In: D.C. Munthali, J.D.T. Kumwenda and F. Kisyombe (Eds.) Proceedings of the Conference on Agricultural Research for Development. Lilongwe and Zomba, Malawi: Department of Agricultural Research and Chancellor College.

# CHAPTER 5

## Genotype x environment interactions and stability analysis for tropical and sub-tropical maize genotypes in Malawi

### 5.1 Abstract

Maize, which is the staple food crop in Malawi, is widely cultivated in both marginal and favourable arable land, resulting in low yields in some environments with a high GEI. In this study 45 maize genotypes were evaluated across eight locations for two years using an (0.1) alpha lattice design with three replications. The objective was to study the GEI and stability of the tropical and sub-tropical maize genotypes. In the AMMI biplot, genotypes LPHpop21, VPO52, VPO72, VPO744 and VPO96 were identified as stable. VPO97 was identified as the most unstable genotype. Chitala optimal site was identified as the most discriminating environment for the genotypes, while Chitedze optimal was identified as a suitable environment. Clustering of genotypes at cut off point 1.0 indicated a cophenetic correlation of $r_{cop} = 0.82$ with four clusters and the results were similar to that of AMMI such that cluster III was comprised of genotypes that were stable, except LPHpop21 which was in its own cluster and was considered to be the most stable and best performer in terms of grain yield. Similarly clustering of environments at cut off point 1.0 indicated a cophenetic correlation of $r_{cop} = 0.84$ with three clusters that grouped the lowest pH sites in cluster I and the second most low pH sites in cluster II. All optimal sites were grouped in the third cluster. Clustering identified the low nitrogen site as similar to the lowest pH sites in terms of its environmental mean. The stable genotypes identified in this study will be used as base populations in the breeding programmes to generate new inbred lines.

### 5.2 Introduction

Maize is an important staple food and world-wide it is a widely grown cereal crop ranging from $58^{o}$ north to $40^{o}$ south with respect to latitude, from sea level to 3808 masl in terms of

altitude and under 25.4 to 1016 cm annual rainfall (Brewbaker, 1985; Hallauer and Miranda, 1988). According to "The Guide to Agricultural Production for Malawi" (MOA, 1994), there are two agro-ecologies for maize cultivation in the country namely: low-land or low-altitude (<600 masl) and mid-altitude areas. The low-altitude area mostly covers the lakeshore districts and the Shire Valley Districts. This region has its own challenges which include prolonged dry spells, early cessation of rains, high temperatures and floods. The mid-altitude areas is the main ecology in terms of size and it is 600 - 1300 masl. This is where most of the maize is cultivated and the major environmental challenges include fungal diseases, low pH, low N and witch weed, which is associated with low-soil fertility.

The challenge is to develop varieties of maize with a high grain yield and stable performance in the low pH areas. Some genotypes tend to exhibit good performance in some environments but not in others (Ramagosa and Fox, 1993). The basic cause of differences in yield stability between genotypes is the wide occurrence of GEI. These interactions can be partly understood as a result of different genotypes responding differently to different environmental stresses such as low pH, diseases and other factors. Plant breeders endeavour to develop improved genotypes that are superior not only in grain yield but also in a number of other agronomic and quality characteristics over a relatively wide range of environmental conditions. This interaction is important to geneticists and plant breeders because of the magnitude of the interaction components which provides information concerning the adaptation of a given crop variety (Myers, 2004).

GEI may alter the performance or development of a crop variety, thus the extent of the environmental effect on a trait determines the importance of replicating in time and space such as testing over years and locations. The multilocation evaluation, however, results in GEIs which are difficult to interpret by plant breeders and agronomists and this often reduces the efficiency in selecting the best genotypes (Annicchiarico and Perenzin, 1994). The presence of GEI may mean that a superior variety in one location is not necessarily the best in another environment. Kang *et al.* (1991) suggested that selection based on yield only may not always be adequate when GEI is significant. The analysis of GEI is regarded as an important strategy used by plant breeders to evaluate crop varieties for adaptation and also for making selections

for parents for base populations (Aina *et al.,* 2007). The development of new crop varieties is expensive and time consuming because of the procedure involved in making sure a stable variety is identified.

According to Myers (2004) stability refers to the character of a crop variety that withstands fluctuations of environments. The stability analysis for the interpretation of GEI was first proposed by Yates and Cochran in 1938. Their proposed methodology was based on linear regression of variety yield on experimental mean yield in order to observe varietal stability across varying environments (Finlay and Wilkinson, 1963; Eberhart and Russell 1966). Stability analysis has been adapted for use in comparing agronomic treatments across different environments consisting of the linear regression of treatment mean yield on the environmental mean (Raun *et al*., 1993). The concept of stability has been defined in many ways by many researchers and several biometrical methods, including univariate and multivariate (Lin *et al.,* 1986; Becker and Leon, 1988; Crossa, 1990). Stability indices are usually univariate while a genotype's response to different environments is considered to be multivariate (Lin *et al*., 1986). Through multivariate analysis, genotypes with similar responses are observed to cluster together (Crossa, 1990). There are two types of biplots that have been widely used to visualize GEI and these are the AMMI and, genotype and genotype x environment interaction (GGE) biplots (Gauch, 1988; Gauch and Zobel, 1997; Yan *et al.*, 2000; Ma *et al.,* 2004). The main difference between the two approaches is that GGE biplot analysis is based on location centred PCA while AMMI analysis is observed as double centred PCAs. When a number of environments and genotypes are involved it is not always easy to visualize 'which won where' in the AMMI biplot and at times it could be deceptive, as suggested by Yan *et al.* (2007). Still AMMI is regarded as a better tool for presenting conclusions rather than a tool for determining "which won where".

To ensure that suitable varieties are recommended for cultivation by farmers in the country, the Agricultural Technology Clearing Committee (ATTC) developed guidelines for release of varieties in Malawi. The most important rule in relation to GxE is that the candidate variety must have been evaluated for three years and shown stable performance at both on-farm and on-station trials. If it is an introduction, it must have two years of data for on-farm and on-

station trials in the country, supported by regional data. In addition to this rule, the variety release dossiers should clearly specify the environment it is suited for e.g. low-altitude or mid-altitude. In this case, multivariate stability analysis like AMMI and GGE are important tools in selecting a stable variety and making recommendations as to where it is suitable for cultivation.

Stable performance of a variety is also dependent on certain genetic properties. Zivanovic *et al.* (2004) indicated that breeding of $F_1$ hybrids of maize is successful because it exploits heterosis and increases homogeneity. The uniformity of hybrids consists of: (i) genetic homogeneity and (ii) genetic stability. Genetic homogeneity is focused on maintenance of the identity of genotypes, while genetic stability tends to maintain homeostasis (phenotypic uniformity) in different environments. The level of yield depends on genetic yield potential (all favourable genes incorporated into a cultivar during a breeding process). Stability of yield or of any other trait depends on the ability of a given cultivar to react to changes in the environment which it is subjected to; this is termed as phenotypic plasticity (Frey, 1983). In the present study, the objective was to study the GxE and stability of the tropical and sub-tropical maize genotypes in low pH, low N and optimal conditions.

### 5.3 Materials and methods

The experimental design, experimental materials and site description are given in Chapter 4 Section 4.3. The low N trial of 2012 was destroyed by livestock just before harvest, hence cluster analysis alone combining with low N data of 2013 was possible using environmental means. The reason for evaluating low N tolerance was to check if other genotypes had additional attributes for this stress apart from that which were pre-described as originating from a low N tolerant source e.g. LOW N POOL C3-B. A genotype which has additional attributes is better placed for high adoption by farmers e.g. a released variety ZM523 is drought tolerant with low N tolerance as an additional attribute and is recognised through the quantities of annual certified seed sales, as widely cultivated compared to other OPVs available in the country.

## 5.4 Data analysis

### 5.4.1 Analysis of variance

Statistical analyses were performed using various software packages: GenStat 16th Version (2013), Agrobase (2010) and NCSS (Hintze, 2007). The AMMI model, which combines ANOVA with PCA, was used to study the nature of GEI. GxE was partitioned into sources of variation (i) additive main effects for genotypes and environment and (ii) non-additive main effect due to GEI.

### 5.4.2 Stability analysis

AMMI analysis for mean yield was performed using Agrobase (2010). GGE biplot analysis was conducted using the GGE biplot in GenStat (2013). The model for GGE biplot (Yan and Hunt, 2002) based on single value decomposition (SVD) of the first two principal components (PC) was used.

## 5.5 Results

### 5.5.1 Analysis of variance for additive main effects multiplicative interaction

The combined ANOVA of the 45 maize genotypes evaluated for two years across eight locations according to the AMMI model is presented in Table 5.1. The ANOVA indicated highly significant effects ($p \leq 0.01$) for environments, genotypes and GEI. The IPCA's were ordered according to decreasing importance. The F-test was highly significant ($p \leq 0.01$) for the first six IPCA axes and at $p \leq 0.05$ for the seventh IPCA. The total variation explained ranged from 2.5% for genotypes, 59.4% for environments and 17.5% for GxE. The variation due to GxE was over five times the variation due to genotypes as main effects. The first six IPCA axes explained 75.3% of the GEI. The first IPCA captured 32.8% of the total interaction sum of squares in 8.8% of the interaction degrees of freedom (GxE).

**Table 5.1 AMMI Analysis of variance for grain yield for two years 2011/12 and 2012/13**

| Sources | DF | SS | MS | Total variation explained (%) | Eigenvalues | % GxE Explained | Cumulative % |
|---|---|---|---|---|---|---|---|
| Total | 2159 | 5033813782 | | | | | |
| Environments | 15 | 2989647437 | 199309829.1** | 59.4 | | | |
| Reps within Env | 32 | 159985978.2 | 4999561.8 | | | | |
| Genotype | 44 | 124590289.1 | 2831597.5** | 2.5 | | | |
| Genotype x Env | 660 | 879765257.9 | 13329877.7** | 17.5 | | | |
| IPCA 1 | 58 | 288728372.6 | 4978075.4** | | 96242790.9 | 32.82 | 32.82 |
| IPCA 2 | 56 | 136931066 | 2445197.6** | | 456436688.7 | 15.56 | 48.38 |
| IPCA 3 | 54 | 88841154.8 | 1645206.6** | | 29613718.3 | 10.10 | 58.48 |
| IPCA 4 | 52 | 75415838.9 | 1450304.6** | | 25138613.0 | 8.57 | 67.05 |
| IPCA 5 | 50 | 72193861.2 | 1443877.2** | | 24064620.4 | 8.21 | 75.26 |
| IPCA 6 | 48 | 54027784.3 | 1125578.8** | | 18009261.4 | 6.14 | 81.40 |
| IPCA 7 | 46 | 47403253.8 | 1030505.5* | | 15801084.6 | 5.39 | 86.79 |
| Residual | 1408 | 879824820.1 | 624875.58 | | | | |

**Grand mean- 2516.39, R- Squared 0.8252, CV = 31.4%, *P≤0.05, **P≤0.01; IPCA= Interaction principal component axis CV = coefficient of variation,**

The second IPCA explained 15.6% of the interaction sum of squares in 8.5% of the interaction degrees of freedom (GxE) (Table 5.1).

Results for IPCA1 and IPCA2 are presented in Table 5. 2 and Table 5.3 and are sorted in terms of environmental mean. G20 ranked first overall. In the biplot in Figure 5.1, low pH environments: Bembeke Trurn Off (BKET), Bembeke Office, (BKEO), Lunyangwa (LUN) and Tsangano (TSA) were distributed with the lower yielding environments in quadrants 1 (top left) and IV (bottom left) (Figure 5.1), while optimal environments: Chitala (CLA), Chitedze (CZE), Meru (MRU) and Baka (BKA) were positioned with the high yielding environments in quadrant II (top right) and III (bottom right). The genotypes categorised under favourable environments with above average means were G20, G18, G13, G26 and G41. Among them G20 was found to be most stable. G42 was identified as the most unstable genotype (quadrant IV) and the other genotypes under low yielding environments are shown in the lower left quadrant of the biplot. With respect to the environments, closer relationships were observed among Bembeke Turn off (BKET), Bembeke Office (BKEO), Lunyangwa (LUN) and Tsangano (TSA). Chitedze (CZE) was identified as a suitable environment as its IPCA score and vector was near to the origin (zero).

### 5.5.2 Genotype and GEI scatter biplot and polygon view of grain yield across eight environments for 20011/12 and 2012/13

The polygon was constructed from genotypes G20, G45, G42, G2, G40, G16 and G8 as markers (Figure 5.2). Eight lines were drawn starting from the origin and extended beyond the polygon such that the biplot was divided into eight sectors and environments fell into three of them. Bembeke Turn off (BKET) fell in sector 1 delineated by rays 1 and 2 and the vertex genotype was G16. Similarly one environment, Bembeke Office (BKEO) fell into sector three and the vertex genotypes were G28 and G8. All optimal sites fell into sector four and were delineated by rays four and five and the vertex genotype was G20. The remaining two low pH sites: Tsangano (TSA) and Lunyangwa (LUN) fell just at the origin.

**Table 5.2 IPCA1 and IPCA2 scores for the top 20 genotypes based on mean grain yield at eight locations for two seasons**

| No | Entry code | Mean yield kg ha$^{-1}$ | IPCA1 | IPCA2 |
|---|---|---|---|---|
| 1 | G20 | 2977 | 23.25322 | 3.15773 |
| 2 | G27 | 2833 | 7.16857 | -6.46885 |
| 3 | G30 | 2729 | 18.05689 | -16.53917 |
| 4 | G8 | 2728 | 18.77411 | -10.69649 |
| 5 | G5 | 2719 | 15.12165 | -8.60019 |
| 6 | G22 | 2663 | -4.61057 | 2.08058 |
| 7 | G33 | 2646 | 19.09816 | -2.1516 |
| 8 | G28 | 2620 | 0.96947 | -4.78308 |
| 9 | G39 | 2614 | 5.95664 | 2.00067 |
| 10 | G32 | 2595 | 5.91891 | 13.04379 |
| 11 | G36 | 2594 | 2.29902 | 17.73102 |
| 12 | G26 | 2593 | 3.39991 | 1.41781 |
| 13 | G45 | 2591 | 5.21745 | 9.87007 |
| 14 | G18 | 2586 | 0.03059 | 3.77821 |
| 15 | G43 | 2584 | 3.63716 | 14.94491 |
| 16 | G6 | 2580 | -7.02094 | -12.23653 |
| 17 | G10 | 2565 | 10.19885 | 2.24328 |
| 18 | G12 | 2552 | 5.78089 | 13.91971 |
| 19 | G15 | 2532 | -1.59902 | -5.52944 |
| 20 | G44 | 2522 | 11.0564 | 12.81569 |

**Table 5.3 IPCA1 and IPCA2 scores for the eight environments, ranked based on environmental mean for two seasons**

| Environment | Environmental mean | IPCAe[1] | IPCAe[2] |
|---|---|---|---|
| MRU | 3964 | 22.77 | 14.34 |
| CLA | 3618 | 47.07 | -9.58 |
| BKA | 3350 | 10.59 | 44.64 |
| CZE | 2802 | -31.12 | 2.85 |
| BKET | 2461 | 14.44 | -38.27 |
| BKEO | 1927 | -20.15 | -8.73 |
| TSA | 718 | -21.26 | -0.35 |
| LUN | 516 | -22.35 | -4.89 |

**MRU = Meru, CLA = Chitala, BKA = Baka, CZE = Chitedze, BkeT = Bembeke Turn Off, BkeO = Bembeke Office, TSA = Tsangano Low pH site, LUN = Lunyangwa**

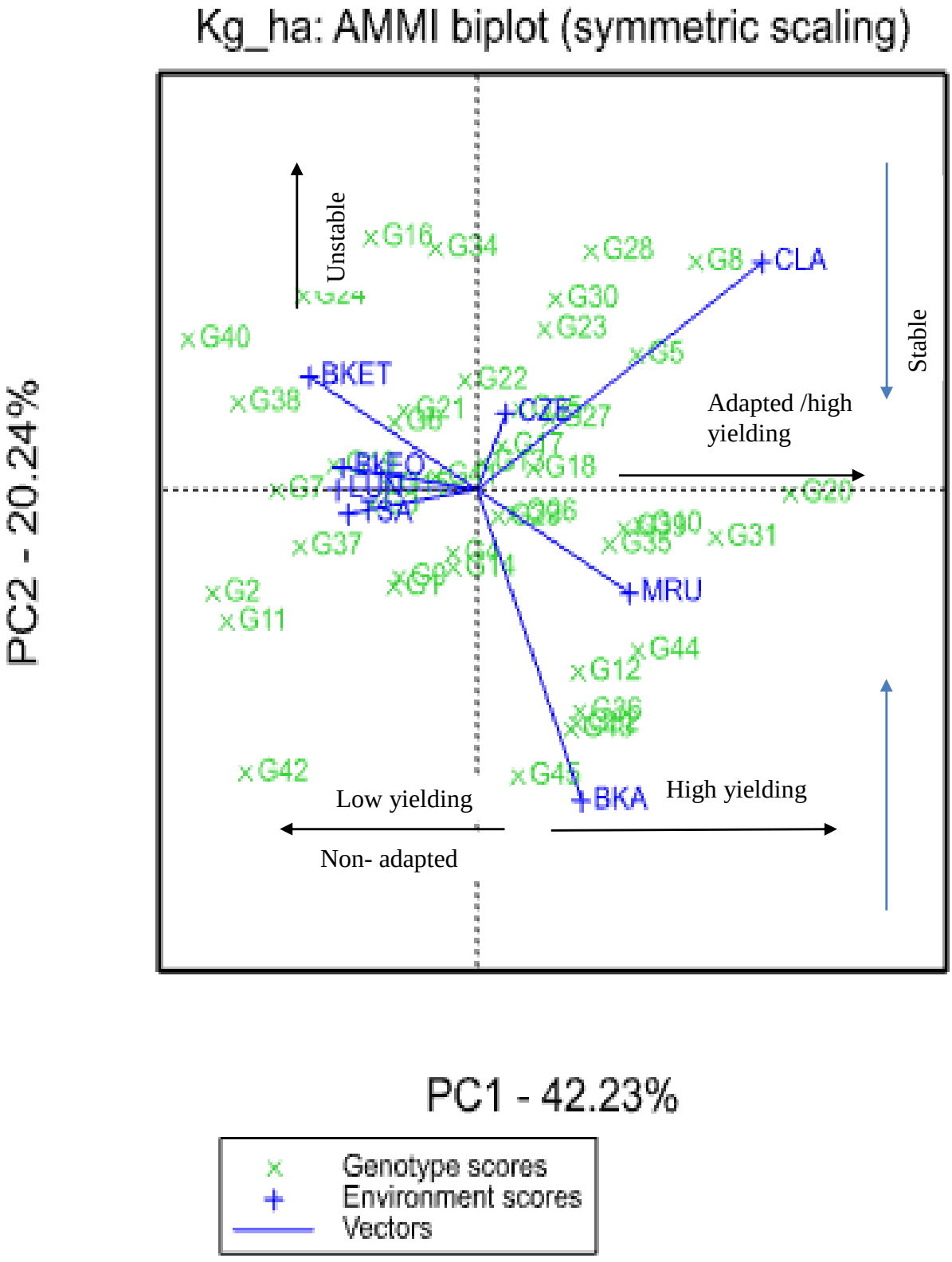


**Figure 5.1 AMMI biplot for yield for genotypes and environments across two seasons 2011/12 and 2012/13**

**MRU = Meru, CLA = Chitala, BKA = Baka, CZE = Chitedze, BkeT = Bembeke Turn Off, BkeO = Bembeke Office, TSA = Tsangano Low pH site, LUN = Lunyangwa**

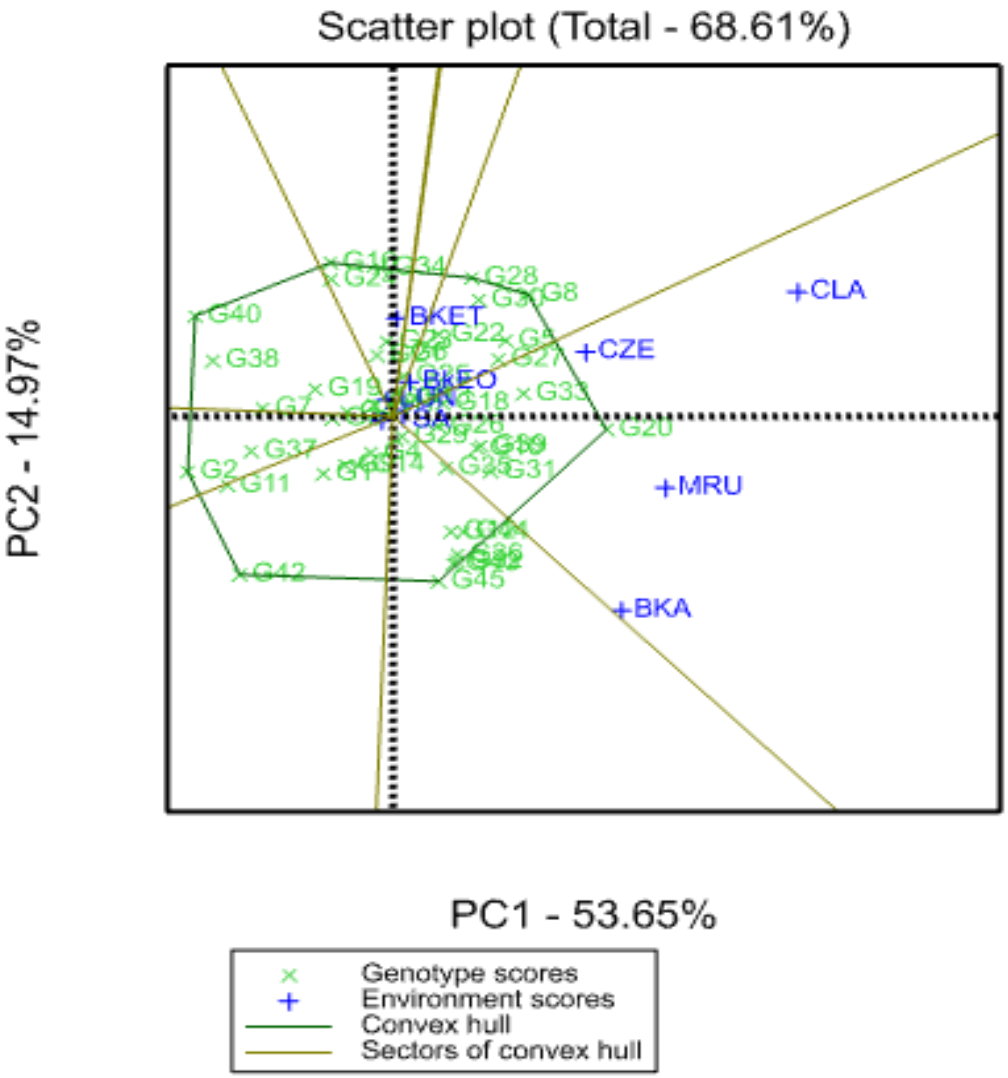


**Figure 5.2 Genotype and GEI scatter biplot and polygon view of grain yield across eight environments for 20011/12 and 2012/13 seasons**

**MRU = Meru, CLA = Chitala, BKA = Baka, CZE = Chitedze, BkeT = Bembeke Turn Off, BkeO = Bembeke Office, TSA = Tsangano Low pH site, LUN = Lunyangwa**

### 5.5.3 GGE comparison biplot across optimal and low pH environments combined for two seasons

The GGE biplot for ranking of environments based on discriminating ability and the representativeness across environments relative to yield performance is presented in Figure 5.3. The ideal environment was positioned near the centre of the average environment axis (AEA) which is represented by a small circle near the end of the arrow. The arrow at the end of AEA points towards a direction indicating the most informative location. The biplot indicated that environment Chitedze (CZE) was the most representative and discriminative in terms of grain yield performance based on AEA. In terms of genotypes G38, G18 and G26 were close to the small circle (ideal environment).

### 5.5.4 Ranking of genotypes based on both mean yield and stability view of the GGE biplot

GGE biplot of the genotypes based on both the mean and stability showed the relative mean performance and stability of hybrids across seasons (Figure 5.4). The genotypes G20 and G33 were high yielding based on average environment coordination abscissa (AECa) and average environment coordination ordinate (AECo). The genotypes G18, G13, G26 were near to the AEA which shows that they are very stable but not the highest yielding genotypes.

### 5.5.5 Cluster analysis of maize genotypes and environments

Clustering of genotypes at cut off point of 1.0 produced four clusters (Figure 5.5). Cluster I consisted of 10 genotypes (G1, G14 up to G9) and cluster II consisted of seven genotypes (G11, G2 up to G7), cluster III consisted of 27 genotypes (G10, G12 to G8) and cluster IV consisted of one genotype G20 which was ranked number one by AMMI in terms of mean grain yield performance. Cluster analysis of environments (Figure 5.6) at cut off point 1.0 with a cophenetic correlation ($r_{cop}$ = 0.84) produced three clusters. Cluster I consisted of three stress sites, the low N site, Lunyangwa and Tsangano. Cluster II consisted of two low pH stress sites Bembeke Office and Bembeke Turn Off, Cluster III consisted of four optimal sites Baka, Chitedze, Chitala and Meru.

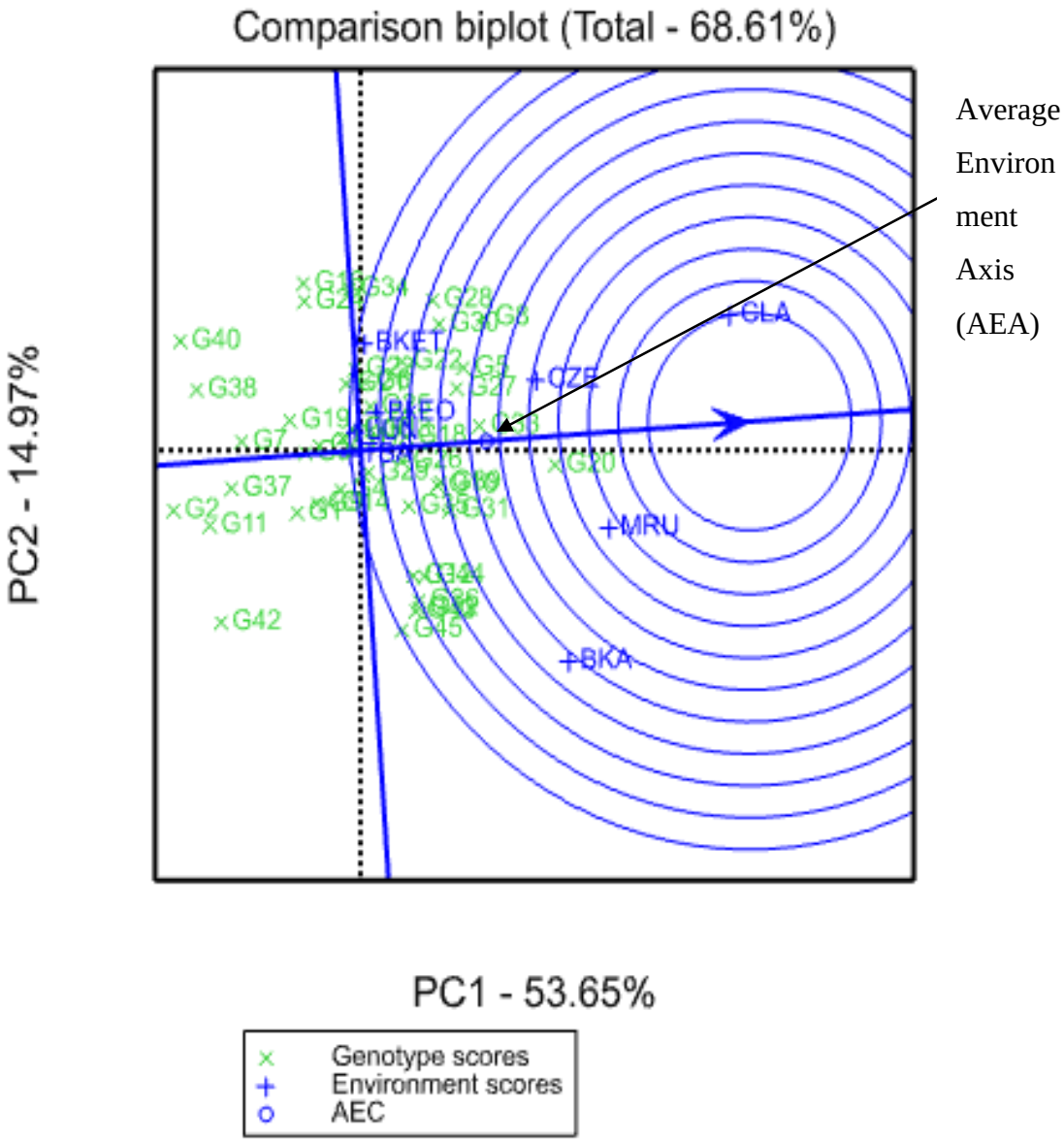


**Figure 5.3 Genotype and GEI comparison biplot of grain yield across eight environments for 2011/12 and 2012/13**

**MRU = Meru, CLA = Chitala, BKA = Baka, CZE = Chitedze, BkeT = Bembeke Turn Off, BkeO = Bembeke Office, TSA = Tsangano Low pH site, LUN = Lunyangwa**

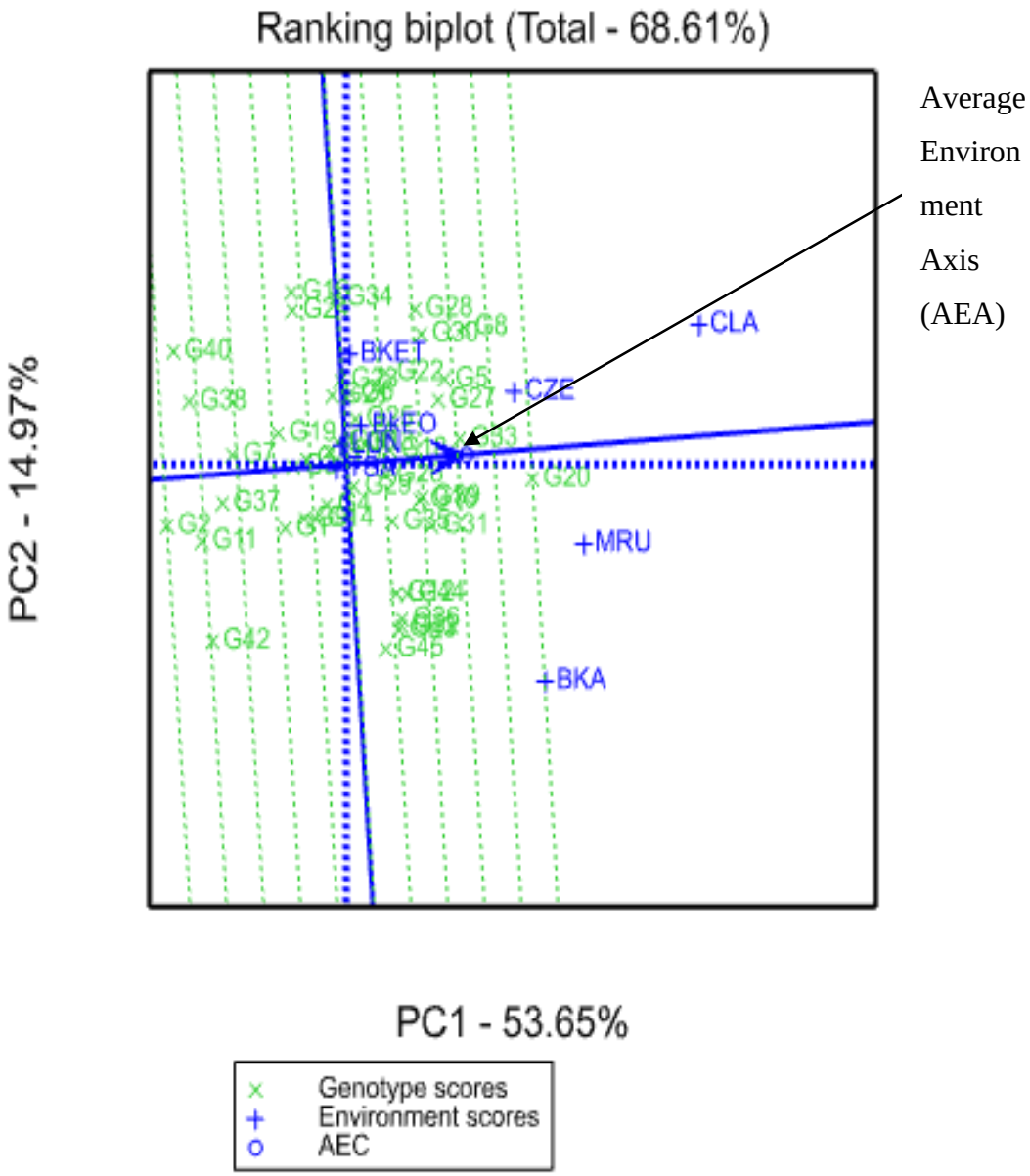


**Figure 5.4 Ranking of genotypes based on both mean yield and stability view of the GGE biplot**

**MRU = Meru, CLA = Chitala, BKA = Baka, CZE = Chitedze, BkeT = Bembeke Turn Off, BkeO = Bembeke Office, TSA = Tsangano Low pH site, LUN = Lunyangwa.**

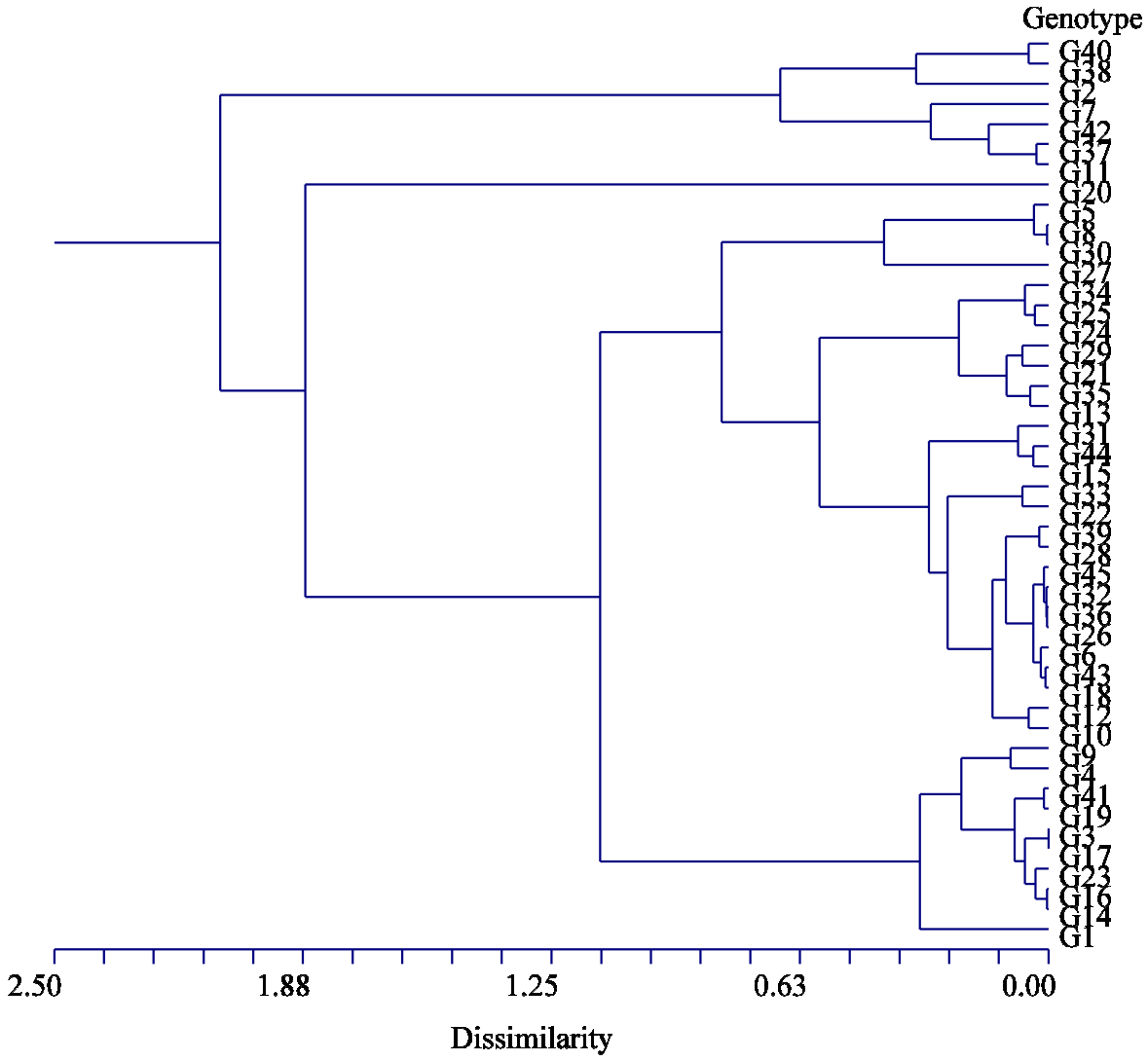


**Figure 5.5 Dendrogram of 45 maize genotypes as revealed by UPGMA cluster analysis based on AMMI adjusted mean yields combined for two seasons using Euclidean distance and standard deviation as scaling method**

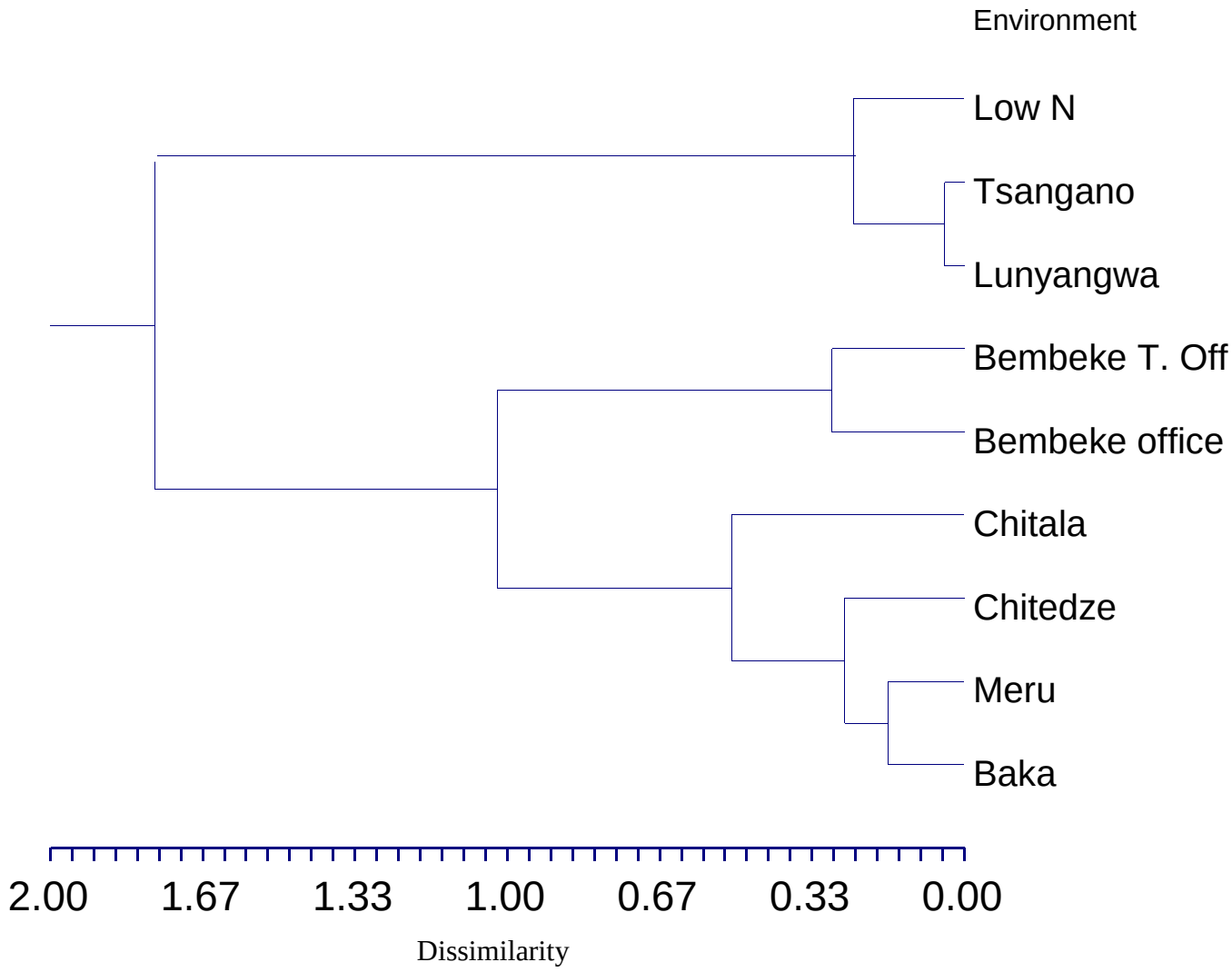


**Figure 5.6 Dendrogram of nine environments as revealed by UPGMA cluster analysis based on environmental means and Euclidean distance and standard deviation as scaling method**

## 5.6 Discussion

Environments and genotypes were both plotted as vectors and points respectively on the AMMI biplot. Genotypes and environments that were in close proximity are considered to be similar in terms of performance and discrimination of genotypes. The angle between two vectors indicated the degree of association or correlation. Small angles indicated similarity, a $90^{o}$ angle indicated orthogonality and no association and an angle $>90^{o}$ indicated a negative correlation. The sites Lunyangwa and Tsangano were close to each other and these had the lowest pH. Genotypes G8 (LPHpop9), G28 (LPHpop10) and G30 (LPHpo3) were in close proximity and these were low pH tolerant populations from CIMMYT-Colombia and this demonstrated similarity of the genotypes. The orthogonal projections of genotypes on environment vectors indicate the relative performance of genotypes in a given environment: that is, the greater the projection of the genotype in the positive direction, the better the performance of that genotype in that environment. Drought tolerant (DT) genotypes were close to each other [G44 (ZM523), G12 (TZE YDT STR C4-B), G43 (ZM309) and ZM721]. These genotypes are likely to have some genes in common that were at play. Tsangano, Lunyangwa and Bembeke Office sites were close to each other and these were classified in one group as acidic sites, by use of the Soil Interpretation Guide (Horneck *et al*., 2011). These sites are also associated with poor performance in terms of maize yields such that 85% yield reduction was reported for Lunyangwa (Munthali and Chilimba, 2004).

When the environment contributes a large percentage of variation, it implies that it was a major factor that influenced yield performance (Issa, 2009). When plotting the genotypes and the environments on the same graph, the association between the hybrids and the environments can be seen clearly. IPCA scores of a genotype in the AMMI analysis are an indication of the stability of a genotype over environments (Gauch and Zobel, 1996; Purchase, 1997). The greater the IPCA scores, either positive or negative, the more specifically adapted a genotype is to certain environments sampled. For instance G27 (Low N Pool C3-B) was close to CZE (Chitedze), indicating that it is a low N tolerant genotype and is able to do much better under ideal conditions probably because of its high N use efficiency (NUE). The present study recorded genotype contribution to total sum of squares as very low at 2.5% and was consistent with findings by Babic *et al.* (2010) who reported

2.2% but was not consistent with findings by Mitrović *et al.* (2011) who reported a somewhat higher 9.17% contribution.

The genotypes categorised under favourable environments with above average means were G20, G18, G13, and G41. Among them G20 (LPHpop21) was found to be more stable and this was from the low pH tolerant populations from CIMMYT-Colombia. Its tolerance to low pH might have contributed to its stable performance across seasons and all locations tested. Genotypes grouped under low yielding environments are shown at the lower left quadrant (IV) of the biplot. G42 (VPO97) from CIMMYT-Zimbabwe was the most unstable genotype identified by the AMMI model (Figure 5.1). Genotypes that are close to each other tend to have similar performance and those that are close to a specific environment indicate their better adaptation to that particular environment. The five IPCA axes can be taken as adequate dimensions of the data, however, only the first two IPCA axes were plotted on the biplots to help investigate the GEI pattern for each genotype. The biplot showed that Chitala was the most discriminating environment for the genotypes as indicated by the longest distance between its marker and the origin and gave information of the performance of the genotypes. This site was associated with genotype G8 (LPHpop 9) which might be specifically adapted to this site. Chitala was used as an optimal site in terms of pH but it is used as random drought screening site classified as low-land tropical zone E by CIMMYT (2008). G8 (LPHpop9) coincidentally was among the low pH tolerant populations from CIMMYT-Colombia and it might be tolerant to random drought. Piñeros *et al.* (2005) and Hartwig *et al.* (2007) reported that low pH negatively influences the use of soil nutrients and induces plants to be more susceptible to drought. It implies that a genotype which is tolerant to low pH is likely to be less susceptible to random drought. However, due to its high IPCA scores, genotype variability at this environment may not exactly reflect the average genotype performance across environments. This is consistent to the findings by Arulselvi and Selvi (2010). For the environments, a closer relationship was observed between Bembeke Turn Off, Bembeke Office, Lunyangwa and Tsangano low pH site. Chitedze was identified as a stable environment as its IPCA score and vector is near to the origin (zero). This site is in the mid-altitude ecology and is in the arable land of Lilongwe Plain with a longer rainfall season than Chitala and these results have confirmed that the country's best yields are obtained in the mid-altitude ecology (MOA, 1994). Generally genotypes with a smaller vector angle have a similar projection, which

designate their proximity in grain yield and performance. Those genotypes that are clustered close to the centre tend to be stable and those far apart unstable.

The GGE biplot construction is carried out by plotting the first PC scores of the genotypes and the environments against their respective scores for PC2 that result from SVD of environment-centered or environment-standardised genotype-by-environment data (GED) (Yan *et al*., 2000; Setimela *et al.*, 2007). According to Setimela *et al.* (2007), the purpose of the polygon view of the biplot is basically to show which hybrids won in which environments. The genotypes located furthest from the biplot origin demarcate the corners of the polygon. The perpendicular lines that are drawn from the biplot origin divide the biplot into sectors or mega environments. The environments are contained into different sectors such that different sectors contain different winner genotypes (Yan *et al*., 2007).

The results showed that the polygon was constructed from genotype markers G20, G45, G42, G2, G40, G16 and G8. Among these markers, G40 in the upper left quadrant (I) marked the unstable environment while G42 in the lower bottom left (IV) marked the low yielding environment. Depending on the objective of the research, selection could be carried out in the quadrant with markers G20 (stable environment) and G45 (high yielding environment). Eight lines were drawn starting from the origin and extended beyond the polygon such that the biplot was divided into eight sectors and environments fell into three of them. Bembeke Turn off fell in sector 1 delineated by rays 1 and 2 and the vertex genotypes were G16. Similarly environment Bembeke Office, fell into sector three where the vertex genotypes were G28 and G8. All optimal sites fell into sector four and were delineated by rays four and five and the vertex genotypes was G20. The remaining two low pH sites: Tsangano and Lunyangwa fell just at the origin.

The construction of GGE comparison biplots is done with the aim of ranking environments based on discriminating ability and the representativeness across environments relative to yield performance (Setimela *et al.*, 2007). In this type of biplot, the ideal environment is one positioned near the centre of the AEA which is represented by a small circle near the end of the arrow as indicated in Figure 5.3. The tiny circle in the biplot represents the average environment and is defined by the average PC1 and PC2 scores across the environments. In the present study, the biplot indicated that environment Chitedze was the

most representative and discriminative in terms of grain yield performance based on the AEA and genotypes G38, G18 and G26 were close to the small circle showed that they were stable but not the highest yielding genotypes.

The AEA is the average environment axis and the projection of the genotypes onto this line represents the main effects of the genotypes (Setimela *et al.,* 2007) therefore the AEAa ranks the genotypes according to the mean performance where by a small a is for abscissa . Usually ranking of the genotypes on the AEA is associated with the genotype main effect that is, the AECa approximates the contribution of each genotype to the main effects of genotypes. Similarly, AECo expresses the genotype contributions to GxE and thus it represents the genotype stability across environments where by a small o is for ordination. The AEA from the biplots points towards maize genotypes with high and stable mean grain yield across environments. The genotypes G20 and G33 are high yielding based on AECa and AECo. An "ideal" genotype may not exist in practice but it can be used as a reference for genotype evaluation (Mitrović *et al.,* 2011). A genotype is more desirable if it is located closer to the "ideal" genotype (Kaya *et al*., 2006). Plant breeders prefer genotypes that are high yielding and also stable across environments. In this ranking biplot, G42 was identified as the most unstable genotype as it was located far from the "ideal genotype".

The GGE biplot explained 68.6% of the G+GE variation. According to Yan *et al.* (2007), the greater the contribution, the more confidence the researcher would have in the interpretations based on the biplot. However, if a smaller portion of the total variation is explained, it does not necessarily mean that the biplot is useless. GGE biplots provide more information than AMMI biplots while the latter gives important details in the ANOVA, making both useful and both should be used in stability analyses.

According to Ghaderri *et al.* (1980) cluster analysis is the most widely used technique for classifying environments or genotypes into homogeneous groups. It operates on a matrix of dissimilarity or dissimilar indexes for all possible pairs of genotypes or pairs of environments, on which it is being clustered. In the present study, cluster analysis was performed to study the pattern of groupings and environments. The hierarchical clustering report indicated that cluster I consisted of 10 genotypes (G1, G14 up to G9) and cluster II consisted of seven (G11, G2 up to G7), cluster III consisted of 27 genotypes (G10, G12 up

to G8) and cluster IV consisted of one genotype, G20 which was ranked number one by AMMI in terms of mean grain yield performance. Therefore both methods could be used to identify stable genotypes.

Cluster analysis of environments at cut off point 1.0 with a cophenetic correlation of $r_{cop}$ = 0.84 produced three clusters (Figure 5.6). The hierarchical clustering report indicated that cluster I consisted of three environments, low N site, Lunyangwa and Tsangano. Cluster II consisted of two low pH stress sites, Bembeke Office and Bembeke Turn Off. Cluster III consisted of four optimal sites Baka, Chitedze, Chitala and Meru environments. This technique could be useful in general grouping of locations that have stresses and further analysis is required to identify specific stresses at play.

## 5.7 Conclusions

The low pH soil environment had an effect on grain yield performance such that the low pH sites were positioned in the low yielding area in the AMMI biplot. Chitala optimal site was identified as the most discriminating environment for the genotypes, and the most stable environment. Genotypes G20 (LPHpop21), G18 (VPO52), G13 (VPO721) and G41 (VPO96) were positioned in the favourable environments with above average means. Cluster analysis results were similar to AMMI results such that cluster III comprised of genotypes that were stable, except for G2O (LPHpop21) the most stable, which was in its own cluster. G42 (VPO97) was identified as the most unstable genotype.

GGE biplots explained more variation and gave more information than AMMI while the latter gave important details on the ANOVA, making them both useful and both should be used in stability analyses. Similarly clustering of environments classified the lowest pH sites in cluster I and intermediate pH sites in cluster II. All optimal sites were positioned in the third cluster. Clustering identified the low N site as similar to the lowest pH sites in terms of its environmental mean.

## 5.8 References


AGROBASE 2010. Agronomix Software, Inc. Generation II user's Manual. Version II. Revised Edition. www.agronomix. Agronomix software, Winnipeg, M.B, Canada.

Aina, O.O., A.G.O. Dixon and E.A. Akinrinde. 2007. Additive main effects and multiplicative interaction (AMMI) analysis for yield of cassava in Nigeria. Journal of Biological Sciences 7: 796-800.

Annicchiarico, P. and M. Perenzin. 1994. Adaptation patterns and definition of macro environment for selection and recommendation of common wheat in Italy. Plant Breeding 113: 197-205.

Arulselvi S. and B. Selvi, 2010. Grain yield stability of single cross maize (*Zea mays* L.) hybrids over three different environments. Electronic Journal of Plant Breeding 1: 577-584.

Babic, V., M. Babic, M. Ivanovic, M. Kraljevic-Balalic and M. Dimitrijevic., 2010. Understanding and utilization of Genotype by Environment Interaction in Maize Breeding. Genetika 42: 79-90.

Becker, H.C. and J. Leon. 1988. Stability analysis in plant breeding. Plant Breeding 101: 1-23.

Brewbaker, J.L. 1985. The Tropical environment for maize cultivation. In: A. Brandolini and F. Salamini (Eds.) Breeding Strategies for Maize Production Improvement in the Tropics. Food and Agriculture Organisations and Instituto Agronomico I'Oltremarc, Firenze, Italy, pp. 47-77.

CIMMYT, 2008. Characterisation of Maize Germplasm Grown in Eastern and Southern Africa. Results of the 2008 Regional Trials Coordinated by CIMMYT. Harare.

Crossa, J. 1990. Statistical analysis of multilocation trials. Advances in Agronomy 44: 55-85.

Eberhart, S.A. and W.A. Russel, 1966. Stability parameters for comparing varieties. Crop Science 6: 36-40.

Finlay, K.W. and G.N. Wikinson, 1963. The analysis of adaptation in plant breeding programme. Australian Journal of Agricultural Research 14: 742-754.

Frey, K.J. 1983. Plant population Management and breeding. In: D.R. Wood (Ed.) Crop Breeding, ASA, Madison, USA, pp.55-88.

Gauch, H.G. 1988. Model selection and validation for yield trials with interaction. Biometrics 44: 705-715.

Gauch, H.G. and R.W. Zobel. 1996. AMMI analysis of yield trials. In: M.S. Kang and H.G. Gauch (Eds.) Genotype by environment interaction pp85-122.CRC Press, Boca Raton, New York.

Gauch, H.G. and R.W. Zobel. 1997. Identifying mega–environment and targeting genotypes. Crop Science 37: 311-326.

GenStat. 2013. Introduction to GenStat for Windows 16.1th Edition. VSN International, Hemel Hempstead, Hertfordshire HPI. IES, UK.

Ghaderri, A., E.H. Everson and C.E. Cress. 1980. Classification of environments and genotypes in wheat. Crop Science 20: 707-710.

Hallauer, A. R. and J. B. Miranda. 1988. Quantitative genetics in maize breeding. Iowa State Univ. Press. Ames, IA.

Hartwig, I., A.C. Oliveira, F.I.F. Carvalho, I. Bertan, J.A.G. Silva, D.A.M. Schnidt, I.P. Valerio, L.C. Maia, D.A.R. Fonseca and C.E.S. Reis. 2007. Mecanismos associados à tolerância ao alumínio em plantas. Semina: Ciências Agrárias 28: 219-228.

Hintze, J.L., 2007**.** Number Cruncher Statistical System (NCSS). Statistical System for Windows. Kaysville, Utah.

Horneck, D.A., D.M. Sulivan, J.S. Owen and J.M. Hart., 2011. Soil Test Interpretation Guide. Oregon State University Extension Service.

Issa, A.H. 2009. Genotype by environment interaction and yield stability of maize of maize hybrids evaluated in Ethiopia. MSc thesis submitted to the University of Free State. South Africa.

Kang, M.S., D.P. Gorman and H.N. Pham. 1991. Application of a stability statistics to international maize yield trials. Theoretical and Applied Genetics 81: 162-165.

Kaya, Y., M. Akcura and S. Taner. 2006. GGE biplot analysis of multi-environment yield trials in bread wheat. Turkish Journal of Agriculture and Forestry 30: 325-337.

Lin, C.S., M.R. Binns, and L.P. Lefkovitch, 1986. Stability analysis: Where do we stand? Crop Science 26: 894-900.

Ma, B.L., W. Yan, L.M. Dwyer, J. Fregeau-Reid, H.D. Voldeng, Y. Dion and H. Nass. 2004. Graphic analysis of genotype, environment, nitrogen fertilizer and their interaction on spring wheat yield. Agronomy Journal 96: 169-180.

Malawi Government. 1994. Guide to Agricultural production in Malawi 1994. Extension Aids Branch. Ministry of Agriculture. Lilongwe.

Mitrović, B., D.S. Tanisavljevi, S. Treski, M. Stojaković, M. Ivanović, G. Bekavac, M. Rajković, 2011. Evaluation of Experimental Maize Hybrids Tested in Multi-location Trials using AMMI and GGE Biplot Analyses. Turkish Journal of Field Crops 17: 35-40.

Munthali, M.W. and A.D.C. Chilimba. 2004. Effects of composting materials and methods of composting on quality of compost and maize yields. In: 2004 Annual Report of Soils and Agricultural Engineering Commodity Group, Ministry of Agriculture, Chitedze Research Station, Lilongwe, Malawi. pp. 52.

Myers, G.O. 2004. Estimation of potential breeding value and genotype stability. http//www.cottoninc.com.

Piñeros, M.A., J.E. Shaff, H.S. Manslank, V.M. Carvalho Alves and L.V. Kochian. 2005. Aluminum Resistance in Maize Cannot Be Solely Explained by Root Organic Acid Exudation. A Comparative Physiological Study. Plant Physiology 137: 231-241.

Purchase, J.L., 1997. Parametric analysis to describe G x E Interaction and yield stability in winter wheat. PhD Thesis. Department of agronomy, Faculty of Agriculture, University of Free State, Bloemfontein, South Africa.

Raun, W.R., H.J. Barreto and R.L. Westerman, 1993. Use of stability for long term soil fertility experiments. Agronomy Journal 85: 159-167.

Ramagosa, I. and P.N. Fox, 1993. Genotype x Environmental interaction and adaptation. In: M.D. Hayward, N.O. Bosemark and I. Ramagosa (Eds.) Plant Breeding: Principles and prospects. Chapman and Hall, London, pp. 373-390.

Setimela, P.S., B. Vivek, M. Bänziger, J. Crossa and F. Maideni. 2007. Evaluation of early to medium maturing open pollinated maize varieties in SADC region using GGE biplot based on SREG model. Field Crops Research 103: 161-169.

Yan, W. and L.A. Hunt. 2002. Biplot analysis of diallel data. Crop Science 42: 21-30.

Yan, W. and N.A. Tinker. 2006. Biplot analysis of multi-environment trial data: Principles and applications. Canadian Journal of Plant Science 86: 623-645.

Yan, W., L.A. Hunt, Q. Sheng, and Z. Szlavnics. 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot. Crop Science 40: 596-605.

Yan, W., M.S. Kang, B. Ma, S. Woods and P.L. Conrnelius. 2007. GGE Biplots vs AMMI analysis of genotype by environment data. Crop Science 41: 656-663.

Yates F. and Cochran W. 1938. The analysis of groups of experiments. Journal of Agricultural Science 28: 556-580.

Zivanovic, T., I. Maja Vracarevic, S. Krstanovic and G. Surlan-Momirovic. 2004 Selection on Uniformity and Yield Stability in Maize. Journal of Agricultural Sciences 49: 117-130.

# CHAPTER 6

## Evaluation of diallel crosses for combining ability between selected tropical and sub-tropical maize lines for low pH tolerance

### 6.1 Abstract

This study was conducted to assess the GCA effects of parental maize inbred lines and SCA effects for the diallel crosses for yield and yield related traits and explore their use in hybrid development for low pH tolerance. Sixty six $F_1$s generated by crossing 12 inbred lines were evaluated alongside two hybrid checks at four locations in Malawi. The experimental design was a (0.1) alpha lattice with three replications. Positive and highly significant GCA effects for grain yield were observed for inbred line CZL999601 across low pH and optimal conditions. Negatively and significant GCA effects for grain yield were observed for inbred line CML161 across low pH and optimal conditions. Single cross hybrids CZL999601/CML144, CML144/CML202, CML481/CML288 and CML161/CM172 were identified as good specific combiners for grain yield. The estimates of broad sense heritability were high for days to 50% anthesis, anthesis-silking interval, grain yield and plant vigour. At a cut-off point of 1.0 the UPGMA clustered the inbred lines based on GCA for grain yield into two main clusters through use of Euclidean distance and standard deviation as type of scale. There was a high cophenetic correlation of $r_{cop} = 0.87$ and the pattern mostly followed the origin of the maize inbred lines such that six out of seven inbred lines from CIMMYT-Colombia (tropical) were grouped in the second cluster. The inbred lines and specific combinations identified in this study will be used in the National Maize Breeding Programme for development of genotypes tolerant to low pH and diseases for yield improvement and subsequent food security in the country.

### 6.2 Introduction

Maize is the world's most widely grown cereal and is the primary staple food in many developing countries (Morris *et al*., 1999). In Malawi, two main types of maize cultivars are cultivated by farmers, hybrids and OPVs. The OPVs include synthetics, composites,

and local types which are locally called Chamakolo. In these types of maize, hybrids have the highest yielding potential, followed by synthetics and composites and then lastly local varieties. The differences are based on the breeding process in case of hybrids, synthetics and composites. The performance of maize genotypes used as parents is evaluated based on the performance of the cross progeny. With respect to hybrids, the parental lines are chosen based on their SCA as measured in their hybrid offspring. Usually two or three selected inbred lines are used in developing single-cross and three-way cross hybrids, respectively.

Synthetics are developed by inter-crossing a larger number of selected parental lines of known superior combining ability, for example inbred lines which are known to give superior hybrid performance when crossed in all combinations. A composite is developed by selecting parental lines of relatively similar maturity periods and mixing the seed from the individuals. In both cases, seed is maintained by allowing full-sib pollination (or plant to plant pollination in the same population). These types are also referred to as open-pollinated because there is no control of pollen movement when planted in isolation for seed increase (bulking), especially for basic and certified seed multiplication. In other words, some form of inbreeding occurs as there is no de-tasselling of the male flowers of the female parent as in hybrid crosses. Hence farmers in Malawi are advised to recycle the OPVs for two seasons and the third season they should look for new seed because of inbreeding depression and genetic drift which occurs with time of recycling the seed and reception of foreign genes from other varieties.

Crop estimates for 2012 showed that hybrids contributed 56.5% to the national total production while composites and synthetics contributed 30.5% and local varieties the least at 13%. In terms of hectarage, hybrids contributed 40%, composites/synthetics 30% and local varieties 30% (MOA, 2012). Combining ability is considered in hybrids more than in synthetics which are based only on GCA. The most well-known synthetic and composite varieties released by the National Maize Breeding Programme in Malawi are Masika and Chitedze Composite A, respectively. In terms of hybrids, it is Malawi maize hybrids number 17 and 18 (MH17, MH18) and these are the first flint three-way cross hybrids which are preferred because of their good pound ability. The two hybrids had a common male parent which is very flint and was identified as a good combiner for flintness.

The concept of GCA and SCA was introduced by Sprague and Tatum (1942) and its mathematical modelling was done by Griffing (1956). The value of any population depends on its potential *per se* and it's combining ability in crosses (Vacaro *et al*., 2002). The variances of GCA and SCA are related to the type of gene action involved. Variance for GCA includes the additive portion while that of SCA includes the non-additive portion of total variance arising largely from dominance and epistatic deviations (Rojas and Sprague, 1952). GCA and SCA are powerful tools used by plant breeders in selecting the best parents for further crosses. Studies on combining ability help breeders in identifying parental lines with good GCA and in detecting hybrids with good SCA (Ndhela, 2012). Devi and Singh (2011) indicated that the best performing genotypes ought to show stable performance across environments in multi-environment trials. However, it is important to bear in mind that heritability is not only influenced by the trait under consideration but is also influenced by the population and environmental conditions which individuals are exposed to, as well as the method of data collection used (Falconer and Mackay, 1996).

In terms of types of genotypes, reports indicate that researchers in the late 1950s and early 1960s recommended the use of maize genotypes with a broader genetic base, because they are more tolerant to stresses than the narrow genetic base genotypes. Lerner (1954), Lewontin (1957) and Allard and Bradshaw (1964) reported that yield stability is influenced in part by the genetic structure of the variety such that more heterogeneous varieties are less affected by environmental differences. Sprague and Federer (1951) found that maize double-cross (DC) hybrids have smaller GEIs and are more stable than single-cross hybrids. Valdivia-Bernal and Hallauer (1991) also reported that more homogeneous generations, inbred lines and $F_1$'s had larger GEIs than more heterogeneous generations, $F_2$ and backcross populations. DC hybrids are rarely used nowadays because of the cost of producing the seed, but with the current maize production constraints, DC hybrids and OPV populations are better placed and the procedure should be to select suitable single-crosses from a diallel trial for the formation of double crosses and also good combiners (high GCA) for formation of synthetics.

Diallel crosses have been widely used in genetic research to investigate the inheritance of important traits among sets of genotypes. These were devised specifically to investigate

the combining ability of the parental lines for the purpose of identifying superior parents for use in hybrid development programmes. It is advisable to carry out indirect selection for related traits which show close correlation with yield and exhibit high heritability because yield is considered a polygenic trait. Analysis of diallel data is usually conducted according to the methods of Griffing (1956) which partition the total variation of diallel data into GCA of the parents and SCA of the crosses (Yan and Hunt, 2002).

A diallel is simple to manipulate in maize and supplies important information to plant breeders about the studied populations for various genetic parameters (Vacaro *et al*., 2002). In Malawi there is no known maize inbred line or variety that is tolerant to low pH, hence the objective of this study was to evaluate the performance of diallel crosses made with 12 maize inbred lines. Seven were from CIMMYT-Colombia, four were from CIMMYT-Zimbabwe and a well-adapted line from Malawi.

## 6.3 Materials and Methods

### 6.3.1 Experimental materials description

The experimental materials comprised of seven low pH tolerant maize inbred lines from CIMMYT-Colombia and five well adapted lines in Malawi from CIMMYT-Zimbabwe (Table 6.1). Seed increase of the parental lines was done at Chitala Research Station in the winter of 2010. Hand pollination by selfing and bulking eight to 10 plants from each parental line was done. Diallel crosses without reciprocals were made during the 2010/11 season at Chitedze Research Station in Lilongwe in summer and at Chitala Research Station and Bwanje Irrigation Scheme during winter by stagger planting. The single crosses pedigrees have a slash separating female and male parent. For example a single cross S410 has a pedigree CML144/CML288. This means that the female was parent number four which was CML144 and the male was parent number 10 which was CML288. The male is always to the right hand side. Even in a three-way cross the male is to the right hand side and the only difference is the double slashes before the male. For instance CML144/CM288// CML481 implies that CML481 which is to the right hand side after two slashes is the male. This was adopted from CIMMYT (CIMMYT, 2012). The trial was

planted at four sites which included Lunyangwa low pH site, Tsangano low pH site, Bembeke low pH site and Chitedze optimal site.

**Table 6.1 Description of 12 maize parental lines used in the diallel crosses and their origin**

| NO. | Parental line | Origin | Traits |
|---|---|---|---|
| 1 | CZL999601 | CIMMYT-ZIMBABWE | GLST, LBT, MSVT |
| 2 | CML481 | CIMMYT-COLOMBIA | Low pH |
| 3 | CML359 | CIMMYT-COLOMBIA | Low pH |
| 4 | CML144 | CIMMYT-COLOMBIA | Low pH |
| 5 | CML161 | CIMMYT-COLOMBIA | Low pH |
| 6 | CML172 | CIMMYT-COLOMBIA | Low pH |
| 7 | CML448 | CIMMYT-COLOMBIA | Low pH |
| 8 | CML312 | CIMMYT-ZIMBABWE | GLST, LBT, MSVT |
| 9 | ZL130-23 | MALAWI | GLST, LBT, MSVT |
| 10 | CML288 | CIMMYT-COLOMBIA | Low pH |
| 11 | CML202 | CIMMYT-ZIMBABWE | GLST, LBT, MSVT |
| 12 | CML539 | CIMMYT-ZIMBABWE | DT, GLST, LBT, MSVT |

**GLST = gray leaf spot tolerant, LBT = leaf blight tolerant, MSVT = maize streak virus tolerant, DT = drought tolerant**

### 6.3.2 Experimental procedures and design

Sixty six single-cross hybrids plus two checks were laid out in a (0.1) alpha lattice design (0,1) with three replications. Plot size was two rows of 5.1 m per plot with 17 stations per row, one seed was planted per station and two at both ends of the row.

### 6.3.3 Description of sites

The description of sites as well as management of the trials was given in the materials and methods section 4.3 of Chapter 4. The list of phenotypic and agronomic traits investigated and measuring procedures are the same as in Table 4.1 (Chapter 4).

## 6.4. Data analysis

Across site analysis was performed using GenStat (2013). Combining ability analyses were carried out using Statistical Analysis Software (SAS, 2013). Genotypes were considered fixed. Dendrogram construction was carried out in NCSS (Hintze, 2007) using UPGMA. Clustering was based on GCA effects for the inbred lines for grain yield, Euclidean distance and standard deviation as scale type.

## 6.5 Results

### 6.5.1 Performance of diallel crosses

Mean squares for performance of diallel crosses for grain yield and other agronomic traits are presented in Table 6.2. Across site analysis for optimal and three low pH sites indicated that all the sources of variation against the measured traits were significant with the exception of the interaction of genotype for shelling percentage and MSV for site. The mean performance across all four sites showed that hybrid CZL999601/CML144 (2.4 t $ha^{-1}$) was the best performer, followed by CZL999601/CML202 (2.1 t $ha^{-1}$), CZL999601/ZL130-23 and CML481/CML288 (2.0 t $ha^{-1}$) (Table 6.3). Across the three low pH sites, CML288/CML202 (1.04 t $ha^{-1}$), CML359/CML448 (1.0 t $ha^{-1}$) and CML481/CML288 (0.9 t $ha^{-1}$) performed relatively better than the other hybrids (Table 6.4). At the optimal site CZL999601/CML144 (7.0 t $ha^{-1}$), CZL999601/CML202 (5.4 t $ha^{-1}$), CML172/ZL130-23 (5.0 t $ha^{-1}$) and CML481/CML288 (4.5 t $ha^{-1}$) were among the top ten yielding hybrids (Table 6.5). Hybrids CML481/CML288 showed some consistency in performance across environments while CZL999601/CML144 was suited for optimal conditions. Grain yield was reduced by 78.2%, ear height by 55.3%, number of ears per plant by 54.5%, grain texture by 15.3%, plant height by 41.7%, 100 seed weight by 36.3%, shelling percentage by 18.8% and plant vigour by 62.5% (Table 6.6). Grain yield and plant vigour were the most reduced traits under low pH. Grain texture exhibited the lowest percentage reduction among the measured traits.

### 6.5.2 Genetic variances, phenotypic variances and heritability estimates for the diallel crosses across optimal and three low pH environments in 2011/12

Results for the diallel crosses are presented in Table 6.7. High broad sense heritability were recorded for anthesis date (0.93), anthesis-silking interval (0.87), grain yield (0.86) and leaf blight (0.86). The lowest heritability value was recorded for number of ears per plant (0.14)

**Table 6.2 Mean squares for diallel crosses across optimal and three low pH environments for grain yield and agronomic traits in 2011/12**

| Source | Site | Genotype | G x E | MSE | LSD | CV% |
|---|---|---|---|---|---|---|
| GY | 4.78E+08** | 1.47E+06** | 1.07E+06** | 3.50E+05 | 474.8 | 12.9 |
| AD | 34.87** | 34.87** | 8800** | 2.866 | 2.716 | 2.15 |
| ASI | 599.97** | 1.81** | 1.888** | 0.575 | 0.61 | 30.7 |
| PH | 496823** | 460.8** | 495.9* | 259.4 | 25.8 | 12.9 |
| EH | 160708** | 280.5** | 250.8** | 129.1 | 18.22 | 21.1 |
| EPP | 32.2** | 0.072** | 0.093** | 0.204 | 0.31 | 29 |
| RL | 1322.7** | 10.76** | 10.4** | 5.87 | 2.25 | 118 |
| SL | 21.9** | 4.5** | 4.1** | 2.56 | 1.82 | 114 |
| GLS | 81.8* | 0.99** | 0.748** | 0.18 | 0.39 | 25 |
| LB | 82.2** | 1.49* | 1.26** | 0.21 | 0.43 | 26.4 |
| MSV | 0.0001 | 0.31** | 0.42** | 0.16 | 0.08 | 36.8 |
| RUST | 219.3** | 0.48* | 0.43** | 0.15 | 0.36 | 21.1 |
| GT | 106.1** | 0.88** | 1.1** | 0.27 | 0.59 | 25.5 |
| SH | 15036** | 617.9 | 620.3** | 478 | 24.8 | 31.4 |
| VIG | 569.76** | 1.22** | 1.38** | 0.31 | 0.64 | 16.4 |
| SWT | 10523** | 94.8** | 77.2** | 24.8 | 5.66 | 19 |

****P≤0.01; *P≤0.05; G = genotype, E = environment, MSE = Mean square error, LSD = Least significant difference, CV = coefficient of variation, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), PH = plant height (cm), EH = ear height (cm), EPP = ears per plant (#), RL = root lodging (#), SL = stem lodging (#), GLS = gray leaf spot disease (1-5), LB = leaf blight disease (1-5), MSV = maize streak virus disease (1-5), Rust = rust disease (1-5), GT = grain texture (1-5), SH = shelling percentage, VIG = vigour (1-5), SWT = 100 seed weight (g), # = number.**

**Table 6.3 Mean performance of diallel crosses across optimal and low pH environments in 2011/12 season**

| | Code | GY | AD | ASI | DS | EH | EPP | LB | GLS | GT | MSV | PH | RL | RUST | SWT | SH | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Top 10 Genotypes | G3 | 2379 | 80.5 | 1.1 | 82.6 | 56.9 | 0.6 | 1.3 | 1.7 | 2.4 | 1.0 | 126.8 | 2.2 | 1.8 | 24.4 | 70.9 | 2.4 | 3.0 |
| | G10 | 2075 | 78.2 | 1.3 | 80.3 | 48.2 | 0.6 | 2.3 | 1.2 | 2.0 | 1.1 | 119.1 | 2.2 | 2.1 | 24.9 | 74.8 | 1.9 | 3.7 |
| | G8 | 1984 | 80.2 | 1.4 | 82.5 | 55.0 | 0.7 | 2.3 | 1.6 | 2.0 | 1.0 | 125.8 | 5.2 | 1.9 | 27.1 | 73.4 | 1.8 | 2.7 |
| | G19 | 1919 | 76.3 | 1.7 | 78.7 | 58.8 | 0.6 | 1.3 | 1.9 | 1.8 | 1.0 | 130.3 | 0.8 | 1.4 | 27.2 | 71.5 | 1.2 | 2.8 |
| | G48 | 1913 | 78.8 | 2.0 | 81.5 | 60.0 | 0.8 | 2.0 | 2.4 | 2.4 | 1.0 | 131.3 | 3.2 | 2.3 | 28.1 | 72.8 | 0.8 | 3.5 |
| | G39 | 1837 | 79.0 | 1.4 | 81.1 | 57.8 | 0.6 | 3.0 | 2.1 | 2.4 | 1.0 | 120.1 | 4.0 | 1.7 | 27.1 | 74.3 | 1.4 | 3.0 |
| | G2 | 1811 | 77.8 | 1.6 | 80.2 | 56.1 | 0.6 | 2.3 | 2.6 | 1.7 | 1.0 | 132.3 | 1.7 | 2.3 | 29.8 | 70.5 | 1.3 | 3.0 |
| | G16 | 1808 | 80.3 | 1.3 | 82.0 | 46.7 | 0.6 | 1.7 | 1.6 | 2.2 | 1.2 | 105.5 | 8.0 | 1.8 | 27.1 | 69.8 | 1.3 | 2.7 |
| | G7 | 1657 | 78.3 | 1.9 | 80.7 | 45.7 | 0.6 | 2.7 | 1.8 | 1.9 | 1.1 | 121.7 | 4.2 | 1.5 | 24.5 | 70.8 | 2.1 | 3.7 |
| | G24 | 1631 | 79.1 | 1.9 | 81.8 | 51.4 | 0.9 | 1.3 | 1.9 | 1.9 | 1.7 | 120.0 | 1.3 | 1.8 | 23.5 | 66.0 | 0.9 | 2.8 |
| Bottom 10 Genotypes | G57 | 965.8 | 79.8 | 1.7 | 82.3 | 59.5 | 0.7 | 1.3 | 2.0 | 1.9 | 1.0 | 130.0 | 3.5 | 2.3 | 26.8 | 67.1 | 0.4 | 3.4 |
| | G54 | 963 | 81.8 | 1.2 | 83.9 | 61.5 | 0.6 | 2.0 | 1.0 | 2.1 | 1.3 | 131.7 | 1.3 | 1.7 | 35.7 | 74.8 | 0.9 | 3.3 |
| | G47 | 943 | 80.2 | 2.1 | 82.5 | 57.6 | 0.7 | 1.0 | 1.8 | 2.3 | 1.0 | 124.9 | 2.5 | 2.2 | 25.1 | 75.3 | 0.8 | 3.8 |
| | G55 | 940.8 | 80.3 | 1.7 | 82.8 | 56.7 | 0.6 | 3.0 | 2.0 | 1.3 | 1.2 | 129.4 | 2.7 | 2.0 | 26.4 | 70.1 | 0.4 | 3.4 |
| | G60 | 842.8 | 78.5 | 1.8 | 81.1 | 55.0 | 0.7 | 1.0 | 1.6 | 1.8 | 1.0 | 130.1 | 4.5 | 1.8 | 20.1 | 71.8 | 2.6 | 4.6 |
| | G62 | 780.3 | 80.6 | 2.2 | 83.5 | 53.3 | 0.7 | 1.0 | 1.7 | 1.6 | 1.0 | 122.5 | 1.0 | 1.7 | 27.2 | 66.4 | 1.8 | 3.7 |
| | G41 | 778 | 80.3 | 1.8 | 82.6 | 46.4 | 0.6 | 4.0 | 1.7 | 2.3 | 1.0 | 113.6 | 2.3 | 1.7 | 24.8 | 68.5 | 0.4 | 4.0 |
| | G44 | 733 | 79.5 | 0.9 | 81.4 | 65.3 | 0.7 | 4.0 | 1.7 | 2.2 | 1.0 | 133.7 | 4.8 | 2.2 | 23.2 | 61.3 | 0.4 | 3.4 |
| | G43 | 711 | 82.0 | 2.2 | 84.9 | 48.1 | 0.7 | 2.0 | 1.7 | 1.7 | 1.1 | 123.9 | 0.5 | 1.7 | 28.2 | 65.0 | 1.7 | 3.8 |
| | G40 | 646 | 77.5 | 1.9 | 80.2 | 47.8 | 0.7 | 2.0 | 1.0 | 2.3 | 1.0 | 124.8 | 1.2 | 1.3 | 27.4 | 60.9 | 0.7 | 4.3 |
| | **Mean** | **1366** | **79** | **2** | **82** | **54** | **1** | **1.0** | **2** | **2** | **1** | **125** | **3** | **2** | **26** | **70** | **1** | **3** |
| | **LSD** | **478.8** | **1.4** | **0.6** | **1.4** | **9.1** | **0.2** | **1.7** | **0.4** | **0.6** | **0.6** | **12.9** | **2.3** | **0.6** | **8.4** | **17.7** | **1.5** | **0.6** |
| | **MSE** | **3.50E+05** | **2.9** | **0.6** | **3.2** | **129.1** | **0.0** | **0.4** | **0.2** | **0.3** | **0.2** | **259.** | **5.9** | **0.2** | **24.8** | **620.3** | **2.6** | **0.3** |

**LSD = Least significant difference, MSE = Mean square error, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease, (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, SL= stem lodging (#), VIG = vigour (1-5), # = number.**

**Table 6.4 Mean performance of diallel crosses across three low pH environment in 2011/2012 season**

| | Entry | GY | AD | ASI | DS | EH | EPP | LB | GLS | GT | MSV | PH | RL | RUST | SWT | SH | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Top 10 | G64 | 1040.7 | 77.7 | 2.7 | 80.3 | 34.1 | 0.4 | 2.0 | 2.3 | 1.5 | 1.0 | 101.0 | 0.5 | 1.8 | 16.5 | 65.6 | 2.5 | 5.0 |
| Genotypes | G25 | 1007.7 | 81.9 | 3.4 | 85.3 | 32.6 | 0.8 | 1.7 | 1.3 | 2.2 | 1.0 | 92.7 | 0.5 | 2.0 | 21.8 | 70.3 | 1.3 | 4.7 |
| | G19 | 999.3 | 77.8 | 3.0 | 80.8 | 47.8 | 0.5 | 1.3 | 2.3 | 1.7 | 1.0 | 113.1 | 0.5 | 1.6 | 21.6 | 66.8 | 1.5 | 4.3 |
| | G10 | 970.7 | 79.6 | 2.6 | 82.1 | 40.4 | 0.5 | 2.3 | 1.3 | 1.9 | 1.0 | 104.1 | 0.5 | 2.6 | 20.4 | 69.5 | 2.3 | 5.0 |
| | G18 | 958.3 | 83.0 | 3.2 | 86.2 | 44.4 | 0.5 | 2.0 | 2.0 | 1.9 | 1.1 | 109.7 | 0.5 | 2.0 | 17.2 | 65.0 | 1.5 | 4.3 |
| | G6 | 953.0 | 77.4 | 3.0 | 80.4 | 43.8 | 0.5 | 2.7 | 2.1 | 2.6 | 1.0 | 113.4 | 0.5 | 2.3 | 18.9 | 73.6 | 1.0 | 5.0 |
| | G8 | 945.3 | 82.9 | 3.1 | 86.0 | 41.5 | 0.5 | 2.3 | 1.8 | 2.1 | 1.0 | 103.6 | 0.5 | 2.3 | 24.0 | 70.2 | 1.5 | 4.3 |
| | G51 | 896.0 | 80.3 | 3.0 | 83.3 | 45.0 | 0.6 | 3.0 | 2.0 | 2.1 | 1.0 | 100.4 | 0.5 | 2.5 | 20.3 | 65.4 | 1.0 | 4.0 |
| | G1 | 894.3 | 83.4 | 2.9 | 86.3 | 46.8 | 0.5 | 2.3 | 1.3 | 2.2 | 1.0 | 109.8 | 0.5 | 2.4 | 22.7 | 62.0 | 2.2 | 4.3 |
| | G20 | 872.0 | 79.3 | 2.9 | 82.2 | 43.6 | 0.6 | 2.7 | 2.1 | 2.1 | 1.0 | 110.5 | 0.5 | 2.3 | 23.0 | 73.4 | 1.2 | 4.3 |
| Bottom10 | G50 | 478.0 | 81.0 | 2.7 | 83.7 | 35.6 | 0.5 | 4.0 | 1.5 | 2.0 | 1.0 | 95.3 | 0.5 | 2.3 | 20.0 | 50.0 | 1.5 | 5.0 |
| Genotypes | G57 | 471.7 | 81.0 | 3.0 | 84.0 | 50.3 | 0.6 | 2.0 | 2.5 | 1.6 | 1.0 | 113.8 | 1.0 | 3.0 | 25.0 | 63.0 | 0.5 | 4.0 |
| | G47 | 468.3 | 83.7 | 2.7 | 86.3 | 55.0 | 0.6 | 3.0 | 1.8 | 2.2 | 1.0 | 112.2 | 0.5 | 2.8 | 23.8 | 72.8 | 1.0 | 4.0 |
| | G46 | 463.7 | 79.3 | 2.7 | 82.0 | 44.1 | 0.4 | 2.0 | 2.0 | 2.6 | 1.0 | 113.9 | 1.0 | 3.0 | 25.6 | 35.9 | 3.0 | 5.0 |
| | G44 | 458.3 | 80.7 | 2.3 | 83.0 | 46.4 | 0.6 | 2.0 | 2.0 | 2.3 | 1.0 | 105.8 | 0.5 | 2.8 | 20.5 | 57.5 | 0.5 | 4.0 |
| | G41 | 435.0 | 83.0 | 3.0 | 86.0 | 33.3 | 0.4 | 4.0 | 2.0 | 2.3 | 1.5 | 94.4 | 0.5 | 2.0 | 22.2 | 65.2 | 0.5 | 5.0 |
| | G56 | 426.3 | 79.3 | 3.7 | 83.0 | 36.0 | 0.5 | 1.0 | 1.8 | 1.9 | 1.0 | 86.7 | 0.5 | 2.0 | 12.7 | 62.5 | 1.0 | 4.0 |
| | G54 | 373.3 | 83.0 | 2.7 | 85.7 | 47.3 | 0.4 | 1.0 | 1.5 | 1.9 | 1.0 | 111.7 | 0.5 | 2.0 | 32.4 | 69.8 | 1.0 | 5.0 |
| | G58 | 360.3 | 85.0 | 2.3 | 87.3 | 38.3 | 0.7 | 3.0 | 1.5 | 2.2 | 1.0 | 102.5 | 1.0 | 2.0 | 17.1 | 61.4 | 1.0 | 5.0 |
| | G62 | 266.0 | 82.7 | 3.3 | 86.0 | 35.7 | 0.6 | 4.0 | 2.0 | 1.6 | 1.0 | 98.3 | 0.5 | 2.0 | 25.0 | 61.6 | 2.5 | 5.0 |
| | **Mean** | **699.9** | **81.0** | **2.9** | **83.9** | **41.1** | **0.5** | **2.1** | **1.9** | **2.0** | **1.1** | **105.5** | **0.6** | **2.2** | **22.2** | **65.7** | **1.6** | **4.6** |
| | **LSD** | **293.3** | **3.1** | **0.7** | **0.4** | **12.9** | **0.3** | **0.5** | **0.8** | **0.8** | **0.7** | **19.3** | **0.3** | **0.7** | **6.9** | **57.8** | **1.6** | **0.6** |
| | **MSE** | **100135** | **3.7** | **0.5** | **4.0** | **61.4** | **0.0** | **0.2** | **0.2** | **0.3** | **0.2** | **145.1** | **0.0** | **0.2** | **18.3** | **1295** | **1.0** | **0.1** |
| | **CV (%)** | **45.2** | **2.4** | **24.6** | **2.4** | **19.0** | **39.3** | **26.9** | **25.0** | **26.0** | **42.5** | **11.4** | **36.4** | **19.4** | **19.0** | **52.1** | **63.8** | **7.7** |
| | **SE** | **316.4** | **1.9** | **0.7** | **2.0** | **7.8** | **0.2** | **0.4** | **0.5** | **0.5** | **0.5** | **12.1** | **0.2** | **0.4** | **4.3** | **36.0** | **1.0** | **0.4** |
| | **Min** | **266.0** | **77.3** | **2.1** | **80.3** | **28.7** | **0.4** | **1.0** | **1.0** | **1.0** | **1.0** | **86.7** | **0.5** | **1.5** | **12.7** | **35.9** | **0.5** | **4.0** |
| | **Max** | **1040.7** | **85.7** | **3.9** | **88.4** | **57.7** | **0.8** | **4.0** | **3.0** | **2.9** | **3.5** | **123.2** | **1.0** | **3.0** | **32.4** | **83.2** | **3.5** | **5.0** |

**LSD = Least significant difference, MSE = Mean square error, CV = coefficient of variation, SE = error, Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour (1-5), # = number.**

**Table 6.5 Mean performance of diallel crosses at the optimal environments in 2011/12**

| | Entry | GY | AD | ASI | DS | EH | EPP | GLS | GT | MSV | PH | RL | RUST | SWT | SH | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Top 10 | G3 | 6955 | 74.0 | 0.7 | 74.7 | 89.4 | 1.2 | 1.8 | 2.8 | 1.0 | 173.3 | 3.0 | 1.2 | 42.7 | 81.9 | 4.7 | 1.0 |
| genotypes | G10 | 5386 | 74.0 | 1.0 | 75.0 | 71.3 | 1.0 | 1.0 | 2.3 | 1.2 | 163.8 | 3.7 | 1.0 | 38.6 | 85.3 | 1.0 | 2.3 |
| | G48 | 5218 | 74.0 | 2.0 | 76.0 | 85.9 | 1.1 | 1.3 | 2.3 | 1.0 | 180.4 | 5.0 | 1.5 | 37.0 | 80.7 | 1.3 | 2.0 |
| | G2 | 5210 | 73.0 | 0.3 | 73.3 | 82.7 | 1.0 | 2.7 | 2.3 | 1.0 | 178.1 | 5.7 | 1.8 | 38.0 | 82.7 | 0.3 | 2.0 |
| | G8 | 5099 | 72.0 | 0.0 | 72.0 | 95.6 | 1.2 | 1.2 | 1.8 | 1.0 | 191.7 | 8.3 | 1.0 | 36.3 | 83.9 | 2.3 | 1.0 |
| | G39 | 5026 | 75.0 | 1.3 | 76.3 | 98.1 | 1.0 | 1.3 | 2.7 | 1.0 | 194.8 | 4.0 | 1.0 | 40.7 | 83.8 | 0.3 | 1.0 |
| | G16 | 4976 | 76.0 | 0.3 | 76.3 | 70.8 | 1.0 | 1.0 | 2.3 | 1.0 | 124.2 | 1.3 | 1.2 | 38.2 | 79.9 | 1.0 | 1.3 |
| | G45 | 4713 | 74.0 | 2.0 | 76.0 | 88.2 | 1.1 | 1.0 | 1.8 | 1.0 | 174.1 | 9.7 | 1.2 | 34.0 | 82.3 | 0.0 | 2.3 |
| | G19 | 4676 | 72.0 | 0.3 | 72.3 | 92.0 | 1.0 | 1.3 | 2.2 | 1.0 | 181.8 | 5.7 | 1.0 | 43.8 | 86.8 | 0.7 | 1.2 |
| | G24 | 4640 | 73.3 | 2.7 | 76.0 | 81.1 | 1.3 | 1.3 | 1.8 | 1.0 | 168.9 | 5.0 | 1.0 | 37.5 | 78.3 | 1.7 | 1.0 |
| Bottom10 | G62 | 2323 | 74.3 | 1.7 | 76.0 | 106.2 | 1.1 | 1.0 | 1.5 | 1.0 | 194.7 | 4.7 | 1.0 | 33.8 | 80.6 | 0.3 | 2.3 |
| genotypes | G55 | 2239 | 77.0 | 0.0 | 77.0 | 92.9 | 1.1 | 1.0 | 2.2 | 1.0 | 186.3 | 2.7 | 1.0 | 31.7 | 75.6 | 0.3 | 2.8 |
| | G31 | 2142 | 71.0 | 0.0 | 71.0 | 101.0 | 1.0 | 1.7 | 2.7 | 1.0 | 187.7 | 4.3 | 1.0 | 32.5 | 83.1 | 0.7 | 2.3 |
| | G35 | 1835 | 76.0 | 0.7 | 76.7 | 95.8 | 1.2 | 1.0 | 1.7 | 1.2 | 174.3 | 10.0 | 1.2 | 33.7 | 74.5 | 0.0 | 2.2 |
| | G41 | 1805 | 72.0 | 0.3 | 72.3 | 85.5 | 1.0 | 1.0 | 2.5 | 1.2 | 170.7 | 2.3 | 1.2 | 29.8 | 75.1 | 0.3 | 3.0 |
| | G60 | 1622 | 69.0 | 1.3 | 70.3 | 84.0 | 1.0 | 1.2 | 2.2 | 1.2 | 172.7 | 10.3 | 1.0 | 27.7 | 75.2 | 0.7 | 4.2 |
| | G44 | 1556 | 76.0 | 0.7 | 76.7 | 122.2 | 1.1 | 1.0 | 2.0 | 1.0 | 216.9 | 1.0 | 1.0 | 31.5 | 72.5 | 0.3 | 2.8 |
| | G61 | 1456 | 74.0 | 0.0 | 74.0 | 104.8 | 1.0 | 1.3 | 1.7 | 1.0 | 190.3 | 8.0 | 1.3 | 24.5 | 77.0 | 0.0 | 4.2 |
| | G43 | 1381 | 74.0 | 0.7 | 74.7 | 84.3 | 1.0 | 1.0 | 2.2 | 1.0 | 180.2 | 3.0 | 1.0 | 29.5 | 79.4 | 0.0 | 3.5 |
| | G40 | 757 | 72.0 | 3.7 | 75.7 | 88.1 | 0.9 | 1.0 | 2.2 | 1.0 | 177.9 | 8.0 | 1.0 | 27.9 | 70.0 | 0.0 | 4.5 |
| | **Mean** | **3450.8** | **73.6** | **1.0** | **74.6** | **91.0** | **1.1** | **1.3** | **2.2** | **1.0** | **179.1** | **5.3** | **1.1** | **34.5** | **79.4** | **0.8** | **2.3** |
| | **LSD** | **1649.9** | **0.8** | **1.4** | **1.3** | **328.2** | **0.2** | **0.5** | **0.8** | **0.4** | **38.7** | **6.7** | **1.1** | **10.2** | **10.5** | **3.8** | **1.1** |
| | **P** | **0.001** | **0.001** | **0** | **0** | **0.63** | **0.165** | **0.001** | **0.36** | **0.16** | **0.75** | **0.002** | **0.078** | **0.001** | **0.05** | **0.35** | **0.001** |
| | **CV (%)** | **31.9** | **0.7** | **74.7** | **0.8** | **19.7** | **12.4** | **22.8** | **23.7** | **21.3** | **13.2** | **82.9** | **0.2** | **18.0** | **8.0** | **230.1** | **30.8** |
| | **Min** | **757.0** | **69.0** | **0.0** | **70.3** | **70.8** | **0.9** | **1.0** | **1.5** | **1.0** | **124.2** | **1.0** | **1.0** | **24.5** | **70.0** | **0.0** | **1.0** |
| | **Max** | **6955.0** | **77.0** | **3.7** | **77.0** | **122.2** | **1.3** | **2.7** | **2.8** | **1.2** | **216.9** | **10.3** | **1.8** | **43.8** | **86.8** | **4.7** | **4.5** |

**LSD = Least significant difference, CV = coefficient of variation, Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour (1-5), # = number.**

**Table 6.6 Estimated percent reduction for salient phenotypic traits for diallel crosses under low pH versus optimal conditions**

| Trait | Low pH | Optimal | Percentage of optimal | % Reduction |
|---|---|---|---|---|
| GY | 699.9 | 3205.2 | 21.8 | 78.2 |
| EH | 41.1 | 92.0 | 44.7 | 55.3 |
| EPP | 0.5 | 1.1 | 45.5 | 54.5 |
| GT | 1.9 | 2.2 | 84.7 | 15.3 |
| PH | 105.5 | 180.9 | 58.3 | 41.7 |
| SWT | 22.2 | 34.9 | 63.7 | 36.3 |
| SH | 65.7 | 81.0 | 81.2 | 18.8 |
| VIG | 4.6 | 2.2 | 37.5 | 62.5 |

**GY = grain yield (kg ha$^{-1}$), EH = ear height (cm), EPP = ears per plant (#), GT = grain texture (1-5), PH = plant height (cm), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number.**

**Table 6.7 Genetic variances, phenotypic variances and heritability estimates for the diallel crosses across optimal and three low pH environments in 2011/12**

| Trait | Genetic variance ($\delta^2g$ ) | Phenotypic variance($\delta^2p$) | Heritability($H^2b$) |
|---|---|---|---|
| GY | 311866.67 | 361866.73 | 0.86 |
| AD | 10.67 | 11.53 | 0.93 |
| ASI | 0.41 | 0.47 | 0.87 |
| DS | 10.65 | 11.71 | 0.91 |
| EH | 50.37 | 65.43 | 0.77 |
| EPP | 0.01 | 0.07 | 0.14 |
| LB | 0.42 | 0.49 | 0.86 |
| GLS | 0.27 | 0.33 | 0.82 |
| GT | 0.2 | 0.27 | 0.74 |
| MSV | 0.05 | 0.11 | 0.45 |
| PH | 47.1 | 67.16 | 0.70 |
| RL | 1.63 | 1.97 | 0.83 |
| Rust | 0.11 | 0.17 | 0.65 |
| SH | 31.57 | 46.63 | 0.68 |
| SL | 1.96 | 3.03 | 0.65 |
| SWT | 21.33 | 28.39 | 0.75 |
| VIG | 0.30 | 0.36 | 0.83 |

**$\sigma^2_g$ = genotypic variance, $\sigma^2_p$ = phenotypic variance, $H^2b$ = broad sense heritability, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SH = shelling percentage, SL = stem lodging (#), SWT = 100 seed weight (g), VIG = vigour (1-5), # = number**

### 6.5.3 Combining ability and inheritance

Combined ANOVA results across all sites are presented in Table 6.8. Environment mean squares were significant for all traits measured except for maize streak virus. Genotype mean squares were significant for all traits excluding root and stem lodging as well as for grain texture and shelling percentage. GCA was significant for grain yield, anthesis date, anthesis-silking interval, days to silking, plant and ear height, and gray leaf spot, leaf blight, maize streak virus, rust, and plant vigour. The interaction of GCA by site was significant for grain yield, anthesis date, root lodging, gray leaf spot, leaf blight, maize streak virus, rust, grain texture, shelling percentage and plant vigour. SCA was significant for all traits measured except shelling percentage. The interaction between SCA effects and site was again significant for all traits apart from number of ears per plant, stem lodging and 100 seed weight. The calculated ratios of GCA/SCA were either higher or closer to 1.0 for the individual traits (Tables 6.8 and 6.9) suggesting the presence of additive and non-additive gene action. Under low pH soil environments (Table 6.9) additive gene action was predominant in the inheritance of grain yield, number of ears per plant, shelling percentage, 100 seed weight and plant vigour because the GCA/SCA ratios were greater than unity while non-additive gene action was predominant in the inheritance of anthesis-silking interval, plant and ear height, grain texture, stem and root lodging, gray leaf spot disease and rust disease. However, the SCA effects were not significant for shelling percentage and ears per plant.

The mean squares due to GCA and SCA were higher under optimal than under low pH conditions and across sites (Table 6.10). However, the mean squares due to GCA and SCA was higher under low pH than under optimal conditions except for root and stem lodging. With respect to the relative contribution of GCA and SCA to total variation, GCA sum of squares for grain yield contributed relatively more to variation under optimal conditions (32.2%) than across environments (28.1%) (Table 6.11). Similarly the sum of squares due to SCA contributed the highest amount of variation under optimal (67.8%) compared to low pH conditions and across sites. A similar trend was observed for other traits. Under low pH the percentage contribution ranged from 0.01 to 9.21 (Table 6.11).

**Table 6.8 Combined analysis of variance for GCA and SCA for diallel crosses for grain yield and other agronomic traits across optimal and three low pH environments in 2012**

| Source | Site | Genotypes | GCA | GCA x Site | SCA | SCA x Site | Error | GCA/SCA ratio |
|---|---|---|---|---|---|---|---|---|
| DF | 3 | 65 | 11 | 33 | 54 | 162 | 195 | |
| GY | 833.60** | 2.94** | 12.40** | 1.86** | 3.53** | 1.44** | 0.45 | 3.51 |
| AD | 345.02** | 3.92** | 4.36** | 3.90** | 4.87** | 6.20** | 10.16 | 0.90 |
| ASI | 81605.70** | 8.35** | 16.43** | -0.70 | 13.31** | 7.53** | 3.51 | 1.23 |
| DS | 258820** | 11.10** | 109.24** | -18.89 | 36.38** | 5.66** | 1.24 | 3.00 |
| PH | 1709.46** | 1.93** | 1.74** | 1.77 | 2.13** | 1.76** | 279.90 | 0.82 |
| EH | 1132.16** | 2.54** | 1.76** | 1.92 | 2.15** | 1.89** | 132.80 | 0.82 |
| EPP | 38.90** | 1.58** | 1.66 | -7.40 | 1.71** | -18.16 | 89.27 | 0.97 |
| RL | 118.80** | 1.24 | 1.23 | 1.83** | 1.89** | 1.46** | 7.65 | 0.65 |
| SL | 44.70** | 1.27 | 1.61 | 1.69 | 1.17* | 1.10 | 2.00 | 1.38 |
| GLS | 429.14** | 4.91** | 5.72** | 5.49** | 5.38** | 3.62** | 0.19 | 1.06 |
| LB | 251.47** | 3.76** | 3.86** | 4.88** | 3.70** | 3.70** | 0.32 | 1.04 |
| MSV | 0.02 | 1.72** | 2.17** | 3.94** | 1.85** | 2.58** | 0.015 | 1.17 |
| RUST | 1394.02** | 3.09** | 3.76** | 2.12** | 3.30** | 2.94** | 0.15*** | 1.14 |
| GT | 28.55** | 1.01 | 1.05 | 1.76** | 1.46* | 1.47** | 3.92 | 0.72 |
| SH | 36.10** | 1.29 | 1.61 | 2.16** | 1.17 | 1.35** | 599.50 | 1.38 |
| SWT | 277.60** | 1.68** | 1.12 | 0.450 | 2.30** | 0.48 | 44.76 | 0.49 |
| VIG | 1316.1** | 2.38** | 1.93* | 3.19** | 2.91** | 3.24** | 0.43 | 0.66 |

*****P≤0.001; **P≤0.01; *P≤0.05; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), PH = plant height (cm), EH = ear height (cm), EPP = ears per plant (#), RL = root lodging (#), SL = stem lodging (#),GLS = gray leaf spot disease (1-5), LB = leaf blight disease, MSV = maize streak virus disease (1-5), Rust = rust disease (1-5), GT = grain texture (1-5), SH = shelling percentage, SWT = 100 seed weight (g), VIG = vigour (1-5), # = number.**

**Table 6.9 Combined analysis of variance for GCA and SCA for diallel crosses for grain yield and other agronomic traits across three low pH environments in 2012**

| Source | Site | Genotypes | GCA | GCA x Site | SCA | SCA x Site | Error | GCA/SCA Ratio |
|---|---|---|---|---|---|---|---|---|
| DF | 2 | 65 | 11 | 22 | 54 | 108 | | |
| GY | 223.70** | 0.48** | 1.09** | 0.32** | 0.57* | 0.05* | 0.18 | 1.92 |
| AD | 573.40** | 43.88** | 45.70** | 53.50** | 44.30** | 89.30** | 11.34 | 1.03 |
| ASI | 379684.90** | 36.59** | 16.00** | 13.95** | 44.20** | 38.40** | 3.65 | 0.36 |
| DS | 471947.80** | 28.80** | 52.70** | 29.90** | 34.98** | 34.40** | 7.44 | 1.51 |
| PH | 331735.00** | 601.70** | 154.57 | 686.00** | 686.70** | 503.90** | 172.90 | 0.23 |
| EH | 49538.45** | 367.60** | 307.40** | 150.70** | 379.70** | 203.60** | 62.37 | 0.81 |
| EPP | 159.00** | 35.70 | 40.00 | 54.00* | 34.90 | 41.45 | 32.68 | 1.15 |
| RL | 44.40** | 2.94** | 2.16** | 0.97 | 3.15** | 1.50** | 7.70 | 0.69 |
| SL | 172.70** | 0.56** | 0.18 | 0.27 | 0.64** | 0.31** | 2.00 | 0.28 |
| GLS | 115.10** | 0.92** | 0.80* | 0.76** | 0.96** | 0.47** | 0.21 | 0.83 |
| LB | 114.96** | 1.036** | 1.23** | 1.32** | 1.01** | 0.68** | 0.33 | 1.22 |
| MSV | 0.20** | 0.17** | 0.28** | 0.24** | 0.15** | 0.19** | 0.03 | 1.87 |
| Rust | 317.50** | 2.50** | 1.60 | 2.40* | 2.70** | 1.90* | 1.40 | 0.59 |
| GT | 152.00** | 0.99** | 0.80** | 0.60** | 1.06** | 0.60** | 0.49 | 0.75 |
| SH | 2679.30* | 877.93 | 851.16 | -315.60 | 839.61 | -357.79 | 749.20 | 1.01 |
| SWT | 5964.70** | 76.39** | 120.42** | -50.39 | 74.15** | -21.60 | 22.39 | 1.62 |
| VIG | 429.10** | 2.16** | 61.23** | 1.97** | 45.39* | 1.98** | 1.80 | 1.35 |

****P≤0.01; *P≤0.05; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), PH = plant height (cm), EH = ear height (cm), EPP = ears per plant (#), RL = root lodging (#), SL = stem lodging (#), GLS = gray leaf spot disease (1-5), LB = leaf blight disease, MSV = maize streak virus disease (1-5), Rust = rust disease (1-5), GT = grain texture (1-5), SH = shelling percentage, SWT = 100 seed weight (g), VIG = vigour (1-5), # = number.**

**Table 6.10 Mean squares for GCA and SCA effects under different environments**

| Trait | Across | | Optimal | | Low pH | |
|---|---|---|---|---|---|---|
| | **GCA** | **SCA** | **GCA** | **SCA** | **GCA** | **SCA** |
| GY | 6.19** | 1.76** | 2423935.00** | 1039389.32** | 1.09** | 0.57* |
| AD | 43.63** | 49.41** | 6.23** | 6.96** | 45.70** | 44.30** |
| ASI | 57.76** | 46.70** | 0.71** | 0.82** | 16.00** | 44.20** |
| DS | 135.50 | 45.13** | 7.77** | 6.48** | 52.7** | 34.98** |
| EH | 234.33 | 284.98** | 107.00 | 100.53 | 154.57 | 34.90 |
| EPP | 148.24 | 152.50** | 0.01 | 0.01 | 40.00 | 34.90 |
| LB | 1.25** | 1.51** | 0.49 | 0.73** | 1.23** | 1.01** |
| GLS | 1.08** | 1.02** | 0.30** | 0.17** | 0.80* | 0.96** |
| GT | 4.11 | 5.74** | 0.11 | 0.10 | 0.99** | 1.06** |
| MSV | 0.33** | 0.28** | 0.02 | 0.02 | 0.28** | 0.15** |
| PH | 488.42 | 596.17** | 190.78 | 159.43 | 601.70** | 686.00** |
| RL | 9.41 | 14.46** | 11.23* | 10.26** | 2.16** | 3.15** |
| RUST | 0.58** | 0.51 | 0.02 | 0.03 | 2.50** | 2.70** |
| SWT | 50.18 | 103.27** | 18.40 | 39.90 | 120.40** | 74.2** |
| SH | 964.10 | 704.60** | 32.96** | 17.05 | 851.16 | 839.61 |
| SL | 3.24 | 2.34 | 3.05 | 1.82 | 0.18 | 0.64** |
| VIG | 0.84** | 1.26** | 0.68 | 0.72** | 61.23** | 45.39** |

****P≤0.01; *P≤0.05; GSA = general combining ability, SCA = specific combining ability, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour (1-5), # = number.**

**Table 6.11 Relative percent contribution of sum of squares for GCA and SCA to total sum of squares across environments**

| Trait | Environment | Sum of squares GCA | Total SS | Percentage of total SS | SCA | Total SS | Percentage of total SS |
|---|---|---|---|---|---|---|---|
| **GY** | Across | 68.10 | 242.00 | 28.10 | 95.10 | 242.00 | 39.30 |
| | Optimal | 26663289.00 | 82760312.20 | 32.20 | 56127023.00 | 82760312.20 | 67.80 |
| | Low pH | 1.09 | 54.96 | 2.00 | 0.57 | 54.96 | 1.03 |
| **EH** | Across | 2577.70 | 67027.00 | 3.80 | 15389.00 | 67027.00 | 23.00 |
| | Optimal | 1177.20 | 6605.90 | 17.80 | 5428.70 | 6605.90 | 82.20 |
| | Low pH | 307.40 | 8915.74 | 3.44 | 379.70 | 8915.74 | 4.30 |
| **EPP** | Across | 1630.60 | 6680.30 | 24.40 | 8236.20 | 6680.30 | 123.30 |
| | Optimal | 0.10 | 0.50 | 17.40 | 0.40 | 0.50 | 82.80 |
| | Low pH | 40.00 | 8003.60 | 0.45 | 34.90 | 8003.60 | 0.01 |
| **GT** | Across | 45.20 | 1519.30 | 3.00 | 309.80 | 1519.30 | 20.40 |
| | Optimal | 1.20 | 6.40 | 19.30 | 5.20 | 6.40 | 80.70 |
| | Low pH | 0.80 | 8766.00 | 0.50 | 1.06 | 8766.00 | 0.01 |
| **PH** | Across | 5372.60 | 133576.10 | 4.00 | 32192.90 | 133576.10 | 24.10 |
| | Optimal | 2098.60 | 10707.80 | 19.60 | 8609.30 | 10707.8.00 | 80.40 |
| | Low pH | 154.57 | 108297.00 | 0.14 | 686.70 | 108297.00 | 0.63 |
| **SWT** | Across | 552.00 | 10894.20 | 5.10 | 5576.40 | 10894.20 | 51.20 |
| | Optimal | 202.40 | 2357.20 | 8.60 | 2154.80 | 2357.20 | 91.40 |
| | Low pH | 120.42 | 8770.00 | 1.37 | 74.15 | 8770.00 | 0.85 |
| **SH** | Across | 10605.10 | 222803.70 | 4.80 | 38049.10 | 222803.70 | 0.40 |
| | Optimal | 362.50 | 1282.90 | 28.30 | 920.40 | 1282.9 | 71.70 |
| | Low pH | 851.16 | 9116.80 | 9.34 | 839.61 | 9116.8 | 9.210 |
| **VIG** | Across | 9.20 | 168.20 | 5.50 | 68.00 | 168.20 | 40.40 |
| | Optimal | 7.50 | 46.20 | 16.20 | 38.70 | 46.20 | 83.80 |
| | Low pH | 61.23 | 5597.50 | 1.09 | 45.39 | 5597.50 | 0.81 |

**GY = grain yield (kg ha$^{-1}$), EH = ear height (cm), EPP = ears per plant (#), GT = grain texture (1-5), PH = plant height (cm), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5).**

Twelve maize inbred lines were clustered based on the GCA effects for grain yield. Two main clusters were observed (Figure 6.1) with a high cophenetic correlation of $r_{cop}$ = 0.87. The pattern mostly followed the origin of the maize inbred lines such that six out of seven inbred lines from CIMMYT-Colombia (tropical) were grouped in the second cluster. The first cluster comprised of inbred lines with low GCA for grain yield while the second cluster was comprised of inbred lines of medium GCA and the third cluster had CZL999601 which had the highest GCA for grain yield.

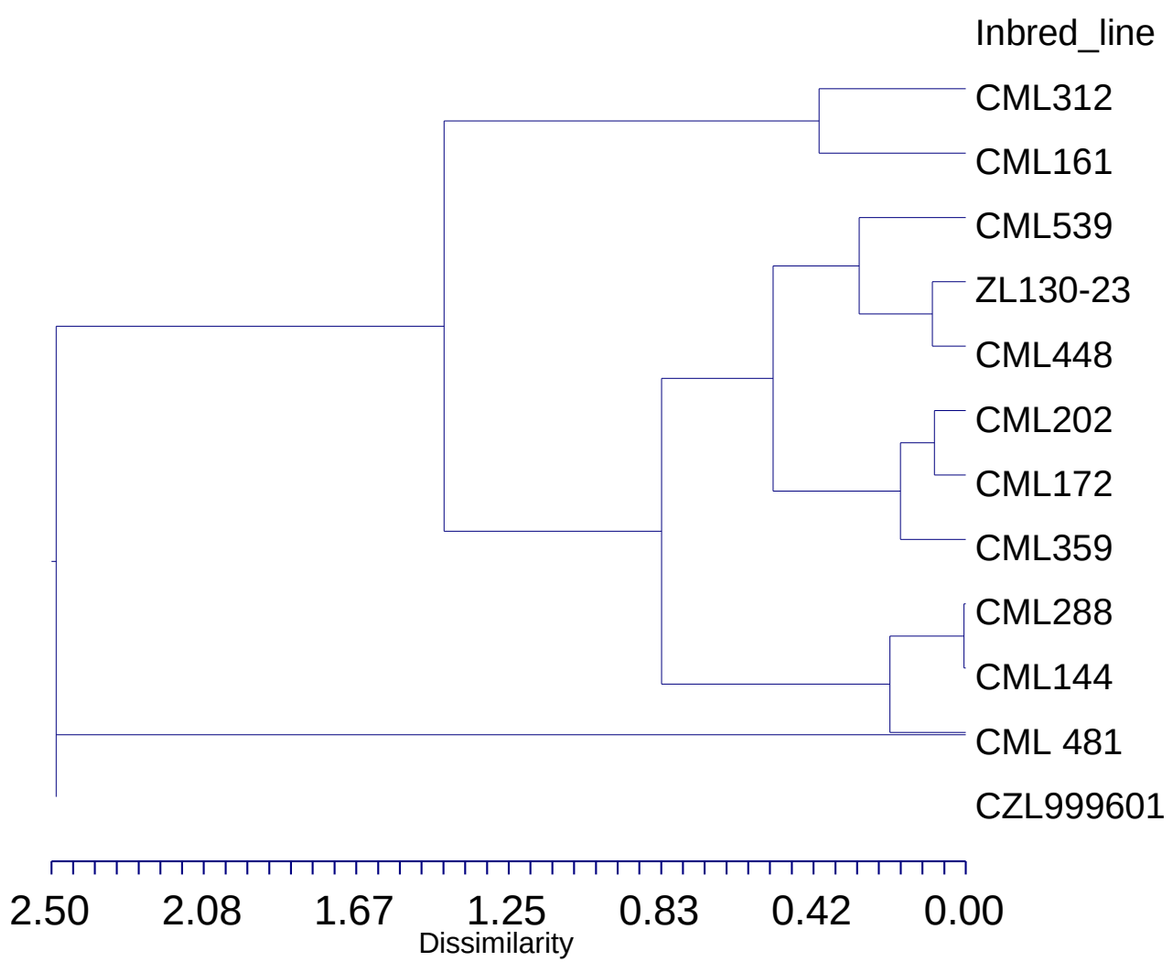


**Figure 6.1 Dendrogram of 12 maize inbred lines based on GCA effects for grain yield across four environments for 2011/12 season**

#### 6.5.3.1 Estimated general combining ability effects for 12 inbred lines for grain yield and agronomic traits across low pH and optimal environments in 2011/12

A positive, high and significant GCA effect for yield was recorded for inbred line CZL999601 (0.55) (Table 6.12). Also positive and high but not significant values were observed for grain yield for inbred lines by CML481 (0.18) followed by CML144 (0.13) and CML 288 (0.13) and significant negative GCA was recorded for inbred line CML161 (-0.38). For days to anthesis positive and significant GCA values were observed for lines ZL130-23 (1.2) and CML312 (1.15). Negative and highly significant GCA was recorded for inbred line CML288 (-0.73). Selecting for earliness to maturity should be done by selecting inbred lines with low and negative GCA effects. Positive and high values for GCA effects were observed for anthesis-silking interval for inbred lines CML288 (1.06) and CML481 (0.75). Negative and lowest GCA values were recorded for inbred lines CML161 (-1.1) and CML172 (-0.9). For stress tolerance breeding, lines with negative GCA for this trait would be preferred.

Positive and high GCA effects were observed for number of ears per plant in lines CZL999601 (1.26), CML481 (1.24), ZL130-23 (1.12) and CML288 (1.08). When selecting for prolificacy, lines with high and positive GCA for this trait would be preferred. Positive and high GCA effects were observed for grain texture for inbred lines ZL130-23 (0.36) followed by CML312 (0.17). When selecting for flint and semi-flintiness, lines with negative GCA should be selected since a score of 1 is better than a score of 5 in 1-5 scale. In terms of diseases, positive and high GCA effects were observed for gray leaf spot for lines CML172 (0.15), CML288 (0.13) and CML202 (0.11). Inbred line CML448 (-0.16) had negative and significant GCA. Selecting for tolerance to this disease should be done by selecting lines with negative GCA. Positive and significant GCA effects were observed for MSV in lines CML288 (0.10). Positive GCAs values were also observed for inbred lines CML161 (0.08) and CML35 (0.08). The lowest and negative GCA was observed for lines (CML202 (-0.08), CZL999601 (-0.06) and CML539 (-0.04). Selecting lines for tolerance to this disease could be achieved by selection lines with negative GCA. For leaf blight disease, high and positive GCA's were recorded for inbred lines CML172 (1.7) followed by CML481 (1.2) and the lowest GCA was recorded for line CML539 (-3.3).

**Table 6.12 Estimated general combining ability effects for 12 inbred lines for grain yield and agronomic traits across low pH and optimal environments in 2011/12**

| Line | Name | GY | AD | ASI | DS | EH | EPP | GLS | GT | LB | MSV | PH | RL | Rust | SWT | SH | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G1 | CZL999601 | 0.55** | -0.21 | -0.17 | -0.53 | -0.43 | 1.26 | 0.05 | -0.13 | -0.4 | -0.06 | 0.71 | 0.18 | 0.04 | 0.68 | 5.19 | 0.22 | -0.04 |
| G2 | CML481 | 0.18 | -0.26 | 0.75 | -1.26 | 1.21 | 1.24 | -0.02 | -0.24 | 1.2 | -0.04 | 1.25 | 0.39 | -0.08 | -0.25 | -3.31 | 0.38* | -0.2 |
| G3 | CML359 | 0.04 | -0.63 | 0.6 | -0.18 | 0.44 | 0.43 | -0.03 | -0.05 | 0.4 | 0.08 | 3.42 | -0.21 | -0.03 | -0.48 | -4.12 | 0.23 | -0.06 |
| G4 | CML144 | 0.13 | -0.32 | 0.69 | -1.25 | 1.04 | 0.29 | 0.03 | -0.28 | 1.0 | -0.02 | 1.19 | -0.36 | -0.06 | 0.96 | -0.34 | 0.02 | -0.05 |
| G5 | CML161 | -0.38** | 0.12 | -1.1 | 0.93 | 0.69 | -1.21 | 0.01 | 0.22 | 0.7 | 0.08 | -1.62 | -0.23 | -0.06 | -0.51 | -0.18 | -0.16 | 0.16 |
| G6 | CML172 | -0.02 | -0.13 | -0.91 | 1.06 | 1.69 | -1.19 | 0.15 | -0.09 | 1.7 | 0.03 | -0.58 | 0.33 | 0.09 | 0.56 | 6.27* | -0.02 | -0.06 |
| G7 | CML448 | -0.15 | -0.27 | -0.29 | -0.08 | -1.73 | 0.48 | -0.16* | -0.12 | -1.7 | -0.04 | -2.3 | -0.41 | -0.04 | 1.1 | -1.81 | -0.16 | 0.05 |
| G8 | CML312 | -0.28 | 1.15* | 0.45 | 0.67 | -0.38 | -2.29 | 0.00 | 0.17 | -0.4 | 0.00 | -0.16 | 0.44 | 0.1 | -0.58 | 1.34 | 0.07 | 0.24 |
| G9 | ZL130-23 | -0.13 | 1.20* | -0.87 | 2.01 | 1.11 | 1.12 | -0.02 | 0.36 | 1.1 | -0.01 | -0.45 | -0.06 | 0.09 | -0.45 | -0.63 | -0.18 | 0.02 |
| G10 | CML288 | 0.13 | -0.73** | 1.06 | -1.64 | -0.9 | 1.08 | 0.13 | -0.07 | -0.9 | 0.10* | 0.97 | 0.26 | -0.15 | 0.68 | -1.6 | -0.11 | 0.07 |
| G11 | CML202 | 0.01 | -0.29 | 0.04 | -0.47 | 0.56 | -0.2 | 0.11 | 0.05 | 0.6 | -0.08 | 1.97 | -0.43 | 0.05 | -0.62 | -1.46 | -0.16 | -0.01 |
| G12 | CML539 | -0.07 | 0.39 | -0.24 | 0.74 | -3.31 | -1.01 | -0.23 | 0.16 | -3.3 | -0.04 | -45 | 0.09 | 0.04 | -1.09 | 0.65 | -0.14 | -0.11 |

****P≤0.01; *P≤0.05; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), LB = leaf blight disease, MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#) VIG = vigour (1-5), # = number.**

Similarly, selecting for tolerance to this disease could be done by selecting lines with negative GCA effects. With respect to rust, positive and high GCA effects were observed for lines CML312 (0.1), CML172 (0.09) and ZL130-23 (0.09). The lowest and negative GCA was observed for line CM288 (-0.15). Selecting lines for tolerance to this disease would be achieved by selecting lines with negative GCA.

High GCA effects were observed for plant height in inbred lines CML359 (3.42), CML202 (1.97), followed by CML481 (1.25). The negative and lowest GCA was observed for line CML539 (-45.0). For ear height a high GCA effects were observed for inbred lines CML172 (1.69) followed by CML481 (1.21). Negative and lowest GCA was observed for line CML539 (-3.31). Where tall varieties are preferred, lines with high and positive GCA could be preferred. Positive and significant value for GCA effects was observed for stem lodging in inbred lines CML481 (0.38), inbred line CML359 (0.23) also had a high value. The lowest and negative GCA values were recorded for lines ZL130-23 (-0.18) followed by CML448, CML202 and CML161 all with a value of -0.16. High GCA effects were observed for root lodging for CML312 (0.44), CML481 (0.39) and CML172 (0.33). The lowest and negative GCA were recorded for lines CML202 (-0.43) and CML448 (-0.41). When selecting for tolerance for both root lodging and stem lodging, lines with negative GCA would be preferred. High GCA effects were observed for plant vigour for inbred lines CML312 (0.24), CM161 (0.16), and negative and lowest GCA was recorded for CML539 (-0.11). In terms of 100 seed weight, high GCA effects were observed for inbred lines CML448 (1.1), CML144 (0.96) and CML288 (0.68). The lowest and negative GCA values were observed for lines CML539 (-0.09), CML202 (-0.62). With respect to shelling percentage, high GCA effects were observed for inbred line CML172 (6.27), followed by CZL999601 (5.19). The lowest and negative GCA was observed for lines CML359 (-4.12) and CML481 (-3.3). For plant vigour, 100 seed weight, and shelling percentage, inbred lines with higher and positive GCAs would be preferred.

### 6.5.3.2 Estimated specific combining ability effects for 12 inbred lines for grain yield and agronomic traits across low pH and optimal environments in 2011/12

Results for the estimated SCA effects in the diallel crosses are presented in Appendix 12. The promising specific combinations for grain yield were CZL999601/CML144 (0.94), CML144/CML202 (0.73) and CML481/CML288 (0.70). The poorest combinations were CZL130-23/CML202 (-0.65) and CZL999601/CML481 (-0.65). When breeding for high yield, positive SCA values are desirable. For days to 50% pollen shedding, the best specific combinations were CML161/CML288 (4.03), CML144/ZL130-23 (3.8), followed by CML312/CML288 (3.09). The poor combinations were CML359/CM288 (-6.71), CML202/CML539 (-3.7) and CML161/ZL130-23 (-2.56). Selecting for earliness to maturity should be done by selecting inbred lines and hybrids with low and negative GCA and SCA effects, respectively. The highest SCA effects were observed for anthesis-silking interval for crosses and the best combinations were CML161/CML288 (4.14), CML359/CML288 (3.9) and CML144/CML539 (3.39). Low SCA values were recorded for the following hybrids: CML288/CML539 (-3.55), ZL130-23/CML288 (-3.5), CML288/CML202 (-3.12) and CML144/CML161 (-2.9). For stress tolerance, hybrids with negative SCA for this trait would be preferred.

Positive and high SCA effects were observed for number of ears per plant for hybrids CML448/CML288 (16.6) CML144/CML202 (7.4) and ZL130-23/CML288 (6.37) and the poor combinations were CZL999601/CML481 (-5.37), ZL130-23/CML288 (-4.91) and CML481/CML448 (-4.51). When selecting for prolificacy, lines and hybrids with high and positive GCA and SCA for this trait would be preferred. Significant and high SCA effects were observed for grain texture for hybrids ZL130-23/CML539 (2.75), CML161/CML202 (2.51) followed by CML312/ZL130-23 (2.19). The poorest combinations were ZL130-23/CML202 (-0.95), CML481/ZL130-23 (-0.84) and CML161/CML539 (-0.83) but when selecting for flint and semi-flintiness, lines and hybrids with negative GCA and SCA, respectively, could be selected. In terms of diseases, positive and high GCA effects were observed for gray leaf spot for hybrids CZL999601/CML359 (0.86), CM172/ZL130-23 (0.64), and CML144/CML202 (0.62). Hybrids CZL999601/CML202 (-0.61), CML161/CML448 (-0.52) and CZL999601/CML481 (-0.48) had negative SCA. Selecting for tolerance to this disease could be done by selecting lines and hybrids with negative

GCA and SCA, respectively. Positive and high SCA effects were observed for MSV in hybrids CML359/CML288 (0.92), CML161/CML172 (0.47) and CML172/ZL130-23(0.23). The lowest and negative SCA was observed for CML161/CML288 (-0.27), CML359/CML161 (-0.25), and CML359/CML172 (-0.20). Selecting hybrids for tolerance to this disease could be achieved by selection the lines and hybrids with negative GCA and SCA, respectively. For leaf blight disease, high and positive SCA's were recorded for hybrids CML481/CML144 (0.88) and CML172/CML202 (0.83) followed by CML172/CML312 (0.77) and the lowest SCA's were recorded for hybrids CML312/CML202 (-0.6), CML481/CML288 (-0.6) and ZL130-23/CML288 (-0.59). Similarly, selecting for tolerance to this disease could be done by selecting lines and hybrids with negative GCA and SCA effects, respectively. With respect to rust disease, positive and high SCA effects were observed in hybrids CML172/CML448 (0.51), CZL999601/CML359 (0.44) and CML202/CML539 (0.42). The lowest and negative SCA's were observed for hybrid CML448/ZL130-23 (-0.49), CZL999601/CML312 (-0.46) and CML144/CML202 (-0.44). Selecting lines for tolerance to this disease could be achieved by selection hybrids with negative SCA.

Positive and high SCA effects were observed for plant height in hybrids CML144/CML202 (18.64), CML448/CML288 (13.18), followed by CML448/CML202 (12.83). Negative and lowest SCA's were observed for hybrid CML481/CML448 (-16.84), CML202/CML539 (-13.13) and CML144/ZL130-23 (-13.03). For ear height, positive and high SCA effects were observed for hybrids CML448/CML288 (12.49) followed by CML448/CML202 (8.12) and CML172/CML288 (7.96). Negative and lowest SCAs were observed for hybrids CML161/CML312 (-8.88), CML288/CML539 (-8.39) and CML202/CML539 (-8.15). Where tall varieties are preferred, lines and hybrids with high and positive GCA and SCA could be preferred. In terms of lodging, positive and high SCA effects were observed for stem lodging in hybrids CM481/CML359 (2.38) followed by CML202/CML539 (1.24) and CZL999601/CML144 (1.20). The lowest and negative SCA were recorded for hybrids CZL999601/CML481 (-0.72), CZL999601/CML359 (-0.68) and CML481/CML288 (-0.61). Positive and high SCA effects were observed for root lodging for CML172/CML448 (3.29), CML481/CML448 (2.82) and CML144/CML288 (2.35). The lowest and negative SCA were recorded for hybrids CML172/CML539 (-2.60), CML161/CML448 (-0.70) and CML481/CML228 (-1.60). When selecting for tolerance

for both root lodging and stem lodging, inbred lines and hybrids with negative GCA and SCA, respectively could be preferred.

Positive and high SCA effects were observed for plant vigour for hybrids, Z130-23/CML288 (1.08), CML312/CML539 (1.04), CZL999601/CML448 (0.99) and negative and lowest SCA's were recorded for hybrids CZL999601/ZL130-23 (-0.70), CML172/CML481 (-0.60) and CML481/ZL130-23 (-060). In terms of 100 seed weight, positive and high SCA effects were observed for hybrid CML288/CML539 (9.44). Also high and positive values were observed for inbred lines CML312/CML202 (5.84), CML359/CML161 (5.57), and CML448/ZL130-23 (5.04). The lowest and negative SCA were observed for hybrids ZL130-23/CML539 (-6.05), CML448/CML539 (-4.86) and CML161/CML202 (-4.81). With respect to shelling percentage, positive and high SCA effects were observed for hybrids, CZL999601/CML172 (41.02) followed by CML481/CML144 (10.49) and CML288/CML539 (9.86). The lowest and negative SCAs were observed for hybrids CML172/CML448 (-15.15), CML448/CML288 (-12.54) and CZL999601/CML539 (-10.72). For plant vigour, 100 seed weight, and s1 helling percentage inbred lines and hybrids with higher and positive GCA's and SCA's, respectively, would be preferred.

### 6.5.4 Pearson's correlation coefficients for diallel crosses between grain yield and other agronomic traits at optimal environment

Pearson correlation was carried out to study the associations between grain yield and some agronomic traits as well as among themselves. The results are presented in Table 6.13. Grain yield was positively and significantly correlated with anthesis date (0.23), days to 50% silking (0.22) and highly significantly correlated with 100 seed weight (0.31). It was highly significantly negatively correlated with leaf blight disease (r = -0.29). In terms of diseases, gray leaf spot was positively and highly significantly correlated with rust (r = 0.34). Plant vigour showed positive and significant correlation with leaf blight disease (0.40). Days to 50% pollen shed (days to anthesis) was highly significantly and positively correlated with 100 seed weight across optimal (r = 0.27).

**Table 6.13 Pearson's correlations coefficients under optimal conditions**

| | GY | AD | ASI | DS | PH | EH | RL | SL | EPP | SH | GT | LB | GLS | Rust | MSV | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AD | 0.23* | | | | | | | | | | | | | | | |
| ASI | -0.01 | -0.16 | | | | | | | | | | | | | | |
| DS | 0.22* | 0.90** | 0.25* | | | | | | | | | | | | | |
| PH | -0.19* | -0.07 | 0.08 | -0.04 | | | | | | | | | | | | |
| EH | -0.11 | -0.03 | 0.01 | -0.03 | 0.80** | | | | | | | | | | | |
| RL | -0.03 | -0.02 | 0.03 | 0.00 | -0.04 | -0.1 | | | | | | | | | | |
| SL | 0.05 | -0.01 | -0.08 | -0.04 | -0.12 | -0.1 | -0.13 | | | | | | | | | |
| EPP | -0.14 | -0.01 | -0.07 | -0.04 | -0.06 | -0.06 | 0.03 | 0.05 | | | | | | | | |
| SH | 0.20 | -0.26** | -0.03 | -0.27** | -0.13 | -0.12 | 0.12 | 0.00 | -0.06 | | | | | | | |
| GT | -0.10 | -0.01 | -0.04 | -0.03 | -0.01 | -0.01 | -0.12 | 0.05 | -0.01 | 0.02 | | | | | | |
| LB | -0.29** | -0.11 | -0.03 | -0.12 | 0.07 | 0.08 | 0.19 | 0.17 | 0.02 | 0.09 | -0.01 | | | | | |
| GLS | 0.10 | -0.26** | 0.01 | -0.25 | 0.01 | -0.05 | 0.08 | 0.00 | -0.06 | 0.16 | 0.23 | -0.06 | | | | |
| Rust | 0.06 | 0.02 | 0.00 | 0.02 | 0.04 | 0.00 | 0.03 | 0.23 | 0.01 | 0.11 | 0.11 | -0.05 | 0.34** | | | |
| MSV | -0.18 | 0.11 | -0.06 | 0.09 | -0.05 | -0.12 | 0.16 | -0.04 | 0.04 | 0.02 | -0.01 | 0.21 | -0.05 | -0.06 | | |
| VIG | -0.49** | -0.14 | -0.02 | -0.14 | 0.12 | 0.04 | 0.06 | 0.06 | 0.15 | -0.09 | 0.15 | 0.40** | -0.22 | 0.00 | 0.24 | |
| SWT | 0.31** | 0.27** | -0.06 | 0.24 | -0.06 | -0.05 | -0.21 | 0.11 | 0.16 | -0.03 | 0.07 | -0.24 | -0.02 | -0.02 | -0.05 | -0.29** |

****P≤0.01; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), PH = plant height (cm), EH= ear height (cm), RL = root lodging (#), SL= stem lodging (#), EPP = ears per plant (#), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), LB = leaf blight disease, MSV = maize streak virus disease (1-5), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number.**

### 6.5.5 Pearson's correlation coefficients for diallel crosses between grain yield and other agronomic traits at low pH environments

Results are given in Table 6.14. Grain yield was positively and significantly correlated with shelling percentage (r = 0.28), 100 seed weight (r = 0.57), plant height (r = 0.81), ear height (r = 0.64), stem lodging (r = 0.35) and grain texture (r = 0.34). GY was negatively but significantly correlated with anthesis date (r = -0.31), anthesis-silking interval (r = 0.70), root lodging (r = -0.32), and plant vigour (r = -0.46). With respect to plant vigour, the lower the score the better the plant vigour while the higher the grain weight the higher the yield. So with correlation analysis this is negative association while in real sense genotypes with high plant vigor (low score) gives higher yield and this is a positive association. Correlation among other traits showed that plant height was correlated with ear height (r = 0.85), 100 seed weight (r = 0.59) but was negatively and significantly correlated with plant vigour (r = -0.46), root lodging (r = -0.26). Grain texture was positively and significantly correlated with shelling percentage (r = 0.36), 100 seed weight (0.3). It was negatively correlated with plant vigour (r = -0.52), and rust disease (r = -0.37). Shelling percentage was positively and significantly correlated with 100 seed weight (r = 0.54), but was negatively and significantly correlated with root lodging (r = -0.30), rust disease (r = -0.23), and plant vigour (r = -0.4).

## 6.6 Discussion

Effective selection of inbred lines for the production of maize hybrids requires prior information of the inbred line *per se* and the behaviour of the line in a particular hybrid combination. Malawi has a humid sub-tropical climate, while Colombia has a tropical climate. In this study, both inter and intra-cross combinations from tropical and sub-tropical maize inbred lines indicated good yield performance under optimal condition and across sites. The top yielding hybrid was a cross between sub-tropical and tropical inbred lines. Under low pH conditions, the top yielding hybrid was a cross involving tropical inbred lines, suggesting that tropical germplasm was more tolerant to low pH than sub-tropical germplasm. The results were similar to what was reported by Magnavaca *et al*. (1987) who reported that Brazilian maize inbred lines (tropical) were generally more

**Table 6.14 Pearson's correlation coefficients and level of significance under low pH for diallel crosses**

| | GY | AD | ASI | DS | PH | EH | RL | SL | GT | LB | GLS | Rust | MSV | VIG | SWT | EPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AD | -0.31** | | | | | | | | | | | | | | | |
| ASI | -0.70** | 0.25** | | | | | | | | | | | | | | |
| DS | -0.48** | 0.96** | 0.50** | | | | | | | | | | | | | |
| PH | 0.81** | -0.20** | -0.68** | -0.35** | | | | | | | | | | | | |
| EH | 0.64** | -0.10** | -0.47** | -0.25** | 0.85** | | | | | | | | | | | |
| RL | -0.32** | 0.13** | 0.56** | 0.27** | -0.26** | -0.02 | | | | | | | | | | |
| SL | 0.35** | -0.09 | -0.05 | -0.10* | 0.34** | 0.33** | 0.33** | | | | | | | | | |
| GT | 0.34** | -0.09 | -0.39** | -0.19** | 0.25** | 0.07 | -0.47** | -0.16** | | | | | | | | |
| LB | 0.66** | -0.20** | -0.42** | -0.26** | 0.63** | 0.60** | 0.12** | 0.47** | 0.09 | | | | | | | |
| GLS | 0.64** | -0.20** | -0.36** | -0.25** | 0.65** | 0.69** | 0.19** | 0.42** | 0.03 | 0.77** | | | | | | |
| Rust | -0.05 | 0.06 | 0.38** | 0.16** | -0.04 | 0.22** | 0.79** | 0.38** | -0.37** | 0.33** | 0.41** | | | | | |
| MSV | 0.34** | -0.06 | -0.04 | -0.06 | 0.30** | 0.42** | 0.40** | 0.39** | -0.11 | 0.57** | 0.64** | 0.60** | | | | |
| VIG | -0.46** | 0.13** | 0.69** | 0.31** | -0.46** | -0.15** | 0.86** | 0.23** | -0.52** | -0.03 | 0.04 | 0.82** | 0.36** | | | |
| SWT | 0.57** | -0.20** | -0.50** | -0.28** | 0.59** | 0.45** | -0.23** | 0.19** | 0.30** | 0.43** | 0.44** | -0.10 | 0.20** | -0.40** | | |
| EPP | 0.04 | 0.40** | 0.01 | 0.36** | 0.16** | 0.14** | -0.01 | 0.05 | 0.07 | 0.00 | 0.04 | 0.01 | 0.02 | -0.08 | -0.02 | |
| SH | 0.28** | -0.03 | -0.28** | -0.10* | 0.29** | 0.19** | -0.30** | 0.01 | 0.36** | 0.11 | 0.08 | -0.23** | -0.03 | -0.40** | 0.54** | 0.14** |

****P≤0.01; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), PH = plant height (cm), EH= ear height (cm), RL = root lodging (#), SL= stem lodging (#), EPP = ears per plant (#), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), LB = leaf blight disease, MSV = maize streak virus disease (1-5), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour (1-5), # = number.**

tolerant than USA inbred lines to Al effects. In terms of grain yield for the hybrids *per se*, the results were similar to what was reported by Pérez (2008).

Maize yields were greatly reduced across low pH sites (78.2%), followed by plant vigour (62.5%) and ear height (55.3%). The results for grain yield reduction were consistent with findings from other researchers. Welcker *et al*. (2005) reported that soil acidity reduces maize yields by up to 70% on 8 million hectares in developing countries and that on these soils maize yield is reduced due to Al or Mn toxicity and Ca, Mg, P and Mo deficiencies (Aldrich *et al*., 1975; Granados *et al*, 1993).

The results for combining ability and inheritance studies showed that both additive and non-additive gene action were involved and this is consistent with what was reported by Badawy (2013) who indicated that the ratio of GCA and SCA revealed the presence of additive and non-additive types of gene action. The concept of the ratio of GCA/SCA was described by Baker (1978) that when this ratio is more than a unit, there is preponderance of additive gene action, but if it is less than a unit the preponderance is towards non-additive gene action. However, the results were not consistent with what was reported by Iqbal *et al*. (2007) who indicated that none of the cross combinations exhibited desirable significant SCA effects for all the characters measured. In this study higher GCA than SCA effects for grain yield were observed in both sub-tropical and tropical inbred lines CZL999601 and CML481, respectively. In addition these two lines had good GCA effects for other traits, for instance, CZL999601 was also a good general combiner for number of ears per plant and shelling percentage while CML481 was also a good general combiner for traits such as ear height, ears per plant and plant height. While for other traits some inbred lines showed higher GCA effects for plant vigour (CML312), 100 seed weight (CML448) and shelling percentage (CML172), gray leaf spot (CML202) as well as anthesis dates (ZL130-23) which were either sub-tropical in the case of CML312, CML202 and ZL130-23 or tropical inbred lines in the case of CML448 and CML172. This suggested the breeding of DC hybrids as an option to combine a number of important traits for low pH tolerance.

At a cut of point of 1.0, the UPGMA clustered the inbred lines into two main clusters through use of GCA effects for the inbred lines for grain yield with Euclidean distance and standard deviation as scale type. At a high cophenetic correlation of $r_{cop} = 0.87$, the pattern

mostly followed the origin of the maize inbred lines such that six out of seven inbred lines from CIMMYT-Colombia (tropical) were grouped in the second cluster. Srdic *et al.* (2007) reported similar results, that cluster analysis using SCA effects was in good agreement with the origin of ten inbred lines, and was very useful in confirming predicted heterotic patterns.

With respect to SCA, the higher specific combinations for yield, plant vigour and 100 seed weight were observed in inter-crosses; CZL999601/CML144 and CML144/CML202. The former had a negative SCA for gray leaf spot disease, stem lodging implying that it was tolerant while the latter was also a good specific combination for plant height, ear height and number of ears per plant. This also suggested the breeding of DC hybrids as an option to combine a number of important traits for low pH tolerance which could broaden the genetic base.

It was found that under stress the relationship between characteristics is affected by the environment at phenotypic level (Chaubey and Singh, 1994; Ojo et al., 2006). In this study, grain yield at optimal environment was positively and significantly correlated with anthesis date, shelling percentage, stem lodging and 100 seed weight. Late maturing genotypes have adequate time to accumulate carbohydrates, leading to high yields. Shelling percentage and 100 seed weight are yield related traits such that high yielding genotypes tend to show high values for these traits. These results were consistent with what was reported by Chinnadurai and Nagarajan (2011), while under low pH grain yield was negatively correlated with anthesis date. The results under low pH were consistent with findings from other researchers (Magorokosho et al., 2003; Kaonga *et al.*, 2007; Ndhela, 2012) who reported negative correlation under drought stress. Under stress silk emergence is delayed, increasing the anthesis-silking interval (Kaonga and Nhlane, 2004). In the present study, it could be due to cold stress associated with low pH sites so that the plants require a higher number of days to attain the required heat units (day degree concept) which delays flowering but is not related to the amount of carbohydrate accumulation in the grain as is the case with late maturing maize genotypes.

Grain yield was negatively correlated with root lodging and leaf blight disease. In the case of root lodging, Al toxicity causes short, thick and under developed roots and plants, thus

reducing nutrient uptake (Sasaki *et al*., 1996). Other findings indicate that Al toxicity is the main problem because it inhibits maize root growth, reducing the water and nutrient uptake and interferes in different physiological processes of crop development (Roy *et al*., 1988). Foy *et al.* (1978) reported that low pH contributes to solubilise Al and make it available in the soil for plant assimilation, causing severe damage to non-adapted genotypes. In this case highly susceptible varieties are likely to have low yield and be susceptible to lodging. Diseases affect photosynthetic area and result in low carbohydrate accumulation in the grain, hence the negative correlation.

Correlation among the traits showed that grain texture was significantly and positively correlated with shelling percentage but was negatively and significantly correlated with plant vigour. Grain texture, refers to hardness (flintiness) or softness (dent) of the kernel. Flint kernels have higher percentage of amylopectin starch formed by branched chain of glucose molecules of high molecular weight. Branching reinforces the caryopsis while soft kernels have relatively higher percentage of amylose starch formed by straight chain of glucose molecules. Regular corn contains 72-76% amylopectin and 24-28% amylose (International Starch Institute, 2001). In terms of diseases, gray leaf spot was positively and significantly correlated with rust. This is a common scenario where different disease pathogens tend to occur together and this calls for breeding for horizontal resistance through the use of inbred lines with negative GCA for such diseases. Plant vigour was positively correlated with leaf blight at optimal conditions but was significantly and negatively correlated with 100 seed weight. In other words it was positively correlated with 100 seed weight as a score of 1.0 for plant vigour is better than a score of 5. The results are consistent with Welcker *et al*. (2005) who reported positive correlation under acid soils. Plant vigour is likely to have been affected in a similar manner to grain yield under low pH soils such that hybrids that had good vigour produced relatively better yields than those with low vigour. Low plant vigour under low pH results in low biomass. Kochian et al. (2005) indicated symptoms of Al toxicity as reductions in biomass and the number as well as the length of the roots, often combined with an increase in the mean radius and root volume; and the uptake of water and mineral nutrients, resulting in severe losses of root elongation and ultimately productivity.

## 6.7 Conclusions

Low pH soil is one of the most important abiotic factors contributing to low maize yields in some parts of Malawi. In this study, inbred lines CZL999601 and CML481 were identified to have higher GCA for grain yield. Inbred lines CML312, CML448, CML172, and CML202 were also identified to have the desired GCA for salient traits like plant vigour, 100 seed weight, shelling percentage and gray leaf spot disease respectively. Single cross hybrids CML99601/CML144, CML144/CML202, CML481/ CML288 and CML161/CM172 were identified as good specific combinations for grain yield and could be used in the formation of DCs which are more resilient to stress. The inbred lines and specific combinations identified in this study will be used in the development of maize hybrids and synthetics tolerant to low pH and diseases.

## 6.8 References


Aldrich, S.R., Scott, W.O. and E.R. Leng. 1975. Modern corn production. A & L Publication Champaign, IL

Allard, R.W. and A.D. Bradshaw. 1964. Implications of genotype-environment interactions in applied plant breeding. Crop Sci.4: 503–508.

Badawy, M.E.M. 2013. Heterosis and Combining Ability in Maize using Diallel Crosses among Seven New Inbred Lines. Asian Journal of Crop Science 5:11-13

Baker, R.J. 1978. Issues in Diallel Analysis. Crop Science 18: 533-536.

Chaubey P.K. and R.P. Singh.1994. Genetic variability, correlation and path analysis of filled components in rice. Mandras Agr. J. 81:438-470.

Chinnadurai, I.S. and P. Nagarajan. 2011. Interrelationship and Path-coefficient Studies for Qualitative Traits, Grain Yield and other Yield Attributes among Maize (*Zea mays L.*). International Journal of Plant Breeding and Genetics 5: 209-223.

Devi, P. and N.K. Singh., 2011. Heterosis, molecular diversity, combining ability and their interrelationships in short duration maize (*Zea mays*) across the environments. Euphytica 178: 71-81

Falconer, D.S. and T.F.C. Mackay. 1996. Introduction to quantitative genetics (fourth edition). Longman Group Limited, England.

Foy, C. D., R. L. Chaney and M.C. White.1978. The physiology of metal toxicity in plants. Annu. Rev. Plant Physiol. 29: 511-566.

GenStat. 2013. Introduction to GenStat for Windows. 16.1th edition. VSN International, Hemel Hempstead, Hertfordshire HPI. IES, UK.

Granados, G., S. Pandey and H. Ceballos. 1993. Response to selection for tolerance to acid soils in a tropical maize population. Crop Science 33: 936-940.

Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. Australian Journal of Biological Science 9: 463-493.

Hintze, J.L. 2007. Number Cruncher Statistical System (NCSS). Kaysville, Utah. USA. International starch Institute, 2001. Maize (corn). Science Park Aarhus, Denmark.

Iqbal, A.M., F.A. Nebvi, S.A. Wani, R. Oadil and Z.A. Dar. 2007. Combining Ability Analysis and Yield Related Traits in Maize. International Journal of Plant Breeding and Genetics1: 101-105.

Kaonga, K.K.E. and W.G. Nhlane. 2004. Evaluation of Early Maturing Maize hybrids for Low Altitude Areas of Malawi. In: D. Polland, M. Sawkins, J.M. Ribaut and D. Hoisington (Eds.) Resilient Crops for Water Limited Environments: Proceedings of a workshop held at Cuernavaca, Mexico. 24 – 28 May 2004, CIMMYT D.F., Mexico. pp. 104-105.

Kaonga, K.K.E., D.M. Lungu and R.P. Ganunga. 2007. Expressivity of Opaque 2 mutant gene in maize genotypes under low nitrogen soil and moisture stressed conditions. MSc Dissertation submitted to the University of Zambia. Lusaka, Zambia.

Kochian, L.V., M.A., Peneros, O.A. Hoekenga. 2005. The physiology, genetics and molecular biology of plant aluminium resistance and toxicity. Plant and Soil 274: 75-195.

Lerner, I M. 1954. Genetic Homeostasis. Oliver and Boyd, Edinburgh.

Lewontin, R C. 1956. Studies on homeostasis and heterozygosity. Amer. Nat. 90: 237–256.

Lewontin, R.C. 1957. The adaptation of populations to varying environments. Cold spring Harb. Symp. Quant. Biol. 22: 395-408.

Magnavaca, R., C.O. Gardner and R.B. Clark. 1987. Evaluation of inbred maize lines for aluminum tolerance in nutrient solution. Genetic Aspects of plant Mineral Nutrition. Martinus Nijhoff, Dordrecht, The Netherlands, pp. 255-265.

Magorokosho, C., K.V. Pixley and P. Tongoona. 2003. Selection for drought tolerance in two tropical maize populations. African Crop Science 11: 151-161.

MOA (Ministry of Agriculture). 2012. Crop Estimates for 2012. Lilongwe. Malawi

Morris, M.L., J. Risopoulos and D. Beck. 1999. Genetic changes in farmer– recycled maize seed: A review of the evidence. CIMMYT Econ. Working Paper No. 99–107. Mexico, D.F., CIMMYT.

Ndhela, T. 2012. Improvement strategies for yield potential, disease resistance and drought tolerance of Zimbabwe maize inbred line. A PhD thesis submitted to the University of the Free State, South Africa.

Ojo, D.K., O.A. Omikunle, M.O. Ajala and S.A. Ogubayo. 2006. Heritability, character correlation and path coefficient analysis among six inbred lines of maize. World Journal of Agricultural Science 2: 352-358.

Pérez, V. J.C. 2008. Adaptation of maize to aluminium toxic soils". Part of a thesis presented to the University of São Paulo, ESALQ/ USP, in partial fulfilment of the requirements for a doctoral degree in Agronomy.

Rojas, B.A. and G.F. Sprague. 1952. A comparison of variance components in corn yield trials: III. General and specific combining ability and their interaction with locations and years. Agron. J. 44: 462–466.

Roy, A.K., A. Sharma and G. Taludker. 1988. Some aspects of aluminium toxicity in plants. Bot. Review 54: 145-147.

Sasaki, M., Y. Yamamoto and H. Matsumoto. 1996. Lignin deposition induced by aluminium in wheat (*Triticum aestivum*) roots. Physiol. Plant. 96: 193–198.

Sprague, G.F. and L.A. Tatum. 1942. General vs. specific combining ability in single crosses of corn. Journal of the American Society of Agronomy 34: 923–932.

Sprague, G.F. and W.T. Federer. 1951. A comparison of variance components in corn yield trials II. Error, year x variety, location x variety components. Agronomy Journal 43: 535-541.

Srdic, J., Z. Pajic and S. Drinid-Mladenovic. 2007. Inheritance of maize grain yield components. Maydica 52: 261–264.

Statistical Analysis Software (SAS). 2013. Statistical Analysis Software (SAS) for Windows 9.0 ed., SAS, Cary, NC, USA.

Vacaro, E., J. Fernandes, B. Neto, D.G. Pegoraro, C.N. Nuss and L.H. Conceicao. 2002. Combining ability of twelve maize populations. Pesq. Agropec. Bras. Brasilia 37: 67-72.

Valdivia-Bernal, R. and A.R. Hallauer. 1991. Estimates of Genetic homeostasis in maize. In Rev. Brazil Genet. 14:483-500.

Welcker, C. 2005. Heterosis and Combining Ability for Maize Adaptation to Tropical Acid Soils. Crop Science 45:2405-2413.

Yan, W. and L.A. Hunt. 2002. Biplot analysis of diallel data. Crop Science 42: 21-30.

# CHAPTER 7

## General conclusions and recommendations

Maize is the number one food crop in Malawi with an annual requirement of 2.4 million tons per year. Its production is constrained by a number of abiotic factors and most of them are edaphic factors like low pH soils. This study looked at the performance of maize genotypes from different genetic backgrounds for tolerance to acid soils. The genotypes were obtained from two breeding institutions in the tropical and sub-tropical regions. Two approaches were employed to evaluate their performance under low pH soil environments. These involved the use of potassium aluminium sulphate [$KAl(SO_4)_2$] in a nutrient solution in a glasshouse hydroponic experiment and field trials. Significant differences were observed among the genotypes tested using $KAl(SO_4)_2$ such that IWDC3SYNF2-B, VPO52 and LPHpop4 were found to be tolerant to low pH. The field trial results indicated that low pH soils made a significant contribution to the yield and yield component reduction of 69.9%. Some genotypes that were among the top ten for field trials were also listed among the top ten in the hydroponic experiment. Phenotypic traits associated with grain yield, like plant vigour, 100 seed weight and numbers of ears per plant were negatively affected by the low pH soil environment and can be used alongside grain yield when selecting maize genotypes which are tolerant to acid soils. Soil analysis identified Lunyangwa Research Site soils as the most acidic of the low pH sites characterised. However, Tsangano Research Site was at a higher altitude than Lunyangwa (1524 masl versus 1342 masl) and was cooler than the latter (28.8$^{o}$C versus 32.0$^{o}$C max temperatures). In view of this, dendrogram clustering based on environmental means generated by AMMI identified Tsangano as the most stressed site of the two most acidic sites, i.e., Tsangano and Lunyanwa. As a recommendation, field trials should be accompanied by glasshouse screening for effective selection for tolerance to acid soils bearing in mind the complexity of the field environment.

With respect to GxE and stability analysis, genotypes LPHpop21, VPO52, VPO72, VPO744 and VPO96 were stable across low pH and optimal soil conditions. While genotype VPO97 was identified as the most unstable genotype. Chitala optimal low-land site was identified as the most discriminating environment for the genotypes as it was

located at the longest distance between its marker and the origin on the GGE biplot. Chitedze optimal was identified as a stable environment as its IPCA score and vector was near to the origin (zero).

Inheritance studies identified inbred lines CZL999601 and CML481 which had good GCA for grain yield. It was found that additive and non-additive gene action was the mode of genetic inheritance for tolerance to acid soils for grain yield and some yield related traits, recording a GCA/SCA ratio above unity while characteristics such as grain texture, stem and root lodging, gray leaf spot disease and rust disease recorded a GCA/SCA ratio below unity. SCA analysis identified four specific combinations CML99601/CML144, CML144/CML202, CML481/ CML288 and CML161/CM172 as good combinations for acid tolerance and these single-cross hybrids will be used in the development of three way and double crosses for further low pH research projects.

## SUMMARY

In Malawi maize is grown even in marginal lands, on steep slopes, wet lands, rocky areas and low pH soils due to the high human population which excert pressure on the land. The objectives of this study were to investigate genetically diverse maize genotypes for tolerance to low pH soil conditions. In the hydroponic experiment genotypes IWDC3SYNF2-B, VPO52, and LPHpop 4 had relatively higher nett seminal root length and were considered tolerant, and DT-YSTR SYNTHETIC-B, TZE-WPOPDTC2STR-B, TZE-YDTSTRC4-B, LPHpop3, LPHpop13, and LPHpop14 were sensitive or susceptible to Al toxicity. Under field conditions, genotypes LPHpop16, LPHpop3, VPO739, VPO5173 and LOW N POOL C3-B were identified to be relatively tolerant to low pH soil conditions. SYNDTE–STY-W-B ranked first in terms of root tolerant index (RTi) with a good NSRL in the glasshouse hydroponic experiment and this was followed by VPO717 which also had a relatively a better root tolerance index and nett seminal root length.

Phenotypic traits associated with grain yield, such as plant vigour, seed size (100 seed weight), shelling percentage, number of ears per plant, ear height and plant height can be used alongside grain yield when selecting germplasm for tolerance to low pH stress. In general, the effects of low pH soil conditions contributed to reduction in grain yields and yield components. The combined mean yield reduction due to low pH soil in this study was 69.9%. From AMMI and GGE analysis, genotypes LPHpop21, VPO52, VPO72, VPO744 and VPO96 were identified as the most stable. VPO097 was identified as an unstable genotype. Chitala low-land optimal site was identified as the most discriminating environment in terms of genotypes while Chitedze mid-altitude optimal environment was identified as a stable environment.

The diallel study revealed that additive and non-additive gene actions were at play in the expression of some of the traits like grain yield, number ears per plant, shelling percentage, 100 seed weight and plant vigour, while non-additive gene action was predominant in the inheritance of characteristics such as anthesis-silking interval, plant and ear height, grain texture, stem and root lodging and gray leaf spot disease. Positive and highly significant GCA effects for grain yield were observed for inbred line CZL999601 across low pH and optimal conditions. While negative and significant GCA effects for grain yield were

observed for inbred line CML161 across low pH and optimal conditions. SCA results indicated that single-cross hybrids CML999601/CML144, CML144/CML202, CML481/CML288 and CML161/CM172 were best for grain yield across low pH and optimal conditions. At a cut-off point of 1.0 with a cophenetic correlation of $r_{cop} = 0.87$, the UPGMA clustered the inbred lines based on GCA for grain yield into two main clusters through use of Euclidean distance and standard deviation as type of scale. The pattern mostly followed the origin of the maize inbred lines such that six out of seven inbred lines from CIMMYT-Colombia (tropical) were grouped in the second cluster. The open pollinated inbred line varieties and specific combinations (single-crosses generated) identified in this study will be used in the National Maize Breeding Programme for development of genotypes tolerant to low pH and diseases for yield improvement and subsequent food security in the country.

**Key words:** low pH**,** hydroponic, cophenetic correlation, diallel crosses, phenotypic traits, GCA, SCA

## OPSOMMING

In Malawi word mielies selfs in marginale grond, op steil hellings, vleilande, klipperige gebiede en in lae pH grond verbou, weens die hoë bevolking wat druk op die land plaas. Die doelwitte van hierdie studie was om geneties diverse mielie genotipes vir verdraagsaamheid vir lae pH grondtoestande te ondersoek. In die hidroponiese eksperiment het genotipes IWDC3SYNF2-B, VPO52 en LPHpop4 relatiewe hoër netto seminale wortel lengtes gehad en word as verdraagsaam beskou en DT-YSTR SYNTHETIC-B, TZE-WPOPDTC2STR-B, TZE-YDTSTRC4-B, LPHpop 3, LPHpop13, en LPHpop14 was sensitief of vatbaar vir Al toksisiteit. Onder veldtoestande, is genotipes LPHpop16, LPHpop3, VPO739, VPO5173 en LOW N POOL C3-B as relatief verdraagsaam vir lae pH grondtoestande geïdentifiseer. In die glashuis hidroponiese eksperiment was SYNDTE-STY-W-B eerste in terme van wortel tolerante indeks met 'n netto seminale wortel lengte van 2.5 cm en is gevolg deur VPO717 met ’n wortel tolerante indeks van 1.0 en netto seminale wortel lengte van 1.7 cm.

Fenotipiese eienskappe wat geassosieer word met graanopbrengs, soos groeikrag, saadgrootte (100 saad gewig), saad persentasie, die aantal koppe per plant, kop hoogte en plant hoogte kan gebruik word saam met graanopbrengs wanneer kiemplasma geselekteer word vir verdraagsaamheid vir lae pH stres. In die algemeen dra die effek van lae pH grondtoestande by tot die verlaging in graanopbrengste en opbrengs komponente. Die gekombineerde gemiddelde opbrengs verlaging as gevolg van lae pH grond in hierdie studie was 69.9%. Deur die AMMI en GGE analise is LPHpop21, VPO52, VPO72 is VPO744 en VPO96 geïdentifiseer as die mees stabiele genotipes. VPO097 is geïdentifiseer as 'n onstabiele genotipe. Chitala lae-ligging optimale omgewing is geïdentifiseer as die mees onstabiele omgewing in terme van genotipes terwyl Chitedze middel-ligging optimale omgewing geïdentifiseer is as 'n stabiele omgewing.

Die dialleel studie het getoon dat beide additiewe en nie-additiewe geenaksie ’n rol gespeel het by die uitdrukking van die eienskappe soos graanopbrengs, aantal koppe per plant, saad persentasie, 100 saad gewig en groeikrag, terwyl nie-additiewe geenaksie oorheersend was in die oorerwing van eienskappe soos antese-baard interval, plant en kop hoogte, graantekstuur, stam en wortel omval en blaarvlek siekte. Positiewe en hoogs betekenisvolle

algemene kombineervermoë (GCA) vir graanopbrengs is in die lae pH en optimale omgewings, vir ingeteelde lyn CZL999601 waargeneem, terwyl negatief en betekenisvolle GCA effekte vir graanopbrengs waargeneem is vir ingeteelde lyn CML161 vir lae pH en optimale toestande. Resultate vir spesifieke kombineervermoë (SCA) het aangedui dat enkelkruisbasters CML99601/CML144, CML144/CML202, CML481/ CML288 en CML161/CM172 die beste graanopbrengs oor lae pH en optimale toestande gelewer het. By 'n afsny punt van 1.0 met 'n ko-fenetiese korrelasie van $r_{cop}$ = 0.87, het die UPGMA kluster, deur die gebruik van Euklidiese afstand en standaardafwyking as skaal tipe, die ingeteelde lyne gebaseer op GCA vir graanopbrengs in twee hoof groepe verdeel. Die groepering het die oorsprong van die ingeteeldelyne gevolg, sodanig dat ses uit sewe ingeteelde lyne van CIMMYT-Kolombië (tropiese) in die tweede kluster groepeer. Die OPVs, ingeteelde lyne en spesifieke kombinasie enkelkruisings wat geïdentifiseer is in hierdie studie sal gebruik word in die Nasionale Mielie Teelprogram vir die ontwikkeling van genotipes tolerant vir lae pH en siektes en om opbrengs te verbeter sodat voedselsekuriteit in die land verseker kan word.

**Sleutel woorde**: lae pH, hidroponiese, ko-fenetiese korrelasie, dialleel kruise, fenotipiese eienskappe, GCA, SCA

**Appendix 1 Root length measurements and derived data before and seven days after transplanting a glasshouse hydroponic experiment**

| | Pedigree | Initial cm | Final cm | Control cm | Rti | % response | RSRLCtrl (cm) | RSRLTrtd(cm) | NSRL cm |
|---|---|---|---|---|---|---|---|---|---|
| 1 | 99TZEFY-STR QPM CO-B | 2.8 | 5.0 | 6.7 | 0.7 | -25.9 | 2.03 | 1.19 | 2.2 |
| 2 | DT-WSTR SYNTHETIC-B | 8.7 | 7.4 | 9.1 | 0.8 | -18.0 | 0.08 | -0.12 | 0.9 |
| 3 | DT-YSTR SYNTHETIC-B | 2.9 | 1.7 | 4.3 | 0.4 | -59.3 | 0.50 | -0.39 | 0.6 |
| 4 | EVDT-Y2000 STR QPM CO-B | 6.3 | 7.5 | 8.9 | 0.8 | -15.7 | 0.41 | 0.19 | 1.2 |
| 5 | EVD-W 99 STR QPM CO-B | 7.2 | 8.5 | 10.8 | 0.8 | -20.9 | 0.50 | 0.19 | 1.2 |
| 6 | IAR-FLINT-Q-B | 2.4 | 2.2 | 3.5 | 0.6 | -36.2 | 0.50 | -0.04 | 1.0 |
| 7 | IWD C3 SYN F2-B | 1.4 | 3.5 | 5.1 | 0.7 | -32.1 | 3.20 | 2.02 | 3.0 |
| 8 | LOW N POOL C3-B | 6.1 | 4.3 | 6.1 | 0.7 | -29.4 | 0.06 | -0.28 | 0.7 |
| 9 | MULTICOB EARLY DT-B | 7.6 | 6.4 | 7.8 | 0.8 | -17.4 | 0.04 | -0.14 | 0.9 |
| 10 | OBA SUPER1[9021-18(IITA)]-B | 2.5 | 2.1 | 4.1 | 0.5 | -46.5 | 0.67 | -0.07 | 0.9 |
| 11 | OBATANPA/IWDC2SYNF2/IWDC2SY | 1.4 | 2.9 | 4.0 | 0.7 | -27.8 | 1.83 | 1.06 | 2.1 |
| 12 | OBATANPA/IWDC2SYNF2/IWDC2SYNF2-B | 3.9 | 2.8 | 4.5 | 0.6 | -36.2 | 0.19 | -0.27 | 0.7 |
| 13 | OBATANPA/TZLCOMP4C3F2/TZLC | 7.0 | 5.8 | 8.5 | 0.7 | -28.2 | 0.21 | -0.16 | 0.8 |
| 14 | OBATANPA/TZLCOMP4C3F2/TZLCOMP4C3F2-B | 3.8 | 2.6 | 4.8 | 0.6 | -43.8 | 0.36 | -0.26 | 0.7 |
| 15 | POP66 SR/DMR-LSRY/DMR-LSRY | 2.6 | 2.1 | 3.9 | 0.6 | -44.7 | 0.50 | -0.17 | 0.8 |
| 16 | POP66 SR/TZUTSR-WSGY/T | 5.2 | 7.5 | 9.0 | 0.8 | -16.1 | 0.74 | 0.47 | 1.5 |
| 17 | SYN DTE STR-Y-B | 1.7 | 2.4 | 3.5 | 0.7 | -29.1 | 1.24 | 0.55 | 1.6 |
| 18 | SYN DTE STY-W-B | 3.4 | 8.5 | 8.2 | 1.1 | 5.4 | 1.39 | 1.49 | 2.5 |
| 19 | TZE COPM3 DTV C2 F2-B | 1.4 | 1.8 | 2.9 | 0.7 | -34.7 | 1.02 | 0.27 | 1.3 |
| 20 | TZE E-WPOP X LD(SET2)-B | 1.3 | 2.7 | 3.7 | 0.7 | -26.4 | 1.97 | 1.21 | 2.2 |
| 21 | TZE-W POP DTC2 STR-B | 4.5 | 2.7 | 5.6 | 0.5 | -51.0 | 0.26 | -0.39 | 0.6 |
| 22 | TZE-WDT STR QPM-CO-B | 8.5 | 9.4 | 11.5 | 0.8 | -18.2 | 0.37 | 0.11 | 1.1 |
| 23 | TZE-YDT STR C4-B | 5.2 | 3.2 | 4.7 | 0.8 | -20.4 | -0.07 | -0.38 | 0.6 |
| 24 | TZE-YPOP DTC2 STR-B | 1.8 | 2.5 | 3.0 | 0.8 | -17.5 | 0.70 | 0.39 | 1.4 |
| 25 | VPO0721 | 6.1 | 7.6 | 9.2 | 0.8 | -15.8 | 0.50 | 0.26 | 1.3 |
| 26 | VPO5148 | 2.8 | 3.2 | 5.2 | 0.6 | -37.1 | 1.16 | 0.46 | 1.5 |

**Appendix 1 continue**

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 27 | VPO5173 | 2.0 | 2.5 | 3.8 | 0.7 | -33.2 | 1.37 | 0.57 | 1.6 |
| 28 | VPO5179 | 4.8 | 3.5 | 5.8 | 0.6 | -38.5 | 0.23 | -0.24 | 0.8 |
| 29 | VPO5187 | 3.3 | 4.6 | 5.7 | 0.8 | -18.0 | 0.78 | 0.43 | 1.4 |
| 30 | VPO52 | 1.4 | 3.4 | 4.4 | 0.8 | -21.1 | 3.30 | 2.47 | 3.5 |
| 31 | VPO627 | 1.7 | 3.3 | 4.5 | 0.7 | -27.6 | 1.68 | 0.95 | 1.9 |
| 32 | VPO630 | 1.5 | 2.5 | 3.9 | 0.6 | -37.0 | 1.79 | 0.73 | 1.7 |
| 33 | VPO710 | 5.9 | 4.8 | 7.7 | 0.6 | -38.4 | 0.34 | -0.17 | 0.8 |
| 34 | VPO712 | 2.4 | 2.7 | 4.2 | 0.7 | -33.8 | 0.77 | 0.16 | 1.2 |
| 35 | VPO716 | 2.3 | 2.8 | 3.9 | 0.7 | -27.9 | 0.79 | 0.27 | 1.3 |
| 36 | VPO717 | 2.9 | 4.9 | 4.8 | 1.0 | 0.5 | 0.66 | 0.70 | 1.7 |
| 37 | VPO738 | 1.9 | 3.5 | 4.2 | 0.8 | -16.6 | | | 2.0 |
| 38 | VPO739 | 5.6 | 4.8 | 7.3 | 0.7 | -31.7 | 0.31 | -0.12 | 0.9 |
| 39 | VPO741 | 6.5 | 6.6 | 8.7 | 0.8 | -23.3 | 0.36 | 0.03 | 1.0 |
| 40 | VPO743 | 3.2 | 3.5 | 4.7 | 0.7 | -26.1 | 0.65 | 0.21 | 1.2 |
| 41 | VPO744 | 2.2 | 2.1 | 3.5 | 0.6 | -38.7 | 0.66 | 0.02 | 1.0 |
| 42 | VPO76 | 10.1 | 10.0 | 11.1 | 0.9 | -9.0 | 0.11 | -0.01 | 1.0 |
| 43 | VPO86 | 4.2 | 5.4 | 7.0 | 0.8 | -23.3 | 0.86 | 0.42 | 1.4 |
| 44 | VPO96 | 3.4 | 4.8 | 6.6 | 0.7 | -26.8 | 0.99 | 0.46 | 1.5 |
| 45 | VPO97 | 2.4 | 3.3 | 4.4 | 0.8 | -23.4 | 0.86 | 0.43 | 1.4 |
| 46 | LPHpop 4 | 1.4 | 4.0 | 5.7 | 0.7 | -27.8 | 3.31 | 1.99 | 3.0 |
| 47 | LPHpop 3 | 5.7 | 3.4 | 6.1 | 0.6 | -42.7 | 0.09 | -0.41 | 0.6 |
| 48 | LPHpop 6 | 1.8 | 3.1 | 4.8 | 0.7 | -30.9 | 1.73 | 0.69 | 1.7 |
| 49 | LPHpop 8 | 1.7 | 2.0 | 2.9 | 0.7 | -30.8 | 0.83 | 0.23 | 1.2 |
| 50 | LPHpop 9 | 6.0 | 5.6 | 7.1 | 0.8 | -20.0 | 0.20 | -0.05 | 0.9 |
| 51 | LPHpop 10 | 5.3 | 8.1 | 8.0 | 1.0 | 4.0 | 0.50 | 0.56 | 1.6 |
| 52 | LPHpop 11 | 8.2 | 7.9 | 10.4 | 0.8 | -23.9 | 0.29 | -0.02 | 1.0 |
| 53 | LPHpop 13 | 4.3 | 2.3 | 4.4 | 0.5 | -46.8 | 0.06 | -0.44 | 0.6 |
| 54 | LPHpop 14 | 6.2 | 4.0 | 6.4 | 0.6 | -35.5 | 0.03 | -0.36 | 0.6 |
| 55 | LPHpop 15 | 2.2 | 2.6 | 3.7 | 0.7 | -29.9 | 0.78 | 0.24 | 1.2 |
| 56 | LPHpop 16 | 3.3 | 3.8 | 5.0 | 0.8 | -21.7 | 0.50 | 0.17 | 1.2 |
| 57 | LPHpop 17 | 2.8 | 2.7 | 4.2 | 0.7 | -35.0 | 0.50 | -0.03 | 1.0 |

| | Appendix 1 continue | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 58 | LPHpop 18 | 1.4 | 2.4 | 4.0 | 0.6 | -38.4 | 2.74 | 1.10 | 2.1 |
| 59 | LPHpop 19 | 7.4 | 7.2 | 9.4 | 0.8 | -22.7 | 0.29 | -0.02 | 1.0 |
| 60 | LPHpop 20 | 1.9 | 2.9 | 3.5 | 0.8 | -17.0 | 0.98 | 0.65 | 1.7 |
| 61 | LPHpop 21 | 2.7 | 3.6 | 5.0 | 0.7 | -29.0 | 0.91 | 0.38 | 1.4 |
| 62 | LPHpop 23 | 1.5 | 1.7 | 3.2 | 0.5 | -46.2 | 1.25 | 0.24 | 1.2 |
| 63 | LPHpop 1 | 3.2 | 3.0 | 4.8 | 0.6 | -37.7 | 0.50 | -0.07 | 0.9 |
| 64 | LPHpop 2 | 1.4 | 2.1 | 3.7 | 0.6 | -41.9 | 1.64 | 0.50 | 1.5 |
| 65 | LPHpop 7 | 1.8 | 1.5 | 2.7 | 0.5 | -45.5 | 0.50 | -0.18 | 0.8 |
| 66 | LPHpop 12 | 4.4 | 3.9 | 5.6 | 0.7 | -29.3 | 0.30 | -0.07 | 0.9 |
| 67 | ZM309 | 0.8 | 1.8 | 3.4 | 0.6 | -38.5 | 3.82 | 1.50 | 2.5 |
| 68 | ZM523 | 3.3 | 2.5 | 4.5 | 0.5 | -46.3 | 0.41 | -0.25 | 0.7 |
| 69 | ZM623 | 3.2 | 3.7 | 5.7 | 0.7 | -33.8 | 0.80 | 0.19 | 1.2 |
| 70 | ZM721 | 3.4 | 4.0 | 6.3 | 0.7 | -32.0 | 0.93 | 0.26 | 1.3 |
| | **Mean** | **3.73** | 4.08 | **5.6** | **0.7** | **-29.1** | **0.89** | **0.32** | **1.3** |
| | **LSD** | **0.95** | 1.2 | **1.87** | **0.22** | **22.01** | **1.27** | **0.88** | **0.88** |
| | **Prob** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** |
| | **CV (%)** | **15.8** | 18.3 | **20.5** | **19.2** | **46.9** | **88.3** | **171.5** | **41.5** |
| | **Min** | **0.8** | 1.5 | **2.7** | **0.4** | **-59.3** | **-0.07** | **-0.44** | **0.6** |
| | **Max** | **10.1** | 10 | **11.5** | **1.1** | **5.4** | **3.82** | **2.47** | **3.5** |
| | **R-Squared** | **0.96** | 0.92 | **0.85** | **0.53** | **0.54** | **-** | **-** | **0.69** |
| | **Heritability** | **0.98** | 0.96 | **0.91** | **0.56** | **0.58** | **-** | **-** | **0.74** |

**ISRL = initial seminal root length, FSRL = final seminal Root length, Zero Al = Zero Aluminium or control, RTi = root tolerance index, RSRLzero Al = relative seminal root length with zero Aluminium, RSRLTRTD = relative seminal root length treated with Aluminium and NSRL = net seminal root length, LSD = Least significant difference, CV = coefficient of variation, Min = minimum, Max = maximum.**

**Appendix 2 Maize genotypes evaluated in the field trials 2011/12 and 2012/13**

| Genotype number | Genotype |
|---|---|
| G1 | DT-WSTR SYNTHETIC-B |
| G2 | EVD-W 99 STR QPM CO-B |
| G3 | IAR-FLINT-Q-B |
| G4 | IWD C3 SYN F2-B |
| G5 | MULTICOB EARLY DT –B |
| G6 | SYN DTE STY-W-B |
| G7 | OBA SUPER1(9021-18(IITA))-B |
| G8 | LPHpop 9 |
| G9 | POP66 SR/DMR -LSRY/DMR-LSRY |
| G10 | POP66 SR/TZUTSR-WSGY/T |
| G11 | LPHpop 7 |
| G12 | TZE-YDT STR C4-B |
| G13 | VPO0721 |
| G14 | TZE E -WPOP X LD(SET2)-B |
| G15 | VPO5173 |
| G16 | VPO717 |
| G17 | VPO5187 |
| G18 | VPO52 |
| G19 | VPO630 |
| G20 | LPHpop 21 |
| G21 | VPO741 |
| G22 | VPO739 |
| G23 | LPHpop 18 |
| G24 | LPHpop 16 |
| G25 | VPO743 |
| G26 | VPO744 |
| G27 | LOW N POOL C3-B |
| G28 | LPHpop 10 |
| G29 | VPO76 |
| G30 | LPHpop 3 |
| G31 | LPHpop 20 |
| G32 | LPHpop 2 |
| G33 | VPO710 |
| G34 | VPO712 |
| G35 | LPHpop 8 |
| G36 | OBATANPA/TZLCOMP4C3F2/TZLCOMP4C3F2-B |
| G37 | VPO738 |
| G38 | LPHpop 13 |
| G39 | LPHpop 15 |
| G40 | VPO86 |
| G41 | VPO96 |
| G42 | VPO97 |
| G43 | ZM309 Check 1 |
| G44 | ZM523 Check 2 |
| G45 | ZM721 Check 3 |

## Appendix 3 Soil sampling data

| Lab no. | Location | Depth (cm) | pH | %OC | %OM | %N | P(µg $g^{-1}$) | Ca(µg $g^{-1}$) | Mg(µg/g) | % Al |
|---|---|---|---|---|---|---|---|---|---|---|
| 97135 | Tsangano | 0-15 | 5.27 | 0.20 | 0.35 | 0.02 | 16.30 | 1.72 | 0.29 | 0.4 |
| 97136 | " " | 15-30 | 5.23 | 1.78 | 3.06 | 0.15 | 5.68 | 1.80 | 0.29 | 0.8 |
| 97137 | " " | 0-15 | 5.35 | 1.69 | 2.91 | 0.15 | 28.32 | 2.51 | 0.39 | 0.4 |
| 97138 | " " | 15-30 | 5.41 | 2.16 | 3.72 | 0.19 | 46.77 | 2.48 | 0.47 | 2.4 |
| 97139 | " " | 0-15 | 5.44 | 1.81 | 3.11 | 0.16 | 5.64 | 1.84 | 0.44 | 0.4 |
| 97140 | " " | 15-30 | 5.49 | 1.98 | 3.41 | 0.17 | 5.36 | 2.25 | 0.34 | 0.8 |
| 97141 | Bvumbwe | 0-15 | 5.65 | 1.49 | 2.56 | 0.13 | 44.32 | 3.22 | 0.98 | 0.6 |
| 97142 | " " | 15-30 | 5.74 | 1.05 | 1.81 | 0.09 | 62.34 | 2.90 | 0.79 | 0.6 |
| 97143 | " " | 0-15 | 5.67 | 1.46 | 2.51 | 0.13 | 69.11 | 3.03 | 0.81 | 0.6 |
| 97144 | " " | 15-30 | 5.57 | 1.40 | 2.41 | 0.12 | 41.40 | 2.46 | 0.56 | 0.2 |
| 97145 | " " | 0-15 | 5.68 | 1.17 | 2.01 | 0.10 | 80.30 | 3.88 | 1.06 | 0.6 |
| 97146 | " " | 15-30 | 5.67 | 1.02 | 1.76 | 0.09 | 83.79 | 3.08 | 0.87 | 0.2 |
| 97147 | Lunyangwa | 0-15 | 4.38 | 1.83 | 3.16 | 0.16 | 21.86 | 0.65 | 0.13 | 1.2 |
| 97148 | " " | 15-30 | 4.62 | 1.57 | 2.71 | 0.14 | 11.92 | 0.60 | 0.11 | 1.0 |
| 97149 | " " | 0-15 | 4.59 | 0.87 | 1.51 | 0.08 | 30.52 | 0.71 | 0.13 | 0.8 |
| 97150 | " " | 15-30 | 4.42 | 0.70 | 1.21 | 0.06 | 12.56 | 0.44 | 0.101 | 0.2 |
| 97151 | " " | 0-15 | 5.11 | 1.81 | 3.11 | 0.16 | 20.53 | 2.08 | 0.36 | 0.6 |
| 97152 | " " | 15-30 | 4.49 | 0.87 | 1.51 | 0.08 | 6.90 | 0.69 | 0.13 | 0.6 |
| 97153 | Bembeke | 0-15 | 5.10 | 1.98 | 3.41 | 0.17 | 20.77 | 2.00 | 0.41 | 0.8 |
| 97154 | " " | 15-30 | 4.95 | 0.84 | 1.46 | 0.07 | 7.17 | 0.65 | 0.11 | 0.6 |
| 97155 | " " | 0-15 | 5.15 | 1.66 | 2.86 | 0.14 | 11.83 | 2.09 | 0.43 | 0.4 |
| 97156 | " " | 15-30 | 5.06 | 1.81 | 3.11 | 0.16 | 20.10 | 1.98 | 0.38 | 1.0 |
| 97157 | " " | 0-15 | 5.14 | 1.63 | 2.81 | 0.14 | 15.53 | 2.05 | 0.46 | 1.0 |
| 97158 | " " | 15-30 | 5.10 | 1.60 | 2.76 | 0.14 | 18.57 | 2.28 | 0.49 | 1.0 |

## Appendix 4 Eigenvectors for the measured and derived data at low pH environments across two seasons

| | AD | ASI | DS | EH | EPP | LB | GLS | GT | HC | GY | MSV | PH | RE | RL | RUST | SH | SL | SWT |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AD | 1.000 | -0.045 | 0.941 | -0.032 | 0.058 | -0.059 | -0.081 | 0.000 | 0.137 | 0.047 | -0.123 | -0.069 | -0.042 | 0.087 | 0.187 | 0.058 | 0.044 | -0.010 |
| ASI | -0.045 | 1.000 | 0.295 | 0.008 | 0.035 | 0.050 | 0.091 | 0.000 | 0.176 | -0.091 | 0.095 | -0.023 | -0.130 | -0.072 | 0.021 | 0.037 | 0.044 | -0.030 |
| DS | 0.941 | 0.295 | 1.000 | -0.028 | 0.067 | -0.039 | -0.046 | 0.000 | 0.191 | 0.014 | -0.085 | -0.074 | -0.084 | 0.059 | 0.186 | 0.068 | 0.057 | -0.010 |
| EH | -0.032 | 0.008 | -0.028 | 1.000 | 0.018 | 0.022 | -0.076 | 0.000 | 0.012 | -0.026 | 0.058 | 0.680 | 0.042 | -0.082 | -0.040 | 0.016 | 0.004 | 0.182 |
| EPP | 0.058 | 0.035 | 0.067 | 0.018 | 1.000 | 0.016 | -0.125 | 0.000 | -0.149 | 0.653 | -0.082 | 0.061 | -0.068 | -0.132 | -0.073 | 0.993 | -0.030 | -0.130 |
| LB | -0.059 | 0.050 | -0.039 | 0.022 | 0.016 | 1.000 | 0.380 | 0.000 | -0.063 | 0.059 | 0.229 | 0.008 | -0.095 | 0.025 | 0.031 | 0.013 | -0.080 | -0.030 |
| GLS | -0.081 | 0.091 | -0.046 | -0.076 | -0.125 | 0.380 | 1.000 | 0.000 | -0.031 | -0.048 | 0.249 | -0.119 | -0.036 | 0.100 | 0.040 | -0.124 | 0.038 | -0.220 |
| GT | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 1.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| HC | 0.137 | 0.176 | 0.191 | 0.012 | -0.149 | -0.063 | -0.031 | 0.000 | 1.000 | -0.225 | -0.113 | 0.039 | 0.066 | 0.135 | 0.176 | -0.144 | 0.052 | 0.094 |
| GY | 0.047 | -0.091 | 0.014 | -0.026 | 0.653 | 0.059 | -0.048 | 0.000 | -0.225 | 1.000 | -0.091 | 0.007 | -0.113 | -0.103 | -0.101 | 0.643 | 0.007 | -0.210 |
| MSV | -0.123 | 0.095 | -0.085 | 0.058 | -0.082 | 0.229 | 0.249 | 0.000 | -0.113 | -0.091 | 1.000 | -0.071 | -0.084 | 0.044 | -0.132 | -0.087 | -0.140 | 0.048 |
| PH | -0.069 | -0.023 | -0.074 | 0.680 | 0.061 | 0.008 | -0.119 | 0.000 | 0.039 | 0.007 | -0.071 | 1.000 | 0.040 | -0.010 | -0.127 | 0.062 | -0.020 | 0.163 |
| RE | -0.042 | -0.130 | -0.084 | 0.042 | -0.068 | -0.095 | -0.036 | 0.000 | 0.066 | -0.113 | -0.084 | 0.040 | 1.000 | -0.001 | 0.033 | -0.067 | -0.000 | 0.096 |
| RL | 0.087 | -0.072 | 0.059 | -0.082 | -0.132 | 0.025 | 0.100 | 0.000 | 0.135 | -0.103 | 0.044 | -0.010 | -0.001 | 1.000 | 0.181 | -0.143 | -0.020 | 0.061 |
| RUST | 0.187 | 0.021 | 0.186 | -0.040 | -0.073 | 0.031 | 0.040 | 0.000 | 0.176 | -0.101 | -0.132 | -0.127 | 0.033 | 0.181 | 1.000 | -0.070 | 0.142 | 0.175 |
| SH | 0.058 | 0.037 | 0.068 | 0.016 | 0.993 | 0.013 | -0.124 | 0.000 | -0.144 | 0.643 | -0.087 | 0.062 | -0.067 | -0.143 | -0.070 | 1.000 | -0.030 | -0.120 |
| SL | 0.044 | 0.044 | 0.057 | 0.004 | -0.035 | -0.085 | 0.038 | 0.000 | 0.052 | 0.007 | -0.135 | -0.016 | -0.003 | -0.023 | 0.142 | -0.027 | 1.000 | 0.123 |
| SWT | -0.006 | -0.026 | -0.014 | 0.182 | -0.132 | -0.034 | -0.217 | 0.000 | 0.094 | -0.211 | 0.048 | 0.163 | 0.096 | 0.061 | 0.175 | -0.119 | 0.123 | 1.000 |

**AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), HC = husk cover, GY = grain yield (kg ha$^{-1}$), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SH = shelling percentage, SL = stem lodging (#), SWT = 100 seed weight (g), # = number.**

## Appendix 5 Eigenvectors from the principal component analysis for grain yield and agronomic at optimal environments across two seasons

| | GY | AD | DS | EH | EPP | LB | GLS | GT | HC | MSV | PH | RL | RE | RUST | SH | SL | SWT | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AD | -0.06 | 1.00 | 0.98 | 0.13 | 0.09 | -0.03 | 0.00 | -0.04 | 0.06 | -0.07 | 0.07 | -0.04 | -0.05 | -0.06 | 0.01 | -0.03 | -0.09 | 0.11 |
| DS | -0.04 | 0.98 | 1.00 | 0.14 | 0.08 | -0.04 | 0.02 | -0.06 | 0.08 | -0.07 | 0.06 | -0.04 | -0.03 | -0.05 | 0.01 | -0.01 | -0.09 | 0.28 |
| EH | -0.05 | 0.13 | 0.14 | 1.00 | 0.04 | -0.07 | -0.03 | 0.05 | -0.15 | 0.06 | 0.63 | -0.02 | 0.10 | -0.07 | -0.04 | -0.04 | 0.12 | 0.21 |
| EPP | -0.08 | 0.09 | 0.08 | 0.04 | 1.00 | 0.14 | 0.06 | -0.31 | -0.01 | 0.09 | 0.08 | 0.04 | -0.17 | -0.03 | -0.04 | 0.09 | 0.02 | 0.00 |
| LB | -0.09 | -0.03 | -0.04 | -0.07 | 0.14 | 1.00 | 0.21 | 0.03 | -0.02 | -0.15 | -0.01 | -0.04 | 0.05 | 0.17 | 0.02 | -0.05 | -0.07 | -0.51 |
| GLS | 0.01 | 0.00 | 0.02 | -0.03 | 0.06 | 0.21 | 1.00 | -0.02 | -0.04 | -0.11 | 0.15 | 0.06 | -0.02 | -0.09 | 0.01 | -0.01 | -0.06 | 0.00 |
| GT | 0.04 | -0.04 | -0.06 | 0.05 | -0.31 | 0.03 | -0.02 | 1.00 | -0.04 | -0.12 | 0.05 | 0.00 | 0.01 | -0.07 | 0.01 | -0.12 | -0.10 | 0.00 |
| HC | 0.10 | 0.06 | 0.08 | -0.15 | -0.01 | -0.02 | -0.04 | -0.04 | 1.00 | -0.16 | -0.19 | 0.17 | 0.11 | 0.06 | 0.01 | 0.00 | -0.06 | 0.00 |
| GY | 1.00 | -0.06 | -0.04 | -0.05 | -0.08 | -0.09 | 0.01 | 0.04 | 0.10 | 0.12 | -0.09 | -0.01 | 0.03 | 0.09 | 0.10 | -0.05 | 0.25 | 0.11 |
| MSV | 0.12 | -0.07 | -0.07 | 0.06 | 0.09 | -0.15 | -0.11 | -0.12 | -0.16 | 1.00 | 0.05 | -0.04 | 0.00 | -0.16 | -0.05 | 0.01 | 0.14 | 0.00 |
| PH | -0.09 | 0.07 | 0.06 | 0.63 | 0.08 | -0.01 | 0.15 | 0.05 | -0.19 | 0.05 | 1.00 | -0.02 | -0.07 | -0.20 | -0.05 | -0.03 | 0.13 | 0.00 |
| RL | -0.01 | -0.04 | -0.04 | -0.02 | 0.04 | -0.04 | 0.06 | 0.00 | 0.17 | -0.04 | -0.02 | 1.00 | -0.04 | -0.03 | -0.03 | -0.07 | -0.10 | 0.13 |
| RE | 0.03 | -0.05 | -0.03 | 0.10 | -0.17 | 0.05 | -0.02 | 0.01 | 0.11 | 0.00 | -0.07 | -0.04 | 1.00 | 0.07 | 0.03 | -0.01 | -0.05 | 0.00 |
| RUST | 0.09 | -0.06 | -0.05 | -0.07 | -0.03 | 0.17 | -0.09 | -0.07 | 0.06 | -0.16 | -0.20 | -0.03 | 0.07 | 1.00 | 0.01 | -0.12 | 0.21 | 0.69 |
| SH | 0.10 | 0.01 | 0.01 | -0.04 | -0.04 | 0.02 | 0.01 | 0.01 | 0.01 | -0.05 | -0.05 | -0.03 | 0.03 | 0.01 | 1.00 | 0.11 | -0.04 | -0.09 |
| SL | -0.05 | -0.03 | -0.01 | -0.04 | 0.09 | -0.05 | -0.01 | -0.12 | 0.00 | 0.01 | -0.03 | -0.07 | -0.01 | -0.12 | 0.11 | 1.00 | 0.17 | -0.32 |
| SWT | 0.25 | -0.09 | -0.09 | 0.12 | 0.02 | -0.07 | -0.06 | -0.10 | -0.06 | 0.14 | 0.13 | -0.10 | -0.05 | 0.21 | -0.04 | 0.17 | 1.00 | 0.00 |
| VIG | 0.11 | 0.11 | 0.28 | 0.21 | 0.00 | -0.51 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.13 | 0.00 | 0.69 | -0.09 | -0.32 | 0.00 | 1.00 |

**GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), HC = husk cover, MSV = maize streak virus (1-5), PH = plant height (cm), RL = root lodging (#), RE = rotten ears (#), Rust = rust disease (1-5), SH = shelling percentage, SL = stem lodging (#), SWT = 100 seed weight (g), VIG = vigor, # = number.**

## Appendix 6 Soil analytical data interpretation guide

Threshold values

**i) Phosphorus ug $g^{-1}$ (Mehlich3) rating**

| | |
|---|---|
| <8 | very low |
| 9 - 18 | low |
| 19 - 25 | medium (adequate range) |
| 25 - 33 | high (adequate range) |
| >34 | very high |

**ii) Potassium cmol $kg^{-1}$(Mehlich3) rating**

| | |
|---|---|
| <0.05 | very low |
| 0.06 - 0.10 | low |
| 0.11 - 0.04 | medium (adequate range) |
| 0.50 - 0.80 | high |
| >1.00 | very high |

**iii) Zinc ug $g^{-1}$ (Mehlich3) rating**

| | |
|---|---|
| <1.00 | very low |
| 1.00 - 1.50 | low |
| 1.60 - 2.50 | medium (adequate range) |
| 2.5 - 3.00 | high (adequate range) |
| >2.5 | very high |

**iv) Boron ug $g^{-1}$ (Mehlich3) rating**

| | |
|---|---|
| <0.70 | low |
| 0.8 - 1.40 | medium |
| 1.40 - 2.50 | high |
| >2.5 | very high |

**v) Copper ug $g^{-1}$ (Mehlich3) rating**

| | |
|---|---|
| <0.30 | low |
| 0.4 - 0.8 | medium |
| 0.9 - 2.50 | high |
| >2.5 | very high |

**vi) Manganese cmol $kg^{-1}$ (Mehlich3) rating**

| | |
|---|---|
| <0.20 | very low |
| 0.2 - 0.5 | low |
| 0.6 - 3.9 | high |
| >4.0 | very high |

**Appendix 6 continued**

NB: Critical levels for Mn is 3.0 ug $g^{-1}$ and Ca is 2.0 cmol $kg^{-1}$ using Mehlich3 (Melich 1984)

**vii) Soil pH**

| In water | In $CaCl_2$ | Rating |
|---|---|---|
| <4.5 | <4.0 | very strongly acid |
| 4.5 - 5.0 | 4.0 - 4.45 | strongly acid |
| 5.1 - 5.5 | 4.5 - 4.95 | acid |
| 5.6 - 6.05 | 0 - 5.45 | moderately acid |
| 6.1 - 6.5 | 5.5 - 5.95 | slightly acid |
| 6.6 - 7.0 | 6.0 - 6.45 | almost neutral |
| 7.1 -7.5 | 6.5 - 6.95 | very slightly alkaline |
| 7.6 - 8.0 | 7.0 - 7.45 | slightly alkaline |
| >8.0 | -7.45 - 7.95 | alkaline / moderately alkaline |
| >8.5 | >8.00 | strongly alkaline |

| **vii) Total Nitrogen%** | **Rating** |
|---|---|
| <0.08 | very low |
| 0.08 - 0.12 | low |
| 0.12 - 0.2 | medium |
| 0.20 - 0.30 | high |
| >0.3 | very high |

| **vii) % Carbon** | **organic matter %** | **Rating** |
|---|---|---|
| <0.88 | 1.5 | low |
| 0.88 - 2.35 | 1.5 - 4.0 | medium |
| >2.35 | >4.0 | high |

Notes: Soil reaction (pH) is determined in water. Non acidifying fertilisers such as CAN are recommended below pH 5.5 in water (4.5 in $CaCl_2$). Dolomitic lime application (1-2 t $ha^{-1}$).

Farm yard manure is recommended at 5 tons per ha if the soil test measures less than 1.0% OM (0.58% OC) and 2.5 tons per ha when the soil test is between 1.0 and 1.5% OM (0.58-0.87% OC).

**Appendix 7 Mean performance for grain yield across four optimal environments combined for 2011/12 and 2012/13 seasons**

| Genotypes | GY | AD | ASI | DS | EH | EPP | LB | HC | GLS | GT | MSV | PH | RE | RL | Rust | SL | SWT | SH% | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G1 | 3100 | 66.1 | 2.9 | 67.8 | 75 | 1.0 | 1.8 | 1.2 | 1.7 | 1.6 | 1.1 | 171 | 0.6 | 0.1 | 1.7 | 0.2 | 30.8 | 77.3 | 2.3 |
| G2 | 2326 | 62.1 | 1.2 | 64.5 | 69 | 1.0 | 2.0 | 1.3 | 1.9 | 1.8 | 1.3 | 156 | 1.0 | 0.5 | 1.5 | 1.5 | 29.3 | 67.4 | 2.1 |
| G3 | 3014 | 64.1 | 0.8 | 65.7 | 75 | 1.2 | 1.4 | 1.3 | 1.7 | 1.6 | 1.3 | 163 | 0.7 | 0.5 | 1.5 | 1.0 | 30.1 | 76.4 | 2.0 |
| G4 | 3311 | 65.0 | 1.3 | 66.9 | 73 | 1.1 | 1.9 | 1.2 | 1.3 | 1.8 | 1.1 | 165 | 0.6 | 0.3 | 1.7 | 0.2 | 28.3 | 80.6 | 2.0 |
| G5 | 3921 | 68.3 | 1.0 | 70.0 | 87 | 1.1 | 1.9 | 1.9 | 1.5 | 1.9 | 1.1 | 189 | 0.7 | 0.8 | 1.4 | 1.0 | 32.1 | 79.6 | 1.9 |
| G6 | 3505 | 67.2 | 0.8 | 69.0 | 85 | 1.2 | 2.0 | 1.4 | 1.9 | 2.0 | 1.1 | 185 | 0.8 | 0.9 | 1.6 | 0.6 | 31.2 | 79.6 | 1.9 |
| G7 | 2663 | 65.6 | 1.4 | 67.6 | 78 | 1.1 | 1.9 | 0.9 | 1.4 | 2.0 | 1.3 | 171 | 0.8 | 0.7 | 1.5 | 0.6 | 30.9 | 80.0 | 2.0 |
| G8 | 3965 | 65.9 | 1.1 | 67.6 | 85 | 1.2 | 1.9 | 1.6 | 1.9 | 1.7 | 1.2 | 182 | 0.7 | 1.4 | 2.0 | 1.2 | 30.1 | 80.9 | 1.9 |
| G9 | 3254 | 66.0 | 0.9 | 67.4 | 80 | 1.1 | 1.9 | 1.2 | 1.5 | 2.0 | 1.3 | 175 | 0.9 | 0.6 | 1.6 | 0.7 | 29.3 | 75.7 | 1.9 |
| G10 | 3817 | 67.7 | 2.0 | 70.2 | 86 | 1.1 | 2.0 | 0.9 | 1.9 | 2.0 | 1.2 | 183 | 0.8 | 0.6 | 1.7 | 0.2 | 31.1 | 81.8 | 2.0 |
| G11 | 2517 | 67.8 | 1.0 | 69.4 | 76 | 1.1 | 2.0 | 1.3 | 1.8 | 1.8 | 1.4 | 169 | 0.7 | 0.6 | 1.6 | 0.5 | 26.7 | 77.5 | 2.1 |
| G12 | 3687 | 66.3 | 1.1 | 68.0 | 78 | 1.1 | 1.9 | 1.1 | 1.8 | 1.8 | 1.1 | 173 | 0.7 | 0.4 | 1.9 | 0.0 | 26.1 | 78.3 | 2.0 |
| G13 | 3444 | 66.5 | 0.8 | 68.1 | 82 | 1.2 | 1.6 | 1.4 | 2.1 | 1.8 | 1.2 | 173 | 1.4 | 0.8 | 1.3 | 0.2 | 28.6 | 80.8 | 2.2 |
| G14 | 3189 | 65.5 | 1.7 | 67.9 | 82 | 1.0 | 2.0 | 1.1 | 1.8 | 1.8 | 1.0 | 177 | 1.1 | 0.9 | 1.6 | 0.2 | 30.2 | 79.4 | 2.0 |
| G15 | 3319 | 63.6 | 1.3 | 65.6 | 73 | 1.1 | 2.0 | 1.7 | 1.7 | 1.8 | 1.1 | 165 | 0.9 | 1.2 | 1.8 | 0.9 | 29.5 | 79.0 | 2.3 |
| G16 | 2901 | 63.2 | 0.8 | 64.9 | 80 | 1.0 | 1.8 | 2.1 | 1.8 | 1.8 | 1.1 | 173 | 0.8 | 0.5 | 1.8 | 0.6 | 32.3 | 77.7 | 2.0 |
| G17 | 3143 | 65.3 | 1.3 | 67.3 | 75 | 1.2 | 1.8 | 1.5 | 1.3 | 1.6 | 1.1 | 164 | 0.5 | 0.3 | 1.4 | 0.8 | 26.2 | 83.4 | 2.4 |
| G18 | 3633 | 63.3 | 1.2 | 65.3 | 79 | 1.2 | 1.4 | 1.1 | 1.5 | 1.7 | 1.1 | 173 | 1.1 | 0.9 | 1.5 | 1.0 | 32.1 | 80.8 | 2.1 |
| G19 | 3179 | 64.9 | 1.0 | 66.8 | 79 | 1.1 | 1.9 | 2.0 | 1.8 | 2.0 | 1.1 | 167 | 0.8 | 1.5 | 2.1 | 0.6 | 29.4 | 86.5 | 2.1 |
| G20 | 4489 | 65.0 | 1.0 | 66.7 | 81 | 1.1 | 1.9 | 1.3 | 1.5 | 1.8 | 1.2 | 173 | 1.1 | 1.4 | 1.3 | 0.4 | 32.0 | 83.0 | 1.5 |
| G21 | 3307 | 65.1 | 1.0 | 66.7 | 83 | 1.2 | 2.4 | 1.5 | 1.6 | 1.8 | 1.0 | 176 | 0.7 | 1.1 | 1.7 | 1.8 | 30.9 | 80.3 | 2.0 |
| G22 | 3573 | 62.7 | 1.4 | 64.7 | 75 | 1.1 | 1.9 | 1.2 | 1.5 | 1.8 | 1.3 | 170 | 0.8 | 0.2 | 1.7 | 0.7 | 30.3 | 80.1 | 2.5 |
| G23 | 3160 | 61.6 | 1.2 | 63.4 | 70 | 1.1 | 2.1 | 1.1 | 1.9 | 2.0 | 1.0 | 163 | 0.7 | 0.6 | 2.0 | 0.6 | 28.6 | 79.0 | 2.0 |
| G24 | 2983 | 59.1 | 1.3 | 61.1 | 72 | 1.1 | 2.2 | 1.8 | 1.3 | 2.0 | 1.1 | 167 | 0.7 | 0.7 | 1.7 | 0.8 | 29.1 | 75.9 | 2.2 |
| G25 | 3396 | 63.3 | 0.9 | 65.2 | 82 | 1.1 | 1.7 | 1.7 | 1.7 | 2.1 | 1.4 | 177 | 1.5 | 0.7 | 1.8 | 0.7 | 30.7 | 81.0 | 1.7 |
| G26 | 3611 | 64.4 | 1.2 | 66.2 | 75 | 1.1 | 2.1 | 1.3 | 1.6 | 2.0 | 1.1 | 174 | 1.3 | 0.8 | 1.5 | 0.2 | 30.5 | 77.4 | 1.9 |
| G27 | 3965 | 66.4 | 1.4 | 68.4 | 82 | 1.2 | 1.9 | 1.6 | 1.7 | 2.1 | 1.2 | 179 | 0.8 | 0.3 | 1.6 | 0.1 | 30.7 | 79.8 | 1.9 |
| G28 | 3727 | 62.0 | 1.0 | 63.8 | 75 | 1.1 | 2.0 | 1.3 | 1.8 | 2.1 | 1.2 | 171 | 0.5 | 1.0 | 1.7 | 0.5 | 27.4 | 82.6 | 1.9 |
| G29 | 3384 | 66.8 | 1.3 | 68.3 | 78 | 1.1 | 2.0 | 1.6 | 1.5 | 2.0 | 1.4 | 176 | 0.9 | 0.6 | 1.6 | 0.5 | 29.7 | 79.3 | 2.1 |

**Appendix 7 continued**

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G30 | 3693 | 65.7 | 0.9 | 67.3 | 82 | 1.1 | 1.9 | 1.5 | 1.8 | 1.8 | 1.2 | 179 | 0.8 | 0.4 | 1.6 | 0.4 | 30.9 | 79.2 | 2.0 |
| G31 | 3820 | 64.8 | 1.0 | 66.6 | 82 | 1.1 | 2.2 | 1.3 | 1.8 | 1.8 | 1.2 | 176 | 0.8 | 0.3 | 1.7 | 1.0 | 27.6 | 80.4 | 2.0 |
| G32 | 3744 | 62.2 | 1.0 | 64.0 | 80 | 1.1 | 2.0 | 1.8 | 1.5 | 1.9 | 1.4 | 178 | 0.5 | 0.6 | 1.6 | 0.6 | 28.6 | 85.4 | 2.0 |
| G33 | 4003 | 61.3 | 1.2 | 63.4 | 75 | 1.2 | 1.8 | 1.5 | 1.4 | 1.9 | 1.6 | 168 | 0.7 | 1.0 | 1.7 | 0.9 | 29.5 | 82.1 | 1.9 |
| G34 | 3223 | 60.7 | 0.9 | 62.5 | 78 | 1.2 | 2.2 | 1.3 | 1.6 | 2.7 | 1.0 | 174 | 0.7 | 1.8 | 1.9 | 0.3 | 25.9 | 80.2 | 2.1 |
| G35 | 3563 | 64.2 | 1.0 | 65.9 | 81 | 1.1 | 1.8 | 2.6 | 1.6 | 2.0 | 1.1 | 178 | 0.7 | 0.7 | 1.6 | 1.2 | 29.9 | 77.8 | 2.0 |
| G36 | 3757 | 62.9 | 1.1 | 64.9 | 83 | 1.1 | 1.9 | 1.3 | 1.6 | 2.0 | 1.3 | 179 | 0.8 | 0.8 | 1.9 | 0.7 | 28.6 | 79.5 | 2.0 |
| G37 | 2594 | 65.3 | 1.3 | 67.2 | 66 | 1.1 | 1.7 | 1.0 | 1.5 | 2.1 | 1.2 | 162 | 0.6 | 0.2 | 1.9 | 0.9 | 30.4 | 74.1 | 2.0 |
| G38 | 2413 | 69.0 | 1.1 | 70.3 | 78 | 1.0 | 1.9 | 1.0 | 1.4 | 1.9 | 1.4 | 175 | 0.5 | 0.8 | 1.4 | 0.8 | 30.5 | 72.8 | 2.0 |
| G39 | 3902 | 64.1 | 0.6 | 65.6 | 70 | 1.1 | 2.0 | 1.2 | 1.5 | 1.9 | 1.1 | 161 | 0.9 | 0.6 | 1.8 | 0.8 | 31.4 | 79.3 | 2.1 |
| G40 | 2295 | 66.5 | 1.1 | 68.0 | 73 | 1.1 | 1.9 | 1.2 | 1.4 | 1.9 | 1.2 | 169 | 0.8 | 0.6 | 1.4 | 0.5 | 33.2 | 77.8 | 2.0 |
| G41 | 3130 | 60.4 | 0.6 | 62.0 | 70 | 1.0 | 1.5 | 1.3 | 1.4 | 1.5 | 1.0 | 164 | 0.9 | 0.2 | 1.9 | 0.3 | 27.5 | 82.2 | 2.3 |
| G42 | 2996 | 63.2 | 1.0 | 64.9 | 71 | 1.0 | 1.8 | 0.9 | 1.6 | 1.7 | 1.2 | 168 | 0.5 | 1.6 | 1.7 | 0.5 | 31.3 | 78.7 | 2.2 |
| G43 | 3750 | 61.9 | 0.9 | 63.8 | 69 | 1.1 | 2.0 | 1.3 | 1.6 | 1.9 | 1.2 | 162 | 0.9 | 0.2 | 1.7 | 1.7 | 31.0 | 77.4 | 1.9 |
| G44 | 3685 | 64.3 | 1.2 | 66.5 | 75 | 1.0 | 2.0 | 1.4 | 1.8 | 1.7 | 1.2 | 172 | 0.8 | 0.5 | 1.5 | 1.0 | 32.1 | 79.4 | 2.0 |
| G45 | 3735 | 66.2 | 0.8 | 68.0 | 89 | 1.1 | 1.8 | 1.4 | 1.3 | 2.5 | 1.7 | 186 | 0.7 | 0.2 | 1.8 | 0.9 | 33.7 | 76.7 | 1.8 |
| **Mean** | **3373** | **64.5** | **1.1** | **66.3** | **77.6** | **1.1** | **1.9** | **1.4** | **1.6** | **1.9** | **1.2** | **172.3** | **0.8** | **0.7** | **1.7** | **0.7** | **29.9** | **79.2** | **2.0** |
| **LSD** | **608** | **1.7** | **1.3** | **1.7** | **8** | **0.1** | **0.3** | **0.8** | **0.3** | **0.5** | **0.3** | **12** | **0.4** | **1.2** | **0.3** | **0.7** | **2.9** | **5.9** | **0.3** |
| **CV** | **31.8** | **4.6** | **194** | **4.6** | **18.2** | **15** | **27.1** | **103** | **36** | **40** | **35.9** | **12.1** | **80** | **302** | **31.3** | **169** | **16.8** | **13.1** | **27.3** |
| **SE** | **1072** | **3.0** | **2.2** | **3.1** | **14.1** | **0.2** | **0.5** | **1.4** | **0.6** | **0.9** | **0.4** | **20.8** | **0.7** | **2.1** | **0.5** | **1.2** | **5.1** | **10.4** | **0.6** |
| **Min** | **2295** | **59** | **1** | **61** | **66** | **1** | **1** | **1** | **1** | **1** | **1** | **156** | **1** | **0** | **1** | **0** | **26** | **67** | **2** |
| **Max** | **4489** | **69** | **3** | **70** | **89** | **1** | **2** | **3** | **2** | **3** | **2** | **189** | **2** | **2** | **2** | **2** | **34** | **86** | **2** |

**LSD = Least significant difference, CV = coefficient of variation, SE = error , Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL = stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour, # = number.**

**Appendix 8 Mean performance for grain yield and other agronomic traits across four low pH environments combined for 2011/12 and 2012/13 seasons**

| Genotypes | GY | AD | ASI | DS | EH | EPP | LB | HC | GLS | GT | MSV | PH | RE | RL | Rust | SL | SWT | SH% | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G1 | 1417 | 84.1 | 2.8 | 87.0 | 52.0 | 0.9 | 2.1 | 1.3 | 2.4 | 2.4 | 1.2 | 136 | 1.4 | 1.7 | 1.2 | 1.2 | 23 | 67 | 2.8 |
| G2 | 1282 | 82.4 | 2.3 | 84.8 | 48.2 | 0.8 | 2.4 | 1.6 | 1.8 | 2.4 | 1.2 | 127 | 0.9 | 2.5 | 1.4 | 1.7 | 22 | 65 | 3.0 |
| G3 | 1562 | 81.4 | 2.5 | 84.0 | 49.4 | 0.8 | 2.1 | 1.7 | 2.0 | 2.5 | 1.2 | 132 | 0.8 | 1.9 | 1.1 | 1.7 | 26 | 75 | 2.6 |
| G4 | 1372 | 83.5 | 3.4 | 87.3 | 48.6 | 0.8 | 2.3 | 2.2 | 2.2 | 2.7 | 1.1 | 127 | 1.7 | 1.8 | 1.4 | 0.9 | 23 | 68 | 2.4 |
| G5 | 1517 | 85.9 | 2.0 | 87.9 | 44.3 | 0.8 | 2.3 | 2.1 | 1.9 | 2.4 | 1.2 | 129 | 1.2 | 1.8 | 1.3 | 1.5 | 24 | 71 | 2.2 |
| G6 | 1655 | 82.0 | 2.0 | 83.1 | 44.4 | 0.9 | 2.4 | 1.3 | 2.7 | 2.8 | 1.2 | 129 | 1.6 | 1.4 | 1.2 | 0.7 | 22 | 68 | 2.7 |
| G7 | 1527 | 80.4 | 3.3 | 83.0 | 46.2 | 0.8 | 2.3 | 1.2 | 2.1 | 2.7 | 1.2 | 301 | 1.4 | 1.7 | 1.1 | 1.1 | 24 | 73 | 2.9 |
| G8 | 1488 | 83.3 | 2.5 | 85.8 | 45.4 | 0.8 | 2.7 | 1.1 | 2.0 | 2.6 | 1.2 | 128 | 0.9 | 1.4 | 1.0 | 1.8 | 23 | 65 | 2.6 |
| G9 | 1537 | 84.6 | 2.3 | 86.9 | 46.9 | 0.9 | 2.2 | 0.8 | 1.9 | 2.5 | 1.2 | 132 | 1.0 | 1.4 | 1.4 | 1.0 | 22 | 66 | 2.9 |
| G10 | 1314 | 84.6 | 2.8 | 87.5 | 46.2 | 1.0 | 2.3 | 1.4 | 2.1 | 2.9 | 1.3 | 123 | 0.9 | 2.3 | 1.4 | 1.3 | 19 | 68 | 2.5 |
| G11 | 1502 | 82.7 | 2.1 | 84.8 | 38.0 | 0.8 | 2.1 | 1.5 | 2.3 | 2.5 | 1.2 | 120 | 0.9 | 1.2 | 1.3 | 1.5 | 20 | 72 | 2.8 |
| G12 | 1417 | 82.5 | 2.7 | 85.0 | 43.8 | 0.9 | 2.4 | 1.3 | 2.7 | 2.9 | 1.3 | 129 | 1.3 | 1.7 | 1.5 | 1.0 | 20 | 68 | 3.1 |
| G13 | 1489 | 82.0 | 3.5 | 85.8 | 50.1 | 0.9 | 2.4 | 1.9 | 2.1 | 2.8 | 1.3 | 127 | 1.4 | 1.4 | 1.2 | 2.2 | 22 | 69 | 3.0 |
| G14 | 1362 | 83.6 | 2.7 | 86.3 | 46.5 | 0.8 | 2.2 | 2.5 | 2.3 | 2.3 | 1.2 | 148 | 0.9 | 2.0 | 1.0 | 1.3 | 22 | 68 | 2.7 |
| G15 | 1746 | 82.5 | 3.5 | 86.0 | 48.6 | 0.9 | 2.3 | 1.7 | 2.4 | 2.7 | 1.1 | 132 | 1.2 | 2.2 | 1.5 | 1.4 | 22 | 70 | 2.8 |
| G16 | 1650 | 80.8 | 3.1 | 82.9 | 38.9 | 0.8 | 1.9 | 1.9 | 2.1 | 2.6 | 1.3 | 116 | 1.0 | 1.3 | 1.4 | 1.6 | 24 | 71 | 2.7 |
| G17 | 1434 | 82.9 | 3.4 | 86.3 | 46.0 | 0.9 | 2.4 | 1.9 | 2.3 | 2.7 | 1.2 | 124 | 1.5 | 2.0 | 1.2 | 1.5 | 23 | 71 | 2.9 |
| G18 | 1539 | 83.3 | 2.0 | 85.3 | 50.4 | 0.8 | 2.2 | 1.6 | 1.9 | 2.5 | 1.2 | 128 | 0.9 | 1.6 | 1.2 | 2.2 | 22 | 70 | 2.6 |
| G19 | 1501 | 82.9 | 1.7 | 84.3 | 48.8 | 0.8 | 2.2 | 1.6 | 2.2 | 2.8 | 1.2 | 127 | 1.2 | 2.0 | 1.4 | 1.4 | 21 | 74 | 3.2 |
| G20 | 1466 | 84.2 | 2.6 | 87.1 | 45.7 | 0.8 | 1.8 | 1.9 | 2.3 | 2.6 | 1.2 | 122 | 0.9 | 1.7 | 1.2 | 1.3 | 24 | 72 | 2.4 |
| G21 | 1602 | 83.8 | 2.8 | 86.6 | 42.6 | 0.9 | 2.3 | 1.7 | 2.0 | 2.9 | 1.1 | 126 | 1.0 | 1.8 | 1.4 | 1.0 | 22 | 71 | 2.6 |
| G22 | 1753 | 81.6 | 2.5 | 84.8 | 48.2 | 0.9 | 2.2 | 2.1 | 2.1 | 2.4 | 1.2 | 126 | 1.2 | 1.7 | 1.2 | 1.1 | 23 | 70 | 2.7 |
| G23 | 1496 | 82.6 | 2.1 | 85.4 | 43.8 | 0.9 | 2.2 | 1.8 | 2.2 | 2.3 | 1.3 | 122 | 1.6 | 2.2 | 1.2 | 1.2 | 24 | 71 | 3.0 |
| G24 | 1792 | 79.7 | 3.0 | 83.0 | 51.2 | 0.8 | 2.4 | 1.6 | 2.3 | 2.4 | 1.1 | 134 | 1.4 | 2.3 | 1.5 | 1.2 | 24 | 73 | 2.7 |
| G25 | 1401 | 84.5 | 2.7 | 86.4 | 50.8 | 0.9 | 2.2 | 1.5 | 1.9 | 2.5 | 1.2 | 141 | 1.1 | 1.5 | 1.3 | 1.1 | 23 | 69 | 2.5 |

**Appendix 8 continued**

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G26 | 1575 | 84.5 | 3.2 | 87.7 | 47.5 | 0.8 | 2.6 | 2.2 | 2.1 | 1.9 | 1.3 | 125 | 1.2 | 1.3 | 1.2 | 0.9 | 23 | 68 | 2.7 |
| G27 | 1701 | 84.7 | 2.0 | 86.7 | 49.8 | 0.9 | 2.1 | 1.0 | 1.9 | 2.8 | 1.2 | 129 | 1.2 | 1.3 | 1.1 | 1.7 | 27 | 69 | 2.4 |
| G28 | 1513 | 84.5 | 2.3 | 86.8 | 47.9 | 0.8 | 2.1 | 1.7 | 2.1 | 3.0 | 1.2 | 127 | 0.9 | 2.0 | 1.4 | 1.1 | 24 | 67 | 2.7 |
| G29 | 1491 | 85.2 | 2.4 | 87.4 | 52.4 | 0.9 | 2.2 | 2.4 | 1.8 | 2.4 | 1.5 | 139 | 1.0 | 1.3 | 1.1 | 1.4 | 22 | 70 | 3.2 |
| G30 | 1765 | 82.5 | 2.9 | 85.4 | 44.0 | 0.9 | 1.9 | 2.4 | 2.1 | 2.3 | 1.3 | 119 | 1.1 | 2.0 | 1.3 | 0.6 | 24 | 74 | 2.1 |
| G31 | 1195 | 80.3 | 2.6 | 82.9 | 45.4 | 0.9 | 2.0 | 2.3 | 2.1 | 2.6 | 1.3 | 123 | 1.3 | 2.2 | 1.3 | 0.9 | 22 | 64 | 3.1 |
| G32 | 1448 | 80.7 | 2.7 | 83.8 | 51.6 | 0.8 | 2.1 | 1.0 | 2.1 | 2.7 | 1.4 | 132 | 1.3 | 1.8 | 1.2 | 1.1 | 23 | 68 | 2.7 |
| G33 | 1385 | 83.0 | 3.0 | 86.5 | 46.6 | 0.8 | 2.0 | 1.2 | 2.1 | 2.5 | 1.2 | 127 | 1.0 | 2.4 | 1.3 | 1.3 | 22 | 70 | 2.5 |
| G34 | 1599 | 81.6 | 3.0 | 84.0 | 44.7 | 0.8 | 2.0 | 1.1 | 1.8 | 1.8 | 1.3 | 123 | 0.9 | 1.7 | 1.3 | 1.1 | 22 | 70 | 2.7 |
| G35 | 1396 | 86.3 | 3.0 | 89.3 | 45.2 | 0.8 | 2.1 | 2.3 | 2.3 | 3.2 | 1.1 | 126 | 1.4 | 2.0 | 1.2 | 1.1 | 26 | 69 | 2.8 |
| G36 | 1432 | 83.6 | 3.2 | 86.4 | 46.0 | 0.7 | 2.3 | 1.9 | 2.3 | 2.3 | 1.3 | 123 | 1.5 | 2.4 | 1.5 | 0.9 | 21 | 70 | 2.6 |
| G37 | 1409 | 82.5 | 2.2 | 85.1 | 47.1 | 0.8 | 1.9 | 2.6 | 2.1 | 2.8 | 1.2 | 129 | 1.1 | 1.3 | 1.3 | 1.4 | 20 | 71 | 2.7 |
| G38 | 1436 | 85.8 | 1.6 | 87.4 | 46.8 | 0.8 | 2.2 | 1.9 | 2.1 | 2.2 | 1.3 | 121 | 1.5 | 1.5 | 1.1 | 1.1 | 22 | 71 | 2.6 |
| G39 | 1429 | 82.5 | 3.4 | 86.1 | 49.6 | 0.8 | 2.0 | 1.3 | 2.2 | 2.4 | 1.3 | 130 | 1.2 | 2.7 | 1.2 | 1.7 | 22 | 68 | 2.8 |
| G40 | 1475 | 84.8 | 2.3 | 87.3 | 47.4 | 0.8 | 2.2 | 2.1 | 1.8 | 2.3 | 1.2 | 130 | 0.9 | 2.3 | 1.3 | 0.7 | 21 | 69 | 2.5 |
| G41 | 1376 | 80.3 | 2.8 | 83.5 | 40.6 | 0.8 | 2.0 | 1.9 | 3.7 | 2.6 | 1.3 | 118 | 1.0 | 1.8 | 1.2 | 1.0 | 21 | 67 | 2.8 |
| G42 | 1406 | 82.7 | 2.8 | 85.9 | 53.9 | 0.8 | 2.3 | 1.8 | 1.6 | 2.5 | 1.2 | 139 | 1.5 | 1.8 | 1.2 | 1.2 | 22 | 68 | 3.2 |
| G43 | 1418 | 84.6 | 3.1 | 89.0 | 39.5 | 0.9 | 2.1 | 2.6 | 2.0 | 2.0 | 1.4 | 121 | 1.3 | 1.6 | 1.2 | 1.0 | 22 | 66 | 3.2 |
| G44 | 1359 | 83.9 | 2.4 | 86.7 | 48.1 | 0.9 | 2.1 | 1.2 | 2.1 | 2.4 | 1.3 | 135 | 0.9 | 1.8 | 1.4 | 1.0 | 23 | 67 | 3.3 |
| G45 | 1447 | 83.8 | 2.9 | 86.7 | 45.4 | 0.8 | 1.9 | 1.5 | 1.9 | 2.4 | 1.2 | 133 | 1.0 | 1.3 | 1.1 | 0.7 | 25 | 66 | 2.5 |
| **Mean** | **1491** | **83.1** | **2.7** | **85.8** | **46.8** | **0.9** | **2.2** | **1.7** | **2.1** | **2.5** | **1.2** | **131.9** | **1.2** | **1.8** | **1.3** | **1.2** | **22.6** | **69.3** | **2.7** |
| **LSD** | **358** | **2.4** | **1** | **2.4** | **7.7** | **0.3** | **0.4** | **0.8** | **0.7** | **0.4** | **0.3** | **58** | **0.7** | **0.9** | **0.3** | **0.9** | **3** | **8** | **0.4** |
| **CV** | **42.4** | **5.1** | **67** | **5** | **28** | **54** | **35** | **83** | **59** | **28** | **37** | **77** | **103** | **92.1** | **44.6** | **127.6** | **20.3** | **19** | **27.4** |
| **SE** | **631** | **4.2** | **1.8** | **4.3** | **13.6** | **0.5** | **0.8** | **1.4** | **1.3** | **0.7** | **0.5** | **101.5** | **1.2** | **1.7** | **0.6** | **1.6** | **4.6** | **13** | **0.8** |
| **Min** | **1195.0** | **79.7** | **1.6** | **82.9** | **38.0** | **0.7** | **1.8** | **0.8** | **1.6** | **1.8** | **1.1** | **116.0** | **0.8** | **1.2** | **1.0** | **0.6** | **19.0** | **64.0** | **2.1** |
| **Max** | **1792.0** | **86.3** | **3.5** | **89.3** | **53.9** | **1.0** | **2.7** | **2.6** | **3.7** | **3.2** | **1.5** | **301.0** | **1.7** | **2.7** | **1.5** | **2.2** | **27.0** | **75.0** | **3.3** |

**LSD = Least significant difference, CV = coefficient of variation, SE = error, Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), HC = husk cover, GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RE = rotten ears (#), RL = root lodging (#), Rust = rust disease (1-5), SL = stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, VIG = vigour, # = number.**

**Appendix 9 Mean performance for grain yield and agronomic traits for low N environment 2012/13 season**

| Genotypes | GY | Rank | AD | ASI | DS | EH | EPP | LB | GLS | GT | HC | PH | RL | RUST | SL | SWT | SH% |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G1 | 826 | 12 | 68.7 | 2.3 | 71.0 | 33.6 | 0.8 | 3.5 | 1.0 | 2.3 | 0.3 | 77.3 | 6.3 | 1.0 | 3.3 | 32.0 | 64.5 |
| G2 | 614 | 27 | 65.3 | 2.0 | 67.3 | 19.3 | 0.7 | 4.0 | 1.7 | 2.2 | 0.3 | 60.7 | 8.3 | 1.0 | 0.3 | 25.7 | 59.0 |
| G3 | 467 | 37 | 66.3 | 3.0 | 67.0 | 38.3 | 1.1 | 3.0 | 2.0 | 2.3 | 1.7 | 73.0 | 5.0 | 1.2 | 1.0 | 27.0 | 60.0 |
| G4 | 465 | 38 | 67.0 | 1.0 | 69.7 | 32.0 | 0.8 | 3.7 | 1.5 | 2.2 | 0.7 | 77.7 | 6.0 | 1.0 | 0.3 | 29.7 | 50.0 |
| G5 | 396 | 42 | 72.3 | 1.7 | 75.0 | 38.6 | 0.6 | 2.2 | 1.2 | 2.0 | 0.0 | 72.7 | 3.3 | 1.0 | 1.7 | 29.0 | 51.0 |
| G6 | 493 | 33 | 68.3 | 1.7 | 74.0 | 31.0 | 0.6 | 3.0 | 1.5 | 2.2 | 0.7 | 76.3 | 1.7 | 1.0 | 1.0 | 29.7 | 43.0 |
| G7 | 721 | 22 | 68.0 | 3.0 | 70.0 | 37.6 | 0.7 | 3.3 | 1.8 | 2.0 | 0.0 | 74.3 | 6.0 | 1.0 | 1.7 | 30.7 | 56.7 |
| G8 | 504 | 31 | 68.0 | 2.3 | 71.0 | 37.6 | 0.8 | 2.8 | 1.0 | 1.5 | 0.0 | 80.7 | 1.0 | 1.0 | 0.3 | 35.4 | 52.2 |
| G9 | 1146 | 1 | 68.0 | 2.0 | 70.3 | 56.6 | 0.9 | 3.2 | 1.3 | 1.7 | 1.3 | 108.3 | 2.3 | 1.0 | 2.0 | 30.0 | 74.5 |
| G10 | 1145 | 2 | 72.3 | 1.3 | 73.0 | 37.3 | 0.8 | 2.8 | 1.5 | 1.7 | 0.0 | 72.3 | 4.3 | 1.0 | 1.0 | 34.4 | 70.8 |
| G11 | 744 | 21 | 69.7 | 2.7 | 71.0 | 43.0 | 0.8 | 3.3 | 1.7 | 2.0 | 0.0 | 88.3 | 5.0 | 1.0 | 2.0 | 25.7 | 68.9 |
| G12 | 471 | 34 | 67.7 | 2.3 | 70.3 | 44.0 | 0.8 | 3.3 | 1.8 | 2.3 | 0.0 | 77.3 | 7.3 | 1.0 | 1.7 | 24.7 | 57.2 |
| G13 | 1113 | 3 | 69.0 | 1.3 | 71.3 | 35.6 | 0.7 | 3.3 | 1.7 | 2.2 | 0.7 | 82.3 | 4.7 | 1.0 | 0.7 | 28.7 | 70.3 |
| G14 | 640 | 25 | 66.3 | 1.7 | 67.7 | 34.3 | 0.7 | 2.7 | 1.3 | 2.5 | 0.0 | 78.0 | 3.0 | 1.0 | 1.0 | 28.0 | 63.9 |
| G15 | 377 | 43 | 66.0 | 2.3 | 67.7 | 32.6 | 0.5 | 3.5 | 1.3 | 2.0 | 0.0 | 69.3 | 2.0 | 1.0 | 1.7 | 27.7 | 62.4 |
| G16 | 788 | 18 | 65.7 | 3.3 | 68.0 | 31.0 | 0.7 | 3.0 | 1.7 | 1.5 | 2.3 | 62.7 | 6.0 | 1.0 | 2.3 | 30.0 | 59.2 |
| G17 | 820 | 14 | 66.3 | 0.7 | 69.7 | 43.0 | 0.8 | 3.0 | 1.8 | 2.2 | 0.0 | 86.0 | 1.7 | 1.0 | 0.0 | 28.4 | 69.4 |
| G18 | 432 | 39 | 65.7 | 2.7 | 66.3 | 22.3 | 0.6 | 3.3 | 1.2 | 1.7 | 0.7 | 59.7 | 6.0 | 1.0 | 2.0 | 30.4 | 60.8 |
| G19 | 974 | 6 | 67.7 | 2.0 | 70.3 | 41.3 | 1.0 | 4.0 | 1.2 | 2.0 | 2.3 | 81.3 | 2.7 | 1.0 | 2.3 | 31.4 | 63.9 |
| G20 | 959 | 7 | 65.7 | 1.3 | 67.7 | 45.3 | 0.7 | 3.0 | 1.8 | 2.7 | 1.0 | 92.0 | 6.3 | 1.0 | 1.3 | 30.0 | 56.7 |
| G21 | 938 | 8 | 66.0 | 1.0 | 67.3 | 33.3 | 0.7 | 3.2 | 2.2 | 1.5 | 0.3 | 70.0 | 4.7 | 1.0 | 2.3 | 28.7 | 68.3 |
| G22 | 678 | 24 | 63.3 | 1.3 | 64.3 | 49.6 | 0.8 | 3.7 | 1.3 | 1.5 | 0.7 | 100.0 | 3.7 | 1.0 | 4.0 | 28.0 | 63.3 |
| G23 | 324 | 44 | 62.0 | 1.3 | 63.3 | 35.6 | 0.7 | 3.5 | 1.2 | 2.0 | 0.7 | 69.7 | 7.3 | 1.0 | 4.0 | 25.7 | 55.6 |
| G24 | 1008 | 4 | 62.3 | 1.0 | 63.7 | 36.6 | 0.8 | 2.5 | 1.7 | 2.5 | 0.0 | 65.0 | 1.7 | 1.0 | 0.0 | 28.7 | 67.3 |
| G25 | 790 | 16 | 64.0 | 2.7 | 65.0 | 32.3 | 1.0 | 2.8 | 1.3 | 2.2 | 0.0 | 67.7 | 2.7 | 1.0 | 1.3 | 34.4 | 65.5 |

**Appendix 9 continued**

| | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G26 | 502 | 32 | 68.3 | 1.3 | 71.0 | 35.3 | 0.6 | 2.7 | 1.3 | 2.5 | 0.0 | 80.7 | 1.3 | 1.0 | 2.3 | 30.0 | 57.2 |
| G27 | 924 | 10 | 68.0 | 1.3 | 69.3 | 43.3 | 0.8 | 3.3 | 1.5 | 2.3 | 1.3 | 88.7 | 4.3 | 1.0 | 0.3 | 28.4 | 67.9 |
| G28 | 799 | 15 | 66.0 | 2.3 | 67.3 | 43.3 | 0.9 | 3.3 | 1.8 | 3.0 | 0.3 | 95.0 | 6.3 | 1.0 | 2.3 | 27.4 | 58.3 |
| G29 | 506 | 29 | 71.3 | 0.7 | 73.7 | 18.6 | 0.6 | 2.7 | 1.0 | 1.7 | 0.3 | 45.7 | 4.0 | 1.0 | 1.7 | 26.7 | 61.6 |
| G30 | 820 | 13 | 67.7 | 3.0 | 70.7 | 47.0 | 0.6 | 3.3 | 1.3 | 1.8 | 0.7 | 81.3 | 7.0 | 1.0 | 0.0 | 30.0 | 61.1 |
| G31 | 538 | 28 | 68.0 | 2.3 | 71.0 | 33.6 | 1.3 | 3.5 | 1.2 | 2.0 | 0.0 | 79.0 | 5.7 | 1.0 | 2.7 | 26.7 | 51.8 |
| G32 | 431 | 40 | 63.7 | 2.3 | 66.0 | 33.0 | 0.9 | 3.2 | 1.5 | 2.0 | 0.0 | 67.3 | 2.3 | 1.0 | 1.0 | 24.7 | 46.7 |
| G33 | 755 | 20 | 65.7 | 0.7 | 68.0 | 39.3 | 0.6 | 3.2 | 1.2 | 2.7 | 0.0 | 87.3 | 3.0 | 1.0 | 2.0 | 23.0 | 61.7 |
| G34 | 398 | 41 | 65.0 | 1.3 | 65.7 | 38.0 | 0.9 | 3.7 | 1.5 | 2.5 | 0.0 | 87.0 | 7.3 | 1.2 | 1.7 | 30.7 | 53.3 |
| G35 | 900 | 11 | 65.0 | 2.0 | 66.3 | 45.6 | 0.9 | 3.5 | 1.3 | 2.2 | 0.0 | 94.0 | 4.3 | 1.0 | 0.3 | 28.0 | 70.0 |
| G36 | 789 | 17 | 65.3 | 1.0 | 67.3 | 36.6 | 0.6 | 2.7 | 1.5 | 2.3 | 0.0 | 65.3 | 3.7 | 1.0 | 2.0 | 27.7 | 62.0 |
| G37 | 469 | 36 | 64.3 | 2.0 | 65.3 | 39.3 | 0.9 | 2.5 | 1.5 | 2.2 | 0.3 | 66.3 | 1.3 | 1.0 | 1.7 | 29.4 | 65.3 |
| G38 | 505 | 30 | 69.0 | 1.3 | 71.0 | 26.6 | 0.7 | 2.3 | 1.2 | 2.0 | 0.0 | 56.0 | 0.3 | 1.0 | 0.0 | 31.7 | 65.9 |
| G39 | 615 | 26 | 65.0 | 2.7 | 66.3 | 31.6 | 0.8 | 3.0 | 1.5 | 2.5 | 0.3 | 64.3 | 5.0 | 1.0 | 1.7 | 26.7 | 59.3 |
| G40 | 469 | 35 | 66.7 | 1.3 | 67.7 | 34.3 | 0.9 | 2.3 | 1.3 | 1.8 | 0.3 | 68.7 | 2.7 | 1.0 | 0.7 | 30.7 | 51.9 |
| G41 | 1000 | 5 | 64.0 | 0.0 | 65.3 | 48.6 | 0.9 | 3.5 | 1.3 | 1.7 | 0.0 | 93.3 | 2.7 | 1.0 | 1.3 | 24.0 | 68.3 |
| G43 | 690 | 23 | 55.0 | 2.7 | 64.3 | 34.0 | 1.0 | 2.7 | 1.7 | 1.8 | 0.3 | 65.7 | 2.7 | 1.0 | 1.0 | 29.4 | 63.3 |
| G44 | 762 | 19 | 65.9 | 1.6 | 57.7 | 47.3 | 0.8 | 3.0 | 1.7 | 2.5 | 0.0 | 91.3 | 2.7 | 1.0 | 1.3 | 27.0 | 68.9 |
| G45 | 938 | 9 | 72.3 | 2.7 | 67.4 | 38.1 | 0.8 | 3.4 | 1.0 | 1.6 | 0.2 | 69.2 | 4.8 | 1.0 | 1.4 | 28.4 | 61.4 |
| **MEAN** | **696** | | **66.5** | **1.8** | **68.3** | **37.2** | **0.8** | **3.1** | **1.5** | **2.1** | **0.4** | **76.6** | **4.1** | **1.0** | **1.5** | **28.7** | **61.1** |
| **P** | **0.73** | | **0.0** | **0.1** | **0.0** | **0.3** | **0.3** | **0.0** | **0.1** | **0.3** | **0.3** | **0.3** | **0.0** | **0.5** | **0.2** | **0.3** | **0.8** |
| **LSD** | **695.8** | | **3.1** | **1.9** | **3.7** | **19.6** | **0.4** | **0.9** | **27.5** | **0.6** | **1.6** | **32.8** | **4.4** | **0.1** | **2.4** | **7.1** | **0.4** |
| **CV** | **61.8** | | **2.9** | **63.8** | **3.3** | **32.3** | **31.3** | **18.7** | **0.7** | **27.5** | **246.7** | **26.4** | **65.7** | **6.0** | **102.0** | **15.3** | **31.3** |
| **Min** | **324.3** | | **55.0** | **0.0** | **57.7** | **18.6** | **0.5** | **2.2** | **1.0** | **1.5** | **0.0** | **45.7** | **0.3** | **1.0** | **0.0** | **23.0** | **43.0** |
| **Max** | **1146** | | **72.3** | **3.3** | **75.0** | **56.6** | **1.3** | **4.0** | **2.2** | **3.0** | **2.3** | **108.3** | **8.3** | **1.2** | **4.0** | **35.4** | **74.5** |

**LSD = Least significant difference, CV = coefficient of variation, Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), HC = husk cover, PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SL = stem lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, # = number.**

**Appendix 10 Mean performance combined across two years and across optimal and low pH environment for 2011/12 and 2012/13 seasons**

| Genotypes | GY | AD | ASI | DS | PH | EH | EPP | RL | SL | GLS | LB | MSV | RUST | GT | SH% | VIG | RE | HC | SWT |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G1 | 2060.1 | 75.9 | 2.2 | 77.9 | 143.0 | 58.3 | 1.0 | 2.3 | 1.5 | 1.0 | 2.3 | 1.1 | 1.6 | 2.0 | 70.3 | 2.7 | 0.9 | 1.2 | 27.2 |
| G2 | 1368.4 | 73.4 | 1.5 | 75.2 | 136.5 | 57.6 | 0.9 | 3.0 | 1.2 | 1.0 | 2.4 | 1.1 | 1.7 | 2.8 | 58.7 | 2.8 | 1.1 | 1.0 | 23.5 |
| G3 | 2240.9 | 72.4 | 1.4 | 73.9 | 136.4 | 59.7 | 1.1 | 2.2 | 1.3 | 1.0 | 2.0 | 1.1 | 1.4 | 2.2 | 77.3 | 2.4 | 0.9 | 1.4 | 25.9 |
| G4 | 2159.8 | 73.6 | 2.4 | 75.9 | 136.8 | 57.8 | 1.0 | 2.0 | 0.8 | 1.0 | 2.1 | 1.1 | 1.7 | 2.8 | 72.1 | 2.3 | 1.3 | 1.5 | 24.6 |
| G5 | 2610.7 | 77.9 | 1.1 | 79.1 | 151.0 | 61.0 | 1.0 | 1.1 | 1.2 | 1.0 | 2.0 | 0.9 | 1.6 | 2.3 | 69.1 | 1.9 | 0.9 | 1.5 | 26.9 |
| G6 | 2222.2 | 73.2 | 1.3 | 74.6 | 155.8 | 66.7 | 1.1 | 2.5 | 1.0 | 1.0 | 2.3 | 1.1 | 1.6 | 2.7 | 69.2 | 2.4 | 1.2 | 1.3 | 25.5 |
| G7 | 1454.7 | 73.0 | 2.3 | 75.2 | 273.4 | 58.6 | 1.0 | 1.3 | 1.0 | 1.0 | 2.1 | 1.1 | 1.5 | 2.5 | 71.6 | 2.3 | 1.4 | 1.1 | 29.2 |
| G8 | 2739.4 | 74.7 | 1.8 | 76.5 | 152.8 | 66.0 | 1.1 | 1.5 | 1.6 | 1.0 | 2.5 | 1.0 | 1.4 | 2.0 | 70.1 | 2.4 | 0.9 | 1.4 | 26.3 |
| G9 | 2293.9 | 75.3 | 1.7 | 76.8 | 148.6 | 63.4 | 1.0 | 2.6 | 1.0 | 1.0 | 2.1 | 1.0 | 1.7 | 2.5 | 70.3 | 2.2 | 0.9 | 0.9 | 26.3 |
| G10 | 2529.0 | 77.0 | 2.1 | 79.1 | 147.9 | 64.8 | 1.6 | 1.8 | 1.0 | 1.0 | 1.9 | 1.1 | 1.7 | 3.0 | 73.5 | 2.1 | 1.2 | 0.8 | 26.6 |
| G11 | 1628.9 | 76.3 | 1.4 | 77.6 | 133.0 | 52.6 | 1.0 | 2.7 | 1.2 | 1.0 | 2.0 | 1.1 | 1.7 | 3.2 | 74.3 | 2.8 | 0.3 | 1.2 | 22.3 |
| G12 | 2121.4 | 73.9 | 2.5 | 76.2 | 145.7 | 59.6 | 1.1 | 3.0 | 1.2 | 1.0 | 2.2 | 1.1 | 1.8 | 2.0 | 71.2 | 2.6 | 1.1 | 1.1 | 22.5 |
| G13 | 2511.7 | 74.6 | 2.5 | 77.0 | 142.1 | 62.1 | 1.1 | 1.7 | 1.0 | 1.0 | 2.1 | 1.2 | 1.5 | 3.3 | 74.8 | 2.6 | 1.5 | 1.4 | 25.8 |
| G14 | 2108.0 | 74.2 | 1.9 | 76.1 | 159.2 | 60.0 | 1.0 | 2.0 | 1.3 | 1.0 | 2.1 | 1.1 | 1.4 | 2.5 | 68.3 | 2.1 | 0.7 | 1.3 | 27.5 |
| G15 | 2244.0 | 71.5 | 2.8 | 74.2 | 138.2 | 56.1 | 1.0 | 1.4 | 1.0 | 1.0 | 2.4 | 1.0 | 1.8 | 2.5 | 71.2 | 2.6 | 1.2 | 1.8 | 24.3 |
| G16 | 2131.7 | 69.6 | 2.2 | 71.7 | 136.8 | 58.3 | 1.0 | 1.7 | 1.2 | 1.0 | 2.0 | 1.1 | 1.7 | 3.3 | 71.1 | 2.2 | 1.6 | 2.6 | 27.3 |
| G17 | 2158.6 | 73.8 | 2.5 | 76.3 | 143.6 | 61.7 | 1.1 | 1.8 | 0.9 | 1.0 | 2.1 | 1.0 | 1.5 | 2.3 | 73.8 | 2.6 | 0.9 | 1.6 | 24.1 |
| G18 | 2600.8 | 73.9 | 1.1 | 75.1 | 148.4 | 64.2 | 1.1 | 2.0 | 1.2 | 1.0 | 2.2 | 1.0 | 1.6 | 2.3 | 73.3 | 2.2 | 0.7 | 1.4 | 26.5 |
| G19 | 2223.4 | 74.3 | 1.2 | 75.5 | 142.0 | 60.9 | 1.0 | 1.7 | 1.2 | 1.0 | 2.3 | 1.1 | 1.6 | 1.8 | 75.0 | 2.6 | 0.9 | 2.1 | 25.3 |
| G20 | 2848.8 | 75.6 | 1.9 | 77.4 | 146.5 | 65.9 | 1.0 | 1.7 | 0.8 | 1.0 | 1.9 | 1.1 | 1.6 | 2.7 | 72.9 | 2.0 | 0.9 | 1.8 | 28.1 |
| G21 | 2350.0 | 74.1 | 1.8 | 75.9 | 150.8 | 64.6 | 1.1 | 1.7 | 1.3 | 1.0 | 2.3 | 1.0 | 1.7 | 2.8 | 74.4 | 2.3 | 0.9 | 1.4 | 26.2 |
| G22 | 2389.2 | 71.7 | 2.8 | 74.4 | 146.1 | 61.3 | 1.1 | 2.1 | 1.3 | 1.0 | 2.2 | 1.1 | 1.6 | 2.3 | 72.4 | 2.4 | 1.1 | 1.4 | 25.4 |
| G23 | 2028.7 | 70.5 | 2.4 | 72.8 | 131.5 | 52.3 | 1.0 | 3.2 | 1.6 | 1.0 | 2.3 | 1.1 | 1.8 | 2.5 | 70.1 | 2.8 | 1.6 | 1.1 | 23.7 |
| G24 | 2662.0 | 69.9 | 2.3 | 72.2 | 146.0 | 60.7 | 1.1 | 1.3 | 1.2 | 1.0 | 2.5 | 0.9 | 1.6 | 2.0 | 74.6 | 2.4 | 0.7 | 1.5 | 25.7 |
| G25 | 2473.3 | 72.5 | 0.8 | 73.4 | 146.1 | 63.1 | 1.1 | 1.7 | 1.1 | 1.0 | 2.1 | 1.1 | 1.7 | 2.3 | 73.9 | 2.3 | 1.2 | 1.4 | 26.2 |
| G26 | 2615.8 | 75.8 | 2.5 | 78.1 | 148.1 | 62.9 | 1.0 | 1.0 | 1.1 | 1.0 | 2.1 | 1.1 | 1.5 | 1.7 | 69.6 | 2.3 | 0.9 | 1.3 | 26.2 |
| G27 | 2934.4 | 76.7 | 1.9 | 78.6 | 158.2 | 70.4 | 1.2 | 1.8 | 1.0 | 1.0 | 2.2 | 1.1 | 1.5 | 2.3 | 74.1 | 1.9 | 0.9 | 1.3 | 26.4 |
| G28 | 2698.0 | 72.7 | 2.1 | 74.8 | 149.0 | 65.7 | 1.1 | 2.3 | 1.4 | 1.0 | 2.1 | 1.1 | 1.7 | 2.3 | 72.7 | 2.1 | 0.7 | 0.9 | 25.1 |

**Appendix 10 continued**

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| G29 | 2270.6 | 76.8 | 1.6 | 78.3 | 145.5 | 60.1 | 1.0 | 1.4 | 1.2 | 1.0 | 2.1 | 1.1 | 1.5 | 2.3 | 71.7 | 2.6 | 0.8 | 1.7 | 25.4 |
| G30 | 2554.8 | 74.3 | 2.0 | 76.3 | 147.8 | 66.8 | 1.0 | 2.0 | 0.5 | 1.0 | 2.1 | 1.0 | 1.6 | 2.0 | 73.4 | 2.1 | 0.9 | 1.4 | 25.8 |
| G31 | 2037.4 | 73.0 | 2.1 | 75.1 | 140.1 | 63.4 | 1.1 | 2.4 | 1.2 | 1.0 | 2.1 | 1.1 | 1.7 | 2.3 | 68.6 | 2.5 | 1.1 | 1.3 | 23.0 |
| G32 | 2271.4 | 71.7 | 2.1 | 73.7 | 145.8 | 62.5 | 1.1 | 2.0 | 1.3 | 1.0 | 2.2 | 1.0 | 1.8 | 2.8 | 71.4 | 2.3 | 0.9 | 1.4 | 24.5 |
| G33 | 2424.7 | 71.9 | 2.1 | 74.1 | 146.9 | 63.6 | 1.1 | 2.0 | 1.3 | 1.0 | 2.0 | 1.1 | 1.6 | 1.5 | 72.0 | 2.4 | 1.0 | 1.1 | 23.3 |
| G34 | 2177.4 | 70.3 | 1.8 | 72.0 | 144.2 | 61.0 | 1.2 | 3.6 | 0.9 | 1.0 | 2.4 | 1.1 | 1.7 | 2.0 | 74.2 | 2.7 | 0.8 | 1.2 | 22.9 |
| G35 | 2303.4 | 74.3 | 2.1 | 76.3 | 146.1 | 61.1 | 1.0 | 2.6 | 1.1 | 1.0 | 2.1 | 0.9 | 1.6 | 2.5 | 75.1 | 2.5 | 0.9 | 2.3 | 27.2 |
| G36 | 2509.3 | 72.1 | 2.3 | 74.4 | 147.7 | 63.7 | 1.0 | 1.7 | 1.2 | 1.0 | 2.1 | 1.1 | 1.9 | 1.5 | 73.0 | 2.2 | 1.2 | 1.3 | 25.6 |
| G37 | 1450.0 | 71.5 | 1.8 | 73.3 | 134.9 | 51.8 | 1.1 | 1.5 | 1.0 | 1.0 | 1.9 | 1.1 | 1.6 | 2.2 | 70.1 | 2.8 | 0.7 | 0.8 | 24.9 |
| G38 | 1000.1 | 76.1 | 1.4 | 77.3 | 142.3 | 59.5 | 0.9 | 1.0 | 0.9 | 1.0 | 2.1 | 0.9 | 1.4 | 1.8 | 66.0 | 2.2 | 1.4 | 0.9 | 27.0 |
| G39 | 2518.1 | 71.4 | 1.8 | 73.3 | 137.9 | 55.3 | 1.1 | 2.1 | 1.2 | 1.0 | 2.1 | 1.1 | 1.7 | 3.0 | 74.3 | 2.4 | 0.9 | 1.5 | 26.5 |
| G40 | 1573.2 | 76.7 | 1.7 | 78.3 | 140.0 | 56.7 | 1.0 | 1.1 | 0.5 | 1.0 | 1.9 | 1.1 | 1.4 | 3.0 | 69.6 | 2.5 | 0.7 | 1.3 | 26.9 |
| G41 | 2153.2 | 67.6 | 2.0 | 69.7 | 132.4 | 51.7 | 1.0 | 2.0 | 1.1 | 0.7 | 2.0 | 1.0 | 1.8 | 2.3 | 76.1 | 2.7 | 0.8 | 1.2 | 25.0 |
| G42 | 2109.8 | 73.8 | 2.0 | 75.8 | 138.9 | 57.6 | 1.0 | 1.3 | 1.2 | 0.0 | 2.1 | 1.0 | 1.6 | 2.3 | 71.1 | 2.4 | 1.4 | 0.8 | 25.2 |
| G43 | 2632.7 | 70.4 | 3.1 | 73.4 | 146.3 | 60.1 | 1.0 | 1.7 | 0.9 | 1.0 | 2.0 | 1.0 | 1.8 | 1.7 | 69.5 | 2.5 | 0.9 | 1.4 | 26.5 |
| G44 | 2617.6 | 72.3 | 2.2 | 74.6 | 146.2 | 61.5 | 1.0 | 1.9 | 1.0 | 1.0 | 2.1 | 1.0 | 1.6 | 2.8 | 70.1 | 2.6 | 0.7 | 1.3 | 26.7 |
| G45 | 2764.9 | 75.7 | 1.9 | 77.7 | 148.6 | 64.8 | 1.0 | 1.6 | 0.9 | 1.0 | 1.9 | 1.1 | 1.6 | 2.7 | 71.5 | 2.1 | 0.8 | 1.0 | 28.2 |
| **Mean** | **2261.7** | **73.5** | **2.0** | **70.5** | **147.2** | **60.8** | **1.1** | **1.9** | **1.1** | **71.7** | **2.1** | **1.0** | **1.6** | **2.4** | **71.7** | **2.4** | **1.0** | **1.3** | **25.7** |
| **Min** | **1000.1** | **67.6** | **0.8** | **131.5** | **51.7** | **0.9** | **1.0** | **0.5** | **0.0** | **1.9** | **0.9** | **1.4** | **1.5** | **58.7** | **1.9** | **0.3** | **0.8** | **22.3** | **22.3** |
| **Max** | **2934.4** | **77.9** | **3.1** | **273.4** | **70.4** | **1.6** | **3.6** | **1.6** | **1.0** | **2.5** | **1.2** | **1.9** | **3.3** | **77.3** | **2.8** | **1.6** | **2.6** | **29.2** | **29.2** |

**Min = minimum, Max = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), ), PH = plant height (cm), EH = ear height (cm), EPP = ears per plant (#), RL = root lodging (#), SL = stem lodging (#),GLS = gray leaf spot disease (1-5), LB = leaf blight disease (1-5), MSV = maize streak virus disease (1-5), Rust = rust disease (1-5), GT = grain texture (1-5), SH = shelling percentage, VIG = vigour, RE = rotten ears (#), HC = husk cover, SWT = 100 seed weight (g), # = number..**

## Appendix 11 Genotypes used in genotype x environment interactions and stability analysis

| Genotype code | Pedigree |
|---|---|
| G1 | DT-WSTR SYNTHETIC-B |
| G2 | EVD-W 99 STR QPM CO-B |
| G3 | IAR-FLINT-Q-B |
| G4 | IWD C3 SYN F2-B |
| G5 | MULTICOB EARLY DT -B |
| G6 | SYN DTE STY-W-B |
| G7 | OBA SUPER1(9021-18(IITA))-B |
| G8 | LPHpop 9 |
| G9 | POP66 SR/DMR -LSRY/DMR-LSRY |
| G10 | POP66 SR/TZUTSR-WSGY/T |
| G11 | LPHpop 7 |
| G12 | TZE-YDT STR C4-B |
| G13 | VPO0721 |
| G14 | TZE E -WPOP X LD(SET2)-B |
| G15 | VPO5173 |
| G16 | VPO717 |
| G17 | VPO5187 |
| G18 | VPO52 |
| G19 | VPO630 |
| G20 | LPHpop 21 |
| G21 | VPO741 |
| G22 | VPO739 |
| G23 | LPHpop 18 |
| G24 | LPHpop 16 |
| G25 | VPO743 |
| G26 | VPO744 |
| G27 | LOW N POOL C3-B |
| G28 | LPHpop 10 |
| G29 | VPO76 |
| G30 | LPHpop 3 |
| G31 | LPHpop 20 |
| G32 | LPHpop 2 |
| G33 | VPO710 |
| G34 | VPO712 |
| G35 | LPHpop 8 |
| G36 | OBATANPA/TZLCOMP4C3F2/TZLCOMP4C3F2-B |
| G37 | VPO738 |
| G38 | LPHpop 13 |
| G39 | LPHpop 15 |
| G40 | VPO86 |
| G41 | VPO96 |
| G42 | VPO97 |
| G43 | ZM309 Check 1 |
| G44 | ZM523 Check 2 |
| G45 | ZM721 Check 3 |

**Appendix 12 Estimated specific combining ability effects of 12 inbred lines for grain yield and agronomic traits across low pH and optimal environments**

| Cross | Pedigree | GY | AD | ASI | DS | EH | EPP | LB | GLS | GT | MSV | PH | RL | Rust | SWT | SH% | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S12 | CZL999601/CML481 | -0.646 | 1.74 | -1.71 | 3.57 | 2.14 | -5.37 | -0.40 | -0.48 | 0.33 | 0.07 | -5.04 | 0.47 | 0.22 | -0.25 | -0.76 | -0.72 | 0.00 |
| S13 | CZL999601/CML359 | -0.148 | -0.18 | -1.98 | 1.38 | 3.51 | 3.08 | 0.11 | 0.86 | -0.25 | -0.11 | 5.06 | -0.80 | 0.44 | 1.76 | -4.32 | -0.68 | -0.30 |
| S14 | CZL999601/CML144 | 0.943 | 2.14 | -0.62 | 2.54 | 2.66 | -4.24 | -0.50 | -0.04 | 0.40 | -0.01 | 0.81 | -0.20 | 0.03 | 3.53 | -5.75 | 1.20 | -0.30 |
| S15 | CZL999601/CML161 | -0.13 | -0.57 | -1.20 | 1.13 | -0.74 | 2.61 | -0.20 | -0.07 | -0.16 | -0.11 | -3.89 | -0.10 | 0.09 | 0.05 | -6.84 | -0.28 | -0.10 |
| S16 | CZL999601/CML172 | -0.449 | -1.87 | 1.26 | -1.86 | 0.78 | 2.84 | -0.10 | 0.18 | 0.10 | -0.05 | 3.17 | -0.80 | -0.18 | -2.09 | 41*** | 0.24 | 0.10 |
| S17 | CZL999601/CML448 | -0.097 | -2.54 | -0.45 | -1.17 | 4.05 | -4.36 | 0.82 | 0.16 | 0.23 | 0.02 | 6.48 | -0.50 | 0.07 | -0.54 | -3.28 | 0.16 | 0.99 |
| S18 | CZL999601/CML312 | 0.401 | -1.61 | 0.99 | -2.47 | -6.67 | -1.62 | -0.10 | 0.06 | -0.29 | 0.03 | -1.25 | 0.87 | -0.46 | -0.23 | 2.73 | 0.48 | 0.05 |
| S19 | CZL999601/CZL130-23 | 0.212 | 0.61 | 1.15 | -0.28 | -0.63 | 0.04 | -0.20 | -0.10 | -0.35 | -0.02 | -0.94 | 0.89 | -0.06 | -0.52 | -1.11 | 0.41 | -0.70 |
| S110 | CZL999601/CML288 | -0.361 | 0.37 | 0.95 | -2.40 | -0.92 | 2.66 | 0.69 | 0.15 | 0.37 | -0.01 | -3.07 | 0.36 | 0.01 | -2.47 | -9.89 | -0.22 | 0.47 |
| S111 | CZL999601/CML202 | 0.668 | -0.16 | -0.97 | 0.66 | -4.62 | 1.74 | -0.10 | -0.61 | -0.09 | 0.11 | -5.65 | 0.03 | 0.14 | 2.48 | -1.08 | -0.18 | 0.30 |
| S23 | CML481/CML359 | -0.387 | 0.32 | 0.10 | -0.07 | -0.71 | 2.29 | 0.65 | 0.21 | 0.23 | -0.07 | 0.22 | -1.30 | 0.17 | -3.67 | 2.34 | 2.38 | 0.60 |
| S24 | CML481/CML144 | -0.316 | 0.65 | -1.17 | 1.90 | 0.21 | -4.37 | 0.88 | -0.35 | 0.04 | -0.03 | 0.86 | 1.72 | 0.21 | -1.48 | 10.49 | 0.15 | 0.18 |
| S25 | CML481/CML161 | 0.487 | -2.44 | -0.75 | -1.37 | -2.68 | 4.74 | 0.06 | -0.11 | -0.09 | 0.04 | 1.21 | 1.71 | -0.07 | -1.61 | -3.99 | 0.11 | 0.30 |
| S26 | CML481/CML172 | -0.219 | 0.18 | 1.79 | -0.59 | -2.86 | 4.14 | -0.10 | -0.13 | -0.03 | -0.07 | -1.19 | -1.20 | -0.12 | -3.49 | -6.57 | -0.59 | 0.85 |
| S27 | CML481/CML448 | 0.403 | 2.14 | -0.46 | 1.28 | -6.09 | -4.51 | -0.50 | 0.06 | 0.38 | 0.00 | -16.8 | 2.82 | 0.13 | 1.37 | 7.76 | -0.34 | -0.60 |
| S28 | CML481/CML312 | -0.079 | 2.44 | 1.16 | 1.53 | -1.31 | -1.56 | 0.24 | 0.24 | -0.04 | 0.12 | -3.39 | -1.50 | -0.01 | -0.15 | -7.11 | 0.54 | -0.10 |
| S29 | CML481/CZL130-23 | 0.595 | -0.41 | 2.57 | -2.02 | 3.59 | 3.75 | -0.30 | 0.08 | -0.84 | 0.02 | 11.30 | -0.30 | -0.17 | 3.69 | -2.41 | -0.43 | -0.60 |
| S210 | CML481/CML288 | 0.703 | -2.18 | -1.97 | -1.07 | 4.27 | 0.47 | -0.60 | 0.16 | -0.10 | -0.14 | 7.43 | -1.60 | -0.28 | 3.19 | 1.55 | -0.61 | -0.50 |
| S211 | CML481/CML202 | -0.3 | -0.84 | -1.89 | 1.58 | 0.80 | 3.20 | 0.02 | 0.24 | 0.32 | 0.04 | -0.09 | -0.60 | 0.15 | -0.93 | 6.21 | -0.23 | -0.20 |
| S34 | CML359/CML144 | -0.593 | 1.96 | -2.34 | 5.21 | -2.52 | -3.54 | -0.20 | -0.40 | 0.00 | -0.15 | -1.07 | -0.60 | -0.07 | -0.79 | 6.07 | -0.59 | 0.62 |
| S35 | CML359/CML161 | 0.189 | 0.43 | 0.03 | 0.36 | 6.07 | -2.01 | -0.30 | 0.13 | -0.19 | -0.25 | 5.18 | -0.70 | -0.01 | 5.57 | -2.19 | 0.03 | -0.20 |
| S36 | CML359/CML172 | 0.404 | 0.82 | 0.85 | -0.85 | -3.31 | -1.38 | -0.50 | 0.04 | -0.42 | -0.20 | -5.69 | -0.20 | -0.11 | 2.14 | -7.08 | -0.22 | -0.50 |
| S37 | CML359/CML448 | 0.236 | 2.42 | 0.32 | 1.48 | -2.98 | 3.30 | 0.38 | -0.26 | 0.06 | 0.04 | -7.54 | 1.31 | -0.09 | -2.64 | 7.71 | -0.19 | 0.10 |

**Appendix 12 continued**

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S38 | CML359/CML312 | 0.012 | -1.50 | 0.20 | -2.05 | 6.58 | -0.35 | 0.44 | 0.30 | -0.18 | -0.06 | 6.24 | -1.40 | 0.05 | -1.27 | -1.26 | -0.42 | -0.10 |
| S39 | CML359/CZL130-23 | -0.032 | 0.78 | -1.53 | 0.37 | 3.20 | 1.97 | -0.20 | -0.46 | -0.24 | 0.01 | 3.66 | -0.40 | -0.22 | -2.15 | 2.12 | -0.50 | 0.04 |
| S310 | CML359/CML288 | 0.144 | -6.71 | 3.90 | -5.26 | -6.93 | 1.77 | -0.30 | -0.41 | 0.91 | 0.92 | 0.69 | 0.19 | -0.02 | -2.59 | -4.89 | 0.27 | -0.10 |
| S311 | CML359/CML202 | -0.249 | -0.47 | -0.10 | -0.77 | -0.86 | -3.04 | 0.05 | 0.19 | 0.20 | -0.08 | -2.13 | 0.03 | 0.04 | -0.62 | -0.16 | -0.19 | -0.40 |
| S45 | CML144/CML161 | -0.234 | -1.63 | -2.90 | 0.34 | 4.24 | -1.81 | 0.09 | 0.51 | 0.08 | 0.07 | -2.76 | -0.80 | 0.08 | -0.77 | -0.35 | 0.02 | 0.15 |
| S46 | CML144/CML172 | -0.218 | -1.94 | -0.42 | -1.42 | -5.95 | 3.23 | -0.20 | -0.47 | 0.26 | -0.10 | -2.22 | -0.20 | -0.30 | 1.19 | -5.11 | -0.01 | 0.28 |
| S47 | CML144/CML448 | -0.156 | -2.53 | -2.04 | -0.36 | -5.21 | 3.55 | 0.56 | 0.01 | 0.03 | 0.14 | -7.19 | -1.10 | 0.11 | -1.29 | 6.61 | -0.20 | 0.26 |
| S48 | CML144/CML312 | 0.431 | -1.71 | 1.01 | -2.99 | 2.33 | -0.65 | -0.30 | -0.37 | -0.44 | -0.07 | 0.66 | 2.19 | 0.14 | 3.51 | -0.84 | -0.10 | -0.30 |
| S49 | CML144/ZL130-23 | -0.475 | 3.80 | 2.79 | 0.85 | -6.46 | 1.10 | -0.10 | -0.03 | -0.67 | 0.00 | -13.0 | 1.09 | -0.13 | -1.89 | -8.34 | -0.18 | -0.10 |
| S410 | CML144/CML288 | 0.208 | -1.12 | -0.31 | -0.88 | -0.11 | -3.61 | -0.10 | 0.55 | 0.25 | 0.17 | -6.27 | 2.35 | 0.22 | -1.86 | -3.25 | -0.14 | -0.30 |
| S411 | CML144/CML202 | 0.731 | -1.30 | 2.60 | -4.03 | 7.70 | 7.40 | -0.20 | 0.62 | -0.16 | 0.01 | 18.64 | -0.30 | -0.44 | 3.00 | 0.15 | -0.26 | -0.30 |
| S56 | CML161/CML172 | 0.671 | 0.43 | 0.29 | -0.63 | 0.46 | -0.44 | -0.30 | 0.28 | 0.12 | 0.47 | -4.05 | 1.41 | -0.19 | 0.26 | 2.91 | 0.06 | -0.50 |
| S57 | CML161/CML448 | -0.359 | -0.93 | 0.00 | -0.15 | -6.13 | -1.99 | 0.29 | -0.52 | 0.03 | -0.13 | 2.43 | -1.70 | -0.39 | 1.24 | -2.43 | -0.24 | 0.64 |
| S58 | CML161/CML312 | -0.12 | 0.40 | 1.43 | -0.99 | -8.88 | 0.63 | 0.18 | -0.01 | -0.17 | 0.22 | -11.0 | 0.28 | -0.14 | 0.30 | 2.04 | -0.36 | 0.19 |
| S59 | CML161/CZL130-23 | 0.094 | -2.56 | -1.92 | -1.41 | 2.94 | -2.72 | 0.31 | 0.17 | -0.78 | -0.16 | 4.70 | -0.60 | -0.02 | -3.97 | 4.02 | 0.67 | -0.20 |
| S510 | CML161/CML288 | -0.557 | 4.03 | 4.14 | 0.90 | -6.64 | -2.65 | -0.40 | -0.14 | -0.52 | -0.27 | -2.01 | -1.20 | 0.06 | 2.53 | 8.84 | 0.38 | 0.11 |
| S511 | CML161/CML202 | -0.558 | 1.41 | 0.86 | 0.20 | 4.13 | 3.99 | 0.00 | -0.12 | 2.5*** | -0.09 | -0.89 | 0.11 | 0.35 | -4.81 | -8.44 | -0.13 | -0.10 |
| S67 | CML172/CML448 | -0.185 | -1.34 | -0.68 | -1.45 | -0.41 | -2.13 | 0.16 | 0.01 | 0.50 | -0.02 | 6.91 | 3.29 | 0.51 | -0.25 | -15.15 | 0.40 | -0.10 |
| S68 | CML172/CML312 | -0.301 | 0.57 | -0.26 | 0.30 | 1.31 | 0.76 | 0.77 | 0.02 | 0.17 | -0.12 | -0.73 | 0.32 | 0.15 | -0.41 | 2.33 | -0.51 | 0.24 |
| S69 | CML172/CZL130-23 | 0.521 | -0.89 | -1.03 | 0.46 | 2.25 | -2.58 | -0.20 | 0.64 | -0.10 | 0.23 | 5.94 | -0.80 | 0.33 | 2.40 | 1.80 | 0.08 | 0.13 |
| S610 | CML172/CML288 | -0.107 | 1.54 | -0.04 | 2.03 | 7.96 | -2.56 | -0.30 | -0.22 | -0.29 | -0.05 | 8.02 | -0.40 | -0.05 | 1.04 | -0.67 | 0.46 | -0.50 |
| S611 | CML172/CML202 | -0.013 | 1.59 | -0.10 | 1.27 | -4.40 | -1.29 | 0.83 | -0.43 | -0.08 | -0.03 | -7.51 | 0.31 | -0.08 | -2.44 | -9.69 | 0.06 | 0.58 |
| S78 | CML448/CML312 | 0.225 | -1.04 | -1.79 | 0.78 | -0.07 | -0.95 | -0.50 | 0.16 | 0.16 | -0.04 | 0.09 | -0.80 | 0.12 | 1.21 | -0.48 | -0.03 | -0.40 |
| S79 | CML448/CZL130-23 | 0.13 | 0.25 | 0.60 | -0.14 | -4.27 | -4.33 | 0.00 | -0.11 | -0.49 | 0.08 | -1.35 | 0.12 | -0.49 | 5.04 | 7.08 | 0.12 | -0.40 |
| S710 | CML448/CML288 | -0.06 | 3.53 | 1.27 | 1.06 | 12.49 | 16.6*** | -0.40 | -0.09 | 0.13 | -0.14 | 13.18 | -1.00 | 0.03 | -0.50 | -12.54 | 0.27 | -0.20 |
| S711 | CML448/CML202 | 0.039 | 1.99 | 3.10 | -1.62 | 8.12 | -2.87 | -0.50 | 0.38 | -0.75 | 0.04 | 12.83 | -0.50 | 0.16 | 1.22 | 0.83 | -0.13 | 0.00 |
| S89 | CML312/CZL130-23 | -0.161 | -1.09 | -2.88 | 1.94 | 3.81 | 5.02 | -0.20 | 0.34 | 2.2*** | 0.04 | 4.26 | -0.80 | 0.32 | -0.81 | -4.94 | -0.01 | -0.30 |
| S810 | CML312/CML288 | -0.233 | 3.09 | 2.21 | 0.73 | -2.63 | -1.53 | 0.41 | -0.41 | 0.06 | -0.13 | -6.77 | -0.60 | -0.05 | -4.23 | 0.89 | -0.19 | -0.30 |

**Appendix 12 continued**

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S811 | CML312/CML202 | 0.145 | 2.06 | 0.62 | 2.00 | 1.79 | -0.30 | -0.60 | -0.44 | -0.76 | 0.00 | 3.61 | -1.20 | 0.02 | 5.8** | 2.21 | 0.52 | -0.10 |
| S910 | CZL130-23/CML288 | -0.254 | -0.79 | -3.50 | 2.16 | 5.32 | -4.91 | 0.59 | -0.34 | -0.53 | -0.17 | -0.65 | 0.90 | 0.35 | 1.55 | 7.76 | 0.07 | 1.08 |
| S911 | CZL130-23/CML202 | -0.65 | 1.10 | 1.94 | 0.24 | -3.31 | -3.71 | 0.34 | -0.10 | -0.95 | 0.01 | -5.54 | 1.15 | -0.30 | 2.71 | 3.13 | -0.11 | 0.24 |
| S112 | CZL999601/CML539 | -0.393 | 2.07 | 2.58 | -1.09 | 0.43 | 2.62 | -0.10 | -0.11 | -0.29 | 0.07 | 4.32 | -0.30 | -0.29 | -1.72 | -10.72 | -0.41 | -0.40 |
| S212 | CML481/CML539 | -0.241 | -1.60 | 2.33 | -4.75 | 2.65 | -2.79 | 0.03 | 0.08 | -0.18 | 0.00 | 5.53 | -0.50 | -0.23 | 3.32 | -7.50 | -0.25 | 0.07 |
| S312 | CML359/CML539 | 0.422 | 2.12 | 0.54 | 0.20 | -2.05 | -2.09 | -0.20 | -0.19 | -0.12 | -0.07 | -4.61 | 1.75 | -0.17 | 4.25 | 1.66 | 0.12 | 0.18 |
| S412 | CML144/CML539 | -0.322 | 1.66 | 3.39 | -1.16 | 3.10 | 2.94 | 0.20 | -0.04 | 0.21 | -0.03 | 11.57 | -0.90 | 0.14 | -3.13 | 0.34 | 0.10 | -0.20 |
| S512 | CML161/CML539 | 0.518 | 1.41 | 0.03 | 1.61 | 7.23 | -0.36 | 0.30 | -0.12 | -0.83 | 0.21 | 11.10 | 1.11 | 0.26 | 1.20 | 6.42 | -0.26 | -0.30 |
| S612 | CML172/CML539 | -0.105 | 0.92 | -1.66 | 2.73 | 4.17 | -0.59 | -0.10 | 0.08 | -0.23 | -0.07 | -2.64 | -2.60 | 0.04 | 1.65 | -3.79 | 0.04 | -0.60 |
| S712 | CML448/CML539 | -0.176 | -1.94 | 0.14 | 0.29 | 0.50 | -2.32 | -0.30 | 0.22 | -0.29 | 0.00 | -9.00 | -0.20 | -0.16 | -4.86 | 3.89 | 0.19 | -0.30 |
| S812 | CML312/CML539 | -0.32 | -1.62 | -2.68 | 1.21 | 3.74 | 0.54 | -0.20 | 0.12 | -0.70 | 0.01 | 8.29 | 2.32 | -0.13 | -3.76 | 4.45 | 0.06 | 1.04 |
| S912 | ZL130-23/CML539 | 0.019 | -0.79 | 1.82 | -2.17 | -6.44 | 6.37 | 0.06 | -0.09 | 2.8*** | -0.03 | -8.34 | -1.00 | 0.38 | -6.05 | -9.11 | -0.13 | 0.76 |
| S1011 | CML288/CML202 | 0.053 | -2.46 | -3.12 | 0.05 | -4.41 | -3.54 | 0.19 | 0.48 | -0.09 | -0.05 | -3.79 | 0.17 | -0.23 | -6.1** | 2.35 | -0.07 | 0.36 |
| S1012 | CML288/CML539 | 0.465 | 0.69 | -3.55 | 2.68 | -8.39 | -2.73 | 0.24 | 0.27 | -0.17 | -0.14 | -6.75 | 0.17 | -0.05 | 9. *** | 9.86 | -0.20 | 0.00 |
| S1112 | CML202/CML539 | 0.165 | -3.70 | -1.41 | 0.06 | -8.15 | -3.56 | 0.20 | 0.25 | 0.08 | 0.03 | -13.1 | 1.50 | 0.42 | 1.81 | 2.36 | 1.24 | -0.30 |

**GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour, # = number.**

**Appendix 13 Mean performance of diallel cross progeny across optimal and low pH environments in 2011/12**

| | Pedigree | GY | AD | ASI | DS | EH | LB | EPP | GLS | GT | MSV | PH | RL | Rust | SWT | SH% | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | CZL999601/CML481 | 3809 | 69.0 | 0.0 | 69.0 | 91.1 | 1.5 | 1.0 | 1.2 | 1.8 | 1.2 | 163.5 | 6.0 | 1.2 | 33.2 | 80.0 | 0.7 | 2.0 |
| 2 | CZL999601/CML359 | 5210 | 73.0 | 0.3 | 73.3 | 82.7 | 2.0 | 1.0 | 2.7 | 2.3 | 1.0 | 178.1 | 5.7 | 1.8 | 38.0 | 82.7 | 0.3 | 2.0 |
| 3 | CZL999601/CML144 | 6955 | 74.0 | 0.7 | 74.7 | 89.4 | 1.0 | 1.2 | 1.8 | 2.8 | 1.0 | 173.3 | 3.0 | 1.2 | 42.7 | 81.9 | 4.7 | 1.0 |
| 4 | CZL999601/CML161 | 3740 | 74.0 | 2.0 | 76.0 | 102.8 | 2.3 | 1.0 | 1.0 | 2.0 | 1.0 | 195.9 | 4.3 | 1.2 | 38.4 | 79.1 | 0.0 | 2.2 |
| 5 | CZL999601/CML172 | 3624 | 69.0 | 1.0 | 70.0 | 94.3 | 2.3 | 1.0 | 2.3 | 2.2 | 1.0 | 189.5 | 6.7 | 1.0 | 31.2 | 87.7 | 2.3 | 2.2 |
| 6 | CZL999601/CML448 | 2663 | 70.0 | 2.0 | 72.0 | 89.3 | 4.0 | 1.0 | 1.0 | 2.2 | 1.0 | 174.0 | 3.0 | 1.0 | 33.1 | 80.5 | 2.0 | 3.8 |
| 7 | CZL999601/CML312 | 4024 | 69.3 | 0.7 | 70.0 | 92.7 | 1.5 | 1.0 | 1.2 | 2.0 | 1.0 | 195.2 | 5.0 | 1.2 | 35.5 | 86.5 | 2.7 | 2.7 |
| 8 | CZL999601/ZL130-23 | 5099 | 72.0 | 0.0 | 72.0 | 95.6 | 1.5 | 1.2 | 1.2 | 1.8 | 1.0 | 191.7 | 8.3 | 1.0 | 36.3 | 83.9 | 2.3 | 1.0 |
| 9 | CZL999601/CML288 | 3779 | 74.0 | 0.0 | 74.0 | 90.6 | 3.7 | 1.1 | 1.0 | 2.3 | 1.0 | 169.4 | 10.3 | 1.2 | 36.8 | 83.4 | 0.7 | 2.8 |
| 10 | CZL999601/CML202 | 5386 | 74.0 | 1.0 | 75.0 | 71.3 | 2.0 | 1.0 | 1.0 | 2.3 | 1.2 | 163.8 | 3.7 | 1.0 | 38.6 | 85.3 | 1.0 | 2.3 |
| 11 | CZL999601/CML539 | 3939 | 72.0 | 0.7 | 72.7 | 92.3 | 1.7 | 1.0 | 1.0 | 2.0 | 1.2 | 180.3 | 4.0 | 1.0 | 33.3 | 77.3 | 0.0 | 1.0 |
| 12 | CML481/CML359 | 3128 | 71.7 | 0.7 | 72.3 | 99.2 | 3.2 | 1.0 | 1.3 | 2.3 | 1.2 | 188.0 | 4.7 | 1.5 | 31.7 | 85.0 | 9.3 | 2.8 |
| 13 | CML481/CML144 | 3628 | 74.0 | 1.3 | 75.3 | 96.4 | 3.7 | 1.1 | 1.0 | 1.8 | 1.0 | 179.9 | 1.3 | 1.0 | 28.8 | 79.1 | 3.3 | 2.3 |
| 14 | CML481/CML161 | 3566 | 70.0 | 2.0 | 72.0 | 89.2 | 2.3 | 1.2 | 1.0 | 2.2 | 1.5 | 177.8 | 7.3 | 1.0 | 28.0 | 84.0 | 2.7 | 2.7 |
| 15 | CML481/CML172 | 2349 | 67.3 | 1.0 | 68.3 | 100.6 | 3.3 | 1.0 | 1.2 | 2.0 | 1.0 | 184.8 | 12.0 | 1.0 | 25.2 | 81.9 | 0.3 | 3.0 |
| 16 | CML481/CML448 | 4976 | 76.0 | 0.3 | 76.3 | 70.8 | 1.3 | 1.0 | 1.0 | 2.3 | 1.0 | 124.2 | 1.3 | 1.2 | 38.2 | 79.9 | 1.0 | 1.3 |
| 17 | CML481/CML312 | 2509 | 75.3 | 0.7 | 76.0 | 82.2 | 3.8 | 1.0 | 1.0 | 1.8 | 1.5 | 180.0 | 16.0 | 1.2 | 28.2 | 81.8 | 3.7 | 2.3 |
| 18 | CML481/ZL130-23 | 3612 | 73.3 | 2.3 | 75.7 | 90.8 | 1.7 | 1.1 | 1.2 | 2.2 | 1.0 | 188.0 | 2.0 | 1.0 | 45.2 | 83.6 | 0.3 | 1.0 |
| 19 | CML481/CML288 | 4676 | 72.0 | 0.3 | 72.3 | 92.0 | 1.5 | 1.0 | 1.3 | 2.2 | 1.0 | 181.8 | 5.7 | 1.0 | 43.8 | 86.8 | 0.7 | 1.2 |
| 20 | CML481/CML202 | 2702 | 72.0 | 1.7 | 73.7 | 90.5 | 2.2 | 1.2 | 1.8 | 2.7 | 1.0 | 171.5 | 1.7 | 1.2 | 33.8 | 87.4 | 0.3 | 1.7 |
| 21 | CML481/CML539 | 2509 | 70.0 | 0.7 | 70.7 | 79.3 | 2.0 | 1.0 | 1.0 | 2.3 | 1.0 | 175.6 | 5.7 | 1.0 | 34.9 | 82.3 | 0.7 | 1.7 |
| 22 | CML359/CML144 | 2484 | 72.0 | 2.0 | 74.0 | 90.9 | 1.5 | 1.0 | 1.0 | 2.0 | 1.0 | 190.7 | 2.7 | 1.0 | 34.8 | 80.9 | 0.3 | 2.8 |
| 23 | CML359/CML161 | 2535 | 73.0 | 2.3 | 75.3 | 96.5 | 1.7 | 1.0 | 1.2 | 2.5 | 1.0 | 188.7 | 2.0 | 1.2 | 42.2 | 70.8 | 0.3 | 2.0 |
| 24 | CML359/CML172 | 4640 | 73.3 | 2.7 | 76.0 | 81.1 | 1.3 | 1.3 | 1.3 | 1.8 | 1.0 | 168.9 | 5.0 | 1.0 | 37.5 | 78.3 | 1.7 | 1.0 |
| 25 | CML359/CML448 | 3073 | 76.0 | 0.0 | 76.0 | 93.4 | 3.0 | 1.0 | 1.0 | 2.2 | 1.5 | 185.9 | 2.7 | 1.0 | 39.2 | 82.7 | 1.3 | 2.3 |
| 26 | CML359/CML312 | 2344 | 69.0 | 2.7 | 71.7 | 84.3 | 3.2 | 1.2 | 1.5 | 2.3 | 1.0 | 180.0 | 10.7 | 1.0 | 25.3 | 82.5 | 1.0 | 2.3 |
| 27 | CML359/ZL130-23 | 2722 | 74.0 | 0.0 | 74.0 | 109.7 | 1.3 | 1.0 | 1.0 | 2.5 | 1.2 | 197.3 | 1.7 | 1.0 | 32.9 | 74.7 | 0.3 | 2.8 |
| 28 | CML359/CML288 | 3621 | 70.0 | 2.0 | 72.0 | 81.8 | 1.5 | 1.0 | 1.2 | 1.8 | 1.2 | 173.2 | 3.7 | 1.0 | 38.0 | 81.4 | 1.7 | 2.0 |

**Appendix 13 continued**

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 29 | CML359/CML202 | 3170 | 70.3 | 1.7 | 72.0 | 108.6 | 2.0 | 1.0 | 2.2 | 2.0 | 1.0 | 194.3 | 3.7 | 1.0 | 39.7 | 81.7 | 0.3 | 1.2 |
| 30 | CML359/CML539 | 3353 | 76.0 | 2.0 | 78.0 | 97.4 | 1.5 | 1.0 | 1.2 | 2.2 | 1.2 | 188.6 | 10.0 | 1.0 | 34.0 | 77.6 | 1.3 | 1.8 |
| 31 | CML144/CML161 | 2142 | 71.0 | 0.0 | 71.0 | 101.0 | 2.0 | 1.0 | 1.7 | 2.7 | 1.0 | 187.7 | 4.3 | 1.0 | 32.5 | 83.1 | 0.7 | 2.3 |
| 32 | CML144/CML172 | 2379 | 70.0 | 1.0 | 71.0 | 94.3 | 1.7 | 1.1 | 1.0 | 2.2 | 1.0 | 184.5 | 3.0 | 1.2 | 37.4 | 90.1 | 1.3 | 2.8 |
| 33 | CML144/CML448 | 2513 | 71.3 | 0.3 | 71.7 | 74.1 | 2.3 | 1.0 | 1.7 | 2.0 | 1.5 | 151.3 | 2.0 | 1.0 | 31.8 | 86.3 | 0.0 | 2.3 |
| 34 | CML144/CML312 | 3280 | 74.0 | 0.3 | 74.3 | 86.8 | 1.7 | 1.0 | 1.0 | 2.2 | 1.0 | 172.0 | 2.7 | 1.3 | 46.4 | 83.1 | 0.7 | 2.3 |
| 35 | CML144/ZL130-23 | 1835 | 76.0 | 0.7 | 76.7 | 95.8 | 1.5 | 1.2 | 1.0 | 1.7 | 1.2 | 174.3 | 10.0 | 1.2 | 33.7 | 74.5 | 0.0 | 2.2 |
| 36 | CML144/CML288 | 3210 | 70.0 | 2.0 | 72.0 | 88.5 | 1.7 | 1.1 | 2.3 | 2.5 | 1.0 | 178.6 | 7.3 | 1.8 | 31.5 | 87.2 | 1.0 | 1.5 |
| 37 | CML144/CML202 | 4172 | 70.0 | 1.0 | 71.0 | 91.0 | 1.5 | 1.1 | 2.3 | 2.3 | 1.0 | 184.3 | 5.7 | 1.0 | 38.0 | 83.4 | 0.3 | 1.2 |
| 38 | CML144/CML539 | 2513 | 70.0 | 1.7 | 71.7 | 94.7 | 1.7 | 1.1 | 1.0 | 2.0 | 1.0 | 183.4 | 2.0 | 1.0 | 31.9 | 83.8 | 1.3 | 1.2 |
| 39 | CML161/CML172 | 5026 | 75.0 | 1.3 | 76.3 | 98.1 | 1.2 | 1.0 | 1.3 | 2.7 | 1.0 | 194.8 | 4.0 | 1.0 | 40.7 | 83.8 | 0.3 | 1.0 |
| 40 | CML161/CML448 | 757 | 72.0 | 3.7 | 75.7 | 88.1 | 4.3 | 0.9 | 1.0 | 2.2 | 1.0 | 177.9 | 8.0 | 1.0 | 27.9 | 70.0 | 0.0 | 4.5 |
| 41 | CML161/CML312 | 1805 | 72.0 | 0.3 | 72.3 | 85.5 | 1.3 | 1.0 | 1.0 | 2.5 | 1.2 | 170.7 | 2.3 | 1.2 | 29.8 | 75.1 | 0.3 | 3.0 |
| 42 | CML161/ZL130-23 | 2652 | 75.3 | 0.7 | 76.0 | 85.7 | 2.7 | 1.0 | 1.5 | 1.8 | 1.0 | 167.3 | 3.7 | 1.0 | 28.6 | 80.7 | 0.7 | 1.8 |
| 43 | CML161/CML288 | 1381 | 74.0 | 0.7 | 74.7 | 84.3 | 1.3 | 1.0 | 1.0 | 2.2 | 1.0 | 180.2 | 3.0 | 1.0 | 29.5 | 79.4 | 0.0 | 3.5 |
| 44 | CML161/CML202 | 1556 | 76.0 | 0.7 | 76.7 | 122.2 | 2.7 | 1.1 | 1.0 | 2.0 | 1.0 | 216.9 | 1.0 | 1.0 | 31.5 | 72.5 | 0.3 | 2.8 |
| 45 | CML161/CML539 | 4713 | 74.0 | 2.0 | 76.0 | 88.2 | 1.5 | 1.1 | 1.0 | 1.8 | 1.0 | 174.1 | 9.7 | 1.2 | 34.0 | 82.3 | 0.0 | 2.3 |
| 46 | CML172/CML448 | 2514 | 69.3 | 0.7 | 70.0 | 85.9 | 2.8 | 1.1 | 1.0 | 1.8 | 1.2 | 179.9 | 12.3 | 1.2 | 29.7 | 74.3 | 0.3 | 1.5 |
| 47 | CML172/CML312 | 2365 | 69.7 | 1.3 | 71.0 | 65.2 | 4.0 | 1.0 | 2.0 | 2.7 | 1.0 | 162.9 | 9.0 | 1.0 | 28.9 | 82.7 | 0.3 | 3.7 |
| 48 | CML172/ZL130-23 | 5218 | 74.0 | 2.0 | 76.0 | 85.9 | 2.0 | 1.1 | 1.3 | 2.3 | 1.0 | 180.4 | 5.0 | 1.5 | 37.0 | 80.7 | 1.3 | 2.0 |
| 49 | CML172/CML288 | 3251 | 74.0 | 0.7 | 74.7 | 81.8 | 1.5 | 1.1 | 1.2 | 1.8 | 1.5 | 169.4 | 6.3 | 1.2 | 37.9 | 79.5 | 0.7 | 1.8 |
| 50 | CML172/CML202 | 3649 | 76.0 | 1.3 | 77.3 | 104.2 | 3.2 | 1.0 | 1.5 | 2.2 | 1.0 | 194.3 | 5.3 | 1.2 | 29.0 | 81.4 | 1.3 | 2.8 |
| 51 | CML172/CML539 | 2775 | 78.0 | 2.0 | 80.0 | 95.0 | 1.3 | 1.0 | 1.0 | 2.0 | 1.0 | 173.3 | 0.3 | 1.0 | 45.7 | 77.6 | 0.3 | 1.3 |
| 52 | CML448/CML312 | 2448 | 75.7 | 1.7 | 77.3 | 95.0 | 1.5 | 0.9 | 1.0 | 2.5 | 1.0 | 192.3 | 4.3 | 1.0 | 39.7 | 68.2 | 1.3 | 2.7 |
| 53 | CML448/ZL130-23 | 2882 | 74.0 | 2.0 | 76.0 | 109.2 | 2.0 | 1.0 | 1.2 | 1.7 | 1.3 | 199.4 | 2.7 | 1.2 | 42.6 | 80.2 | 0.0 | 1.2 |
| 54 | CML448/CML288 | 2732 | 78.0 | 0.7 | 78.7 | 104.0 | 1.5 | 1.1 | 1.7 | 2.7 | 1.0 | 191.2 | 3.3 | 1.0 | 39.0 | 84.9 | 0.7 | 1.7 |
| 55 | CML448/CML202 | 2239 | 77.0 | 0.0 | 77.0 | 92.9 | 1.5 | 1.1 | 1.0 | 2.2 | 1.0 | 186.3 | 2.7 | 1.0 | 31.7 | 75.6 | 0.3 | 2.8 |
| 56 | CML448/CML539 | 3243 | 69.0 | 3.7 | 72.7 | 93.6 | 2.0 | 1.1 | 1.0 | 1.7 | 1.0 | 182.0 | 5.3 | 1.0 | 44.8 | 84.9 | 0.3 | 2.2 |
| 57 | CML312/ZL130-23 | 2448 | 76.3 | 1.0 | 77.3 | 86.9 | 1.7 | 1.1 | 1.0 | 3.0 | 1.3 | 178.4 | 5.3 | 1.0 | 32.0 | 79.4 | 0.3 | 2.8 |

## Appendix 13

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 58 | CML312/CML288 | 3737 | 69.0 | 3.0 | 72.0 | 111.3 | 2.3 | 1.0 | 1.2 | 2.2 | 1.2 | 187.1 | 6.0 | 1.2 | 33.7 | 87.6 | 0.0 | 1.8 |
| 59 | CML312/CML202 | 3820 | 72.0 | 0.7 | 72.7 | 97.6 | 1.5 | 1.0 | 1.0 | 2.5 | 1.0 | 182.5 | 1.0 | 1.0 | 42.2 | 86.4 | 1.0 | 2.0 |
| 60 | CML312/CML539 | 1622 | 69.0 | 1.3 | 70.3 | 84.0 | 2.5 | 1.0 | 1.2 | 2.2 | 1.2 | 172.7 | 10.3 | 1.0 | 27.7 | 75.2 | 0.7 | 4.2 |
| 61 | ZL130-23/CML288 | 1456 | 74.0 | 0.0 | 74.0 | 104.8 | 3.8 | 1.0 | 1.3 | 1.7 | 1.0 | 190.3 | 8.0 | 1.3 | 24.5 | 77.0 | 0.0 | 4.2 |
| 62 | ZL130-23/CML202 | 2323 | 74.3 | 1.7 | 76.0 | 106.2 | 1.3 | 1.1 | 1.0 | 1.5 | 1.0 | 194.7 | 4.7 | 1.0 | 33.8 | 80.6 | 0.3 | 2.3 |
| 63 | ZL130-23/CML539 | 2792 | 72.0 | 0.7 | 72.7 | 89.0 | 2.3 | 1.0 | 1.0 | 2.5 | 1.0 | 170.9 | 2.0 | 1.0 | 28.3 | 78.7 | 0.3 | 3.2 |
| 64 | CML288/CML202 | 2653 | 69.7 | 0.7 | 70.3 | 90.7 | 2.7 | 1.3 | 2.7 | 2.2 | 1.2 | 186.3 | 2.7 | 1.0 | 25.4 | 80.9 | 0.7 | 2.7 |
| 65 | CML288/CML539 | 3677 | 75.7 | 0.3 | 76.0 | 83.4 | 1.7 | 1.1 | 1.5 | 2.3 | 1.0 | 181.0 | 2.3 | 1.0 | 48.9 | 81.4 | 0.3 | 1.7 |
| 66 | CML202/CML539 | 3942 | 71.0 | 0.7 | 71.7 | 102.9 | 1.3 | 1.3 | 1.0 | 1.8 | 1.0 | 193.2 | 3.0 | 1.3 | 34.7 | 82.1 | 3.0 | 1.0 |
| 67 | MH27 | 4744 | 74.7 | 1.3 | 76.0 | 86.9 | 1.0 | 1.1 | 1.0 | 2.0 | 1.0 | 192.3 | 5.7 | 1.0 | 34.2 | 77 | 0.7 | 1.3 |
| 68 | MH26 | 6018 | 74.3 | 1.7 | 76.0 | 111.3 | 1.0 | 1.0 | 1.2 | 2.0 | 1.0 | 199.4 | 7.0 | 1.0 | 41.2 | 83 | 0.0 | 1.2 |
| | **Mean** | **3205.2** | **72.6** | **1.2** | **73.8** | **92.0** | **2.1** | **1.1** | **1.3** | **2.2** | **1.1** | **180.9** | **5.0** | **1.1** | **34.9** | **81.0** | **1.0** | **2.2** |
| | **LSD** | **1650** | **0.8** | **1.4** | **1.3** | **328.2** | **0.8** | **0.2** | **0.5** | **0.8** | **0.4** | **38.7** | **6.7** | **1.1** | **10.2** | **10.5** | **3.8** | **1.1** |
| | **MSE** | **4E+06** | **0.3** | **0.8** | **0.6** | **29.3** | **0.3** | **0.0** | **0.1** | **0.3** | **0.1** | **574.1** | **17.2** | **0.5** | **39.5** | **42.3** | **5.6** | **0.5** |
| | **P** | **0.001** | **0.001** | **0.00** | **0** | **0.63** | **0.0** | **0.17** | **0** | **0.4** | **0.2** | **0.75** | **0.00** | **0.08** | **0.001** | **0.05** | **0.35** | **0** |
| | **CV (%)** | **31.9** | **0.7** | **74.7** | **0.8** | **19.7** | **24.3** | **12.4** | **22.8** | **23.7** | **21.3** | **13.2** | **82.9** | **0.2** | **18.0** | **8.0** | **230.1** | **30.8** |

**LSD = Least significant difference, MSE = Mean square error, CV = coefficient of variation, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), LB = leaf blight disease (1-5), EPP = ears per plant (#), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour, # = number.**

**Appendix 14 Mean performances of diallel cross progenies across three low pH environments in 2012**

| | Pedigree | GY | AD | ASI | DS | EH | EPP | LB | GLS | GT | MSV | PH | RL | RUST | SWT | SH% | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | CZL999601/CML481 | 894 | 83.4 | 2.9 | 86.3 | 46.8 | 0.5 | 2.3 | 1.3 | 2.2 | 1.0 | 110 | 0.5 | 2.4 | 22.7 | 62.0 | 2.2 | 4.3 |
| 2 | CZL999601/CML359 | 678 | 79.3 | 3.1 | 82.4 | 47.3 | 0.5 | 2.3 | 2.5 | 1.5 | 1.0 | 117 | 0.7 | 2.5 | 27.0 | 66.4 | 1.8 | 4.0 |
| 3 | CZL999601/CML144 | 853 | 82.7 | 2.6 | 85.2 | 46.1 | 0.4 | 1.3 | 1.7 | 2.2 | 1.0 | 111 | 0.7 | 2.2 | 18.4 | 68.2 | 1.3 | 5.0 |
| 4 | CZL999601/CML161 | 657 | 79.2 | 2.4 | 81.7 | 38.3 | 0.5 | 2.0 | 2.0 | 2.1 | 1.0 | 97 | 0.5 | 2.3 | 23.6 | 78.5 | 1.8 | 4.7 |
| 5 | CZL999601/CML172 | 787 | 78.8 | 3.8 | 82.6 | 42.5 | 0.7 | 2.3 | 1.9 | 2.2 | 1.0 | 108 | 0.7 | 2.2 | 24.6 | 74.0 | 1.3 | 4.7 |
| 6 | CZL999601/CML448 | 953 | 77.4 | 3.0 | 80.4 | 43.8 | 0.5 | 2.7 | 2.1 | 2.6 | 1.0 | 113 | 0.5 | 2.3 | 18.9 | 73.6 | 1.0 | 5.0 |
| 7 | CZL999601/CML312 | 867 | 81.2 | 3.0 | 84.2 | 30.2 | 0.5 | 2.7 | 2.1 | 1.9 | 1.1 | 97 | 0.8 | 1.7 | 20.9 | 65.8 | 1.8 | 4.7 |
| 8 | CZL999601/ZL130-23 | 945 | 82.9 | 3.1 | 86.0 | 41.5 | 0.5 | 2.3 | 1.8 | 2.1 | 1.0 | 104 | 0.5 | 2.3 | 24.0 | 70.2 | 1.5 | 4.3 |
| 9 | CZL999601/CML288 | 821 | 79.6 | 2.2 | 81.8 | 37.5 | 0.5 | 2.7 | 2.5 | 2.3 | 1.2 | 102 | 0.5 | 2.0 | 23.5 | 65.4 | 1.0 | 5.0 |
| 10 | CZL999601/CML202 | 971 | 79.6 | 2.6 | 82.1 | 40.4 | 0.5 | 2.3 | 1.3 | 1.9 | 1.0 | 104 | 0.5 | 2.6 | 20.4 | 69.5 | 2.3 | 5.0 |
| 11 | CZL999601/CML539 | 664 | 83.9 | 2.4 | 86.3 | 35.6 | 0.6 | 2.3 | 1.6 | 1.8 | 1.0 | 105 | 0.7 | 1.9 | 22.7 | 61.7 | 2.0 | 4.7 |
| 12 | CML481/CML359 | 631 | 80.4 | 3.7 | 84.1 | 37.1 | 0.5 | 3.0 | 2.1 | 2.3 | 1.0 | 106 | 0.8 | 2.1 | 16.3 | 59.0 | 2.2 | 4.7 |
| 13 | CML481/CML144 | 670 | 80.8 | 2.7 | 83.4 | 40.7 | 0.5 | 3.0 | 1.5 | 1.6 | 1.0 | 107 | 0.5 | 2.3 | 22.8 | 73.0 | 1.3 | 4.3 |
| 14 | CML481/CML161 | 835 | 78.7 | 2.4 | 81.1 | 39.5 | 0.5 | 3.0 | 1.8 | 1.7 | 1.0 | 105 | 0.5 | 1.9 | 20.5 | 73.4 | 3.0 | 4.7 |
| 15 | CML481/CML172 | 695 | 82.4 | 3.9 | 86.3 | 34.9 | 0.4 | 1.3 | 1.9 | 2.1 | 1.0 | 98 | 0.5 | 2.1 | 20.9 | 58.2 | 1.8 | 5.0 |
| 16 | CML481/CML448 | 752 | 81.8 | 2.1 | 83.9 | 38.6 | 0.5 | 1.7 | 1.8 | 2.2 | 1.0 | 99 | 0.5 | 2.2 | 23.4 | 66.2 | 1.5 | 4.0 |
| 17 | CML481/CML312 | 651 | 84.1 | 3.0 | 87.1 | 39.9 | 0.4 | 1.7 | 2.3 | 2.6 | 1.0 | 110 | 0.5 | 2.2 | 19.7 | 59.5 | 1.8 | 4.3 |
| 18 | CML481/ZL130-23 | 958 | 83.0 | 3.2 | 86.2 | 44.4 | 0.5 | 2.0 | 2.0 | 1.9 | 1.1 | 110 | 0.5 | 2.0 | 17.2 | 65.0 | 1.5 | 4.3 |
| 19 | CML481/CML288 | 999 | 77.8 | 3.0 | 80.8 | 47.8 | 0.5 | 1.3 | 2.3 | 1.7 | 1.0 | 113 | 0.5 | 1.6 | 21.6 | 66.8 | 1.5 | 4.3 |
| 20 | CML481/CML202 | 872 | 79.3 | 2.9 | 82.2 | 43.6 | 0.6 | 2.7 | 2.1 | 2.1 | 1.0 | 111 | 0.5 | 2.3 | 23.0 | 73.4 | 1.2 | 4.3 |
| 21 | CML481/CML539 | 721 | 80.6 | 2.8 | 83.3 | 41.6 | 0.5 | 2.7 | 1.8 | 2.3 | 1.0 | 105 | 0.7 | 1.8 | 21.0 | 56.3 | 1.3 | 4.7 |
| 22 | CML359/CML144 | 643 | 82.1 | 3.8 | 85.9 | 41.5 | 0.5 | 1.0 | 1.4 | 1.7 | 1.0 | 110 | 0.5 | 2.0 | 21.3 | 61.6 | 1.0 | 5.0 |
| 23 | CML359/CML161 | 686 | 80.3 | 3.0 | 83.3 | 50.7 | 0.4 | 1.7 | 2.1 | 2.1 | 1.0 | 115 | 0.5 | 2.0 | 23.9 | 62.4 | 2.2 | 4.7 |
| 24 | CML359/CML172 | 628 | 81.0 | 2.7 | 83.7 | 41.5 | 0.7 | 1.3 | 2.1 | 1.9 | 1.0 | 104 | 0.5 | 2.2 | 18.8 | 62.2 | 0.5 | 4.7 |
| 25 | CML359/CML448 | 1008 | 81.9 | 3.4 | 85.3 | 32.6 | 0.8 | 1.7 | 1.3 | 2.2 | 1.0 | 93 | 0.5 | 2.0 | 21.8 | 70.3 | 1.3 | 4.7 |
| 26 | CML359/CML312 | 685 | 81.3 | 3.3 | 84.7 | 47.8 | 0.8 | 2.0 | 2.2 | 2.2 | 1.2 | 113 | 0.7 | 2.4 | 19.9 | 65.1 | 0.8 | 4.7 |
| 27 | CML359/ZL130-23 | 815 | 81.9 | 2.7 | 84.6 | 43.1 | 0.6 | 2.0 | 1.3 | 2.2 | 1.2 | 112 | 0.5 | 2.0 | 20.6 | 66.5 | 0.5 | 4.0 |
| 28 | CML359/CML288 | 638 | 81.6 | 2.3 | 84.5 | 35.0 | 0.7 | 1.0 | 1.6 | 1.8 | 3.5 | 99 | 0.8 | 2.3 | 20.8 | 58.4 | 1.6 | 4.7 |

**Appendix 14 continued**

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 29 | CML359/CML202 | 569 | 79.8 | 3.2 | 83.0 | 35.4 | 0.5 | 2.0 | 1.8 | 2.6 | 1.0 | 105 | 0.7 | 2.3 | 16.9 | 53.7 | 1.7 | 4.7 |
| 30 | CML359/CML539 | 804 | 82.3 | 2.4 | 84.8 | 30.8 | 0.5 | 1.7 | 1.3 | 2.1 | 1.0 | 93 | 0.7 | 2.0 | 22.1 | 72.3 | 1.7 | 5.0 |
| 31 | CML144/CML161 | 704 | 78.7 | 2.3 | 81.0 | 47.6 | 0.5 | 2.3 | 2.5 | 2.0 | 1.3 | 102 | 0.5 | 2.2 | 26.7 | 64.8 | 1.2 | 5.0 |
| 32 | CML144/CML172 | 821 | 78.7 | 3.2 | 81.9 | 34.6 | 0.6 | 1.7 | 1.6 | 2.0 | 1.0 | 100 | 0.5 | 1.8 | 26.8 | 64.4 | 1.3 | 4.3 |
| 33 | CML144/CML448 | 825 | 77.6 | 3.2 | 80.8 | 38.2 | 0.5 | 2.7 | 1.5 | 1.8 | 1.0 | 103 | 0.5 | 2.3 | 27.5 | 72.2 | 1.7 | 5.0 |
| 34 | CML144/CML312 | 725 | 80.6 | 3.0 | 83.6 | 41.5 | 0.6 | 1.0 | 1.5 | 1.8 | 1.0 | 102 | 0.5 | 2.3 | 21.5 | 74.7 | 1.5 | 4.3 |
| 35 | CML144/ZL130-23 | 827 | 85.7 | 2.8 | 88.4 | 38.0 | 0.5 | 1.7 | 2.0 | 1.7 | 1.0 | 102 | 0.5 | 2.0 | 21.0 | 83.2 | 1.8 | 4.3 |
| 36 | CML144/CML288 | 712 | 79.7 | 2.8 | 82.4 | 39.4 | 0.5 | 1.3 | 2.2 | 1.7 | 1.0 | 102 | 0.5 | 2.1 | 20.0 | 63.6 | 1.7 | 4.7 |
| 37 | CML144/CML202 | 736 | 81.6 | 3.1 | 84.7 | 44.7 | 0.4 | 1.3 | 2.3 | 1.7 | 1.0 | 114 | 0.5 | 1.9 | 26.2 | 72.3 | 3.2 | 5.0 |
| 38 | CML144/CML539 | 821 | 82.8 | 2.8 | 85.6 | 43.0 | 0.6 | 2.3 | 1.6 | 2.4 | 1.0 | 121 | 0.8 | 2.3 | 22.3 | 70.9 | 1.3 | 4.3 |
| 39 | CML161/CML172 | 773 | 80.3 | 2.3 | 82.7 | 44.3 | 0.5 | 3.0 | 2.5 | 2.3 | 2.0 | 95 | 0.5 | 2.0 | 22.5 | 71.2 | 2.0 | 5.0 |
| 40 | CML161/CML448 | 608 | 79.3 | 2.3 | 81.7 | 34.3 | 0.7 | 1.0 | 1.0 | 2.4 | 1.0 | 107 | 0.5 | 1.5 | 27.2 | 57.9 | 1.0 | 4.0 |
| 41 | CML161/CML312 | 435 | 83.0 | 3.0 | 86.0 | 33.3 | 0.4 | 4.0 | 2.0 | 2.3 | 1.5 | 94 | 0.5 | 2.0 | 22.2 | 65.2 | 0.5 | 5.0 |
| 42 | CML161/ZL130-23 | 581 | 78.0 | 2.3 | 80.3 | 51.0 | 0.5 | 3.0 | 2.0 | 1.9 | 1.0 | 116 | 1.0 | 2.3 | 18.0 | 80.5 | 2.5 | 5.0 |
| 43 | CML161/CML288 | 487 | 84.7 | 3.7 | 88.3 | 36.1 | 0.6 | 2.0 | 2.0 | 1.6 | 1.0 | 105 | 0.5 | 2.0 | 27.6 | 61.0 | 2.5 | 4.0 |
| 44 | CML161/CML202 | 458 | 80.7 | 2.3 | 83.0 | 46.4 | 0.6 | 2.0 | 2.0 | 2.3 | 1.0 | 106 | 0.5 | 2.8 | 20.5 | 57.5 | 0.5 | 4.0 |
| 45 | CML161/CML539 | 594 | 82.7 | 2.7 | 85.3 | 50.1 | 0.8 | 4.0 | 1.5 | 1.6 | 1.5 | 117 | 0.5 | 2.5 | 22.2 | 68.9 | 0.5 | 4.0 |
| 46 | CML172/CML448 | 464 | 79.3 | 2.7 | 82.0 | 44.1 | 0.4 | 2.0 | 2.0 | 2.6 | 1.0 | 114 | 1.0 | 3.0 | 25.6 | 35.9 | 3.0 | 5.0 |
| 47 | CML172/CML312 | 468 | 83.7 | 2.7 | 86.3 | 55.0 | 0.6 | 3.0 | 1.8 | 2.2 | 1.0 | 112 | 0.5 | 2.8 | 23.8 | 72.8 | 1.0 | 4.0 |
| 48 | CML172/ZL130-23 | 811 | 80.3 | 3.0 | 83.3 | 51.4 | 0.7 | 2.0 | 3.0 | 2.4 | 1.5 | 115 | 0.5 | 2.8 | 25.1 | 70.1 | 0.5 | 5.0 |
| 49 | CML172/CML288 | 636 | 81.0 | 3.7 | 84.7 | 57.7 | 0.6 | 2.0 | 2.0 | 1.6 | 1.0 | 123 | 0.5 | 2.0 | 22.8 | 64.3 | 2.0 | 4.0 |
| 50 | CML172/CML202 | 478 | 81.0 | 2.7 | 83.7 | 35.6 | 0.5 | 4.0 | 1.5 | 2.0 | 1.0 | 95 | 0.5 | 2.3 | 20.0 | 50.0 | 1.5 | 5.0 |
| 51 | CML172/CML539 | 896 | 80.3 | 3.0 | 83.3 | 45.0 | 0.6 | 3.0 | 2.0 | 2.1 | 1.0 | 100 | 0.5 | 2.5 | 20.3 | 65.4 | 1.0 | 4.0 |
| 52 | CML448/CML312 | 509 | 79.3 | 2.7 | 82.0 | 38.7 | 0.4 | 1.0 | 2.0 | 2.4 | 1.0 | 101 | 0.5 | 2.5 | 21.0 | 62.5 | 0.5 | 4.0 |
| 53 | CML448/ZL130-23 | 554 | 81.7 | 2.7 | 84.3 | 30.3 | 0.5 | 2.0 | 1.5 | 2.0 | 1.0 | 97 | 1.0 | 1.5 | 25.5 | 64.9 | 2.0 | 5.0 |
| 54 | CML448/CML288 | 373 | 83.0 | 2.7 | 85.7 | 47.3 | 0.4 | 1.0 | 1.5 | 1.9 | 1.0 | 112 | 0.5 | 2.0 | 32.4 | 69.8 | 1.0 | 5.0 |
| 55 | CML448/CML202 | 508 | 81.3 | 3.3 | 84.7 | 44.8 | 0.5 | 1.0 | 2.5 | 1.0 | 1.0 | 110 | 0.5 | 2.5 | 23.8 | 67.3 | 0.5 | 4.0 |
| 56 | CML448/CML539 | 426 | 79.3 | 3.7 | 83.0 | 36.0 | 0.5 | 1.0 | 1.8 | 1.9 | 1.0 | 87 | 0.5 | 2.0 | 12.7 | 62.5 | 1.0 | 4.0 |
| 57 | CML312/ZL130-23 | 472 | 81.0 | 3.0 | 84.0 | 50.3 | 0.6 | 2.0 | 2.5 | 1.6 | 1.0 | 114 | 1.0 | 3.0 | 25.0 | 63.0 | 0.5 | 4.0 |

**Appendix 14 continued**

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 58 | CML312/CML288 | 360 | 85.0 | 2.3 | 87.3 | 38.3 | 0.7 | 3.0 | 1.5 | 2.2 | 1.0 | 103 | 1.0 | 2.0 | 17.1 | 61.4 | 1.0 | 5.0 |
| 59 | CML312/CML202 | 589 | 84.7 | 3.3 | 88.0 | 43.4 | 0.5 | 1.0 | 1.5 | 1.4 | 1.0 | 115 | 0.5 | 2.5 | 26.2 | 61.1 | 2.5 | 5.0 |
| 60 | CML312/CML539 | 583 | 81.7 | 3.0 | 84.7 | 45.3 | 0.6 | 1.0 | 1.8 | 1.6 | 1.0 | 116 | 0.5 | 2.3 | 17.6 | 70.6 | 3.5 | 5.0 |
| 61 | ZL130-23/CML288 | 824 | 79.7 | 3.0 | 82.7 | 45.7 | 0.4 | 2.0 | 1.5 | 1.9 | 1.0 | 105 | 1.0 | 2.5 | 28.7 | 67.8 | 1.5 | 5.0 |
| 62 | ZL130-23/CML202 | 266 | 82.7 | 3.3 | 86.0 | 35.7 | 0.6 | 4.0 | 2.0 | 1.6 | 1.0 | 98 | 0.5 | 2.0 | 25.0 | 61.6 | 2.5 | 5.0 |
| 63 | ZL130-23/CML539 | 799 | 81.0 | 3.3 | 84.3 | 39.0 | 0.5 | 2.0 | 1.5 | 2.9 | 1.0 | 104 | 0.5 | 3.0 | 20.2 | 58.9 | 1.5 | 5.0 |
| 64 | CML288/CML202 | 1041 | 77.7 | 2.7 | 80.3 | 34.1 | 0.4 | 2.0 | 2.3 | 1.5 | 1.0 | 101 | 0.5 | 1.8 | 16.5 | 65.6 | 2.5 | 5.0 |
| 65 | CML288/CML539 | 829 | 80.0 | 2.3 | 82.3 | 28.7 | 0.4 | 3.0 | 2.0 | 1.9 | 1.0 | 95 | 0.5 | 2.0 | 27.4 | 70.7 | 3.5 | 5.0 |
| 66 | CML202/CML539 | 847 | 77.3 | 3.3 | 80.7 | 28.7 | 0.4 | 3.0 | 1.5 | 2.2 | 1.0 | 88 | 0.5 | 2.5 | 17.9 | 64.6 | 2.0 | 5.0 |
| 67 | MH27 | 639.5 | 77.7 | 1.3 | 79.0 | 57.0 | 1.0 | 1.7 | 2.0 | 2.0 | 1.0 | 166.3 | 0.0 | 1.0 | 33.6 | 59.9 | 2.2 | 5.0 |
| 68 | MH26 | 879.3 | 78.7 | 1.0 | 79.7 | 65.0 | 1.0 | 1.3 | 2.0 | 2.0 | 1.3 | 171.0 | 0.0 | 1.7 | 29.9 | 63.2 | 3.5 | 4.5 |
| | **Mean** | **701.6** | **80.9** | **2.9** | **83.8** | **41.7** | **0.5** | **2.1** | **1.9** | **2.0** | **1.1** | **107** | **0.6** | **2.2** | **22.5** | **65.6** | **1.6** | **4.6** |
| | **LSD** | **293.3** | **3.1** | **0.7** | **0.4** | **12.6** | **0.3** | **0.5** | **0.8** | **0.8** | **0.7** | **19.3** | **0.3** | **0.7** | **6.9** | **57.8** | **1.6** | **0.6** |
| | **MSE** | **1001** | **3.7** | **0.5** | **4.0** | **61.4** | **0.0** | **0.2** | **0.2** | **0.3** | **0.2** | **145** | **0.0** | **0.2** | **18.3** | **1295.** | **1.0** | **0.1** |
| | **P** | **0.001** | **0.00** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.001** | **0.005** | **0.001** | **0.001** |
| | **CV (%)** | **45.2** | **2.4** | **24.6** | **2.4** | **19.0** | **39.3** | **26.9** | **0.5** | **26.0** | **42.5** | **11.4** | **36.4** | **19.4** | **19.0** | **52.1** | **63.8** | **7.7** |

**LSD = Least significant difference, MSE = Mean square error, CV = coefficient of variation, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour, # = number.**

## Appendix 15 Mean performance of the diallel cross progenies under optimal conditions in 2011/12

| | Pedigree | GY | AD | ASI | DS | EH | LB | EPP | GLS | GT | MSV | PH | RL | RUST | SWT | SH% | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | CZL999601/CML481 | 3809 | 69.0 | 0.0 | 69.0 | 91.1 | 1.5 | 1.0 | 1.2 | 1.8 | 1.2 | 163.5 | 6.0 | 1.2 | 33.2 | 80.0 | 0.7 | 2.0 |
| 2 | CZL999601/CML359 | 5210 | 73.0 | 0.3 | 73.3 | 82.7 | 2.0 | 1.0 | 2.7 | 2.3 | 1.0 | 178.1 | 5.7 | 1.8 | 38.0 | 82.7 | 0.3 | 2.0 |
| 3 | CZL999601/CML144 | 6955 | 74.0 | 0.7 | 74.7 | 89.4 | 1.0 | 1.2 | 1.8 | 2.8 | 1.0 | 173.3 | 3.0 | 1.2 | 42.7 | 81.9 | 4.7 | 1.0 |
| 4 | CZL999601/CML161 | 3740 | 74.0 | 2.0 | 76.0 | 102.8 | 2.3 | 1.0 | 1.0 | 2.0 | 1.0 | 195.9 | 4.3 | 1.2 | 38.4 | 79.1 | 0.0 | 2.2 |
| 5 | CZL999601/CML172 | 3624 | 69.0 | 1.0 | 70.0 | 94.3 | 2.3 | 1.0 | 2.3 | 2.2 | 1.0 | 189.5 | 6.7 | 1.0 | 31.2 | 87.7 | 2.3 | 2.2 |
| 6 | CZL999601/CML448 | 2663 | 70.0 | 2.0 | 72.0 | 89.3 | 4.0 | 1.0 | 1.0 | 2.2 | 1.0 | 174.0 | 3.0 | 1.0 | 33.1 | 80.5 | 2.0 | 3.8 |
| 7 | CZL999601/CML312 | 4024 | 69.3 | 0.7 | 70.0 | 92.7 | 1.5 | 1.0 | 1.2 | 2.0 | 1.0 | 195.2 | 5.0 | 1.2 | 35.5 | 86.5 | 2.7 | 2.7 |
| 8 | CZL999601/ZL130-23 | 5099 | 72.0 | 0.0 | 72.0 | 95.6 | 1.5 | 1.2 | 1.2 | 1.8 | 1.0 | 191.7 | 8.3 | 1.0 | 36.3 | 83.9 | 2.3 | 1.0 |
| 9 | CZL999601/CML288 | 3779 | 74.0 | 0.0 | 74.0 | 90.6 | 3.7 | 1.1 | 1.0 | 2.3 | 1.0 | 169.4 | 10.3 | 1.2 | 36.8 | 83.4 | 0.7 | 2.8 |
| 10 | CZL999601/CML202 | 5386 | 74.0 | 1.0 | 75.0 | 71.3 | 2.0 | 1.0 | 1.0 | 2.3 | 1.2 | 163.8 | 3.7 | 1.0 | 38.6 | 85.3 | 1.0 | 2.3 |
| 11 | CZL999601/CML539 | 3939 | 72.0 | 0.7 | 72.7 | 92.3 | 1.7 | 1.0 | 1.0 | 2.0 | 1.2 | 180.3 | 4.0 | 1.0 | 33.3 | 77.3 | 0.0 | 1.0 |
| 12 | CML481/CML359 | 3128 | 71.7 | 0.7 | 72.3 | 99.2 | 3.2 | 1.0 | 1.3 | 2.3 | 1.2 | 188.0 | 4.7 | 1.5 | 31.7 | 85.0 | 9.3 | 2.8 |
| 13 | CML481/CML144 | 3628 | 74.0 | 1.3 | 75.3 | 96.4 | 3.7 | 1.1 | 1.0 | 1.8 | 1.0 | 179.9 | 1.3 | 1.0 | 28.8 | 79.1 | 3.3 | 2.3 |
| 14 | CML481/CML161 | 3566 | 70.0 | 2.0 | 72.0 | 89.2 | 2.3 | 1.2 | 1.0 | 2.2 | 1.5 | 177.8 | 7.3 | 1.0 | 28.0 | 84.0 | 2.7 | 2.7 |
| 15 | CML481/CML172 | 2349 | 67.3 | 1.0 | 68.3 | 100.6 | 3.3 | 1.0 | 1.2 | 2.0 | 1.0 | 184.8 | 12.0 | 1.0 | 25.2 | 81.9 | 0.3 | 3.0 |
| 16 | CML481/CML448 | 4976 | 76.0 | 0.3 | 76.3 | 70.8 | 1.3 | 1.0 | 1.0 | 2.3 | 1.0 | 124.2 | 1.3 | 1.2 | 38.2 | 79.9 | 1.0 | 1.3 |
| 17 | CML481/CML312 | 2509 | 75.3 | 0.7 | 76.0 | 82.2 | 3.8 | 1.0 | 1.0 | 1.8 | 1.5 | 180.0 | 16.0 | 1.2 | 28.2 | 81.8 | 3.7 | 2.3 |
| 18 | CML481/ZL130-23 | 3612 | 73.3 | 2.3 | 75.7 | 90.8 | 1.7 | 1.1 | 1.2 | 2.2 | 1.0 | 188.0 | 2.0 | 1.0 | 45.2 | 83.6 | 0.3 | 1.0 |
| 19 | CML481/CML288 | 4676 | 72.0 | 0.3 | 72.3 | 92.0 | 1.5 | 1.0 | 1.3 | 2.2 | 1.0 | 181.8 | 5.7 | 1.0 | 43.8 | 86.8 | 0.7 | 1.2 |
| 20 | CML481/CML202 | 2702 | 72.0 | 1.7 | 73.7 | 90.5 | 2.2 | 1.2 | 1.8 | 2.7 | 1.0 | 171.5 | 1.7 | 1.2 | 33.8 | 87.4 | 0.3 | 1.7 |
| 21 | CML481/CML539 | 2509 | 70.0 | 0.7 | 70.7 | 79.3 | 2.0 | 1.0 | 1.0 | 2.3 | 1.0 | 175.6 | 5.7 | 1.0 | 34.9 | 82.3 | 0.7 | 1.7 |
| 22 | CML359/CML144 | 2484 | 72.0 | 2.0 | 74.0 | 90.9 | 1.5 | 1.0 | 1.0 | 2.0 | 1.0 | 190.7 | 2.7 | 1.0 | 34.8 | 80.9 | 0.3 | 2.8 |
| 23 | CML359/CML161 | 2535 | 73.0 | 2.3 | 75.3 | 96.5 | 1.7 | 1.0 | 1.2 | 2.5 | 1.0 | 188.7 | 2.0 | 1.2 | 42.2 | 70.8 | 0.3 | 2.0 |
| 24 | CML359/CML172 | 4640 | 73.3 | 2.7 | 76.0 | 81.1 | 1.3 | 1.3 | 1.3 | 1.8 | 1.0 | 168.9 | 5.0 | 1.0 | 37.5 | 78.3 | 1.7 | 1.0 |
| 25 | CML359/CML448 | 3073 | 76.0 | 0.0 | 76.0 | 93.4 | 3.0 | 1.0 | 1.0 | 2.2 | 1.5 | 185.9 | 2.7 | 1.0 | 39.2 | 82.7 | 1.3 | 2.3 |
| 26 | CML359/CML312 | 2344 | 69.0 | 2.7 | 71.7 | 84.3 | 3.2 | 1.2 | 1.5 | 2.3 | 1.0 | 180.0 | 10.7 | 1.0 | 25.3 | 82.5 | 1.0 | 2.3 |
| 27 | CML359/ZL130-23 | 2722 | 74.0 | 0.0 | 74.0 | 109.7 | 1.3 | 1.0 | 1.0 | 2.5 | 1.2 | 197.3 | 1.7 | 1.0 | 32.9 | 74.7 | 0.3 | 2.8 |
| 28 | CML359/CML288 | 3621 | 70.0 | 2.0 | 72.0 | 81.8 | 1.5 | 1.0 | 1.2 | 1.8 | 1.2 | 173.2 | 3.7 | 1.0 | 38.0 | 81.4 | 1.7 | 2.0 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 29 | CML359/CML202 | 3170 | 70.3 | 1.7 | 72.0 | 108.6 | 2.0 | 1.0 | 2.2 | 2.0 | 1.0 | 194.3 | 3.7 | 1.0 | 39.7 | 81.7 | 0.3 | 1.2 |
| 30 | CML359/CML539 | 3353 | 76.0 | 2.0 | 78.0 | 97.4 | 1.5 | 1.0 | 1.2 | 2.2 | 1.2 | 188.6 | 10.0 | 1.0 | 34.0 | 77.6 | 1.3 | 1.8 |
| 31 | CML144/CML161 | 2142 | 71.0 | 0.0 | 71.0 | 101.0 | 2.0 | 1.0 | 1.7 | 2.7 | 1.0 | 187.7 | 4.3 | 1.0 | 32.5 | 83.1 | 0.7 | 2.3 |
| 32 | CML144/CML172 | 2379 | 70.0 | 1.0 | 71.0 | 94.3 | 1.7 | 1.1 | 1.0 | 2.2 | 1.0 | 184.5 | 3.0 | 1.2 | 37.4 | 90.1 | 1.3 | 2.8 |
| 33 | CML144/CML448 | 2513 | 71.3 | 0.3 | 71.7 | 74.1 | 2.3 | 1.0 | 1.7 | 2.0 | 1.5 | 151.3 | 2.0 | 1.0 | 31.8 | 86.3 | 0.0 | 2.3 |
| 34 | CML144/CML312 | 3280 | 74.0 | 0.3 | 74.3 | 86.8 | 1.7 | 1.0 | 1.0 | 2.2 | 1.0 | 172.0 | 2.7 | 1.3 | 46.4 | 83.1 | 0.7 | 2.3 |
| 35 | CML144/ZL130-23 | 1835 | 76.0 | 0.7 | 76.7 | 95.8 | 1.5 | 1.2 | 1.0 | 1.7 | 1.2 | 174.3 | 10.0 | 1.2 | 33.7 | 74.5 | 0.0 | 2.2 |
| 36 | CML144/CML288 | 3210 | 70.0 | 2.0 | 72.0 | 88.5 | 1.7 | 1.1 | 2.3 | 2.5 | 1.0 | 178.6 | 7.3 | 1.8 | 31.5 | 87.2 | 1.0 | 1.5 |
| 37 | CML144/CML202 | 4172 | 70.0 | 1.0 | 71.0 | 91.0 | 1.5 | 1.1 | 2.3 | 2.3 | 1.0 | 184.3 | 5.7 | 1.0 | 38.0 | 83.4 | 0.3 | 1.2 |
| 38 | CML144/CML539 | 2513 | 70.0 | 1.7 | 71.7 | 94.7 | 1.7 | 1.1 | 1.0 | 2.0 | 1.0 | 183.4 | 2.0 | 1.0 | 31.9 | 83.8 | 1.3 | 1.2 |
| 39 | CML161/CML172 | 5026 | 75.0 | 1.3 | 76.3 | 98.1 | 1.2 | 1.0 | 1.3 | 2.7 | 1.0 | 194.8 | 4.0 | 1.0 | 40.7 | 83.8 | 0.3 | 1.0 |
| 40 | CML161/CML448 | 757 | 72.0 | 3.7 | 75.7 | 88.1 | 4.3 | 0.9 | 1.0 | 2.2 | 1.0 | 177.9 | 8.0 | 1.0 | 27.9 | 70.0 | 0.0 | 4.5 |
| 41 | CML161/CML312 | 1805 | 72.0 | 0.3 | 72.3 | 85.5 | 1.3 | 1.0 | 1.0 | 2.5 | 1.2 | 170.7 | 2.3 | 1.2 | 29.8 | 75.1 | 0.3 | 3.0 |
| 42 | CML161/ZL130-23 | 2652 | 75.3 | 0.7 | 76.0 | 85.7 | 2.7 | 1.0 | 1.5 | 1.8 | 1.0 | 167.3 | 3.7 | 1.0 | 28.6 | 80.7 | 0.7 | 1.8 |
| 43 | CML161/CML288 | 1381 | 74.0 | 0.7 | 74.7 | 84.3 | 1.3 | 1.0 | 1.0 | 2.2 | 1.0 | 180.2 | 3.0 | 1.0 | 29.5 | 79.4 | 0.0 | 3.5 |
| 44 | CML161/CML202 | 1556 | 76.0 | 0.7 | 76.7 | 122.2 | 2.7 | 1.1 | 1.0 | 2.0 | 1.0 | 216.9 | 1.0 | 1.0 | 31.5 | 72.5 | 0.3 | 2.8 |
| 45 | CML161/CML539 | 4713 | 74.0 | 2.0 | 76.0 | 88.2 | 1.5 | 1.1 | 1.0 | 1.8 | 1.0 | 174.1 | 9.7 | 1.2 | 34.0 | 82.3 | 0.0 | 2.3 |
| 46 | CML172/CML448 | 2514 | 69.3 | 0.7 | 70.0 | 85.9 | 2.8 | 1.1 | 1.0 | 1.8 | 1.2 | 179.9 | 12.3 | 1.2 | 29.7 | 74.3 | 0.3 | 1.5 |
| 47 | CML172/CML312 | 2365 | 69.7 | 1.3 | 71.0 | 65.2 | 4.0 | 1.0 | 2.0 | 2.7 | 1.0 | 162.9 | 9.0 | 1.0 | 28.9 | 82.7 | 0.3 | 3.7 |
| 48 | CML172/ZL130-23 | 5218 | 74.0 | 2.0 | 76.0 | 85.9 | 2.0 | 1.1 | 1.3 | 2.3 | 1.0 | 180.4 | 5.0 | 1.5 | 37.0 | 80.7 | 1.3 | 2.0 |
| 49 | CML172/CML288 | 3251 | 74.0 | 0.7 | 74.7 | 81.8 | 1.5 | 1.1 | 1.2 | 1.8 | 1.5 | 169.4 | 6.3 | 1.2 | 37.9 | 79.5 | 0.7 | 1.8 |
| 50 | CML172/CML202 | 3649 | 76.0 | 1.3 | 77.3 | 104.2 | 3.2 | 1.0 | 1.5 | 2.2 | 1.0 | 194.3 | 5.3 | 1.2 | 29.0 | 81.4 | 1.3 | 2.8 |
| 51 | CML172/CML539 | 2775 | 78.0 | 2.0 | 80.0 | 95.0 | 1.3 | 1.0 | 1.0 | 2.0 | 1.0 | 173.3 | 0.3 | 1.0 | 45.7 | 77.6 | 0.3 | 1.3 |
| 52 | CML448/CML312 | 2448 | 75.7 | 1.7 | 77.3 | 95.0 | 1.5 | 0.9 | 1.0 | 2.5 | 1.0 | 192.3 | 4.3 | 1.0 | 39.7 | 68.2 | 1.3 | 2.7 |
| 53 | CML448/ZL130-23 | 2882 | 74.0 | 2.0 | 76.0 | 109.2 | 2.0 | 1.0 | 1.2 | 1.7 | 1.3 | 199.4 | 2.7 | 1.2 | 42.6 | 80.2 | 0.0 | 1.2 |
| 54 | CML448/CML288 | 2732 | 78.0 | 0.7 | 78.7 | 104.0 | 1.5 | 1.1 | 1.7 | 2.7 | 1.0 | 191.2 | 3.3 | 1.0 | 39.0 | 84.9 | 0.7 | 1.7 |
| 55 | CML448/CML202 | 2239 | 77.0 | 0.0 | 77.0 | 92.9 | 1.5 | 1.1 | 1.0 | 2.2 | 1.0 | 186.3 | 2.7 | 1.0 | 31.7 | 75.6 | 0.3 | 2.8 |
| 56 | CML448/CML539 | 3243 | 69.0 | 3.7 | 72.7 | 93.6 | 2.0 | 1.1 | 1.0 | 1.7 | 1.0 | 182.0 | 5.3 | 1.0 | 44.8 | 84.9 | 0.3 | 2.2 |
| 57 | CML312/ZL130-23 | 2448 | 76.3 | 1.0 | 77.3 | 86.9 | 1.7 | 1.1 | 1.0 | 3.0 | 1.3 | 178.4 | 5.3 | 1.0 | 32.0 | 79.4 | 0.3 | 2.8 |
| 58 | CML312/CML288 | 3737 | 69.0 | 3.0 | 72.0 | 111.3 | 2.3 | 1.0 | 1.2 | 2.2 | 1.2 | 187.1 | 6.0 | 1.2 | 33.7 | 87.6 | 0.0 | 1.8 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 59 | CML312/CML202 | 3820 | 72.0 | 0.7 | 72.7 | 97.6 | 1.5 | 1.0 | 1.0 | 2.5 | 1.0 | 182.5 | 1.0 | 1.0 | 42.2 | 86.4 | 1.0 | 2.0 |
| 60 | CML312/CML539 | 1622 | 69.0 | 1.3 | 70.3 | 84.0 | 2.5 | 1.0 | 1.2 | 2.2 | 1.2 | 172.7 | 10.3 | 1.0 | 27.7 | 75.2 | 0.7 | 4.2 |
| 61 | ZL130-23/CML288 | 1456 | 74.0 | 0.0 | 74.0 | 104.8 | 3.8 | 1.0 | 1.3 | 1.7 | 1.0 | 190.3 | 8.0 | 1.3 | 24.5 | 77.0 | 0.0 | 4.2 |
| 62 | ZL130-23/CML202 | 2323 | 74.3 | 1.7 | 76.0 | 106.2 | 1.3 | 1.1 | 1.0 | 1.5 | 1.0 | 194.7 | 4.7 | 1.0 | 33.8 | 80.6 | 0.3 | 2.3 |
| 63 | ZL130-23/CML539 | 2792 | 72.0 | 0.7 | 72.7 | 89.0 | 2.3 | 1.0 | 1.0 | 2.5 | 1.0 | 170.9 | 2.0 | 1.0 | 28.3 | 78.7 | 0.3 | 3.2 |
| 64 | CML288/CML202 | 2653 | 69.7 | 0.7 | 70.3 | 90.7 | 2.7 | 1.3 | 2.7 | 2.2 | 1.2 | 186.3 | 2.7 | 1.0 | 25.4 | 80.9 | 0.7 | 2.7 |
| 65 | CML288/CML539 | 3677 | 75.7 | 0.3 | 76.0 | 83.4 | 1.7 | 1.1 | 1.5 | 2.3 | 1.0 | 181.0 | 2.3 | 1.0 | 48.9 | 81.4 | 0.3 | 1.7 |
| 66 | CML202/CML539 | 3942 | 71.0 | 0.7 | 71.7 | 102.9 | 1.3 | 1.3 | 1.0 | 1.8 | 1.0 | 193.2 | 3.0 | 1.3 | 34.7 | 82.1 | 3.0 | 1.0 |
| 67 | MH27 | 4744 | 74.7 | 1.3 | 76.0 | 86.9 | 1.0 | 1.1 | 1.0 | 2.0 | 1.0 | 192.3 | 5.7 | 1.0 | 34.2 | 77 | 0.7 | 1.3 |
| 68 | MH26 | 6018 | 74.3 | 1.7 | 76.0 | 111.3 | 1.0 | 1.0 | 1.2 | 2.0 | 1.0 | 199.4 | 7.0 | 1.0 | 41.2 | 83 | 0.0 | 1.2 |
| | **Mean** | **3205.2** | **72.6** | **1.2** | **73.8** | **92.0** | **2.1** | **1.1** | **1.3** | **2.2** | **1.1** | **180.9** | **5.0** | **1.1** | **34.9** | **81.0** | 1.0 | 2.2 |
| | **LSD** | **1650** | **0.8** | **1.4** | **1.3** | **328.2** | **0.8** | **0.2** | **0.5** | **0.8** | **0.4** | **38.7** | **6.7** | **1.1** | **10.2** | **10.5** | 3.8 | 1.1 |
| | **MSE** | **4E+06** | **0.3** | **0.8** | **0.6** | **29.3** | **0.3** | **0.0** | **0.1** | **0.3** | **0.1** | **574.1** | **17.2** | **0.5** | **39.5** | **42.3** | 5.6 | 0.5 |
| | **P** | **0.001** | **0.001** | **0.001** | **0** | **0.63** | **0.0** | **0.17** | **0** | **0.36** | **0.16** | **0.75** | **0** | **0.08** | **0.001** | **0.05** | 0.35 | 0 |
| | **CV (%)** | **31.9** | **0.7** | **74.7** | **0.8** | **19.7** | **24.3** | **12.4** | **22.8** | **23.7** | **21.3** | **13.2** | **82.9** | **0.2** | **18.0** | **8.0** | 230.1 | 30.8 |
| | **SE** | **1021** | **0.5** | **0.9** | **1.1** | **18.1** | **0.5** | **0.1** | **0.3** | **0.5** | **0.2** | **24.0** | **4.2** | **25.5** | **6.3** | **6.5** | 2.4 | 0.7 |
| | **MIN** | **757.0** | **67.3** | **0.0** | **68.3** | **65.2** | **1.0** | **0.9** | **1.0** | **1.5** | **1.0** | **124.2** | **0.3** | **1.0** | **24.5** | **68.2** | 0.0 | 1.0 |
| | **MAX** | **6955.0** | **78.0** | **3.7** | **80.0** | **122.2** | **4.3** | **1.3** | **2.7** | **3.0** | **1.5** | **216.9** | **16.0** | **1.8** | **48.9** | **90.1** | 9.3 | 4.5 |

**LSD = Least significant difference, MSE = Mean square error, CV = coefficient of variation, SE = error, MIN = minimum, MAX = maximum, GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), LB = leaf blight disease (1-5), EPP = ears per plant (#), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour, # = number.**

**Appendix 16 Estimated general combining ability effects for 12 inbred lines for grain yield and agronomic traits at low pH environments in 2011/12**

| | | Name | GY | AD | ASI | DS | EH | EPP | GLS | GT | LB | MSV | PH | RL | RUST | SWT | SH% | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | G1 | CZL999601 | 0.12 | -0.07 | -0.37 | 0.13 | -0.15 | 0.30 | 0.01 | 0.01 | 0.07 | -0.06 | 1.06 | 0.02 | -0.05 | 0.95 | 7.60* | 0.05 | -0.51 |
| 2 | G2 | CML481 | 0.03 | 0.28 | 0.11 | 0.24 | 0.22 | 0.44 | 0.02 | -0.11 | 0.03 | -0.02 | 0.93 | 0.16 | -0.20 | -1.03 | -3.22 | -0.01 | -0.89 |
| 3 | G3 | CML359 | 0.03 | -0.61 | 0.16 | -0.33 | -0.85 | 1.62* | -0.08 | 0.09 | -0.04 | 0.06 | 0.25 | -0.18 | 0.37 | -1.81* | -5.18 | 0.00 | 3.16* |
| 4 | G4 | CML144 | 0.17 | 0.05 | 0.16 | -0.16 | 0.00 | -0.14 | -0.04 | -0.17 | -0.21 | -0.02 | 0.71 | -0.01 | -0.22 | 1.36 | 1.16 | -0.05 | -0.65 |
| 5 | G5 | CML161 | -0.19 | -0.31 | -0.23 | -0.69 | 2.00 | -0.75 | 0.08 | 0.05 | 0.20 | 0.19** | 0.23 | -0.08 | -0.15 | 0.92 | 0.41 | 0.05 | -0.64 |
| 6 | G6 | CML172 | -0.04 | -0.18 | -0.38 | 0.52 | 3.51* | -0.06 | 0.16 | 0.10 | 0.08 | 0.07 | 0.79 | -0.20 | 0.06 | 0.43 | 4.23 | 0.02 | -0.57 |
| 7 | G7 | CML448 | -0.09 | -0.67 | -0.52 | -0.18 | -2.28 | -0.71 | -0.16 | 0.07 | -0.32* | -0.10* | -2.10 | -0.25 | -0.11 | 1.51 | -0.20 | -0.05 | -0.67 |
| 8 | G8 | CML312 | -0.20 | 1.69** | 0.67 | 1.10 | 0.98 | -0.70 | 0.05 | 0.04 | -0.08 | -0.02 | 1.13 | -0.21 | 0.07 | -0.97 | -0.59 | 0.07 | -0.81 |
| 9 | G9 | ZL130-23 | 0.03 | 0.82 | 0.28 | 0.60 | 1.69 | 0.12 | 0.05 | 0.02 | 0.05 | 0.02 | 1.20 | 0.01 | 0.05 | 0.42 | -0.10 | -0.01 | -0.65 |
| 10 | G10 | CML288 | 0.11 | -0.90 | 0.75 | -1.86 | -0.43 | -0.11 | 0.11 | -0.09 | 0.05 | 0.03 | -0.83 | 0.21 | 0.17 | 1.39 | 0.89 | 0.06 | 3.24 |
| 11 | G11 | CML202 | 0.00 | -0.42 | -0.18 | -0.12 | -1.91 | -0.75 | 0.04 | -0.13 | 0.07 | -0.10* | -0.62 | 0.34* | 0.03 | -0.56 | -2.98 | -0.12 | -0.44 |
| 12 | G12 | CML539 | 0.03 | 0.32 | -0.44 | 0.73 | -2.78 | 0.74 | -0.24 | 0.14 | 0.10 | -0.03 | -2.74 | 0.19 | -0.01 | -2.62** | -2.01 | -0.01 | -0.57 |

****P≤0.01; *P≤0.05; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), LB = leaf blight disease (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), Rust = rust disease (1-5), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour, # = number.**

**Appendix 17 Estimated specific combining ability effects of 12 inbred lines for grain yield and agronomic traits across low pH environments 2011/12**

| | Cross | Pedigree | GY | AD | ASI | DS | EH | EPP | LB | GLS | GT | MSV | PH | RL | SWT | SH | SL | VIG | Rust |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | S12 | CZL999601/CML481 | -0.09 | 2.45 | 0.77 | 1.73 | 5.68 | -1.53 | -0.02 | -0.66* | 0.35 | 0.00 | 2.70 | 0.31 | 0.56 | -6.96 | -0.04 | 0.60 | 0.41 |
| 2 | S13 | CZL999601/CML359 | -0.31 | -0.78 | -2.28 | 1.64 | 7.20 | 7.76** | 0.05 | 0.69* | -0.53 | -0.09 | 10.37 | 0.48 | 2.01 | -12.58 | -0.05 | -3.78 | -0.07 |
| 3 | S14 | CZL999601/CML144 | -0.03 | 1.89 | -0.39 | 1.80 | 5.23 | -0.88 | -0.28 | -0.18 | 0.04 | -0.01 | 4.25 | -0.52 | -1.24 | -4.42 | 0.33 | 1.03 | 0.18 |
| 4 | S15 | CZL999601/CML161 | -0.02 | -1.19 | -1.33 | 0.00 | -4.54 | -0.22 | -0.36 | 0.03 | 0.09 | -0.22* | -9.72 | 0.05 | -0.66 | -7.01 | 0.06 | 0.69 | 0.19 |
| 5 | S16 | CZL999601/CML172 | -0.13 | -1.76 | 0.48 | -0.65 | -1.94 | -0.73 | -0.07 | -0.14 | -0.08 | -0.09 | 0.94 | 0.00 | 1.61 | 56.17** | -0.07 | 0.62 | -0.10 |
| 6 | S17 | CZL999601/CML448 | 0.36 | -2.61 | -1.04 | -1.18 | 5.18 | -0.16 | 0.49 | 0.36 | 0.09 | 0.07 | 9.28 | -0.29 | -3.26 | -4.19 | -0.17 | 1.05 | 0.24 |
| 7 | S18 | CZL999601/CML312 | 0.37 | -1.19 | 0.88 | -1.79 | -11.74** | -0.22 | 0.26 | 0.15 | -0.15 | 0.08 | -10.29 | 0.35 | -0.84 | -5.34 | 0.21 | 0.85 | -0.61 |
| 8 | S19 | CZL999601/CZL130-23 | 0.08 | 1.35 | 2.27 | -0.40 | -1.12 | -1.16 | -0.04 | -0.10 | 0.12 | -0.04 | -3.80 | -0.20 | 0.32 | -1.89 | -0.04 | 0.36 | 0.08 |
| 9 | S110 | CZL999601/CML288 | -0.24 | -0.27 | -0.87 | -0.39 | -2.89 | -0.94 | 0.13 | 0.50 | 0.35 | 0.09 | -3.55 | -0.90* | -0.49 | -6.47 | -0.11 | -2.86 | -0.38 |
| 10 | S111 | CZL999601/CML202 | 0.30 | -0.75 | -1.38 | -0.02 | 1.48 | -0.22 | -0.06 | -0.59 | 0.00 | 0.07 | -1.42 | 0.46 | -0.02 | 0.35 | -0.10 | 0.82 | 0.35 |
| 11 | S23 | CML481/CML359 | -0.26 | -0.01 | 1.24 | -0.25 | -3.29 | 3.39 | 0.41 | 0.27 | 0.04 | 0.01 | -0.72 | 0.51 | -0.61 | -2.03 | 0.35 | -2.73 | -0.34 |
| 12 | S24 | CML481/CML144 | -0.36 | -0.34 | -0.64 | -0.20 | -0.47 | -1.09 | 0.59 | -0.35 | -0.07 | -0.05 | 0.38 | -0.16 | -0.43 | 6.73 | -0.27 | 0.74 | 0.49 |
| 13 | S25 | CML481/CML161 | 0.27 | -2.09 | -2.25 | -0.22 | -3.80 | -0.42 | 0.18 | -0.14 | -0.42 | 0.00 | -1.26 | 1.58** | -0.71 | 7.38 | -0.37 | 1.07 | 0.01 |
| 14 | S26 | CML481/CML172 | 0.07 | 1.56 | 1.89 | 1.23 | -9.87* | -1.12 | -0.54 | -0.14 | -0.25 | 0.01 | -8.70 | 0.20 | -0.49 | -5.47 | 0.00 | 1.34 | -0.03 |
| 15 | S27 | CML481/CML448 | -0.02 | 1.38 | -0.07 | -0.18 | -0.30 | -0.46 | 0.03 | 0.10 | 0.19 | 0.03 | -4.59 | 0.08 | 0.50 | 4.29 | -0.10 | 0.44 | 0.22 |
| 16 | S28 | CML481/CML312 | 0.07 | 1.36 | 1.51 | -0.12 | -4.78 | -0.50 | -0.21 | 0.39 | 0.38 | -0.04 | -6.05 | 0.05 | 2.31 | -1.81 | 0.11 | -0.76 | 0.04 |
| 17 | S29 | CML481/CZL130-23 | 0.34 | 0.24 | 2.24 | -1.94 | 2.57 | -1.22 | -0.17 | 0.06 | -0.46 | 0.13 | 4.26 | -0.34 | -1.01 | 6.31 | 0.03 | 0.91 | -0.11 |
| 18 | S210 | CML481/CML288 | 0.15 | -2.39 | -3.45 | 1.39 | 6.96 | 5.15** | -0.50 | 0.24 | -0.28 | -0.09 | 7.80 | -0.20 | -2.97 | -1.89 | -0.38 | -3.15 | -0.73 |
| 19 | S211 | CML481/CML202 | 0.01 | -1.32 | -2.08 | 0.54 | 4.22 | -0.38 | 0.14 | 0.15 | 0.38 | 0.03 | 5.04 | -1.34** | 1.90 | 10.37 | 0.47 | 0.54 | 0.25 |
| 20 | S34 | CML359/CML144 | -0.39 | 1.88 | -0.36 | 3.60 | 1.37 | -2.22 | -0.34 | -0.33 | -0.13 | -0.14 | 3.50 | -0.32 | -0.86 | 1.17 | -0.12 | -2.64 | -0.41 |
| 21 | S35 | CML359/CML161 | 0.21 | 0.47 | 0.70 | 0.13 | 8.49 | -1.61 | -0.42 | 0.21 | -0.12 | -0.06 | 9.20 | 0.25 | 3.40 | 2.42 | 0.45 | -2.98 | -0.47 |
| 22 | S36 | CML359/CML172 | -0.12 | 1.00 | -0.38 | 0.14 | -2.25 | 4.25* | -0.47 | 0.13 | -0.46 | -0.22* | -2.58 | -0.47 | -4.15 | -8.57 | -0.35 | -3.05 | -0.51 |
| 23 | S37 | CML359/CML448 | 0.23 | 2.38 | 0.76 | 2.29 | -5.35 | -1.32 | 0.10 | -0.30 | -0.02 | -0.05 | -10.58 | 0.41 | -2.01 | 11.11 | -0.29 | -2.95 | -0.51 |
| 24 | S38 | CML359/CML312 | 0.11 | -0.53 | -2.42 | 2.23 | 6.62 | -1.22 | 0.03 | 0.33 | 0.17 | 0.04 | 6.63 | -0.12 | -1.16 | -4.33 | -0.24 | -2.81 | -0.28 |
| 25 | S39 | CML359/CZL130-23 | 0.15 | 0.89 | -0.81 | 0.73 | 1.14 | -2.31 | -0.10 | -0.59 | 0.03 | 0.26 | 4.89 | -0.67 | 0.09 | 7.17 | -0.32 | -3.64 | -0.67 |
| 26 | S310 | CML359/CML288 | 0.12 | -7.16** | 3.22 | -10.78 | -4.37 | -2.10 | 1.20** | -0.10 | 0.35 | 0.42** | -11.04 | 0.13 | -0.77 | -3.43 | 0.11 | 30.47** | 4.20** |

**Appendix 17 continued**

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 27 | S311 | CML359/CML202 | -0.29 | 0.02 | -0.02 | 0.11 | -2.93 | -1.60 | -0.12 | 0.00 | 0.72* | -0.05 | 0.27 | -0.17 | -2.69 | -2.68 | 0.29 | -3.18 | -0.32 |
| 28 | S45 | CML144/CML161 | -0.11 | -1.86 | -2.30 | -0.04 | 4.52 | 0.18 | 0.09 | 0.59 | 0.14 | 0.07 | -4.48 | -0.42 | 0.91 | -1.06 | 0.00 | 1.16 | 0.28 |
| 29 | S46 | CML144/CML172 | 0.44 | -1.99 | -1.04 | -0.59 | -9.88* | -0.42 | -0.13 | -0.41 | 0.09 | -0.14 | -6.93 | 0.03 | 2.98 | -5.36 | -0.14 | 0.43 | -0.35 |
| 30 | S47 | CML144/CML448 | -0.09 | -2.62 | -1.90 | 0.00 | -0.53 | 0.13 | 0.77* | -0.17 | -0.13 | 0.02 | -1.04 | 0.24 | 3.21 | 8.08 | 0.10 | 1.19 | 0.32 |
| 31 | S48 | CML144/CML312 | 0.02 | -1.97 | -1.09 | -0.72 | -0.57 | 0.20 | -0.29 | -0.38 | -0.10 | -0.05 | -5.16 | -0.12 | -1.48 | 2.69 | 0.15 | 0.66 | 0.22 |
| 32 | S49 | CML144/ZL130-23 | -0.21 | 4.00* | 4.86 | -1.11 | -7.83 | -0.69 | -0.09 | 0.12 | -0.20 | -0.09 | -12.79 | 0.16 | -1.91 | -2.91 | 0.06 | -0.73 | -0.09 |
| 33 | S410 | CML144/CML288 | 0.19 | -0.69 | 0.47 | -1.71 | -1.98 | -0.44 | -0.26 | 0.48 | -0.09 | 0.40** | -7.49 | 0.13 | -3.74 | 0.08 | -0.44 | -3.22 | -0.38 |
| 34 | S411 | CML144/CML202 | 0.75 | 0.08 | 1.27 | -1.33 | 5.38 | 0.27 | -0.25 | 0.63 | 0.03 | 0.02 | 12.05 | 1.52** | 3.79 | -2.25 | -0.06 | 0.96 | -0.47 |
| 35 | S56 | CML161/CML172 | 0.17 | 0.04 | -0.10 | -0.72 | -2.21 | 0.06 | 0.13 | 0.38 | 0.21 | 0.66** | -11.01 | 0.43 | -1.29 | 2.03 | 0.10 | 1.09 | -0.16 |
| 36 | S57 | CML161/CML448 | 0.06 | -0.47 | -0.29 | -0.69 | -6.42 | 0.87 | -0.47 | -0.79* | 0.24 | -0.18 | 3.88 | -0.02 | 2.33 | -6.86 | -0.34 | 0.19 | -0.50 |
| 37 | S58 | CML161/CML312 | 0.00 | 0.84 | 2.53 | -0.97 | -10.68* | 0.64 | 0.79* | 0.00 | 0.26 | 0.25* | -12.02 | -0.55 | -0.14 | 0.91 | -0.45 | 1.32 | -0.18 |
| 38 | S59 | CML161/CZL130-23 | -0.08 | -3.30* | -3.42 | -0.47 | 6.28 | -0.10 | 0.16 | 0.00 | -0.05 | -0.29* | 9.57 | 0.73 | -5.81* | -2.38 | 0.63 | 1.16 | 0.09 |
| 39 | S510 | CML161/CML288 | -0.25 | 5.09** | 6.78 | 0.66 | -6.60 | 0.17 | -0.34 | -0.07 | -0.27 | -0.30* | 0.27 | 0.03 | 2.85 | 3.08 | 0.56 | -3.73 | -0.28 |
| 40 | S511 | CML161/CML202 | -0.18 | 0.61 | -0.63 | 0.58 | 5.22 | 0.85 | -0.36 | 0.01 | 0.43 | -0.18 | 1.06 | -1.11* | -2.34 | -4.43 | -0.26 | -0.05 | 0.62 |
| 41 | S67 | CML172/CML448 | -0.11 | -0.61 | 0.19 | -1.57 | 1.73 | -0.03 | 0.14 | 0.12 | 0.52 | -0.06 | 9.99 | 1.60** | 1.22 | -22.36* | 0.70* | 1.12 | 0.79 |
| 42 | S68 | CML172/CML312 | -0.12 | 1.37 | 0.34 | 0.16 | 9.48 | 0.15 | 0.41 | -0.34 | 0.22 | -0.13 | 5.09 | 0.06 | 1.96 | 4.63 | -0.42 | 0.25 | 0.36 |
| 43 | S69 | CML172/CZL130-23 | -0.01 | -1.10 | -2.27 | 0.99 | 5.11 | -0.58 | -0.22 | 0.91** | 0.24 | 0.33* | 7.68 | -0.65 | 1.81 | 1.46 | -0.34 | 1.09 | 0.39 |
| 44 | S610 | CML172/CML288 | -0.09 | 1.29 | 1.59 | 1.11 | 13.56* | -0.42 | -0.22 | -0.15 | -0.32 | -0.18 | 18.05 | -0.35 | -1.46 | -5.39 | 0.59 | -3.80 | -0.49 |
| 45 | S611 | CML172/CML202 | -0.18 | 0.81 | 0.85 | -0.96 | -6.96 | 0.22 | 0.76* | -0.58 | 0.05 | -0.06 | -9.82 | 0.01 | -2.26 | -15.82 | -0.23 | 0.89 | -0.09 |
| 46 | S78 | CML448/CML312 | 0.23 | -2.47 | -0.85 | -2.14 | -1.07 | 0.77 | -0.19 | 0.24 | 0.24 | 0.03 | -3.02 | -0.39 | -1.94 | -1.29 | -0.35 | 0.35 | 0.28 |
| 47 | S79 | CML448/ZLL130-23 | -0.06 | 0.72 | 0.87 | -0.64 | -10.10* | -0.05 | 0.18 | -0.26 | -0.07 | -0.01 | -7.76 | 0.90* | 1.17 | 0.61 | 0.23 | 1.19 | -0.70 |
| 48 | S710 | CML448/CML208 | -0.29 | 3.78* | -0.60 | 4.15 | 9.01 | 0.18 | -0.32 | -0.32 | 0.04 | -0.02 | 9.60 | -0.80 | 7.05 | 4.55 | 0.16 | -2.70 | -0.32 |
| 49 | S711 | CML448/CML202 | 0.02 | 1.63 | 1.66 | 0.74 | 7.83 | 0.90 | -0.34 | 0.75* | -0.92* | 0.11 | 7.73 | -0.94* | 0.40 | 5.92 | -0.16 | -0.01 | 0.33 |
| 50 | S89 | CML312/ZL130-23 | -0.19 | -2.30 | -3.65 | 1.41 | 6.64 | -0.08 | -0.06 | 0.53 | -0.37 | -0.08 | 6.34 | -0.64 | 3.10 | -0.84 | 0.11 | 0.33 | 0.62 |
| 51 | S810 | CML312/CML288 | -0.37 | 3.42* | 1.88 | 0.54 | -3.24 | 0.21 | 0.45 | -0.53 | 0.40 | -0.09 | -2.96 | -0.34 | -5.80* | -3.42 | 0.04 | -2.56 | -0.51 |
| 52 | S811 | CML312/CM202 | -0.04 | 2.61 | 2.81 | 0.46 | 3.24 | 0.75 | -0.58 | -0.46 | -0.56 | 0.03 | 9.16 | 0.03 | 5.24* | 0.11 | 0.72* | 1.12 | 0.14 |
| 53 | S910 | ZL130-23/CML288 | 0.27 | -1.05 | -3.40 | 2.70 | 3.38 | -0.65 | -0.19 | -0.53 | 0.09 | -0.13 | -0.70 | -0.05 | 4.49 | 2.47 | 0.12 | -2.72 | 0.02 |
| 54 | S911 | ZL130-23/CML202 | -0.59 | 1.47 | 2.86 | -0.71 | -5.13 | -0.08 | 0.79* | 0.04 | -0.20 | -0.01 | -7.57 | 0.81 | 2.69 | 0.17 | -0.20 | 0.96 | -0.33 |
| 55 | S112 | CZL999601/CML539 | -0.32 | 2.85 | 2.88 | -0.75 | -2.54 | -1.70 | -0.09 | -0.06 | -0.27 | 0.15 | 1.26 | 0.28 | 2.01 | -7.66 | -0.04 | 0.62 | 0.15 |

**Appendix 17 continued**

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 56 | S212 | CML481/CML539 | -0.17 | -0.83 | 0.85 | -1.98 | 3.08 | -1.81 | 0.11 | 0.10 | 0.14 | -0.03 | 1.16 | -0.69 | 0.96 | -16.91 | 0.20 | 1.00 | -0.03 |
| 57 | S312 | CML359/CML539 | 0.56 | 1.83 | 0.35 | 0.15 | -6.63 | -3.02 | -0.32 | -0.30 | -0.07 | -0.12 | -9.94 | -0.02 | 6.75* | 11.74 | 0.18 | -2.71 | -0.12 |
| 58 | S412 | CML144/CML539 | -0.21 | 1.62 | 1.13 | 0.31 | 4.74 | 4.96* | 0.19 | 0.00 | 0.43 | -0.04 | 17.72 | -0.52 | -1.23 | -2.76 | 0.40 | 0.43 | -0.04 |
| 59 | S512 | CML161/CML539 | -0.07 | 1.87 | 0.30 | 1.73 | 9.75 | -0.43 | 0.61 | -0.21 | -0.50 | 0.26* | 14.52 | -0.95* | 1.46 | 5.93 | -0.37 | 0.09 | 0.26 |
| 60 | S612 | CML172/CML539 | 0.07 | -0.60 | -1.55 | 0.86 | 3.23 | -1.38 | 0.23 | 0.21 | -0.22 | -0.12 | -2.70 | -0.84 | 0.09 | -1.33 | 0.16 | 0.02 | -0.12 |
| 61 | S712 | CML448/CML539 | -0.34 | -1.11 | 1.26 | -0.78 | 0.02 | -0.83 | -0.37 | 0.28 | -0.19 | 0.04 | -13.48 | -0.79 | -8.67** | 0.13 | 0.23 | 0.12 | 0.04 |
| 62 | S812 | CML312/CML539 | -0.07 | -1.13 | -1.93 | 0.95 | 6.10 | -0.69 | -0.61 | 0.07 | -0.49 | -0.03 | 12.29 | 1.68** | -1.25 | 8.69 | 0.11 | 1.25 | -0.03 |
| 63 | S912 | ZL130-23/CML539 | 0.30 | -0.93 | 0.46 | -0.56 | -0.94 | 6.92** | -0.24 | -0.18 | 0.86* | -0.07 | -0.12 | -0.04 | -4.94 | -10.18 | -0.30 | 1.09 | -0.07 |
| 64 | S1011 | CML288/CML202 | 0.23 | -1.81 | -3.61 | 1.42 | -4.68 | 0.07 | -0.21 | 0.23 | -0.26 | -0.02 | -2.88 | 0.61 | -5.34* | 3.17 | -0.27 | -2.93 | -0.02 |
| 65 | S1012 | CML288/CML539 | 0.28 | -0.21 | -2.01 | 0.90 | -9.15 | -1.24 | 0.26 | 0.26 | -0.03 | -0.08 | -7.09 | 1.76** | 6.19* | 7.25 | -0.38 | -2.80 | -0.08 |
| 66 | S1112 | CML202/CML539 | -0.17 | -4.25 | -0.93 | -1.57 | -8.81 | 1.53 | 0.34 | 0.42 | 0.31 | -0.22 | -18.52 | 0.80 | -1.45 | -2.09 | 0.12 | 4.53 | -0.22 |

****P≤0.01; *P≤0.05; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour, Rust = rust disease (1-5), # = number.**

**Appendix 18 Estimated general combining ability effects for 12 inbred lines for grain yield and agronomic traits for optimal soil conditions in 2011/12**

| | Line | Name | GY | AD | ASI | DS | EH | EPP | GLS | GT | LB | MSV | PH | RL | SWT | SH% | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | G1 | CZL999601 | 1.31** | -0.87** | -0.45** | -1.32** | -2.01 | -1.54 | 0.12* | 0.02 | 0.07 | -0.09 | -1.57 | 0.51 | 1.94 | 3.13 | 0.56 | -0.76 |
| 2 | G2 | CML481 | 0.23 | -0.83** | -0.18 | -1.02** | -3.00 | -1.54 | -0.12* | 0.00 | 0.37** | -0.01 | -7.53 | 0.88 | -0.66 | 3.47 | 1.19 | -0.86 |
| 3 | G3 | CML359 | 0.12 | -0.07 | 0.35* | 0.28 | 1.36 | -1.54 | 0.13* | 0.04 | -0.07 | -0.03 | 4.32 | -0.26 | 1.55 | 0.13 | 0.69 | -0.75 |
| 4 | G4 | CML144 | 0.01 | -0.67** | -0.15 | -0.82** | 0.10 | -1.50 | 0.17** | 0.03 | -0.26* | -0.08 | -2.64 | -1.04 | 1.14 | 3.63 | 0.13 | -0.85 |
| 5 | G5 | CML161 | -0.57** | 0.73** | 0.32* | 1.05** | 3.05 | 1.38 | -0.15* | 0.06 | -0.02 | 0.02 | 4.04 | -0.52 | -3.01* | -4.36* | -0.56 | 1.22 |
| 6 | G6 | CML172 | 0.25 | -0.33** | 0.22 | -0.12 | -2.58 | -1.53 | 0.10 | 0.00 | 0.18 | -0.08 | -0.76 | 1.41 | 0.28 | 2.10 | -0.08 | -0.75 |
| 7 | G7 | CML448 | -0.51** | 0.93** | 0.22 | 1.15** | -1.58 | -1.58 | -0.17** | -0.03 | 0.35** | 0.01 | -4.60 | -0.72 | 2.00 | -0.94 | -0.38 | -0.43 |
| 8 | G8 | CML312 | -0.40* | -0.77** | 0.08 | -0.68 | -4.39 | 1.06 | -0.13* | 0.20* | 0.10 | 0.07 | -0.29 | 1.53* | -1.33 | -1.38 | 0.09 | 0.97 |
| 9 | G9 | ZL130-23 | -0.31 | 1.63** | -0.25 | 1.38** | 3.76 | 4.76** | -0.15* | -0.18 | -0.17 | 0.17* | 2.80 | -0.06 | -2.88* | -5.73** | -0.54 | 1.81* |
| 10 | G10 | CML288 | -0.02 | 0.13 | -0.25 | -0.12 | -0.21 | -1.54 | 0.20** | 0.03 | -0.05 | -0.03 | 1.17 | 0.13 | 1.87 | 3.12 | -0.48 | -0.66 |
| 11 | G11 | CML202 | -0.01 | 0.33** | -0.15 | 0.18 | 6.70* | 1.46 | 0.23** | -0.02 | -0.17 | -0.01 | 7.65 | -1.99* | -1.52 | -0.72 | -0.19 | 0.68 |
| 12 | G12 | CML539 | -0.10 | -0.23** | 0.25 | 0.02 | -1.22 | 2.11 | -0.23** | -0.15 | -0.36 | 0.06 | -2.59 | 0.13 | 0.63 | -2.44 | -0.44 | 0.39 |

****P≤0.01; *P≤0.05; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), LB = leaf blight disease (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour, # = number.**

**Appendix 19 Estimated specific combining ability effects of 12 inbred lines for grain yield and agronomic traits at optimal soil conditions 2011/12**

| | Cross | Pedigree | GY | AD | ASI | DS | EH | EPP | LB | GLS | GT | MSV | PH | RL | SWT | SH% | SL | VIG |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | S12 | CZL999601/CML481 | -0.90 | -1.94** | -0.53 | -2.47** | 4.06 | 1.60 | -1.01** | -0.12 | -0.34 | 0.14 | -8.35 | -0.38 | -2.40 | -6.36 | -2.09 | 0.84 |
| 2 | S13 | CZL999601/CML359 | 0.61 | 1.30** | -0.73 | 0.56 | -8.70 | 1.64 | -0.08 | 1.13** | 0.13 | -0.01 | -5.61 | 0.42 | 0.14 | -0.31 | -1.92 | 0.72 |
| 3 | S14 | CZL999601/CML144 | 2.44** | 2.90** | 0.10 | 3.00** | -0.68 | 1.75 | -0.89** | 0.26 | 0.64** | 0.04 | -3.41 | -1.46 | 5.30 | -4.58 | 2.98* | -0.17 |
| 4 | S15 | CZL999601/CML161 | -0.18 | 1.50** | 0.97* | 2.46** | 9.78 | -1.27 | 0.21 | -0.25 | -0.23 | -0.06 | 12.51 | -0.65 | 5.17 | 0.64 | -1.01 | -1.07 |
| 5 | S16 | CZL999601/CML172 | -1.16* | -2.44** | 0.07 | -2.37** | 6.84 | 1.60 | 0.01 | 0.83** | -0.01 | 0.04 | 10.85 | -0.25 | -5.34 | 2.79 | 0.84 | 0.89 |
| 6 | S17 | CZL999601/CML448 | -1.33* | -2.70** | 1.07* | -1.64** | 0.90 | 1.63 | 1.51** | -0.24 | 0.03 | -0.04 | -0.78 | -1.78 | -5.14 | -1.42 | 0.81 | 2.24 |
| 7 | S18 | CZL999601/CML312 | -0.08 | -1.67** | -0.13 | -1.80** | 7.05 | -0.93 | -0.74* | -0.10 | -0.36 | -0.10 | 16.08 | -2.03 | 0.55 | 5.01 | 1.01 | -0.33 |
| 8 | S19 | CZL999601/CZL130-23 | 0.94 | -1.40** | -0.47 | -1.87** | 1.84 | -4.42 | -0.48 | -0.09 | -0.16 | -0.21 | 9.55 | 2.89 | 2.85 | 6.78 | 1.31 | -2.83 |
| 9 | S110 | CZL999601/CML288 | -0.73 | 2.10** | -0.47 | 1.63** | 0.80 | 1.72 | 1.57** | -0.60** | 0.14 | 0.00 | -11.18 | 4.70* | -1.30 | -2.59 | -0.42 | 1.47 |
| 10 | S111 | CZL999601/CML202 | 0.86 | 1.90** | 0.43 | 2.33** | -25.41** | -1.34 | 0.02 | -0.64** | 0.19 | 0.14 | -23.20 | 0.15 | 3.81 | 3.15 | -0.37 | -0.37 |
| 11 | S23 | CML481/CML359 | -0.41 | -0.07 | -0.67 | -0.74 | 8.83 | 1.68 | 0.79* | 0.03 | 0.14 | 0.07 | 10.25 | -0.95 | -3.56 | 1.66 | 6.44** | 1.66 |
| 12 | S24 | CML481/CML144 | 0.22 | 2.86** | 0.50 | 3.36** | 7.32 | 1.67 | 1.48* | -0.34 | -0.35 | -0.04 | 9.09 | -3.50 | -5.98 | -7.77 | 1.01 | 1.27 |
| 13 | S25 | CML481/CML161 | 0.70 | -2.54 | 0.70 | -1.84 | -2.83 | -1.14 | -0.09 | -0.02 | -0.05 | 0.36 | 0.37 | 1.99 | -2.67 | 5.21 | 1.03 | -0.47 |
| 14 | S26 | CML481/CML172 | -1.35* | -4.14** | -0.20 | -4.34 | 14.13 | 1.64 | 0.71* | -0.10 | -0.16 | -0.04 | 12.17 | 4.72* | -8.63* | -3.44 | -1.79 | 1.82 |
| 15 | S27 | CML481/CML448 | 2.05** | 3.26** | -0.87 | 2.40 | -16.60 | 1.72 | -1.46** | 0.00 | 0.21 | -0.13 | -44.65** | -3.81 | 2.51 | -2.31 | -0.82 | -0.16 |
| 16 | S28 | CML481/CML312 | -0.50 | 4.30** | -0.40 | 3.90 | -2.42 | -0.96 | 1.29** | -0.04 | -0.51 | 0.31 | 6.87 | 8.60** | -4.17 | 0.00 | 1.38 | -0.56 |
| 17 | S29 | CML481/CZL130-23 | 0.52 | -0.10 | 1.60** | 1.50 | -1.97 | -4.56 | -0.61 | 0.15 | 0.19 | -0.29 | 11.78 | -3.81 | 14.40** | 6.11 | -1.32 | -2.73 |
| 18 | S210 | CML481/CML288 | 1.25* | 0.06 | -0.40 | -0.34 | 3.23 | 1.59 | -0.89 | -0.04 | -0.01 | -0.09 | 7.24 | -0.33 | 8.26* | 0.45 | -1.06 | -0.09 |
| 19 | S211 | CML481/CML202 | -0.76 | -0.14 | 0.83 | 0.70 | -5.22 | -1.20 | -0.11 | 0.43* | 0.54* | -0.11 | -9.54 | -2.21 | 1.64 | 4.89 | -1.67 | -0.94 |
| 20 | S34 | CML359/CML144 | -0.83 | 0.10 | 0.63 | 0.73 | -2.54 | 1.59 | -0.25 | -0.59** | -0.21 | -0.03 | 8.03 | -1.03 | -2.24 | -2.53 | -1.49 | 1.65 |
| 21 | S35 | CML359/CML161 | -0.22 | -0.30 | 0.50 | 0.20 | 0.11 | -1.27 | -0.33 | -0.10 | 0.25 | -0.13 | -0.58 | -2.21 | 9.31* | -4.66 | -0.81 | -1.25 |
| 22 | S36 | CML359/CML172 | 1.09* | 1.10** | 0.93 | 2.03 | -9.66 | 1.93 | -0.86 | -0.19 | -0.36 | -0.03 | -15.58 | -1.15 | 1.35 | -3.64 | 0.04 | -0.29 |
| 23 | S37 | CML359/CML448 | 0.26 | 2.50** | -1.73** | 0.76 | 1.64 | 1.67 | 0.64 | -0.25 | 0.01 | 0.39* | 5.19 | -1.35 | 1.26 | 3.82 | 0.01 | 0.72 |
| 24 | S38 | CML359/CML312 | -0.59 | -2.80** | 1.07* | -1.74 | -4.72 | -0.76 | 1.06** | 0.21 | -0.05 | -0.17 | -4.98 | 4.40* | -9.26* | 4.00 | -0.79 | -0.68 |
| 25 | S39 | CML359/CZL130-23 | -0.27 | -0.20 | -1.27* | -1.47 | 12.60 | -4.67 | -0.51 | -0.27 | 0.49 | -0.11 | 9.26 | -3.01 | -0.07 | 0.59 | -0.82 | -1.02 |
| 26 | S310 | CML359/CML288 | 0.33 | -2.70** | 0.73 | -1.97 | -11.33 | 1.60 | -0.46 | -0.45** | -0.38 | 0.10 | -13.28 | -1.20 | 0.25 | -1.62 | 0.44 | 0.62 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 27 | S311 | CML359/CML202 | -0.11 | -2.57** | 0.30 | -2.27 | 8.52 | -1.39 | 0.16 | 0.51** | -0.16 | -0.09 | 1.41 | 0.92 | 5.34 | 2.53 | -1.17 | -1.55 |
| 28 | S45 | CML144/CML161 | -0.52 | -1.70** | -1.33** | -3.04 | 5.80 | -1.30 | 0.20 | 0.36* | 0.43 | -0.08 | 5.39 | 0.90 | 0.06 | 4.08 | 0.09 | -0.81 |
| 29 | S46 | CML144/CML172 | -1.07* | -1.64** | -0.23 | -1.87 | 4.76 | 1.72 | -0.34 | -0.55** | -0.01 | 0.02 | 6.95 | -2.36 | 1.58 | 4.70 | 0.28 | 1.65 |
| 30 | S47 | CML144/CML448 | -0.20 | -1.57** | -0.90* | -2.47 | -16.41 | 1.63 | 0.16 | 0.38* | -0.15 | 0.44* | -22.37 | -1.23 | -5.67 | 3.86 | -0.76 | 0.83 |
| 31 | S48 | CML144/CML312 | 0.45 | 2.80** | -0.77 | 2.03 | -0.96 | -1.00 | -0.25 | -0.32* | -0.21 | -0.12 | -6.02 | -2.81 | 12.21** | 1.08 | -0.56 | -0.57 |
| 32 | S49 | CML144/ZL130-23 | -1.10* | 2.40** | -0.10 | 2.30 | -0.07 | -4.54 | -0.15 | -0.30 | -0.33 | -0.06 | -6.78 | 6.10* | 1.11 | -3.10 | -0.59 | -1.58 |
| 33 | S410 | CML144/CML288 | 0.03 | -2.10** | 1.23** | -0.87 | -3.38 | 1.66 | -0.10 | 0.68** | 0.29 | -0.02 | -0.84 | 3.25 | -5.83 | 0.69 | 0.34 | 0.23 |
| 34 | S411 | CML144/CML202 | 0.99 | -2.30** | 0.13 | -2.17 | -7.79 | -1.29 | -0.15 | 0.65** | 0.18 | -0.04 | -1.62 | 3.70 | 3.98 | 0.81 | -0.61 | -1.45 |
| 35 | S56 | CML161/CML172 | 2.14* | 1.96** | -0.37 | 1.60 | 5.61 | -1.35 | -1.08** | 0.10 | 0.45 | -0.08 | 10.57 | -1.88 | 9.38* | 6.29 | -0.04 | -2.25 |
| 36 | S57 | CML161/CML448 | -1.36* | -2.30** | 1.97** | -0.34 | -5.42 | -1.31 | 1.92** | 0.03 | -0.01 | -0.16 | -2.52 | 4.25 | -5.42 | -4.43 | -0.07 | 0.93 |
| 37 | S58 | CML161/CML312 | -0.44 | -0.60* | -1.23** | -1.84 | -5.21 | -3.86 | -0.83** | 0.00 | 0.09 | -0.05 | -14.00 | -3.66 | -0.23 | 1.10 | -0.21 | -1.97 |
| 38 | S59 | CML161/CZL130-23 | 0.34 | 0.33 | -0.57 | -0.24 | -13.15 | -7.57 | 0.77* | 0.51** | -0.20 | -0.33 | -20.46 | -0.75 | 0.13 | 11.11 | 0.76 | -3.98* |
| 39 | S510 | CML161/CML288 | -1.22* | 0.50 | -0.57 | -0.07 | -10.53 | -1.28 | -0.68* | -0.34* | -0.07 | -0.12 | -5.99 | -1.60 | -3.66 | 0.90 | 0.03 | 0.16 |
| 40 | S511 | CML161/CML202 | -1.43* | 2.30** | -0.33 | 1.96 | 21.48** | 25.24** | 0.11 | -0.37* | -0.44 | 0.86** | 23.01 | -1.48 | -14.06** | -29.65** | 0.24 | 12.77** |
| 41 | S67 | CML172/CML448 | -0.41 | -3.90** | -0.93* | -4.84 | -1.93 | 1.75 | 0.22 | -0.22 | -0.29 | 0.11 | 4.35 | 6.65* | -6.92 | -6.55 | -0.22 | -0.11 |
| 42 | S68 | CML172/CML312 | -0.73 | -1.87** | -0.13 | -2.00 | -19.81* | -0.97 | 1.64** | 0.75** | 0.32 | -0.12 | -16.96 | 1.07 | -4.41 | 2.22 | -0.69 | 0.66 |
| 43 | S69 | CML172/CZL130-23 | 2.09** | 0.06 | 0.87 | 0.93 | -7.26 | -4.62 | -0.09 | 0.10 | 0.36 | -0.23 | -2.56 | -1.35 | 5.22 | 4.61 | 0.94 | -1.85 |
| 44 | S610 | CML172/CML288 | -0.21 | 1.56** | -0.47 | 1.10 | -7.46 | 1.68 | -0.71* | -0.42* | -0.35 | 0.48* | -11.92 | -0.20 | 1.40 | -5.47 | 0.21 | 0.46 |
| 45 | S611 | CML172/CML202 | 0.18 | 3.36** | 0.10 | 3.46 | 8.03 | -1.36 | 1.07** | -0.12 | 0.04 | -0.04 | 6.46 | 0.92 | -4.06 | 0.32 | 0.59 | 0.11 |
| 46 | S78 | CML448/CML312 | 0.17 | 2.86** | 0.20 | 3.06 | 8.95 | -1.05 | -1.03** | 0.01 | 0.19 | -0.20 | 16.28 | -1.46 | 4.72 | -9.19 | 0.61 | -0.66 |
| 47 | S79 | CML448/ZLL130-23 | 0.52 | -1.20** | 0.87 | -0.34 | 14.97 | -4.61 | -0.26 | 0.20 | -0.27 | 0.02 | 20.28 | -1.55 | 9.16* | 7.17 | -0.09 | -3.00 |
| 48 | S710 | CML448/CML208 | 0.09 | 4.30** | -0.47 | 3.83 | 13.74 | 1.74 | -0.88** | 0.35* | 0.52 | -0.10 | 13.65 | -1.06 | 0.82 | 3.01 | 0.51 | -0.03 |
| 49 | S711 | CML448/CML202 | -0.45 | 3.10** | -1.23* | 1.86 | -4.21 | -1.26 | -0.76* | -0.35* | 0.07 | -0.13 | 2.34 | 0.39 | -3.11 | -2.48 | -0.11 | -0.20 |
| 50 | S89 | CML312/ZL130-23 | -0.06 | 2.83** | 0.00 | 2.83 | -4.48 | 19.17** | -0.68* | 0.00 | 0.50 | 0.63* | -5.06 | -1.13 | -10.29* | -17.23** | -0.22 | 8.62** |
| 51 | S810 | CML312/CML288 | 1.86** | -3.00** | 2.00** | -1.00 | 20.73 | -1.04 | -0.63* | -0.35 | -0.12 | 0.09 | 18.97 | -3.15 | 6.13 | 4.93 | -0.62 | -2.09 |
| 52 | S811 | CML312/CM202 | 1.00 | -0.20 | -0.43 | -0.64 | 3.30 | -3.97 | -0.51 | -0.39* | 0.18 | -0.19 | -5.81 | -3.53 | 10.75** | 8.80 | 0.09 | -2.44 |
| 53 | S910 | ZL130-23/CML288 | -1.44** | -0.40 | -0.67 | -1.07 | 9.27 | -4.65 | 1.97** | 0.00 | -0.33 | -0.27 | 5.35 | 2.94 | -8.83* | -0.09 | 0.01 | 0.23 |
| 54 | S911 | ZL130-23/CML202 | -0.55 | -0.27 | 0.90 | 0.63 | 3.69 | -7.60 | -0.41 | -0.37* | -0.45 | -0.29 | 3.30 | 1.72 | 3.81 | 7.35 | 0.06 | -2.95 |
| 55 | S112 | CZL999601/CML539 | -0.47 | 0.46 | -0.30 | 0.16 | 3.52 | -1.97 | -0.12 | -0.17 | -0.01 | 0.07 | 3.54 | -1.63 | -3.63 | -3.10 | -1.12 | -1.41 |
| 56 | S212 | CML481/CML539 | -0.83** | -1.57** | -0.57 | -2.14 | -8.52 | -2.05 | -0.09 | 0.06 | 0.34 | -0.18 | 4.77 | -0.33 | 0.61 | 1.55 | -1.09 | -0.64 |

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 57 | S312 | CML359/CML539 | 0.15 | 3.66** | 0.23 | 3.90 | 5.25 | -2.02 | -0.15 | -0.02 | 0.14 | 0.01 | 5.88 | 5.14* | -2.51 | 0.17 | 0.08 | -0.59 |
| 58 | S412 | CML144/CML539 | -0.41 | -1.74** | 0.73 | -1.00 | 13.95 | -1.89 | 0.29 | -0.22 | -0.27 | -0.11 | 11.58 | -1.58 | -4.52 | 2.75 | -0.69 | -1.07 |
| 59 | S512 | CML161/CML539 | 2.17** | 0.86 | 0.27 | 1.13 | -5.64 | -4.88 | -0.20 | 0.10 | -0.22 | -0.21 | -8.30 | 5.07* | 2.00 | 9.39 | -0.01 | -2.05 |
| 60 | S612 | CML172/CML539 | -0.59 | 5.93** | 0.37 | 6.30 | 6.75 | -2.03 | -0.57* | -0.15 | 0.00 | -0.11 | -4.33 | -6.20* | 10.44* | -1.82 | -0.16 | -1.09 |
| 61 | S712 | CML448/CML539 | 0.65 | -4.34** | 2.03** | -2.30 | 4.35 | -1.91 | -0.07 | 0.11 | -0.30 | -0.19 | 8.24 | 0.94 | 7.80* | 8.52 | 0.14 | -0.57 |
| 62 | S812 | CML312/CML539 | -1.07* | -2.64** | -0.17 | -2.80 | -2.44 | -4.62 | 0.68* | 0.25 | -0.02 | -0.09 | -5.37 | 3.69 | -5.99 | -0.71 | 0.01 | 0.02 |
| 63 | S912 | ZL130-23/CML539 | -0.99 | -2.04** | -1.17* | -3.20 | -15.45 | 28.07** | 0.45 | 0.10 | 0.19 | 1.14** | -24.66 | -2.06 | -17.49** | -23.31** | -0.02 | 11.09** |
| 64 | S1011 | CML288/CML202 | -0.55 | -3.44** | -0.10 | -3.54 | -7.85 | -1.08 | 0.81* | 0.95** | 0.01 | 0.08 | -3.50 | -0.46 | -9.32* | -1.25 | 0.33 | -0.14 |
| 65 | S1012 | CML288/CML539 | 0.58 | 3.13** | -0.83 | 2.30 | -7.22 | -1.94 | 0.00 | 0.25 | 0.31 | -0.15 | 1.50 | -2.91 | 12.08** | 1.02 | 0.24 | -0.84 |
| 66 | S1112 | CML202/CML539 | 1.08 | -1.53** | 0.67 | -0.87 | -7.17 | -0.09 | 0.29 | -0.02 | -0.63 | -0.07 | -2.10 | 2.88 | 1.30 | 4.94 | 3.45* | -1.83 |

****P≤0.01; *P≤0.05; GY = grain yield (kg ha$^{-1}$), AD = days to anthesis (days), ASI = anthesis-silking interval (days), DS = days to silking (days), EH = ear height (cm), EPP = ears per plant (#), LB = leaf blight disease (1-5), GLS = gray leaf spot disease (1-5), GT = grain texture (1-5), MSV = maize streak virus disease (1-5), PH = plant height (cm), RL = root lodging (#), SWT = 100 seed weight (g), SH = shelling percentage, SL = stem lodging (#), VIG = vigour, # = number.**