PhD thesis

Use of exotic germplasm to enhance the performance of local maize

by

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ABSTRACT

Exotic maize germplasm has been used minimally in most maize breeding programmes in Zimbabwe and sub-Saharan Africa (SSA). The major reasons for this include challenges in adaptation and the general tendency by breeders to shun the dilution of their elite breeding material. Breeders often prefer the easier and more predictable option of recycling their elite materials. This has resulted in the loss of genetic diversity, development of breeding bottlenecks and subsequent possibilities of stagnating or deteriorating yield gain. The cost and time constraints, the generally high expectations imposed by industry, and the huge capital outlays required to introduce exotic germplasm further discourages its inclusion in local breeding programmes. Traditionally in most breeding programmes in SSA, exotic germplasm is incorporated through introgression with backcrossing to produce modified local inbred lines. The modified local inbred lines with minor exotic components are then used in the production of three-way hybrids for commercialisation. Only minor modifications to the elite germplasm are accepted by most breeders. The usefulness of an inbred in any breeding programme is dependent upon its performance in combination with other inbreds. In this study, the usefulness of inbred lines was investigated through the production and evaluation of F_1 single-cross hybrids and F_1 three-way hybrids. The general aim of this study was to illustrate quicker and easier ways of identifying usable exotic inbreds in local breeding programmes. The yield *per se* performance of each hybrid in different stress environments was used as the major reference for selection. This study also challenged and allayed the breeders' fears concerning the use of exotic germplasm by identifying superior marketable hybrids without going through the lengthy process of backcrossing. Furthermore, the study demonstrated the huge potential of local x exotic crosses as sources of multiple pedigree starts. All hybrids in this study were evaluated in varied stress environments approximating the local farmers' conditions of low phosphorus, low nitrogen, random stress, high density and optimal conditions. Two hundred and fifty temperate inbreds with expired Plant Variety Protection (ex-PVP) certificates from the United States of America (USA) were crossed with three CIMMYT single-cross testers: CML539/CML442 (A tester), CML444/CZL068 (B tester), and CML312/CML444 (AB tester) to produce three-way hybrids which were evaluated over eight sites. The best inbreds, which were identified for enhancing yield from heterotic group A (SS group) were LH159, LH214, LH23HT, LH213 and MM402A. The best combiners from heterotic group B (NSS group) were HB8229, W8304, LH198, PJH40 and LH190, and from the unclassified lines were PHR58, WIL500, PHK35 and ICI441. The Griffing diallel model 1 method 4 mating scheme was used to evaluate 18 local inbred lines in a local x local diallel scheme and nine selected exotic inbred lines in an exotic x exotic diallel scheme. The North Carolina design II (NCII) was used to evaluate 18 selected local inbreds in combination with 12 selected exotic lines. Highest yielding crosses from the local x local diallel were, L3 x L6 and L4 x L14, and from the exotic x exotic diallel were E7 x E1 and E1 x E9. Inbred lines with the highest GCA from the diallels were L16, L4, E1 and E9. The best crosses from the NCII were N28 x N16 and N21 x N4. Local inbred lines N19, N28 and N30 and exotic inbred N3, N8 and N16 had the highest significant positive GCA effects. Inbred lines from Mexico lowland tropics and Kenya produced the best hybrids in combination with local lines, suggesting them as the most promising future sources of usable germplasm. The leveraging of local single-crosses using exotic tropical germplasm produced 1860 hybrids which were evaluated across eight sites. The outstanding combinations of (local x local) x local hybrids were DJH141028, DJH153523, DJH152318, DJH152580, DJH166030, DJH167263, and DJH168087. The best combinations of (local x local) x exotic hybrids were DJH161178, DJH152183, DJH152552, and DJH168068. The (local x local) x exotic crosses produced equally competitive hybrids as compared to the (local x local) x local. The highest heterosis was generated between the combination of IITA inbred lines and CIMMYT single-crosses, identifying IITA germplasm as the most promising source of tropical exotic germplasm. Overall, this study identified exotic inbred lines that can be used in local breeding programmes to produce hybrids directly and provides an initial step in a possibly bigger and even more comprehensive screening and evaluation programme that can be funded to create a database for the performance of exotic inbred lines in local breeding programmes.

Key words: Exotic germplasm, tropical germplasm, temperate germplasm, germplasm leverage, diallel, North Carolina design II, genetic gain, yield stagnation.

DECLARATION

I, OSWELL FARAYI NDORO, hereby submit this thesis for the degree of Philosophiae Doctor in Plant Breeding to the University of the Free State. I declare that this is my original work, and has not previously in its entirety or in part been submitted to any other university. All sources of materials and financial assistance used in this study have been duly acknowledged. I also agree that the University of the Free State has the sole right to the publication of this thesis.

Oswell Farayi Ndoro Date: December 2018

DEDICATION

This work is dedicated to my sons Takura Munyaradzi Ndoro, Tapiwa Ndoro and Tafadzwa Michael Ndoro. The sky is no longer the limit guys!

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Acronyms and abbreviations

AD	Anthesis date
ANOVA	Analysis of variance
ASI	Anthesis silking interval
CGIAR	Consultative Group on International Agricultural Research
CIMMYT	International Maize and Wheat Improvement Centre
CV	Coefficient of variation
DF	Degrees of freedom
DTMA	Drought tolerant maize for Africa
E	Environment
EA	Ear aspect
EH	Ear height
EPO	Ear position
EPP	Number of ears per plant
ER	Ear rot
ESA	Eastern and southern Africa
exPVP	Expired plant variety protection
FAO	Food and Agriculture Organisation
FAOSTAT	FAO statistical database
GCA	General combining ability
GEI	Genotype by environmental interaction
GLS	Grey leaf spot
GMO	Genetically modified organism
GY	Grain yield
H	Heritability in the broad-sense
h	Heritability in the narrow-sense
ha	Hectare/s
HC	Husk cover
IPP	Intellectual property protection
IITA	International Institute of Tropical Agriculture
ITPGRFA	International Treaty for plant genetic resources for food and agriculture

IO	Iodent
LSD	Least significant difference
m	Metre/s
Masl	Meter above sea level
MARS	Marker assisted recurrent selection
MET	Multi environmental trials
MOI	Moistue
MS	Mean squares
N	Nitrogen
NARS	National agricultural research stations
NSS group	Non-stiff stalk group
NUE	Nitrogen use efficiency
OPV	Open pollinated varieties
P	Phosphorus
PH	Plant height
SCA	Specific combining ability
SEN	Senescence
SL	Stem lodging
SS	Sum of squares
SSA	Sub-Saharan Africa
SS group	Stiff stalk group
TCTemp	Temperate test crosses
$t\ ha^{-1}$	Tonne/s per hectare
TEX	Grain texture
TURC	Turcicum
BLUPs	Best linear unbiased predictors
DTYP	Drought tolerant yellow population
DTWP	Drought tolerant white population
GEM	Germplasm enhancement of maize
GM	Genetically modified
g	gram

GLS	Grey leaf spot
HSD	Honestly significant difference
IMAS	Improved maize for African soils
K	potassium
kg	kilogram
LxT	Line x tester
LAMP	Latin American Maize Project
MOI	Moisture
MSV	Maize streak virus
PVP	Plant Variety Protection
QPM	Quality protein maize
SDG	Sustainable development doals
SNP	single nucleotide polymorphism
S	Sulphur
STMA	Stress tolerant maize for Africa
USA	United States of America
WEMA	Water Efficient Maize for Africa

CHAPTER 1

Introduction

1.1 Significance of maize in eastern and southern Africa

Maize (*Zea mays* L.) is a world source of carbohydrates for human diets and competes with other sources such as wheat, rice and potatoes. For Mexicans, the "children of corn," maize is entwined in life, history and tradition. It is not just a crop; it is central to their identity (Cassman, 1999). The native Americans, the early plant breeders who took care of maize for their survival, referred to maize as the "corn mother, the woman that never dies" (Hallauer, 1978). In Malawi, maize is life; "*Chimanga ndi moyo*" (Smale, 1995). Maize accounts for more than 30% of total calories in human diets in the world and more than 70% in African countries (Shiferaw et al., 2011). Maize alone makes up to 90% of dietary calories in poor households across sub-Saharan Africa (SSA) (Kent and Magrath, 2016).

According to Hassan (2001), *per capita* consumption of maize remains highest in the eastern and southern African (ESA) countries; South Africa (195 kg), Malawi (181 kg), Zambia (168 kg) and Zimbabwe (153 kg). In these countries, maize remains nutritionally and culturally fundamental to the smallholder farm families as the major and more preferred staple (Prasanna, 2012). Most of the maize is consumed as flour used to prepare *sadza, ugali, nshima or pap,* or is used to prepare porridge for babies and children of school going ages. The grain is processed industrially to produce beverages and is also used as an ingredient in an endless list of manufactured products that affect the nutrition of the region's population. Intact fresh cobs are boiled or roasted, and dried grain is mixed, boiled and consumed together with dried pulses especially common beans (*Phaseolus vulgaris L.*) and cowpeas (*Vigna anguiculata L.*).

In most ESA markets, preference of maize for human consumption is based on the kernel colour and kernel hardness. The white flints are more preferred where hand-processing is practiced, and the white dents are preferred where mechanical dry milling is available (De Groote and Kimenju, 2008; Ndhlela, 2012). Yellow maize is generally processed industrially into stock feeds for especially pigs, poultry and dairy cattle. The dried and unprocessed maize crop residue (stover) is a cheap and valuable direct feed for beef cattle during the dry winter seasons for the subsistence of communal and poor communities.

The significance of maize in the ESA region as both an economic and political crop cannot be overemphasised, as it is centrally integrated into both the economic and political fabrics of these countries (Smale et al., 2013). Maize markets play a pivotal role in the regional economies (Kent and Marath, 2016), and offer the greatest opportunity for economic growth for the smallholder farm families (Govereh et al., 2008).

1.2 Meeting future demand for maize in ESA

The global dependence on cultivated maize continues to strengthen as nearly half of the world's population presently relies on maize as the staple food (Conway, 2012). To meet this growing demand for food, feed and industrial use, many researchers agree that the level of maize productivity has to substantially improve, because expanding production by increasing acreage is no longer a feasible option due to limited arable land resources (Tilman et al., 2011; Mandal, 2014). To date, maize production has managed to keep up pace with human demands due mostly to growing yields and the crop's genetic plasticity (Shiferaw et al., 2011). Breeders have managed to exploit this existing genetic variability of maize to continuously produce hybrids that show genetic gain. Nonetheless, the speed of crop productivity growth appears to be slowing down in some maize regions, particularly in parts of Africa, India, China, and the USA (Finger, 2010). There is need to develop more efficient breeding procedures to set new thresholds. The need to deploy enhanced germplasm in order to be able to feed the growing maize dependent population is becoming increasingly apparent.

For a long time, many researchers have acknowledged drought and low soil nitrogen as the major limiting factors to maize production in ESA (Bänziger et al., 2000; Santos et al., 2000; Cooper et al., 2014). Many breeders in ESA and Zimbabwe have been working towards drought tolerance in maize (Bänziger and Diallo, 2004) and recently drought and heat tolerance (Cairns et al., 2013a). This focus was further strengthened when the International Maize and Wheat Improvement Centre (CIMMYT) initiated the Drought Tolerant Maize for Africa (DTMA) project. DTMA was launched in 2007 with an aim to mitigating drought and other stress factors to maize production in SSA. The target was to increase yields by 20 to 30%, benefiting 30 to 40 million people in sub-Saharan Africa (Abate et al., 2013). Other extensive research projects on drought and low nitrogen, similar to the DTMA project, were initiated to cover the whole of Africa. These included the Water Efficient Maize for Africa (WEMA) project, the Improved Maize for African Soils (IMAS) project and most recently the Stress Tolerant Maize for Africa (STMA) project (Edmeades et al., 1997; Santos et al., 2000; Bänziger and Diallo, 2004; Lobell et al., 2011). Subsequently, several drought and low nitrogen tolerant three-way hybrids and open pollinated varieties (OPVs) have been released onto the markets in the ESA region (Abate et al., 2013; Edmeades, 2013; Walker et al., 2015; Masuka et al., 2017a; 2017b). In addition to these projects, government agricultural departments through the National Agricultural Research Stations (NARS) and private seed companies have been also releasing a number of good hybrids onto the market annually.

African maize production represents only 7.9% of world production notwithstanding that the major proportion of the population depends on maize as a single staple (Ranum et al., 2014). The low maize production and low productivity has been attributed to the multiple and simultaneous occurrence of stress factors in the SSA region, mainly drought, low nitrogen and low phosphorous (Ranum et al., 2014; Setimela et al., 2017). Setimela et al. (2005) characterised the SSA region into mega-environments depending on the natural capacity of the environment to support crop production. This natural capability was dependent on the annual distribution and the total amount of rainfall, the soil type and the annual temperatures. Most farm families in ESA are presently found in vulnerable mega-environments with inherently low natural capacity to produce maize. Abiotic and biotic factors pose the greatest challenges in maize productivity in these regions, especially in the maize-dependent and climate change vulnerable countries (Smale et al., 2013). Recent developments clearly indicate that climate change, diseases, and insect pests are now as prominent and equally limiting to maize production as drought and low nitrogen (Cairns et al., 2013b).

Despite the increased exposure and vulnerability of the agriculture systems in ESA, the expectations to provide food for an additional 3.5 billion people by 2050, translating to food increase demand of 70%, remains a reality (Prasanna, 2012). The question that begs answering is; can the future maize requirements be met using the available germplasm?

1.3 Current breeding efforts to mitigate stress factors in Zimbabwe and ESA

The development and introduction of hybrid maize has been described as the greatest single contribution of government research to Zimbabwe’s agricultural industry and the precursor to Zimbabwe’s own green revolution (Alumira and Rusike, 2005). Scientific maize breeding in Zimbabwe started way back in 1904, but a well-coordinated government hybrid breeding programme was only initiated in 1932 (Havazvidi and Tattersfield, 1994). Throughout the years, the maize hybrid breeding programmes made significant advances, which resulted in the release of many hybrids with better yield, grain quality, and better agronomic characteristics. All breeding programmes then derived their parent material from three populations; Southern Cross (SC), Salisbury White (N group) and to a lesser extent Hickory King (Ndhlela, 2012). A milestone was achieved in 1960 when SR52 was released as the world's first commercial single-cross hybrid. This hybrid was based on the inbred lines SC-5-5-2-2 and N3-2-3-3 derived from Southern Cross and Salisbury White, respectively (Weinmann, 1972). The SC and N heterotic groups are considered as the backbone of Zimbabwe's breeding programmes. The unique heterosis between these two groups led to the formation of the legendary SR52.

Although SR52 was initially intended for high and more reliable rainfall areas in Zimbabwe, it was widely adapted to various conditions throughout ESA, particularly in the KwaZulu-Natal region of South Africa. Following the success of SR52, more crosses were made from local inbreds and inbred lines from South Africa, Mexico and Colombia, which led to the development of three-way hybrids. The first three-way short season hybrid was R200 (1970), followed by R201 (1975) and R215 (1976) (Alumira and Rusika, 2005). The R200 series were widely adopted by smallholder farmers throughout ESA, and this propelled Zimbabwe to become the leading exporter of hybrid maize seeds in Africa (Havazvidi and Tattersfield, 1994).

Regionally, CIMMYT has spearheaded the breeding of drought and low nitrogen tolerant maize hybrids targeting the resource poor farmers. The resource poor farmers are situated in mega-environments characterised by acid soils, sandy soils as well as erratic and unpredictable rainfall. The bulk of germplasm from CIMMYT, therefore, is made up of drought and low nitrogen tolerant populations such as the La Posta Seq, Drought Tolerant Yellow Population (DTYP) and Drought Tolerant White Population (DTWP) and marker assisted recurrent selection (MARS) populations (JM pop 1-3, ZIMCM pop 1-6, KEN pop1-3) from which very good hybrids have been produced (Cairns et al., 2013a).

Whereas the Zimbabwean National breeding programmes are based on the SC and N heterotic groups, CIMMYT has used general combining ability (GCA) and specific combining ability (SCA) estimates to establish heterotic patterns among its maize populations and pools, and have categorically placed their material in broad heterotic groups of A and B. Where heterotic tendencies were not consistent with the groups, the materials have been placed in an intermediate AB group. The concepts of GCA and SCA have become useful for characterisation of CIMMYT inbred lines in crosses and often have been included in the description of all publicly available inbred lines (Hallauer et al., 2010). The different heterotic groups give maximum heterosis when crossed and have made considerable contributions to hybrid development in ESA. Hybrids developed from these groups have exhibited high levels of broad adaptation in both high and low potential mega-environments in all ESA countries. Besides the most common CIMMYT group A and B, elsewhere within the region popular heterotic groups include P, I, K, M and F (Table 1.1).

Table 1.1 Main heterotic groups of maize inbred lines used in eastern and southern Africa

Heterotic group	Source population	Examples of public lines
SC	Southern Cross	SC5-5-2-2
N3	Salisbury White	N3-2-3-3
K	K64R/M162W	K64R, M162W
P	Natal Potchefstroom Pearl Elite Selection (NPP ES)	NAW5867
I	NYHT/TY	R118W, I137TN
M	21A2.Jellicorse	M37W
F	F2934T/Teko Yellow	F2834T
CIMMYT- A	Tuxpeno, Kitale, BSSS, N3 (more dent type)	CML442, CML312
CIMMYT- B	ETO, Ecuador 573, Lancaster, SC (more flint type)	CML444, CML395

Adapted from Fasahat et al. (2016)

Most of the maize breeding programmes to date have concentrated on the above locally available germplasm and heterotic groups, with minimal attempts to introduce new genes from other sources. It is envisaged that the concept of heterotic groups and heterosis can be further exploited by the introduction of gene pools from other sources. Sources that can enhance heterosis even more, and lead to the production of superior hybrids. Perhaps it is time the local heterotic groups receive a boost from new and more robust introductions and it is time to generate new heterotic groups that combine well with the existing groups to produce maize hybrids with higher grain yield (GY) potential and higher tolerance to stress. While the USA and other regions might have different classification systems, this study made an attempt to conveniently compress all the heterotic groups and fit them into the CIMMYT heterotic groups A, B and AB.

1.4 Rationale of the study

Many studies have been carried out based on the concept of combining ability and heterosis and have focussed on selecting the best combiners from the existing gene pools. Very few, if any, have emphasised the need for the introduction of new genes to break through the pending genetic thresholds or genetic caps that have probably been created by the continuous selfing and recurrent selection within the same heterotic pools. New genes may reside in exotic germplasm. Exotic germplasm refers to crop varieties unadapted to the breeders' target environment (Holland, 2004; Hallauer et al., 2010). The purpose of this study was to identify and select exotic inbred lines that combine well with CIMMYT inbred lines to produce superior maize hybrids targeted for the heterogeneous ecological zones of the ESA regions. Additionally, new populations for pedigree breeding could be initiated through crossing of selected exotic inbreds with particular local inbreds. In this study, selection of good exotic inbreds for use in the local breeding programme was based on *per se* grain yield (GY) performance of the evaluated single-cross or three-way hybrids across optimal, low nitrogen, low phosphorus, random stress, high plant density and managed drought conditions. The study also aimed at identifying exotic inbred lines with individual or groups of alleles that could confer specific yield enhancing traits as well as consumer traits to local germplasm under the selected environments. Across site within specific stress environments were used to identify inbred lines with specific alleles for stress tolerance for recommendation in target breeding programmes.

By introducing exotic germplasm from diverse sources, new hybrids and populations are generated and identified for commercialisation within a shorter period as compared to the conventional processes. Inclusion of exotic germplasm in the local programmes would be based on high GCA and high SCA as well as GY performance *per se* (Hallauer and Sears, 1972). So far, no studies have reported the advantages of leveraging local germplasm using exotic germplasm. No research has so far described the strength and possible shortcomings of exotic tropical germplasm introductions from diverse sources. Even in the developed world Goodman (1999) reported a small increase in the use of both temperate exotic germplasm (from 0.8% in 1984 to 2.6% in 1996) and tropical exotic germplasm (from 0.1% in 1984 to 0.3% in 1996) in USA maize breeding programmes. The situation has remained similar until now, not only in the US maize seed industry, but also in the European southeastern maize breeding programmes and the developing world (Nastasic et al., 2011). The opportunities for exploiting both the exotic temperate and exotic tropical germplasm are yet to be reported in the ESA region, hence this study.

1.5 Specific objectives of this study were

1. To identify temperate inbred lines with expired Plant Variety Protection (ex-PVP) certificates that combine well to enhance trait and yield *per se* performance of local CIMMYT inbred lines.
2. To identify tropical exotic inbreds from Kenya, Mexico, Colombia and IITA-Nigeria that give the best hybrids with perfect nick with local single-crosses.
3. To identify elite (old) CIMMYT Zimbabwe (CimZim-O), new CIMMYT Zimbabwe (CimZim-N), and exotic inbreds with high GCA effects.
4. To determine combinations of inbreds with high SCA effects among CimZim-N, CimZim-O and exotic inbreds and select new hybrids for immediate commercialisation.
5. To predict the best combinations of both exotic and local inbred lines with the highest possible GY in three-way and double-cross hybrids.
6. To identify specific exotic tropical inbred lines that could be used directly to leverage the local single-crosses and produce hybrids for immediate commercialisation.

1.6 Hypotheses

1. Ex-PVP temperate inbred lines can enhance trait and yield performance of local germplasm
2. Exotic inbred lines can produce superior hybrids (SCA effects) in combination with local inbred lines
3. High GCA inbred lines make the best hybrid combinations in three-way and double-cross combinations
4. New generation CIMMYT inbred lines from Zimbabwe (CimZim-N) have higher GCA effects than elite CIMMYT (CimZim-O) inbred lines
5. Leveraging local germplasm with tropical exotic finished lines can significantly reduce the time taken to produce and release new commercial hybrids

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CHAPTER 2

The need to introduce genetic diversity in maize breeding programmes: A review

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2.0 Introduction

While the use of exotic germplasm is an old and well-known concept, its actual deployment and acceptance by the current crop of conventional maize breeders is largely low, and fundamentally ignored. The slowdown in genetic gain in maize and the threat of yield stagnation have created a new breeding impetus for introducing exotic germplasm into the elite gene pools. Through conventional pedigree breeding, it generally takes eight to 10 years to develop a maize inbred line, and 4-5 years when the winter season is used to advance generations. The advantage of the conventional selfing with recurrent selection is that by the time an inbred line is developed, the breeder will have developed confidence in its performance. Breeders are not keen on introducing new germplasm from other sources, because this involves more work and more time before an inbred line and subsequent hybrids are released. This study explored alternative and pragmatic ways of using developed and successful inbred lines from diverse sources to generate quick-fix hybrids within a shorter period compared to the conventional pedigree method. Furthermore, the materials used to produce these quick-fix hybrids can be selected for conventional pedigree start-up programmes. Notably, general combining ability (GCA) and specific combining ability (SCA), heterosis, the diallel and the North Carolina mating designs were reviewed in the light of their use in the utilisation of exotic germplasm. The review also included the successes and challenges associated with the use of exotic germplasm and the breeders' dilemma emanating from strict industrial demands and expectations. The overall advocacy in this review was to expose faster and easier ways of leveraging breeding programmes on work that has already been done in other regions. After one season, a breeder should be able to evaluate quick-fix hybrids for the market. Why invent the wheel again?

2.1 Sources of increased pressure on productivity of maize in ESA

The demand for maize is expected to increase in developing countries and especially in countries that depend on maize as a single staple (Prasanna, 2011). Sustainability of adequate supplies of maize in the future is confronted by a steady increase in world population, increase in wealth, and a diminishing availability of fertile land and water for agriculture (Pimentel et al., 1999). Whereas the direct *per capita* consumption of maize and coarse grains is declining with increasing incomes, the *per capita* and total meat consumption is growing with improving eating habits of the middle class. More crops are therefore required *per capita* to cater for the adjustments in diets (Rosegrant and Msangi, 2011). The intensification and the discovery of new industrial uses of rough grains such as the manufacture of biofuels have escalated the demand for maize. Thus, besides the normal population growth, other factors like the general improvement in standards of living, the improving economic status, and the improvement in physical health of people worldwide, have added significant pressure on the productivity of maize and other crops.

The inability of production to meet the projected demand will result in malnutrition and subsequent and perpetual poverty as most of the productive time is used to source food, especially in the drought prone sub-tropical regions. Conspicuously the grain yields of maize in these sub-tropics and in developing countries in particular, have remained lower than in the temperate regions and the developed world (Osaki, 1995; Masuka et al., 2017a), a possible indicator of absence of grain yield enhancing genes from the populations. In ESA, the genetic potential of the varieties is hardly exploited to the full by farmers, as indicated by the large existing yield gap (Kurukulasuriya and Rosenthal, 2013). The yield gap is the difference between the genetic potential of a variety and the actual average realised yields on the farmers' fields. Largely the yield gap is higher with poorly resourced farmers and climate vulnerable mega-environments compared to developed and rich regions. The yield gap has been widening due to limited access to advanced technologies and lack of technical exposure prevalent in all developing countries. Average grain yields in poor countries are still below 2 t ha^{-1} while the national averages for grain yield in South America and the USA are above 4.2 t ha^{-1} and 8 t ha^{-1}, respectively (FAOSTAT, 2017). Ostensibly, the yield potential for newly released varieties in all these regions is well above 10 t ha^{-1}, alluding to the fact that there is need to specifically develop hybrids that are more amenable to the rough and heterogeneous environmental conditions of the poorer ecological zones.

Different regions have experienced different rates of maize yield development and subsequent differential rates of genetic gain and yield increases. Cassman (1999) attributed the differences in regional crop yield averages to the differential use of genetic diversity. Traditional maize breeding techniques and continuous selection from the same populations have created genetic uniformity that has led to increased vulnerability of monocultures to crop pathogens, insects, and abiotic factors. Mega-environmental differences have necessitated different emphasis on breeding objectives targeted at specific limiting factors prevalent in each ecological zone. Breeders in the different regions have therefore been challenged to produce crop varieties that maximize crop yields and minimize crop failure in the presence of particular adverse conditions. Maize breeders have continuously recycled their elite germplasm, whose intrinsic genomic capacity to provide the requisite traits for selection, is now threatened by yield stagnation due to their limited inherent capacity. The breeding efforts in stressful environments should therefore target the acquisition and introduction of germplasm that responds to the heterogeneous growing environments as well as varieties that are responsive to the common poor management practices. Often biophysical and socio-economic constraints that cause yield stagnation or deterioration are not mutually exclusive (Pradhan et al., 2015).

2.2 The impact of crop breeding on different crops

Crop improvement has impacted positively and broadly on all crops grown worldwide and will continue to play a critical role in world food security. The steady and significant increase in the yields of most crops and the impact of plant breeding is evident and acknowledged in all domesticated plants (Acquaah, 2012). All the genetic gain achieved so far has come with plant genetic modification and selection. Crop varieties with modified physiology to cope with the environmental variations now exist and exotic crop species can be produced in locations different from their regions of origin (Fischer et al., 2014). Photoperiod and season length adaptation have been successful breeding objectives (Goodman, 2002). Stress tolerance has greatly improved for most crops as newer hybrids out-yield the older ones not only in high yielding environments, but also in stress environments. Newer hybrids are now available that can withstand higher plant densities (Mansfield and Mumm, 2014). The genetic basis for disease resistance and host plant resistance have been successfully exploited in many crops (Kucharik and Ramankutty, 2008).

Examples of breeding successes are plenty. Yields of major crops such as maize, rice, sorghum, wheat, and soybean have recorded significant increases worldwide due the efficient use of nitrogen. The response of grain yield to nitrogen fertiliser in old hybrids is more dependent on uptake of nitrogen rather than the efficiency of nitrogen utilisation, and approximately 65% of genetic gain for grain yield at high nitrogen could be explained by improvements in nitrogen use efficiency (NUE) (Haegele et al., 2013). Selection for desirable plant architecture has been responsible for production of semi-dwarf wheat varieties, more erect maize plants, and fewer leaves in field crops, high harvest index and modified canopy structures (Adams, 1982). This has paved a way for optimizing the plant architecture of crops by even by molecular breeding and has improved grain productivity (Wang and Lee, 2008), and has greatly improved lodging resistance. Harvesting losses have been reduced enormously especially for crops that are machine harvested. Identification of quality traits associated with specific uses has produced quality protein maize (QPM), orange maize, golden rice, sweet corn, and orange potatoes, as classic examples (McGloughlin, 2018).

Significant genetic gain has been reported in all crops across the globe. Recently released soybean varieties are out-yielding the original introductions used in the 1930s by about 25% (Specht et al., 1999). The dry bean breeding programmes have developed early maturing, high yielding varieties that are adapted to various environmental stresses, especially the pinto and navy bean market classes (Specht et al., 1999). Sunflower hybrids that are grown today, yield approximately 35% more than the OPVs that were grown in the 1960s and the average oil content of currently grown hybrids is approximately 10% higher than the average of the early hybrids of the mid-1970s (Garg et al., 2018). The release of the first Mexican semi-dwarf wheat varieties, Penjamo 62 and Pitic 62, together with other varieties dramatically transformed wheat yields in Mexico, eventually making Mexico a major wheat exporting country. Barley improvement programmes have increased grain yield in the US by 60% over the past 20 years (Acquaah, 2012). Sorghum yields increased sharply in the 1950s as hybrid sorghum was adopted (Ganapathy et al., 2012; Rakshit et al., 2014), and in the USA maize grain yields have increased by an average of 4% per year for the period from 1963-1990 (Duvick, 2005; Chavas et al., 2014). Several maize diseases have been successful controlled through breeding for resistance (Williams et al., 2014), where before, in extreme cases, uncontrolled or uncontrollable new strains of disease outbreaks have led to total crop failure (Makone, 2014).

Adoption of genetically modified (GM) crops has been different in different parts of the globe especially for maize. While still very controversial in some European and African countries that originally banned GM maize, this position may be changing as the benefits of Bt maize become accepted (Ranum et al., 2014). Socioeconomic, political and environmental factors as well as factors of religion have played a major part in the adoption and utilisation of GM crops (Connor and Siegrist, 2010; Frewer et al., 2011). Slow ripening climacteric fruits such as tomatoes (Seymour et al., 2013), and *Bt* maize derived from the incorporation of *Bacillus thuringensis* (Qaim and Zilberman, 2003) have met their resistance especially in the conservative developing countries.

All the crop breeding successes have been founded on the availability of yield and trait enhancing genes within the source population in the different regions. Present and future breeding objectives will continue to emphasise the development of crop varieties that combine higher yield with good quality and disease and pest resistance. The genes conferring these attributes may not be inherent within elite germplasm and may need to be introduced from external populations. Breeders all over the world are aware of the existence of genetic diversity in maize (Vigouroux et al., 2008), and are also aware of the fact that improved varieties of the future will likely have a narrower adaptation to more specific environments, and are more likely to contain a higher percentage of desirable exotic genes. Successful transfer of the favourable genes from external populations can uplift the grain yield thresholds of elite populations. Systematic mechanisms have to be devised to identify, extract and transfer these genes from these external populations to the elite gene pools in order to continue with the upward trend in yield and genetic gain.

2.3 Genetic gain and pending yield stagnation in maize

Differential genetic gains using several dissimilar gene pools in maize, have been recorded in different mega-environments, resulting in different hybrid yield potential (Lobell et al., 2009). A study using CIMMYT varieties grown in ESA by Masuka et al. (2017a) showed incremental and continuous genetic gain under optimal conditions, managed drought, random stress, low nitrogen and under maize streak virus (MSV) disease pressure. They estimated the genetic gains to have increased by 109.4, 32.5, 22.7, 20.9 and 141.3 kg ha^{-1} yr^{-1} under the above conditions, respectively, for the period 2004-2014. A similar study on open pollinated varieties (OPVs) concluded that the genetic gain in the early maturity OPVs was 109.9, 29.2, 84.8 and 192.9 kg ha^{-1} yr^{-1} under similar conditions with that of the hybrids, and in intermediate-late maturity OPVs the genetic gain was 79.1, 42.3, 53.0 and 108.7 kg ha^{-1} yr^{-1}, respectively (Masuka et al., 2017b). In another similar study, Laidig et al. (2014) calculated and used percentage rates of genetic gain based on yield levels of a base year extrapolated from regression estimates and their results enabled comparisons of genetic gains across crops. The above studies showed positive genetic gain and continuous yield improvement in both hybrids and OPVs under different environmental stress conditions in the 10 years studied.

Other researchers (Cassman, 1999; Ray et al., 2012; Fischer et al., 2014) have also reported on genetic gain studies and have alluded to the threat of pending yield stagnation in some parts of the maize growing areas, possibly caused by the continuous mining of the same gene pools. Yield stagnation is a phenomenon being experienced in some parts of the globe and is believed to be caused by the combination of both bio-physical and socio-economic factors (Ray et al., 2012). Low genetic potential of available varieties, together with poor farmer management practices, poor soils, and climatic limitations have had an aggregated direct impact on the possible manifestation of yield stagnation.

Using conventional methods, the common procedure of inbred line extraction for hybrid formation is slow in addressing low genetic potential of varieties. While it has been acceptable to go through a 12-year or 12-season cycle to develop and commercialise a hybrid, current trends urgently demand faster turnaround breeding cycles. The use of successful inbreds and hybrids from other regional breeding programmes has been suggested as a plausible way of accelerating the turnaround time for hybrid release. These developed products bring two great advantages in that they have already proved their usability in their areas of origin and they inject genetic variability into the elite gene pools for further exploitation. The period required to commercialise a variety could be shortened significantly by using this approach.

2.4 Creating new diversity in maize germplasm

The motivation for introducing new genes in any breeding programme is to generate new breeding populations that have high proportions of unique alleles. Goodman (2005) justified the use of exotic germplasm as the need to enhance heterosis, increase frequency of alleles that increase yield and introduce genes for specific traits such as disease and pest resistance. Darsana et al. (2004) proposed increasing genetic diversity as a safeguard against unpredictable biological and environmental hazards, while Pollak and Salhuana (2001) concurred and added the direct use of exotic cultivars as local varieties if they were adaptable. While concurring, Mandal (2014), working for the Food and Agriculture Organisation (FAO) in the Democratic Peoples' Republic of Korea, added the prerequisite characteristics for source germplasm as yield *per se*, earliness, delayed senescence, short anthesis to silking interval and high number of ears per plant.

In the early days, maize breeding populations for line extraction were generally OPVs developed by maize breeders, and growers who chose an ear type considered ideal by scorecard standards (Hallauer, 1978). In the 1920s the first commercial hybrids produced and sold were almost exclusively double-crosses. In the 1960s a transition from double-crosses to single-crosses occurred in the USA, because single-crosses out-yielded double-crosses due to maximum heterosis occurring in the F_1 generation. The genetic uniformity of these single-crosses, however, still makes them less suitable for the ESA region, which is characterised by extensive mega-environmental heterogeneity and unpredictable seasonal variations. Three-way hybrids and double-crosses are more capable of withstanding these diverse and adverse conditions and hence their preference over single-crosses.

CIMMYT has a mandate to continuously develop and release new inbred lines onto the market for public consumption. The new releases are expected to have higher yield potential than the current and the old inbreds. Inbred line extraction at CIMMYT and many other breeding programmes has been effected through selective breeding based on defect elimination. Repeated cycles of continuous selection of plants with desirable traits, while omitting the undesirable ones, has so far produced highly productive inbred lines that are genetically identical but with limited genetic diversity, making them susceptible and vulnerable to the ever-changing climate and varied growing environments (Pandey and Gardner, 1992; Bazzaz, 1996).

Technically, pre-breeding programmes are necessary to produce new base populations from different germplasm coming from various sources. Existing information on the breeding value of exotic germplasm is very helpful, but phenotypic evaluation in local target environments, to which the exotic germplasm is not adapted, is more informative and thus more useful (Gracen, 1986). Identification of tropical maize germplasm that can be used in temperate breeding programmes in the USA has been done on a large scale by the Genetic Enhancement of Maize (GEM) project (Pollak et al., 2001) and the (LAMP) project (Salhuana et al., 1998). These were multi-institutional, public-private, cooperative endeavors to quickly inject elite exotic germplasm into public and private breeding programmes. In addition to the LAMP and the GEM projects, the North Carolina State University and the United States Department of Agriculture in conjunction with some private and public partners have spearheaded various studies on the incorporation of tropical germplasm into temperate breeding programmes (Goodman, 1997; 2005; Carena, 2007; Nelson and Goodman, 2008). Carena et al. (2007; 2011) from North Dakota State University have also successfully used exotic short season tropical germplasm to produce unique materials adapted to very short seasons with drought and cold tolerance, fast dry down and enhanced quality. They also have asserted that the environmental challenges experienced in North Dakota were consistent with climate change claims, which justify the need for proactive research to stay ahead of climate change.

2.5 Limitations in the exploitation of exotic germplasm in maize breeding

For years maize breeders from the temperate regions and the USA have encouraged breeding with tropical germplasm, which is the most logical source of added genetic variability (Nelson and Goodman, 2008). Unfortunately, to date, very little tropical germplasm (<5%) is represented in USA maize breeding programmes (Goodman, 2005) indicating limited success in this regard. Nelson and Goodman (2008) advocated for a more committed use of publicly available elite inbreds from different maize breeding programmes to broaden the genetic base of local maize. Nonetheless, the lack of coordinated use and the limited availability of information on which breeders could base parental choices remain the strongest reasons for underuse of exotic germplasm (Goodman, 1997). While recognizing the challenges of incorporating diversity into their elite breeding pools, Fan et al. (2014) showed that there were substantial genetic differences worth exploiting between CIMMYT tropical maize germplasm and temperate maize germplasm from China and the USA, indicative of abundant possibilities of high heterosis.

Limited studies are available that effectively evaluate the usability of exotic temperate germplasm in tropical breeding programmes (Gracen, 1986; Abadassi, 2014). The utilisation path for any introduced germplasm is contingent upon the evaluation outcomes in the target production environment (Prasanna, 2012). The search for superior genotypes regarding yielding ability, disease and pest resistance, stress tolerance or better nutritional quality is very long, hard, competitive and expensive. Wild parents, landraces and exotics that are available in germplasm banks would require a long time and significant financial support to evaluate before they become usable (Goodman, 2002). Materials from gene banks are normally difficult to identify and characterise. Nass et al. (2000) and Goodman (2002) detailed the main factors responsible for the low utilisation of plant genetic resources as lack of documentation, inadequate description of collections, lack of the information desired by breeders, poor adaptability and lack of collection evaluations. Some attempts to incorporate exotic germplasm into elite gene pools have failed due to the major difficulty of identifying superior sources among the overwhelming numbers of samples stored in germplasm banks.

Gepts (2006), additionally alluded to inadequacy or lack of seed regeneration programmes as one of the other major barriers to the use of exotic germplasm.

The hybrid maize breeding industry is competitive and demands tangible results within the shortest possible time, and this exerts excessive pressure on breeders. Private breeders therefore tend to rely almost exclusively on their working collection as opposed to using alien materials, which require a lengthy and expensive programme of pre-adaptation or pre-breeding. Industry should recognise the advantages, challenges and consequences of incorporation or non-incorporation of crop diversity into their elite breeding pools and craft long term breeding strategies that encourage gradual inclusion (Badu-Apraku et al., 2017). This strategy can be implemented through the selection of intermediaries showing the new traits, while maintaining a high amount of the adapted source background. Marshall (1989) concluded that the lack of pre-breeding programmes in maize has been most limiting in the use of both landraces and exotic germplasm. Consequently, for any breeding programme to succeed the source germplasm should have established prerequisite attributes of high yield performance and broad genetic variation for all important agronomic traits. Even on a smaller scale, pre-breeding procedures will remain essential for the creation and establishment of the desired diversity. Pre-breeding programmes can assist in identifying heterotic patterns as well as identifying materials that have special genes. The accomplishments of pre-breeding programmes have been centred on the accurate selection of parents from which superior breeding populations are generated, followed by rigorous selection for a number of generations (Mungoma and Pollak, 1988; Goodman, 2002; 2005; Carena, 2007; Tokatlidis, 2017). Unfortunately, the cost and the technical requirements to run a large pre-breeding programme are highly prohibitive.

2.6 Heritability, testing and evaluation of inbreds and hybrids

Crop genetic improvement involves cycles of creating genetic variability and exploiting that variability to derive improved crop varieties with outstanding performance for specific traits of interest (Hallauer et al., 2010). Progress in genetic gain in all crop characteristics will depend on the variability in populations and on the extent to which the desirable characters are heritable (Bello et al., 2012). Heritability of a trait is a measure of the phenotypic variance attributable to genetic causes and has predictive functions in plant breeding (Holland et al., 2003; Hallauer, 2007). Highly heritable characters can easily be fixed with simple selection, resulting in quick progress (Bello et al., 2012), and the existence of these heritable characters in a source population is therefore a prerequisite for successful plant breeding. Heritability of a trait is mostly measured through the assessment parent-offspring regression or using expected mean squares from the analysis of variance and relating them to the co-variance among relatives as per the mating design used (Hallauer et al., 2010).

General combining ability (GCA) of an inbred and its specific combining ability (SCA) with other inbreds, have also been used extensively in maize breeding. GCA is an estimation of the value of genotypes on the basis of their offspring performance in some definite mating design. It refers to the average performance of an inbred line in crosses. The deviation in performance of a cross from that expected of the average of two parents that constituted it is referred to as SCA (Sprague and Tatum, 1942; Fehr, 1992). The SCA includes not only the non-additive deviations due to dominance and epistasis, but also a considerable portion of the genotype x environment interaction. While the GCA gives an indication of additive gene effects, the SCA is indicative of dominance and epistatic gene effects (Hallauer et al., 2010). Statistically the GCA is a main effect and the SCA is an interaction effect. The concepts of GCA and SCA have become so integrated in hybrid breeding schemes that they have been used comprehensively to characterise inbred lines and establish heterotic patterns among maize populations and pools by many breeding Organisations, including CIMMYT (Crossa et al., 1990).

The importance of GCA and SCA effects has been variable under different environmental conditions as reported by Makumbi et al. (2011). Significant interactions were found between both GCA and SCA effects and the environment by Warburton et al. (2008) and Dehghanpour and Ehdaie (2013). Rankings of GCA and SCA varied across different stress environments and selection would be more effective when based on performance across environments. Although evaluation of hybrids over multiple seasons has been suggested by Nass et al. (2000), the concept of testing under multiple sites in one season has been used extensively at CIMMYT and other breeding organisations following the recommendations of Sprague and Eberhart (1977).

For quick progress in the evaluation of breeding materials, all CIMMYT generated hybrids are tested over at least five sites in stage 1 where 15 to 20% selection intensity is used. The use of a single tester to screen a large number of inbred lines has been used successfully by many breeders and they have concluded that one tester was sufficient for the initial screening (Nelson and Goodman, 2008; Banerjee and Kole, 2009; Badu-Apraku et al., 2017). The selected inbred lines are then crossed with more testers (3 to 5) in stage 2 and 3 and are evaluated again with an increased selection intensity of 10%. After evaluating the hybrids in stage 3 they are then evaluated in regional trials (stage 4) where 150 sites per season are used across the ESA region. The selected hybrids from regional trials are passed on to the on-farm trials (stage 5) where successful hybrids are tested in farmers' fields under the farmers' management practices. The data from the on-farm trials, which show how a variety performs in real life situations, are mandatory for the variety release and registration process in Zimbabwe.

2.7 Strategies for incorporating exotic germplasm

A number of breeding techniques are available that can be used to introduce desired exotic genes into local populations. These include the breeding processes of conversions, introgression and combinations (Bridges and Gardner, 1987). The more preferred techniques are those that are less complex and those that have a shorter duration. Conversions use repeated backcrossing to the recurrent parent with selection for adaptive traits in each succeeding backcross generation (Haussmann and Parzies, 2009). The complete conversion of an introduced maize genotypes for adaptation requires at least five generations of backcrossing to produce populations with 95 to 99% introduced germplasm (Williams et al., 2014). Introgression involves backcrossing a few chromosome segments with easily identifiable effects into elite varieties (Holland et al., 2003). The aim of introgression is to disrupt elite genetic backgrounds as little as possible during the introduction of a relatively small number of desirable alleles (Michelini, 1991). New directions for incorporation and introgression involve use of DNA markers to characterise the value of specific genomic regions in exotic germplasm sources (Bänziger and Diallo, 2004) and the use of multiple trait integration processes (Sun and Mumm, 2015). Combinations are generated by simple crossing of two different sets of germplasm to obtain 50% contribution from either side. This is easily applied where the materials being crossed have limited challenges of adaptation.

Available mating designs and evaluation techniques that can be systematically used to combine and evaluate germplasm include the top cross, the line by tester (LxT), the diallel and the North Carolina II mating schemes (Moreno-Gonzalez and Cubero, 1993). The mating designs are founded on genetic assumptions which were presented by Visscher et al. (2008), and the importance of each mating design were discussed in detail by Nduwumuremyi et al. (2013).

2.7.1 Top cross mating design

Top cross refers to a mating arrangement between a selection, line, clone and a common pollen parent which may be a variety, inbred line or single-cross. A large number of plants are selected and then crossed with one tester, which is normally used as the male parent in open pollination. All the lines being tested are de-tasselled and progenies are tested by simple analysis of variances between and within the families (Nduwumuremyi et al., 2013). Top crosses have been widely used for preliminary evaluation of combining ability of new inbred lines. The major shortfalls of this design are that a single tester may not offer a wide genetic background for testing the inbred lines and the number of crosses becomes large if the test inbred lines are many (Hallauer, 1978).

2.7.2 The diallel mating design

Genetic underpinnings of quantitative traits can be investigated using the diallel mating scheme (Griffing, 1956). A complete diallel allows the parents to be crossed in all possible combinations including selfs and reciprocals, and is required to achieve Hardy-Weinberg equilibrium in a population (Braun et al., 2010). According to Hallauer et al., (2010) the diallel is the most used and abused of all mating designs in obtaining genetic information and much of its abuse probably emanates from the presence of two models for diallel analyses i.e. random and fixed models. A random model involves parents that are random members of a random mating population and are used in the estimation of GCA and SCA variances. In contrast, when parents are considered fixed the aim is to measure the GCA effect for each parent and the SCA effect for each pair of parents (Bridges and Gardner, 1987; Braun et al., 2010). Griffing (1956) further split the diallel into method I (full diallel), method II (without reciprocals), method III (without parents) and method IV (without both parents and reciprocals). The assumptions for the diallel were listed as diploid segregation, no difference between reciprocal crosses, independent action of non-allelic genes, no multiple allelism, homozygous parents and independent distribution of genes between the parents (Griffing, 1956; Hallauer, 1978).

Since Griffing (1956), multiple diallel crosses have been used to evaluate the GCA and SCA effects for several plant characteristics. Many maize breeders have used the diallel to calculate combining abilities of different inbred lines and used the information for selecting good inbred lines for participation in breeding programmes (Gowda et al., 2012; Laude and Carena, 2014; Werle et al., 2014; Abdel-Moneam et al., 2015). Konate et al. (2017) evaluated combining ability and heterotic grouping of early maturing pro-vitamin A maize inbreds across *striga* infested and optimal growing environments. Badu-Apraku et al. (2017) examined the combining ability of the set of early yellow QPM inbreds and classified them into heterotic groups and identified the best testers. Zhang et al. (2016) used the diallel to propose modifications to the heterosis theory.

2.7.3 The North Carolina mating designs

The North Carolina (NC) designs were developed as a modification to the diallel, and are commonly used to estimate additive and dominance variances as well as for the evaluation of full-sib and half-sib recurrent selection. Comstock and Robinson (1952) observed that making crosses in all possible combinations as in the diallel was sometimes not necessary and laborious. They observed that in order to obtain more information about combining ability but without much labour compared to the full diallel, the NC designs I, II, and III could be used.

In the NC II each member of a group of parents used as males is mated to each member of another group of parents used as females. NC II is a factorial mating scheme and is one of the most important in practical plant breeding programmes for selection of test cross performance and is widely used for the evaluation of inbred lines for combining ability. It is similar to the LxT design and can be used for pre-selection of inter-pool three-way and four way hybrids. NC II is most suitable when there is some known basis for grouping lines into males and females, for example heterotic groups or seed production capacity. This method can also be used with materials from different populations and allows the estimation of the genetic variances in an F_2 base population (Hallauer, 1978). Best combiners can be identified from a set of crosses as well as the best hybrids produced from the same set of crosses. According to Hallauer et al., (2010), the male and female main effects and the male x female interactions effects are equivalent to GCA and SCA effects in the diallel. There are two independent estimates of GCA and the two estimates allow determination of maternal effects and calculation of heritability based on the male variance, which is free from maternal effects.

2.8 Predicting inbred line performance in three-way and double-cross hybrids

The amount of work required to develop and evaluate an inbred line and its products is expensive and requires large investment in both time and effort. The overwhelming number of several possible hybrid combinations may never be tested in the field. Breeders have developed statistical techniques of predicting the performance of lines in different hybrid combinations without experimentation. This has allowed the prediction of the performance of all possible three-way or double-crosses between both sets of lines using for example, the Fieldbook formulae, which were largely derived from Jenkins' method C (Vivek et al., 2007). These statistical procedures allow breeders to select with a higher intensity and precision among the predicted hybrids, and thus reduce costs of experimentation and improve genetic gain in crop breeding (Melchinger et al., 1987).

Germplasm so far gathered in ESA countries have managed to mitigate, to a large extent, effects of drought and low nitrogen conditions. Emerging challenges such as heat, low phosphorus and climate change still require augmented gene introgression from external and especially from exotic populations in order for the new hybrids to have the necessary constitution to survive and produce higher yields. While there has been a growing general awareness of these factors, there is very little evidence of concerted efforts to introduce exotic germplasm into the current gene pools to mitigate the growing impact of the less popular abiotic stress factors.

2.9 Conclusion

Breeding crops for abiotic and biotic stress tolerance and breeding crops that are responsive to the production environment such as drought, low nitrogen and low phosphorus (Bänziger et al., 2000) have always been the major objectives in plant breeding that have resulted in improved yield gain in crop productivity. The exploitation of heterosis and heritability has been complemented by the use of improved management and agronomic practices to produce higher yields in maize hybrids (Tollenaar and Lee, 2002; Kucharik and Ramankutty, 2008). Breeders who have been comfortable using their elite materials have, however, noted that, as the genetic gain slows down and stagnation occurs, novel genes have to be imported from exotic populations to rejuvenate the thresholds of the elite material. The easiest sources of exotic novel genes that can be used immediately, reside in inbreds and hybrids. These have already satisfied a market need in their places of origin and thus are ready for immediate deployment, notwithstanding the challenges of adaptation. Faster methods of introducing exotic germplasm are required to improve the turnaround time for inbred line extraction and evaluation. Using the top cross, the diallel model 1 method 4 and the NC II, exotic germplasm can be systematically and efficiently transferred into the local germplasm and enhance yield by creating new and higher yield threshold levels.

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CHAPTER 3

Identification of exotic temperate inbred lines with expired plant variety protection for use in local CIMMYT tropical breeding programmes

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3.0 Abstract

Limited genetic variability of elite tropical maize germplasm raises concern about the potential to breed for new abiotic and biotic challenges. Initiatives over the years around the globe have identified and utilised useful diversity from landraces and wild relatives of maize, but there has been limited exploitation of exotic developed products, such as inbreds and hybrids, to improve the genetic variability of elite maize. The objective of this study was to identify useful temperate inbreds for inclusion in CIMMYT tropical maize breeding programmes. Two hundred and fifty ex-Plant Variety Protection (ex-PVP) temperate inbred lines collected from the USA were top crossed with three CIMMYT single-cross testers, CML539/CML442 (A tester), CML444/CZL068 (B tester) and CML312/CML444 (AB tester). The three-way hybrids were then evaluated using an alpha (0.1) lattice design, with two replications, across eight sites, under optimal, managed drought, random stress, low nitrogen and high density conditions. Significant differences ($p<0.01$) were observed for grain yield (GY), anthesis date (AD), plant height (PH), ear position (EPO) and ear rots (ER). The highest grain yields were obtained under high plant density conditions. The test cross hybrids CML442/CML539//LH159 (7.06 t ha^{-1}), CML444/CZL068//W8304 (6.57 t ha^{-1}) and CML444/CZL068//HB8229 (6.43 t ha^{-1}) had the highest average grain yields among the test cross hybrids across sites. Significant correlations were identified between GY and PH, EPP and AD under low nitrogen and managed drought conditions. Among the top 15 GY performers, 65% involved heterotic group A lines, 30% heterotic group B lines, while only 5% were AB lines. Overall, the results demonstrated that, although the temperate x tropical crosses were susceptible to major local diseases, they were capable of conferring GY comparable to the commercial checks in their test crosses, especially under high plant density conditions. Temperate germplasm also showed genetic promise for other traits such as earliness, lower cob placement and shorter plant height.

3.1 Introduction

Maize (*Zea mays L.)* plays an important role in food security and poverty alleviation in most poor, maize dependent countries of ESA, and has an important role in livelihoods and economies of the region (Bellon et al., 2003). The global demand for food will always increase commensurate with the natural increase in human population and the natural upward dietary preferences with a sharp increase in *per capita* consumption of meat. Increasing animal production, as demand for animal products rises, requires increased grain use for improved animal feeds. Going into the future, the provision of adequate and sustainable food supply will depend more on the productivity of crops rather than on the expansion of land area under crops (Makumbi et al., 2011). One way of ensuring higher crop productivity is through the creation and utilisation of crop genetic diversity in the main food crop varieties (Ray et al., 2012). Genetic diversity is an indicator of the multiplicity of alleles and genotypes present in a population reflected by morphological and physiological differences between individuals (Gracen, 1986; Kumar et al., 2011; Ogunniyan and Olakojo, 2014). Information on genetic variability of maize inbreds and populations is important to breeders who are interested in the ability of the individual inbreds or populations to contribute to the general improvement of the genetics of the maize crop.

Breeding for biotic and abiotic stress, early maturity, grain quality and yield are top priorities to meeting the future demands for food, feed and fuel in the changing environments (Carena, 2011). Regardless of the immense breeding improvements demonstrated so far with adapted breeding materials, current germplasm still faces risks from emerging environmental threats, and this can perhaps be attributed to the existence of a narrow and diminishing genetic base (Goodman, 2004). Arguably, the most commonly used breeding procedures have contributed to the narrowing genetic base and have been responsible for the observed reduced genetic gains in some maize breeding programmes especially in the developing world (Fischer et al., 2014). The scenario demands an imperative need to adopt new breeding strategies that encourage introduction of new genes from other sources. New genes are necessary to mitigate both old and new biotic and abiotic stress factors that are prevalent in different ESA mega-environments as well as mitigate the increasing threat from climate change (Cairns et al., 2013).

Traditionally, wild relatives, germplasm accessions, existing varieties, populations and inbred lines have been used as sources of crop genetic diversity in maize improvement programmes. Hallauer et al., (2010) defined exotic germplasm as crop varieties that are not adapted to a breeder's target environments. Largely, exotic breeding materials now represent one of the most important resources for crop improvement, especially for the tropical breeding programmes (Goodman, 2005; Drinic et al., 2012). Plant breeders with exposure to exotic germplasm overwhelmingly acknowledge the usefulness of inbreds and hybrids as better sources of exotic alleles compared to populations with no history of inbreeding (Goodman, 1999; Nelson and Goodman, 2008; Fan et al., 2010). Maize inbreds and hybrids are therefore the preferred sources of exotic novel genes for inclusion in local breeding programmes because they have already been subjected to multiple cycles of inbreeding and selection.

Introduction of exotic temperate maize genes into tropical breeding programmes has the potential to rejuvenate and improve the agronomic and trait performance of tropical germplasm, and break the impending genetic caps or thresholds. Mature breeding programmes are well grounded on historic and heterotic patterns and not many breeders are willing to destabilise this status quo. Goodman (2005) suggested the introduction of exotic germplasm through slow integration into the established breeding programmes. Some researchers have adopted this slow integration approach for different crops. In wheat, the use of temperate germplasm to introduce useful genetic variation was reported by Trethowan and Mujeeb-Kazi (2008). In maize, Hallauer and Carena (2013) used stratified mass selection at the phenotypic level to successfully generate populations with 25 to 100% tropical germplasm that could be readily used in temperate breeding programmes to achieve new levels of yield potential.

Due to numerous challenges associated with exotic germplasm, many of the uses have been restricted to population development rather than inclusion in the final products. Limited studies exist where temperate germplasm is incorporated into tropical backgrounds, and most of the available research has principally focused on introducing tropical germplasm into temperate breeding programmes (Goodman, 1999; 2005; Nelson and Goodman, 2008). Little is currently known on the usefulness of temperate germplasm in tropical x temperate crosses adapted to tropical conditions. Information deduced from these studies is important in understanding how temperate x tropical hybrids perform under mid-altitude tropical conditions. Furthermore, the success of breeding with exotic germplasm is largely dependent on the choice of parents (Tester and Langridge, 2010). Most of the temperate germplasm are yellow in colour and this has affected the acceptance and adoption rates of these materials in the ESA region where white maize is mostly preferred. In addition, most temperate inbred lines are susceptible to the common diseases, such as maize streak virus (MSV), Northern corn leaf blight (*Exserohilum turcicum)* and grey leaf spot (*Cercospora zea-maydis*).

The availability of exotic inbred lines to plant breeders has always been restricted by the Intellectual Property Protection (IPP) laws, of which Plant Variety Protection Act (PVPA) is the most globally used form. Maize inbred lines with expired PVPA certificates are publicly available and potentially represent a new germplasm bank for many public and private breeding programmes. In order to facilitate easier access to such germplasm, following expiration of their PVP status, the Multilateral System under the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) was established. This treaty is an international agreement adopted under the aegis of the United Nations' Food and Agricultural Organisation (FAO) in 2001. It entered into force in 2004 (Kurtz et al., 2016). The Treaty has created a Multilateral System (MLS) of access and benefit-sharing providing facilitated access to plant genetic resources for food and agriculture. Subsequently, access to exotic germplasm has been greatly facilitated. However, breeders are still faced with the challenge of recognising the best combiners from a myriad of available genotypes from the gene banks for use in local breeding programmes.

The focus of this study was to identify temperate inbred lines that could enhance the grain yield potential and trait performance of adapted tropical germplasm in the presence of biotic and abiotic stress factors and for intensive and large scale incorporation into the CIMMYT tropical breeding programmes. It is hypothesised that temperate maize inbred lines can augment the grain yield potential of local tropical maize germplasm through favourable trait enhancement.

3.2 Materials and methods

3.2.1 Germplasm

A total of 250 temperate inbred lines were collected from the USA through the collaboration of breeders from CIMMYT-Mexico and Cornel University in USA. During the collection process, the collaborators ensured that the selected inbred lines were constituents of previously successful commercial hybrids in the USA and were confirmed as ex-PVP inbreds in order to avoid challenges with IPP laws. Inbred lines were also selected on the basis of some unique characteristic, such as disease and lodging resistance, among other favorable agronomic traits. All the inbred lines were planted in Muzarabani in Zimbabwe (latitude 17^{o}48’ S, longitude, 31^{o}02’ E and altitude, 570 masl) during the winter season of 2015. All the 250 inbred lines flowered and produced enough seed.

The temperate inbred lines belonged to different heterotic groups by USA standards (Table 3.1). USA breeders broadly classify material as either stiff stalk (SS), Iodent (IO) or non-stiff stalk (NSS) (Fasahat et al., 2016). The SS group is further divided into B37, B73 and Amargo, which were assigned to CIMMYT heterotic group A while NSS is further divided into Mo17, OH43, OH7 and LH82 and were assigned to CIMMYT heterotic group B. The rest of the inbreds with mixed or unknown USA heterotic groups were assigned to CIMMYT heterotic group AB.

Table 3.1 Temperate inbred lines and their USA heterotic groups

Ent	Name	HG	Ent	Name	HG	Ent	Name	HG	Ent	Name	HG	Ent	Name	HG
1	PHJ40	SS	51	LH199	B73	101	PHM1	Iodent	151	IB02	Iodent/OH43	201	78371A	NSS
2	PHAA0	SS	52	LH197	B73	102	PHW5	Iodent	152	PHR4	Iodent-Mixed	202	LH85	NSS
3	PHTE4	SS	53	F118	B73	103	PHV57	Iodent	153	8M12	M017	203	LH123H	OH43
4	PHEM9	SS	54	LH209	B73	104	207	Iodent	154	LH21	Mo17	204	PHG47	OH43
5	AQA3	SS	55	NL001	B73	105	PHKE	Iodent	155	LH59	Mo17	205	LH212H	OH43
6	LH223	SS	56	6F629	B73	106	PHFA5	Iodent	156	LH21	Mo17	206	PHK76	OH43
7	PHT69	SS	57	LH193	B73	107	PHAW	Iodent	157	78551	Mo17	207	PHRD6	OH43
8	MQ305	SS	58	LH192	B73	108	3IJI1	Iodent	158	LH18	Mo17	208	ICI581	OH43
9	PHN66	SS	59	LH191	B73	109	91IFC2	Iodent	159	LH18	Mo17	209	PHR30	OH43
10	FBLA	SS	60	LH190	B73	110	PHTM	Iodent	160	LH21	Mo17	210	LH127	OH43
11	PHW51	SS	61	LH220H	B73	111	PHR31	Iodent	161	LH21	Mo17	211	LH211	OH43
12	PHV07	SS	62	LH206	B73	112	PHK74	Iodent	162	Lp21	Mo17	212	LH156	OH43
13	RS 710	SS	63	LH204	B73	113	PHGW	Iodent	163	BCC0	Mo17	213	LH93	OH43
14	1538	SS	64	PHJ70	B73	114	83IBI3	Iodent	164	LH16	Mo17	214	LH82	LH82
15	HB8229	SS	65	4N506	B73	115	PHJ89	Iodent	165	LH16	Mo17	215	LH172	LH82
16	FBHJ	SS	66	W8555	B73	116	PHW8	Iodent	166	E850	Mo17	216	LH166	LH82
17	BO9	SS	67	CR14	B73	117	PHW0	Iodent	167	S8326	Mo17	217	LH167	Mo17/LH
18	PHHB4	B37	68	2369	B73	118	PHP76	Iodent	168	LH65	Mo17	218	LH165	LH82/Mo
19	PHEG9	B37	69	S8324	B73	119	PHK46	Iodent	169	740	Mo17	219	LH184	OH43/Mo
20	PHBB3	B37	70	LH149	B73	120	PHJ65	Iodent	170	MBP	Mo17	220	LH214	OH43/Mo
21	PHMK0	B37	71	W8304	B73	121	PHW4	Iodent	171	LH61	Mo17	221	LH213	OH43/Mo
22	PHEW7	B37	72	793	B73	122	PHT22	Iodent	172	LH60	Mo17	222	LH284	OH43/Mo
23	PHVA9	B37	73	790	B73	123	PHR63	Iodent	173	LH52	Mo17	223	PHR03	Oh7
24	PHT47	B37	74	PB80	B73	124	PHR62	Iodent	174	LH57	Mo17	224	PHN46	Oh7
25	PHP85	B37	75	PHG86	B73	125	PHP60	Iodent	175	LH54	Mo17	225	PHR55	Oh7
26	PHW20	B37	76	LH146H	B73	126	PHP55	Iodent	176	MBN	Mo17	226	PHBA6	Oh7/OH4
27	PHV37	B37	77	794	B73	127	PHN73	Iodent	177	MM5	NSS	227	PHK56	Oh7/OH4
28	PHT55	B37	78	764	B73	128	PHN37	Iodent	178	MM4	NSS	228	899	Mixed
29	807	B37	79	78002A	B73	129	PHM5	Iodent	179	MBW	NSS	229	PHN41	Unknown
30	778	B37	80	78010	B73	130	PHJ75	Iodent	180	LH15	NSS	230	PHHH9	Unknown
31	4676A	B37	81	78004	B73	131	PHJ33	Iodent	181	CS60	NSS	231	904	Unknown
32	6103	B37	82	PHW52	B73/Amarg	132	PHJ31	Iodent	182	PHT7	NSS	232	OQ403	Unknown
33	FAPW	B37	83	OS602	SS/Amargo	133	PHW7	Iodent	183	PHG	NSS	233	ICI 986	Unknown
34	FBLL	B73	84	PHVJ4	SS/Iodent-	134	PHN47	Iodent	184	OQ10	NSS	234	ICI 193	Unknown
35	LH132	B73	85	PHG71	SS/Iodent-	135	IBB14	Iodent	185	LH16	NSS	235	912	Unknown
36	LH208	B73	86	PHRE1	Amargo/SS	136	PHW6	Iodent	186	LIBC	NSS	236	911	Unknown
37	LH202	B73	87	PHBW8	Amargo/SS	137	PHV63	Iodent	187	MBU	NSS	237	PHW30	Unknown
38	LH196	B73	88	PHT11	Amargo/SS	138	PHT77	Iodent	188	MBSJ	NSS	238	PHR58	Unknown
39	LH205	B73	89	PHHV4	Amargo/SS	139	PHN11	Iodent	189	29MI	NSS	239	PHK93	Unknown
40	LH195	B73	90	L 155	Amargo/SS	140	PHK42	Iodent	190	PHM	NSS	240	PHK35	Unknown
41	87916W	B73	91	PHR61	Amargo/SS	141	PHV78	Iodent	191	6M50	NSS	241	L 139	Unknown
2	H8431	B73	92	PHP02	Iodent	142	IBB15	Iodent	192	LH16	NSS	242	L 135	Unknown
43	LH198	B73	93	3IIH6	Iodent	143	PHR36	Iodent	193	WIL9	NSS	243	L 127	Unknown
44	PHJR5	B73	94	PHR25	Iodent	144	PHG72	Iodent	194	WIL9	NSS	244	PHT60	Unknown
45	LH200	B73	95	PHTD5	Iodent	145	PHZ51	Iodent	195	WIL9	NSS	245	PHKM5	Unknown
46	LH224	B73	96	PHN82	Iodent	146	PHG84	Iodent	196	PHM	NSS	246	PHV53	Unknown
47	PHPR5	B73	97	PHN18	Iodent	147	PHG83	Iodent	197	2MA	NSS	247	ICI 740	Unknown
48	CS405	B73	98	IBC2	Iodent	148	IB014	Iodent	198	6M50	NSS	248	ICI 441	Unknown
49	ICI 893	B73	99	PHG29	Iodent	149	G80	Iodent	199	11430	NSS	249	J8606	Unknown
50	LH222	B73	100	PHJ90	Iodent	150	PHN29	Iodent	200	787	NSS	250	WIL500	Unknown

HG-heterotic group, Ent-Entry, SS-stiff stalk, NSS-non-stiff stalk,

3.2.3 Trial evaluation

The test crosses were evaluated alongside eight commercial hybrid checks and nine CIMMYT hybrids (already commercialised varieties that came from the CIMMYT pipeline) at all the sites using an alpha (0.1) lattice design (Patterson and Williams, 1976). While the concept of using a single tester to screen a large number of inbred lines has been deemed adequate for the initial screening (Nelson and Goodman, 2008; Badu-Apraku et al., 2017), the concept of testing under multiple sites in a single season is becoming common following the recommendations of Sprague and Eberhart (1977). All temperate test crosses (TCTemp) with inadequate seed were replaced with CIMMYT hybrids at planting without changing the design. A total of 243 tropical x temperate hybrids had sufficient seed and were evaluated in the 2016 winter season under managed drought at Chiredzi and Chisumbabje, and in the 2016-2017 summer season at the other sites. The total trial had 260 hybrids and was replicated twice on each site. Each replicate accommodated 26 incomplete blocks each with a block size of 10 plots. All test crosses evaluated in this study were 50% temperate x 50% local tropical hybrids. The working assumption was that 50% of the characters of the hybrids were derived from the temperate inbred lines. The conclusions made using the performance data of the hybrids were considered as true representation of the performance of the respective inbred lines.

3.2.4 Trial management

The hybrids were planted in one 4 m row plots with an inter-row spacing of 0.75 m and an in-row spacing of 0.25 m at all sites (Table 3.3), targeting a plant population of about 53 333 plants ha^{-1} (the generally recommended population in commercial production at CIMMYT). Two kernels were planted at each planting station and thinned out at between five and seven-leaf stages to one plant per station, giving 17 plants per row. For the high density trials 80 000 plants ha^{-1} were targeted by systematically thinning out to 25 plants per row. Basal dressing fertiliser [8% nitrogen (N): 14% phosphorus (P): 7% potassium (K)] was applied at a rate of 400 kg ha^{-1} and top dressing feriliser (ammonium nitrate: 34.5% N) was applied at a rate of 300 kg ha^{-1} in all sites. To mitigate randomly occurring pests, two routine sprays of a synthetic pyrethroid, karate (Lambda-cypermethrin) and Belt (Flubendiamide) were effected to control fall army worm (*Spodoptera frugiperda*). African maize stem borer (*Busseola fusca*) was controlled using Dipterex (Trichlorfon) granules (approximately 0.1 g dropped in individual plant funnels immediately after thinning out).

At the random stress site (Kadoma), all randomly occurring stress factors were allowed to affect the maize naturally. These were taken to represent real small scale farmers' field conditions, without irrigation. Optimum sites received supplementary irrigation when necessary, but no supplementary irrigation was applied under random stress. The managed drought sites are located in the southern eastern Lowveld of Zimbabwe (Chiredzi and Chisumbanje). This region does not receive any rainfall during the dry season stretching from May to October. All crop water requirements are therefore supplied through irrigation. Traditionally for drought tolerance evaluation in maize, irrigation is withheld two weeks before anthesis and only resumed two weeks after anthesis. However, light irrigation was done to ensure crop survival when conditions were too dry.

The CIMMYT low nitrogen site was used for the low-N trials. Nitrogen depletion for this site has been achieved through repeatedly and continuously growing of non-leguminous crops on the same plot and the non-use of nitrogenous fertilizers, followed by the removal of crop residues from the plots. This process has been repeated for the past ten years on the same plot. The CIMMYT low phosophorus site that was used for the low-P trials has been depleted for the past seven years through the same process as for the low nitrogen site, by repeatedly growing non-leguminous crops, non-use of phosphate fertilizers and removal of crop residues from the plots immediately after harvesting.

Grain yield and the other agronomic traits recorded are shown in Table 3.3. Diseases were not recorded at the drought sites, because due to low humidity during the dry season, diseases do not normally manifest (Bänziger et al., 2000).

Table 3.2 Agronomic traits measured and derived for the temperate x tropical TCTemp crosses

Trait	Units
Grain yield (GY)	t ha^{-1}
Anthesis date (AD)	Days to 50% pollen shed
Days to silking (SD)	Days to 50% protruding silk by 2-3 cm
Ear aspect (EA)	Scale 1-5 (1 being big, good and disease free)
Plant height (PH)	From ground to first branch of tassel (cm)
Ear height (EH)	From ground to node subtending ear (cm)
Ear position (EPO)	Ratio EH/PH
Ears per plant (EPP)	Total ear number, of ears including secondary ears
Ear rot (ER)	% of rotten cobs as a proportion of total cobs
Husk cover (HC)	Scale 1-5 (1 being completely covered at the tips)
Moisture content (MOI)	% measured using a moisture meter
Texture (TEX)	Scale 1-5 (1 being flint and 5 being dent)
Stem lodging (SL)	% plants with broken stem above ground below the cob

3.2.5 Evaluation sites

The eight sites used in this trial represent the traditional testing sites of CIMMYT, which and ESA (Table 3.3). Yang (2009) recommended breeding for adaptation to be best done under challenging environmental conditions where strengths and weaknesses are quickly identified and most stable genotypes are selected.

Table 3.3 Evaluation sites for the tropical x temperate (TCTemp) test cross trials

Site	Agro-ecological region	Annual rainfall (mm)	Latitude	Longitude	Altitude (masl)	Soil type	Growing environment
ART Farm Harare	IIa	820	17°43’S	31005’E	1 480	Harare 5E series	High density
Chiredzi	V	-	21°02’S	31°58’ E	433	Triangle E series	Managed drought
Chisumbanje	V	-	20°45’S	32°13’ E	540	Chisumbanje Montmorillonite expanding clays	Managed drought
Kadoma	III	800	18°32’S	30°90’ E	1155	Clays	Random stress
CIMMYT Harare-OPT	IIa	820	17°43’S	31^{0}05’E	1 480	Harare 5E series	Optimal
CIMMYT Harare-HD	IIa	820	17°43’S	31^{0}05’E	1 480	Harare 5E series	High density
CIMMYT Harare-HA3LN	IIa	820	17°43’S	31^{0}05’E	1 480	Harare 5E series	Low nitrogen
Ratteray Arnold	IIa	865	17°40’ S	31°05’ E	1369	Harare 5G2 series	Optimal

3.2.6 Data analysis

Preliminary data checking and individual site analysis of variance (ANOVA) were performed using the CIMMYT Fieldbook software (Bänziger and Vivek, 2007). Across-site ANOVA, trial means and mean separation using Tukey’s honestly significant difference test (HSD) also called the Tukey’s studentised range test, were further performed, using the *aov* and HSD test functions, respectively, in the Agricolae R package (R Foundation for Statistical Computing, 2017). Heritability values and the genetic correlations between traits were estimated using the Multi-Environment Trial Analysis with R (META-R) version 5.0 (Alvarado et al., 2015).

3.3 Results

3.3.1 Analysis of variance for grain yield for individual sites

The test cross grain yield performance was highly significantly different ($p<0.01$) for CIMMYT Harare-OPT, CIMMYT Harare-HD, Kadoma-RS, Chiredzi and Rattray Arnold-HD (Table 3.4). Grain yield performance was significant ($p>0.05$) at CIMMYT Harare-LN and ART farm-HD. Non-significant differences for grain yield were noted only at Chisumbanje-MD. Broad-sense heritability (H) for grain yield was high at most growing environments except under managed drought. For instance, H for GY at the Chisumbanje site was 0.05 while Chiredzi showed H of 0.21 for GY.

Table 3.4 Individual site analysis of variance for grain yield of the temperate TCTemp test crosses planted at eight sites during the 2015-2016 seasons in Zimbabwe

Source of Variation	Degrees Freedom	CIMMYT Harare OPT	CIMMYT Harare HD	CIMMYT Harare LN	ART Farm HD	Kadoma RS	Chisumbanje MD	Chiredzi MD	Rattray Arnold OPT
Replication	1	9.43**	0.03*	61.42*	105.6***	13.95***	19.65***	50.53***	156.4***
Entry	259	6.12***	4.98***	3.63*	3.36*	0.95***	0.55	1.17***	8.04***
Block/Replication	50	1.98***	0.91***	1.07	2.46	0.59***	0.76*	2.35***	4.19
Residuals	209	0.89	0.47	0.74	6.5	0.31	0.48	0.54	3.6
Entry Variance		2.26	2.59	1.43	2.43	0.29	0.01	0.07	1.09
Mean		6.76	5.07	4.23	5.54	3.61	1.89	2.67	5.09
LSD		1.43	1.98	1.75	2.29	1.15	1.42	1.58	2.73
CV		10.71	19.77	20.94	20.95	16.16	38.3	30.06	27.21
Heritability (broad-sense)		0.9	0.85	0.79	0.79	0.66	0.05	0.21	0.55

* $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, OPT- optimal, HD-high density, LN- low nitrogen RS- random stress, MD-managed drought, LSD-least significant difference, CV-coefficient of variation ,

3.3.2 Across sites variance components for grain yield and other traits

The mean squares from the analysis of variance across the eight sites showed highly significant differences ($p<0.001$) in entry performance for GY and other agronomic traits (Table 3.5). The mean squares were also significant ($p<0.01$) for HC and only significant ($p<0.05$) for EPP and MOI. Non-significant mean squares were noted for ASI. Interaction effects of entry x environment was highly significant ($p<0.01$) across all sites. Across sites H (the broad-sense) for individual traits ranged from 3% for EPP to 91% for AD.

3.3.3 Mean grain yield performance and agronomic characteristics across sites

The highest mean for GY and the relative grain yield percentage (Table 3.6) expressed as a percentage of the trial mean was obtained from a commercial single-cross check SC727 (8.57 t ha^{-1}). The top five test crosses in terms of grain yield that surpassed the overall grand mean by more than one tonne per hectare of the test crosses of 4.36 t ha^{-1} (Table 3.8) were CML442/CML539//LH159 (7.06 t ha^{-1}), CML444/CZL068//W8304 (6.57 t ha^{-1}), CML444/CZL068//HP8229 (6.43 t ha^{-1}), CML444/CZL068//LH190 (6.11 t ha^{-1}) and CML444/CZL068//PHJ140 (6.05 t ha^{-1}). These competed well with commercial check varieties PAN 53 (7.04 t ha^{-1}) and PHB30G19 (6.19 t ha^{-1}). For the CIMMYT checks, (CZH-CIMMYT Zimbabwe Hybrid), the highest mean GY was recorded for CZH131001 (8.77 t ha^{-1}), CZH131011 (8.74 t ha^{-1}), CZH13113 (8.15 t ha^{-1}) and CZH131007 (8.05 t ha^{-1}) (Appendix 3.1 fives the names and the entry numbers summarised in Table 3.8).

The GY mean differences among the entries are shown as the mean separation using the Tukey-HSD test for GY (for top and bottom 15 entries) across the eight sites (Table 3.7). There was variable GY performance of the test crosses in different environmental conditions (Table 3.8). The highest mean GY was obtained under high density conditions by a commercial single-cross check SC727 (12.6 t ha^{-1}). The lowest average GY was obtained under managed drought with a minimum of 1.03 t ha^{-1} and a maximum grain yield of 3.52 t ha^{-1}. The relative GY rankings of the entries also varied among environmental conditions.

Table 3.5 Analysis of variance and heritability for yield and other traits across eight sites

Source of variation	DF	Grain Yield (t ha^{-1})	Anthesis date	Anthesis silking interval	Plant height	Ear height	Ear position	Stem lodging	Ears per plant	Husk cover	Ear rots	Grain texture	Grain moisture	Ear aspect
Site	7	1320***	2658***	295.02	32822***	101264***	0.314***	49394***	2.85***	2999.8**	76019***	137.6***	2790.5**	230.1***
Replication	1	44.84***	683***	26.598**	2618***	14652***	0.063***	8239***	0.08*	6010.9**	7057***	3.251***	0.8	9.09***
Entry	259	13.96***	103***	27.297	154***	1354***	0.017***	125***	0.02*	166.5**	326***	1.342***	42.6**	1.21***
Replication: Block	50	3.51***	31.3***	28.560	72***	470***	0.007***	322***	0.03***	199.3**	436***	0.781***	14.8**	1.59***
Site: Entry	1813	1.92***	9.1***	28.119	25***	176***	0.004**	124***	0.02	137.8**	168***	0.333***	5.5**	0.51***
Site: Replication: Block	357	2.29***	28.2***	29.805	78***	414***	0.006***	356***	0.03***	197.7***	255***	0.317***	7.3**	0.69***
Residuals	1664	0.81	6.9	25.563	18	141	0.003	3.54	0.02	94.7	141	0.229	1.9	0.32
Heritability (broad-sense)		0.87	0.91	0.55	0.86	0.88	0.77	0.15	0.03	0.16	0.48	0.76	0.87	0.59

* $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$. DF- Degrees of Freedom

Table 3.6 Best Linear Unbiased Predictors for grain yield and other agronomic traits for the top 40 temperate inbreds crossed with CIMMYT testers evaluated across eight sites

Entry	Female	Male	Male	GY %	GY	MOI	AD	ASI	PH	EH	SL	ER	HC	EA
260	SC727	SC727	CC	177	7.83	21.37	67.14	0.79	222.00	120.30	12.05	14.41	9.86	3.42
180	SXTA//LH	LH159	B	150	6.42	17.22	63.84	0.65	189.00	85.38	6.76	18.37	2.24	3.20
258	PAN53	PAN5	CC	141	6.39	20.54	68.94	0.66	204.00	102.40	9.97	14.86	3.54	3.28
15	SXTB//HB	HB822	A	135	6.06	16.82	65.85	0.51	184.00	95.38	8.70	18.16	13.00	3.65
71	SXTB//W8	W8304	A	141	5.97	15.94	66.93	0.43	200.00	104.90	9.76	12.17	6.42	3.74
43	SXTB//LH	LH198	A	124	5.63	17.25	64.22	1.09	176.00	85.07	9.62	6.07	6.31	3.46
220	SXTA//LH	LH214	B	124	5.59	15.47	62.41	1.57	187.00	84.92	7.79	27.49	10.10	4.10
1	SXTB//PH	PHJ40	A	128	5.59	17.37	61.69	1.86	177.00	84.65	13.49	20.51	14.00	3.67
60	SXTB//LH	LH190	A	128	5.57	15.72	66.18	1.28	209.00	105.30	9.95	12.75	7.41	3.64
203	SXTA//LH	LH123	B	121	5.55	16.44	61.95	1.36	191.00	87.74	2.84	25.93	10.90	3.95
39	PHB30G1	PHB3	CC	127	5.53	19.78	67.76	0.15	206.00	107.20	6.70	22.85	2.79	3.27
221	SXTA//LH	LH213	B	127	5.53	16.70	62.64	1.51	193.00	84.00	6.52	34.50	5.75	3.89
128	SC637	SC637	CC	118	5.47	20.14	68.40	0.93	209.00	110.10	7.55	20.16	3.72	3.45
238	SXTAB//P	PHR5	AB	120	5.46	16.42	64.55	0.85	201.00	97.31	14.02	15.88	10.80	3.75
156	SXTB//LH	LH210	A	128	5.41	16.26	63.87	1.07	190.00	90.86	5.20	10.51	4.40	3.51
51	SXTB//LH	LH199	A	125	5.38	16.07	64.40	0.79	188.00	87.79	5.56	13.41	6.31	3.30
12	SXTB//PH	PHV0	A	123	5.33	17.90	68.53	0.51	196.00	107.70	7.18	8.83	3.43	3.08
134	SXTB//PH	PHN4	A	123	5.29	16.36	68.47	0.23	193.00	99.26	3.26	11.15	-0.62	3.91
178	SXTA//M	MM40	B	122	5.28	14.85	63.05	1.37	191.00	79.99	9.96	19.16	7.15	3.96
68	SXTB//23	2369	A	121	5.26	16.49	66.18	0.79	202.00	106.10	14.85	16.94	8.47	3.68
19	SXTB//PH	PHEG	A	117	5.22	16.05	66.13	0.85	200.00	100.40	12.52	12.93	8.25	3.70
195	SXTA//WI	WIL90	B	115	5.20	16.65	63.99	0.93	190.00	89.79	7.63	18.03	8.56	3.49
138	SXTB//PH	PHT77	A	113	5.18	15.46	61.42	1.07	191.00	88.06	9.69	18.35	17.40	3.99
158	SXTB//LH	LH181	A	117	5.17	15.70	62.19	1.52	187.00	86.11	6.18	21.21	0.47	3.44
131	SXTB//PH	PHJ33	A	121	5.17	15.23	63.60	0.72	185.00	92.35	6.11	18.28	6.45	3.87
80	SXTB//78	78010	A	112	5.15	15.10	61.23	1.36	183.00	93.80	11.94	13.02	3.40	3.94
149	SXTB//G8	G80	A	114	5.15	15.39	58.65	1.23	188.00	90.22	10.18	27.76	9.28	4.06

Table 3.6 (cont.) Best Linear Unbiased Predictors for GY and other agronomic traits for the top 40 temperate inbred lines

Entry	Female	Male	Male	GY %	GY	MOI	AD	ASI	PH	EH	SL	ER	HC	EA
170	SXTA//M	MBP	B	116	5.14	14.98	61.61	1.29	199.00	87.60	11.41	16.22	7.10	3.90
65	SXTB//4N	4N506	A	124	5.13	15.42	64.73	0.93	205.00	108.00	8.78	15.14	11.40	3.73
205	SXTA//LH	LH212	B	118	5.11	15.74	61.20	1.35	186.00	88.40	7.09	18.72	6.99	3.68
155	SXTB//LH	LH59	A	119	5.10	16.04	63.90	22.28	193.00	90.08	7.93	21.33	3.16	3.90
84	SXTB//PH	PHVJ4	A	118	5.06	13.57	60.12	1.36	192.00	89.27	9.25	21.89	17.40	3.70
126	SXTB//PH	PHP55	A	118	5.06	15.12	63.87	0.51	192.00	92.16	8.42	22.35	12.10	3.80
86	SXTB//PH	PHRE	A	113	5.05	14.28	58.65	1.35	193.00	96.10	5.51	20.43	10.10	3.92
179	SXTA//M	MBW	B	112	5.04	15.08	61.33	0.35	183.00	87.30	12.47	19.10	8.13	3.92
177	SXTA//M	MM50	B	121	5.04	14.53	60.66	1.50	181.00	75.79	5.43	11.93	6.48	3.74
18	SXTB//PH	PHHB	A	121	5.03	16.34	66.52	1.01	193.00	86.62	11.99	17.92	1.77	3.74
91	SXTB//PH	PHR6	A	115	5.02	15.88	65.27	0.93	201.00	96.90	11.20	11.68	5.18	3.45
127	SXTB//PH	PHN7	A	117	5.00	15.37	61.10	0.93	191.00	90.25	8.57	14.90	6.00	3.75
209	SXTA//PH	PHR3	B	52	2.30	11.39	59.34	0.93	171.00	70.00	6.75	12.77	9.66	3.82
184	SXTA//O	OQ101	B	48	2.10	12.97	54.74	1.28	163.00	68.57	6.99	23.16	10.20	3.98
245	SXTAB//P	PHKM	AB	48	2.08	13.31	55.02	1.02	158.00	69.78	2.37	14.74	3.44	4.00
202	SXTA//LH	LH85	B	48	2.08	13.17	57.92	1.57	165.00	68.14	8.74	16.01	13.40	4.06
182	SXTA//PH	PHT73	B	45	1.98	13.17	57.29	0.22	166.00	63.28	7.59	28.66	7.16	4.15
Site Variance				2.45	3.38	595.70	0.53	0.43	0.00	0.00	0.26	38.92	5.09	179.6
Entry Variance				0.77	6.58	77.06	0.00	0.04	4.79	0.00	0.06	3.07	2.22	71.32
Site x Entry Variance				0.51	0.97	11.59	0.68	0.07	0.06	0.00	0.05	18.04	1.60	6.64
Residual Variance				0.81	6.78	184.90	50.62	0.32	55.30	0.00	0.23	93.61	1.91	140.0
Mean				4.36	62.87	186.70	1.08	3.80	5.45	0.47	3.98	8.41	15.10	88.91
LSD				0.96	2.25	10.41	5.35	0.49	14.90	0.04	0.40	11.46	1.60	8.89
CV				11.18	1.82	2.84	52.79	6.53	138.00	4.62	5.11	69.42	5.43	5.10
Heritability				0.87	0.91	0.86	0. 20	0.59	0.15	0.77	0.76	0.16	0.87	0.88

SXTA-Single-Cross Tester heterotic group A, SXTB- Single-Cross Tester heterotic group B, SXTAB- Single-Cross Tester heterotic group AB, GY- grain yield, MOI-moisture, AD-anthesis date, PH-plant height, EH-ear height, SL-stem lodging, ER-ear rots, HC-husk cover, EA- ear aspect, LSD- Least Significant Difference, CV-coefficient of Variation, CC-commercial check

Table 3.7 Grain yield means (for top and bottom 15 entries) across the eight sites, separated using the Tukey-HSD test

Entry	Yield (t ha^{-1})	Groups	
255	7.896	A	
163	7.893	A	
260	7.713	Ab	
256	7.371	Abc	
233	7.282	Abcd	
211	7.031	Abcde	
252	6.877	Abcdef	
254	6.588	Abcdefg	
180	6.416	Abcdefgh	
251	6.356	Abcdefghi	
258	6.321	Abcdefghij	
15	6.089	Bcdefghijk	
71	5.987	Cdefghijkl	
60	5.653	Cdefghijklm	
39	5.581	Defghijklmn	
1	5.578	defghijklmn	Top 15 hybrids
197	3.079	qrstuvwxyz12345	Bottom 15 hybrids
122	3.043	rstuvwxyz12345	
232	3.037	stuvwxyz12345	
199	3.034	tuvwxyz12345	
13	2.827	uvwxyz12345	
164	2.809	vwxyz12345	
165	2.768	wxyz12345	
192	2.759	wxyz12345	
117	2.634	xyz12345	
87	2.421	yz12345	
209	2.319	z12345	
190	2.292	12345	
184	2.126	2345	
202	2.090	345	
245	2.056	45	

Table 3.8 Mean grain yield performance of temperate x tropical TCTemp test crosses under different environmental conditions (Entry names in Appendix 3.1)

	High density		Optimal conditions		Managed drought		Low Nitrogen		Random stress	
	Entry	(t ha-1)	Entry	(t ha^{-1})	Entry	(t ha^{-1})	Entry	(t ha^{-1})	Entry	(t ha^{-1})
	Top 20 hybrids									
	260	12.6	163	11.91	25	3.52	255	8.98	255	5.1
	255	11.61	256	11.51	195	3.47	163	8.89	91	5.02
	256	10.77	255	10.99	88	3.42	254	8.26	70	4.98
	163	10.52	252	10.97	20	3.39	233	8.24	163	4.98
	233	9.9	233	10.81	222	3.27	252	8.21	71	4.96
	258	9.34	211	10.8	176	3.23	211	7.85	66	4.96
	128	9.17	260	10.38	26	3.12	256	7.72	211	4.9
	180	9.11	254	10.28	179	3.1	258	7.2	42	4.85
	252	8.69	258	9.51	36	3.02	251	6.92	178	4.85
	254	8.66	251	9.26	81	3.02	260	6.77	154	4.82
	211	8.59	15	8.03	232	2.93	43	6.73	92	4.78
	251	8.55	180	8	182	2.91	180	6.63	23	4.75
	71	8.2	203	7.63	246	2.91	1	6.46	147	4.74
	15	8.18	221	7.54	51	2.9	39	6.41	131	4.72
	253	8	220	7.53	15	2.89	238	6.29	138	4.67
	220	7.91	60	7.5	49	2.89	158	6.22	205	4.64
	11	7.87	39	7.49	99	2.89	187	6.15	238	4.59
	134	7.82	71	7.47	43	2.88	178	6.14	1	4.57
	81	7.81	158	7.32	106	2.87	15	6.12	18	4.54
	39	7.79	65	7.3	59	2.86	203	6.12	252	4.54
	Bottom five hybrids									
	190	3.42	190	2.07	256	1.32	209	1.64	165	2.14
	117	3.31	184	1.8	208	1.13	182	1.54	215	2.09
	184	3.28	202	1.74	181	1.08	245	1.51	81	2.08
	202	2.61	182	1.68	13	1.08	184	1.44	174	1.87
	245	2.46	245	1.58	98	1.03	202	1.22	212	1.81
Grand mean		5.93		5.3		2.28		4.23		5.3
Mean (commercial checks)		6.19		5.85		2.06		4.62		3.7
Mean (local checks)		8.05		7.64		1.59		5.47		3
LSD		1.69		1.6		1.03		1.76		1.6
CV		14.49		15.35		22.94		20.9		15
Heritability (broad sense)		0.82		0.89		0.34		0.76		0.9

LSD- Least Significant Difference, CV-coefficient of Variation

3.3.4 Frequency distribution of disease scores, anthesis dates and plant heights across sites

Frequency distributions for disease scores, anthesis dates (Figure 3.1) and plant heights (Figure 3.2) revealed presence of wide variability in their distribution. The best TCTemp hybrid scores for Turcicum (Northern corn leaf blight) were obtained by SXTA//LH60 (2.4), SXTB//LH202 (2.7) and SXTB //PHV07 (2.7). The best test cross scores for grey leaf spot (GLS) was obtained from SXTB//PHN73 (2.3), SXTAB//WIL500 (2.4) and SXTA //LH60 (2.4). MSV scores were less severe and their distribution was less continuous than those of the other diseases. The best test cross scores for MSV were SXTB //807 (2.0) and SXTA//LH60 (2.4) (Appendix 3.1). The highest cob rots recorded were 46% with a minimum of 4%. The best TCTemp hybrids against cob rots were SXTAB//PHHH9 (4.4%), SXTAB//LH60 (5.4%) and SXTB //LH60 (6.4%). The test cross resistance against cob rots was better than all the entries, including commercial checks (Names of entries and commercial checks in Appendix 3.1).

The distribution of anthesis dates ranged from 54 to 70 days with a mean of 62 days. PH was continuous distributed with 75% of the plants under 2 m tall (Figure 3.2).

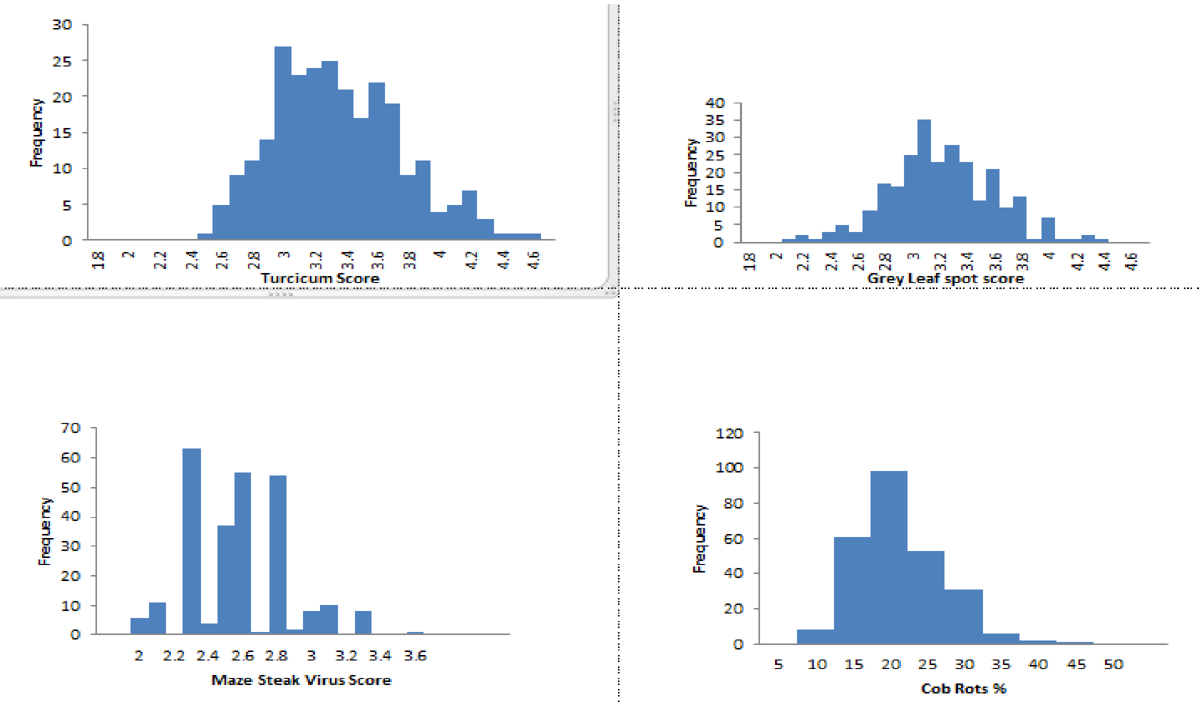

Figure 3.1 Disease reaction variability for temperate x tropical TCTemp test crosses across eight sites

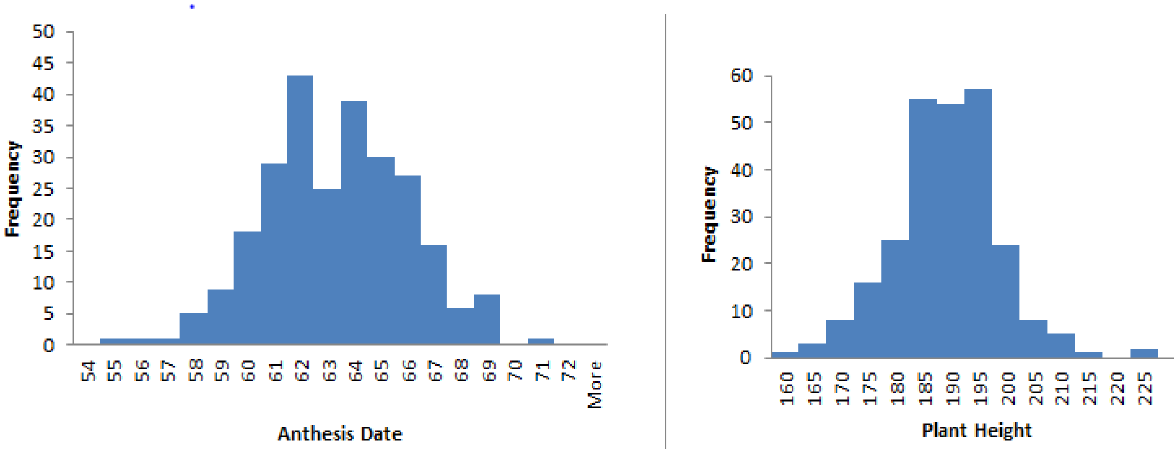

Figure 3.2 Anthesis date and plant height variability for temperate x tropical TCTemp test crosses across eight sites

3.3.5 Genotypic correlations between grain yield and other traits under different environmental conditions

Grain yield exhibited significant (p<0.01) to highly significant (p<0.001) and strong positive correlations (Table 3.9) with EA, ASI, EPO and EH in all the environments, although the relationship was much weaker under managed drought for EH (r=0.18), ASI (r = 0.18) respectively and for EA (r = 0.34). On the other hand, negative and significant correlations were observed between GY and AD under all environmental conditions. Anthesis dates were negatively correlated with yield under high density (p<0.01) as well as under optimal and managed drought conditions (p<0.001). The negative correlation between GY and anthesis date was highest under optimal conditions (r = -0.63). Grain moisture was negatively correlated (p<0.001) with grain yield under all the different stress environments except under managed drought where the relationship was positive (r = 0.19) and highly significant (Table 3.9).

Table 3.9 Genotypic correlations between grain yield and other agronomic traits under optimal, high density, managed drought and low nitrogen conditions

Trait	Optimal conditions	High density	Managed Drought	Low nitrogen
Ear height (cm)	0.58***	0.54**	0.18***	0.51***
Plant height (cm)	0.24***	-0.07**	0.48***	0.07***
Ear position(ratio EH/PH)	0.50***	0.51***	0.27***	0.46***
Grain texture (score)	0.24***	0.35***	0.22***	0.27***
Grain moisture (%)	-0.40***	-0.41***	0.19***	-0.19***
Ear aspect (score)	0.77***	0.74***	0.34***	0.69***
Anthesis dates (days)	-0.63***	-0.43**	-0.48***	-0.28
Anthesis to silking interval (days)	0.58***	0.33*	0.18***	0.33***
Ears per plant (number)	0.01**	0.08***	-0.3***	0.00

***** p≤0.05, ** p≤0.01,*******p≤0.001

3.4 Discussion

The exploitation of genetic variability in local germplasm is one of the most important factors responsible for the observed average increase in genetic gain for maize over the years. While maize GY in Zimbabwe and ESA is improving every year, genetic variability required to maintain this rate of genetic gain has hardly been enhanced. No big efforts have been made to capacitate new hybrid releases to withstand the emerging variable climatic conditions as well as increasing their yield potential. The objective of this study was to identify temperate inbred lines that could be useful in the tropical breeding programmes for GY and trait enhancement. A large number of temperate maize inbreds (250) obtained from the USA was evaluated as three-way test crosses across eight sites.

The different genetic control of the expression of the traits presented in this study was used to identify a number of inbred lines that were capable of directly enhancing GY. In addition, genetic variations for tolerance to high plant density, drought stress and low nitrogen was observed among the test crosses, which is in agreement with other studies (Al-Naggar et al., 2017). High repeatability for GY was exhibited by a high number of the test crosses under different environments, alluding to the possibility of effective direct selection (Ogunniyan and Olakojo, 2014). On the other hand significant correlations between yield and some traits indicated the possibility of effective indirect section, where direct selection could be deemed inefficient, in agreement with Silva et al. (2015). The results presented here confirm the assertion that temperate inbred lines have a diversity of alleles capable of enhancing the GY potential and trait performance of local germplasm.

Nelson and Goodman (2008) reported that temperate germplasm from the USA had higher GY than tropical germplasm even when grown in their respective areas of adaptation. In the present study the GY *per se* and the disease resistance scores of the test cross hybrids were not better than those for check hybrids, indicative of lack of adaptation. A number of TCTemp hybrids however, produced mean GY above 7 t ha^{-1} across environments, which were highly comparable to the mean GY of commercial and local checks. In addition, some inbred lines were identified under different stress environments that could be used to introgress observed novel genes into the local adapted backgrounds (Abadassi and Hervé, 2000).

Although GY is a polygenic character that is prone to the effects of GEI, direct selection for GY can be done if H is high, as postulated by Bello et al. (2012). The high H observed for GY across sites (87%) was also similar to independent research findings for GY reported by Naroui et al. (2013) for wheat and Kumar et al. (2011) for rice. Studies on maize by Bellon et al. (2003) and Meseka et al. (2008) concur with these results, which show that direct selection could be effected for GY under optimal conditions. Superior performance under stressed environments could be identified using yield correlated secondary traits (Silva et al., 2015). Significant positive correlations of GY with EPO, EH and ASI which were observed, suggest that, where H for GY was low, for example under managed drought stress, indirect selection could be more efficient using traits such as EPO and ASI.

Under unfavourable environmental conditions, selection based on GY alone is inefficient due to a decline in H as observed by Rebout et al. (2007), hence the need to use indirect selection through secondary traits. Knowledge of other traits associated with GY and the strength of their correlations with GY has important implication in breeding. These traits could be improved simultaneously with GY or could alternatively be used as secondary traits for indirect selection (Magorokosho et al., 2003; Dao et al., 2017).

High plant density tolerance is a promising phenomenon for achieving higher GY in tropical maize breeding. In this study, the highest yields were obtained under high density conditions, indicating that if tropical populations were bred for tolerance to high density stress, the local grain yields could be raised. These results were corroborated by findings by Isik et al. (2017) who reported highest GY for maize grown under high density conditions in multi-environmental trials (METs).

With more intensification in maize production systems in ESA and the world over, where augmented production through increased acreage is impossible, genotypes that are capable of tolerating high plant density have become a necessity. High plant density tolerance is a trait currently absent in tropical maize germplasm because of their bushy growth habit. Contrary to this, temperate germplasm has fewer leaves and has been associated with improved tolerance to high density stress, apart from improved lodging resistance and earliness (Goodman, 2004).

The frequency distribution of disease tolerance scores showed that most of the test crosses were highly susceptible to *Turcicum,* while the scores for grey leaf spot (GLS) and maize streak virus (MSV) were less severe. Whereas the temperate germplasm could be used to enhance GY in tropical maize, their susceptibility to local diseases is cause for concern. Fortunately, disease resistance can be achieved if the susceptible lines are incorporated into resistant local genetic backgrounds. One or two back crosses to the tropical lines were deemed adequate by Darsana et al. (2004) for the conversion of exotic temperate sources into useful tropical breeding materials. GLS and *Turcicum* tend to attack the maize crop towards the end of the season and perhaps the earliness exhibited by most test crosses allowed them to escape the attack as was also reported by Gouesnard et al. (1996). Based on the current study results, the best resistance for cob rots shown by TCTemp hybrids could be transferred into elite backgrounds to enhance and improve grain storability of local material.

Goodman (2004) reported findings of the Genetic Enhancement for Maize (GEM) programme in the temperate regions that identified about 50% tropical and 50% temperate families tracing back primarily to tropical hybrids that were competitive with commercial checks. Likewise, the TCTemp hybrids and populations could produce higher levels of GY potential in the local CIMMYT breeding programme. Flexibility and greater long-term progress in maize breeding could be achieved through well organised and consistent efforts to incorporate the identified excellent temperate inbred lines such as LH159 into the local breeding programmes.

In nature it is unlikely to find individual stress factors operating independently of each other, hence the proposition here to use METs for screening inbreds. This approach was consistent with other published studies done by Bellon et al. (2003) who screened inbred lines for both yield and diseases under different environments. METs have also been successfully used by Worku et al. (2016) and Isik et al. (2017). Similarly Cairns et al. (2013) screened inbred lines for tolerance to combined drought and heat stress under contrasting environments, as opposed to genetically distinct selections for tolerance to drought or heat stress alone. The screening of large numbers of entries is similar to research done by Zhang et al. (2015) who screened 826 entries for low-P tolerance and Cairns et al. (2013) who screened 806 inbred lines for combined drought and heat stress. These studies shared the same objective of identifying donors of alleles for specific traits. Due to the large number (250) of the inbred lines screened in this study, the use of single testers in each heterotic group was considered sufficient as suggested by Sprague and Tatum (1942), and it was consistent other published studies by Nelson and Goodman (2008) and Cairns et al. (2013).

The results of this study offer information on newly screened temperate germplasm for wider selection and inclusion. The study also provides a fundamental step in a possible bigger pre-breeding perspective, which is currently ignored, but essential. Future GY sustainability for feeding the ever growing human world populations will depend on the creation of new heterotic combinations with enhanced agronomic performance. These results show that in an advanced breeding programme, the direct use of temperate germplasm may often be limited by the lack of adaptability and diseases. However, in the absence of easily identifiable outstanding test cross hybrids from the local x temperate crosses, desirable genes from the temperate inbreds can be introgressed into elite adapted backgrounds. In addition, the strength and usability of the temperate germplasm in producing the final three-way crosses for the market has to be further investigated, especially using the very promising inbreds such as LH159 and HB8229

Although conventional methods of selection are still valuable as used in this study, they should be complemented by faster alternative methods such as marker assisted recurrent selection also reported by Lewis and Goodman (2003), Legesse et al. (2007) and Weber et al. (2012).

3.5 Conclusions

The best exotic inbreds identified for enhancing GY of local germplasm across all stress environments from heterotic group A or the SS group were LH159, LH214, LH23HT, LH213 and MM402A. The best exotic inbreds identified for enhancing GY from heterotic group B or the NSS group were HB8229, W8304, LH198, PJH40 and LH190 and from the unclassified lines were PHR58, WIL500, PHK35 and ICI441. The best GY enhancers under optimal conditions were B09, PHHB4, LH123HT, LH213 and LH214. Inbreds LH98, LH159, PHI40, PHR58 and LH181 were identified as donors for drought tolerance alleles while PHP8525, WIL900, PHT11, PHBB3 and LH384 were identified as donors for low nitrogen tolerance. Inbreds LH159, W8304, HB8229, LH214 and PHW51 were superior under high plant density. The results clearly presented the variability in traits of temperate germplasm, the extent to which these traits were heritable, and the degree to which these characters were inter-related and correlated with GY. Although these temperate inbreds cannot be used directly to produce final hybrids for immediate commercialisation, the GY results and the trait performance indicators show that temperate germplasm can be a useful source of favourable traits for introgression into tropical breeding programmes for improved GY.

3.6 References

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CHAPTER 4

Evaluation of combining ability and usefulness of exotic tropical inbred lines in the CIMMYT Zimbabwe breeding programme

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4.0 Abstract

The creation of suitable and superior maize (*Zea mays* L.) hybrids in the stress prone east and southern African (ESA) region has always been hindered by lack of genetic variability in the local maize germplasm, leading to the limited availability of suitable alleles to confer the desired traits for stress tolerance. In order to guarantee increased productivity in the long run, desirable alleles have to be introduced from exotic maize germplasm to broaden the genetic base and allow greater future flexibility and choice. The objectives of this study were to identify maize inbred lines with high general combining ability (GCA) and parental combinations with high specific combining ability (SCA) effects for grain yield (GY) among exotic tropical inbred lines and CIMMYT Zimbabwe (CimZim) inbred lines using the partial diallel and the North Carolina design II mating schemes. The study also aimed at predicting the GY performance of the possible three-way and double-cross hybrids from the resulting single-crosses. The F_1 hybrids resulting from the local x exotic design II (LEDII), local x local diallel (LLDiallel) and the exotic x exotic diallel (EEDiallel) were evaluated alongside 10 commercial checks using an alpha (0.1) lattice design with two replications, randomised differently on each site. Combined analysis of variance for LEDII crosses depicted highly significant ($p<0.001$) differences among entries and their interactions with the environment for GY. Additive genetic variances were as important as dominant genetic variances for GY. LLDiallel and the EEDiallel experiments also had significant entry x environment interactions that resulted in dissimilar GCA and SCA rankings in different environments. The LEDII identified local inbred lines N19 and N25 with the highest positive GCA across environments. The same lines were also identified through LLDiallel as lines L4 and L16, respectively, and EEDiallel identified inbred lines E1 and E9, both from Mexico, with the highest GCA. LEDII best three-way predictions were derived from local lines N22, N25 and N28, and exotic lines N4 and N5, while the best double-crosses were generated from local lines N22 and N28, and exotic lines N2, N3 and N4. LLDiallel best predicted three-way hybrids were L4/L8//L14 and L3/L5//L6, and best predicted double-crosses were L3/L15//L10/L13 and L10/L13//L15/L16. EEDiallel best predicted three-way hybrids were E7/E9//E1 and E1/E7//E9 while best exotic double-crosses were E1/E2//E7/E9 and E1/E2//E5/E9. Mexico sub-tropical x CIMMYT Zimbabwe new (CimZim-N) hybrid combinations produced the highest yielding test crosses. Overall, the results revealed that some of the single-cross hybrids containing 50% exotic tropical germplasm can produce higher or equivalent GY to local checks.

Key words: *Zea mays* L., exotic germplasm, diallel, North Carolina design II, specific combining ability, general combining ability, diverse sources, stress tolerance.

4.1 Introduction

Maize provides 30% of the caloric requirements for human diets in eastern and southern Africa (ESA), and is grown on 65% of the cultivated land (Cairns et al., 2013). The combined effect of an increasing population and the growing demand for animal protein as dietary habits improve is further intensifying pressure on maize productivity. Despite the incontestable significance of maize in ESA, maize yields have stagnated around 2 t ha^{-1} while in other regions of world, maize yields have increased to 6.8 to 8.0 t ha^{-1} (Masuka et al., 2017). The ESA region is generally known for its semi-arid, harsh and variable sub-tropical hot and dry mega-environments (Setimela et al., 2005; Windhausen et al., 2012). These, coupled with resource constraints, impose severe restrictions to crop productivity and yield improvement in all characteristic farm households in ESA.

The major limitations to increasing maize GY in the ESA region have been drought (Edmeades, 2013; Oyekunle and Badu-Apraku, 2013) and soil fertility, especially nitrogen (Makumbi et al., 2011; Meseka et al., 2013). In addition to drought and poor soil fertility, climate change now poses another serious threat to maize production (Cairns et al., 2013), predominantly through increased unreliability of rainfall and increased temperatures. The current annual yield increases and the current rate of genetic gain for maize are therefore insufficient in view of natural rapid human population growth, dietary preferences and current global environmental changes. Increasing production through increased land area has become progressively impractical because land is not limitless.

Efforts to closing the yield gaps through technological advances to attain higher grain yield (GY) through improved productivity therefore remain the most plausible option to increasing global crop production (Pradhan et al., 2015; Liu and Yang, 2016; Snyder et al., 2017).

Although breeding maize for drought and nitrogen stress tolerance are major objectives for all breeding programmes in ESA, rates of genetic gain remain lowest in the region and the yield gap is the largest compared to the USA and the developed world (Pradhan et al., 2015). Many of the current researchers working on drought and low nirogen tolerance use the conventional guidelines recommended by Bänziger et al. (2000). However other modern breeding techniques that are now available can complement these conventional methods of evaluation. These include, but not limited to genetic analyses as used by Meseka et al. (2013), and marker assisted recurrent selection as used by Bankole et al. (2017) to evaluate genetic gains in yield and yield related traits under drought stress.

High-throughput genotyping and phenotyping technologies together with emerging statistical genomic methods are also now available to competent the conventional methods. These can provide new avenues for efficient exotic germplasm management, characterisation, and utilisation as reported by Wang et al. (2017). Of note is that all the above techniques can only assess available crop variability but do not necessarily generate new variability.

Over the years, breeders have successfully increased maize performance by exploiting local genetic variability and recycling their elite inbred lines, which are often closely related (Lewis and Goodman, 2004). This continuous selective use of highly favoured gene pools has reduced maize genetic variability and has pre-disposed all present-day crop varieties to both new and recurrent abiotic and biotic stress factors (Goodman, 2005). Many of the available studies have been devoted to selecting the best recombinants from the existing gene pools with minimal efforts to expanding the genetic base, for example Cooper et al. (2014), Ogunniyan and Olakojo (2014), Al-Naggar et al. (2017) and Badu-Apraku et al. (2018). Very few reports, if any, are available from the ESA region that targeted the growing or widening of the maize genetic base through the acquisition and incorporation of new genes. The gene base expansion process recruits genes resident in external populations and incorporate them into local gene pools (Bankole et al., 2017) and this process enhances the capacity of any breeding programme to continuously and sustainably generate superior hybrids. This process also culminates in the accumulation and concentration of desired alleles that generate continuous genetic gain (Nelson and Goodman, 2008).

Genetic parameter estimates and identification of superior maize populations (Rovaris et al., 2017), knowledge of genetic variability, and heterotic grouping information of the new breeding materials is important in determining their usability in different hybrid combinations (Henry et al., 2015; Dhoot et al., 2017). Incorporation of exotic germplasm therefore represents a latent and hardly exploited, but important source of genetic variability, which is currently poorly understood, and underutilised by most breeding programmes. Underutilisation of exotic germplasm in the world has been likened by Molin et al. (2013) to the present day underutilisation of landraces.

Breeding processes and procedures needed to transfer the requisite genes from exotic germplasm into local germplasm are premised on the correct identification of source germplasm as well as on the correct deployment of genetic mating schemes (Nduwumuremyi et al., 2013). Only if the source germplasm has the required alleles, as well as the required variability, would selection processes be effective.

Exotic germplasm is most beneficial if adaptable to the local environments, otherwise the best approach would be incorporation into locally adapted backgrounds. Successful projects that have introgressed exotic genes into local germplasm include the Latin American Maize Project (LAMP) (Salhuana et al., 1998), the United Statas of American Germplasm Enhancement of Maize (GEM) project (Goodman, 2005), and the Chinese Maize Germplasm Enhancement, Improvement and Development (Yong et al., 2013). According to Yong et al. (2013), each 1% increase in the genetic contribution of exotic germplasm from Consultative Group on International Agricultural Research (CGIAR) and the United States has increased maize yield in China by 0.025 and 0.01 t ha^{-1}, respectively. Exotic germplasm has introduced lower ear height, earlier maturity and high harvest index, resulting in a gradual increase in plant population density and yield in Chinese maize (Wang et al., 2017).

The process of selecting breeding parents to use in sustaining different breeding objectives has remained a challenging process to many breeding programmes. Most modern breeders reluctantly turn to external sources only when their own germplasm lack sufficient gene frequency of the related genes, or even lack variability for the desired trait (Edmeades et al., 1997). Perhaps the limited success in using exotic germplasm sources in the past can be attributed more to poor choices of parental populations than to the choices of the breeding schemes employed (Nelson and Goodman, 2008). When identified and selected, source germplasm still require extensive evaluation for combining ability or productivity in crosses before they can be used (Cooper et al., 2010). The time and resources involved in this lengthy process have always been restrictive to the use of exotic germplasm.

Combining ability of individual inbreds during the hybridisation process needs to be established beforehand (Fasahat et al., 2016). The use of exotic germplasm in maize breeding programmes has been partial, while the necessity for its use has been escalating. The present study queries the rationale for the continued use of CIMMYT Zimbabwe old or elite (CimZim-O) inbreds and investigates the impact of exotic germplasm inclusion in local breeding programmes. The objectives of this study were to: (i) identify parental lines with high GCA and parental combinations with high SCA effects for GY among exotic tropical inbred lines and CIMMYT Zimbabwe (CimZim) inbred lines using the partial diallel and the North Carolina design II mating schemes, (ii) estimate additive and non-additive gene action and determine the possibility of commercial exploitation of heterosis among the parental lines and (iii) predict the GY performance of three-way hybrids derived from local single-cross x exotic inbreds and double-cross hybrids derived from local single-cross x exotic single-crosses, respectively.

This research was based on the hypothesis that exotic inbred lines developed elsewhere within the tropics could be used in the local breeding programme without further genetic manipulation to produce superior hybrids for immediate commercialisation.

4.2 Materials and methods

This research involved combining ability analysis for GY performance between CIMMYT-Zimbabwe inbreds and exotic tropical inbreds using the North Carolina Design II [local x exotic lines (LEDII)] (Comstock and Robinson, 1952) and two diallel mating schemes (Griffing, 1956, Gilbert, 1958) of local x local lines (LLDiallel) and exotic x exotic lines (EEDiallel). The local inbred lines are the backbone of the local breeding programme. The LLDiallel was therefore included in this study to ensure that the local germplasm is also improved simultaneously with the exotic germplasm so that the identified exotic inbreds will be used with the best local inbreds to give a holistic approach to the breeding programme.

4.2.1 Germplasm

The local inbreds were chosen on the basis of their previous GY performance in test crosses and commercial hybrids. The entries were grouped into old lines (CimZim-O) and new lines (CimZim-N) (Tables 4.1 and 4.2). The exotic inbred lines were obtained from other CIMMYT breeding programmes in Colombia, Kenya, Mexico (lowland tropical and sub-tropical), and from IITA (Nigeria) (Tables 4.1 and 4.3).

4.2.2 Creating the F_1 hybrids

During the 2015 winter season, 12 CIMMYT-Zimbabwe inbreds (females) were crossed with 18 exotic inbreds (males) to produce 153 F_1 single-cross hybrids using the North Carolina Design II (Table 4.1). In the same season, 18 local inbreds (Table 4.2) and nine exotic inbreds (Table 4.3) were separately crossed following procedures of a partial diallel mating scheme.

4.2.3 Experimental designs and testing sites

The F_1 hybrids from the three mating schemes were evaluated in three separate trials using an alpha (0.1) lattice design along with 10 commercial checks. Two replications were used in each trial at all sites. Testing sites were selected to represent the different predominant maize growing environmental conditions in Zimbabwe and ESA (Table 4.4)

Table 4.1 Origin and pedigrees of parental lines used in the local x exotic North Carolina design II LEDII scheme

Entry	Origin	Pedigree of exotic inbred lines
Exotic inbred lines (Males)		
N1	Kenya	((KU1403x1368)-7-2-1-1-BB/CML444)-B-3-2-3-2-2-1-BB
N2	Kenya	((KU1403x1368)-7-2-1-1-BB/CML444)-B-3-3-2-2-3-1-BB
N3	Kenya	((KU1403x1368)-7-2-1-1-BB/CML444)-B-8-5-5-1-1-1-B
N4	Mexico sub-tropical	(43SR-123x43SR-197)-F2-B-6-2-B*5
N5	Kenya	(KU1403x1368)-7-2-1-1-BB/CML444)-B-3-2-3-2-2-1-BB
N6	Kenya	(KU1403x1368)-7-2-1-1-BB/CML444)-B-8-5-5-1-1-1-B
N7	IITA	(TZMI101xTZMI501)-28-1-1-2-1-1-B*10
N8	Colombia	[(P84c3/P63C2HS161-1-3-BB-2-BB-5-1-B*4-1/P62C5HS2-1-2-2-1-1-B-4-BB-3-BB-3-1-1/CML264Q)-B]-1-B*5-1-B
N9	Colombia	[MIRTC5AmF111-3-2-1-2-1/P390amC3/285/287F27-2-1-3)-2-1-B/G18C30HS57-3-2]-1-BBB-1-B
N10	Mexico lowland tropical	CLWN416
N11	Mexico lowland tropical	CLWN507
N12	Mexico lowland tropical	CML549
N13	Kenya	ECAVL17-30-6-1-1-1-1-1-BB
N14	Kenya	ECAVL17-30-6-1-1-2-1-2-B
N15	Mexico sub-tropical	POB501c3F216-5-1-1-B*8
N16	Mexico sub-tropical	NEW-S4/S3-71-2-1-1-B*12
N17	Mexico sub-tropical	POB502c2F215-15-2-1-B*5
N18	Mexico sub-tropical	V305-87-2-2-B*4-1-B
Local inbred lines (Females)		
N19	CimZim-New	([LZ956441/LZ966205]-B-3-4-4-B-5-B*7/LaPostaSeqC7-F71-1-2-1-1-BBB)-1-7-2-2-BB
N20	CimZim-New	([LZ956441/LZ966205]-B-3-4-4-B-5-B*7/LaPostaSeqC7-F71-1-2-1-1-BBB)-1-7-1-1-B
N21	CimZim- New	[[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-2-BB/[CML442/CML197//[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-1-2-BBB]-B-1-1-BBB-B
N22	CimZim-New	[[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-2-BB/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-B//EV7992/EV8449-3-2-2-2-B*5]-B-1-1-BBB-B
N23	CimZim-New	[[LZ956441/LZ966205]-B-3-4-4-B-5-B*5/[CML390/CML206]-BB-2-4-B*4]-B-4-1-1-B*4-B
N24	CimZim-New	[MAS[206/312]-23-2-1-1-B*5/MAS[MSR/312]-117-2-2-1-B*5]-B-10-1-BBB-B
N25	CimZim-New	[P501SRc0-F2-47-3-2-1-B/[CML442/CML197//[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-1-2-BBB]-B-11-1-2-B*4-B
N26	CimZim-Old	CML197
N27	CimZim-Old	CML312
N28	CimZim-Old	CML444
N29	CimZim-Old	CML543
N30	CimZim-Old	CML547

Table 4.2 Pedigrees of the parental lines used in the local x local LLDiallel scheme

Entry	Pedigree of new and old CimZim LLDiallel entries
L1	([CML390/CML206]-BB-2-4-BBB/LaPostaSeqC7-F71-1-2-1-1-BBB)-3-3-1-2-BB
L2	([CML390/CML206]-BB-2-4-BBB/LaPostaSeqC7-F71-1-2-1-1-BBB)-3-3-1-4-BB
L3	([LZ956441/LZ966205]-B-3-4-4-B-5-B*7/LaPostaSeqC7-F71-1-2-1-1-BBB)-1-7-1-3-BB
L4	([LZ956441/LZ966205]-B-3-4-4-B-5-B*7/LaPostaSeqC7-F71-1-2-1-1-BBB)-1-7-2-2-BB
L5	[[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-2-BB/[CML442/CML197//[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-1-2-BBB]-B-1-1-BBB-B
L6	[[CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-2-2-BB/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-B//EV7992/EV8449-3-2-2-2-B*5]-B-1-1-BBB-B
L7	[[LZ956441/LZ966205]-B-3-4-4-B-5-B*5/[CML390/CML206]-BB-2-4-B*4]-B-1-1-1-B*4-B
L8	[[LZ956441/LZ966205]-B-3-4-4-B-5-B*5/[CML390/CML206]-BB-2-4-B*4]-B-4-1-1-B*4-B
L9	[[LZ956441/LZ966205]-B-3-4-4-B-5-B*5/[CML390/CML206]-BB-2-4-B*4]-B-4-1-3-B*4-B
L10	[CML312/[TUXPSEQ]C1F2/P49-SR]F2-45-3-2-1-BB//INTA-F2-192-2-1-1-1-B*4]-1-5-1-1-2-B*8-B
L11	[CML444/DRB-F2-60-1-1-1-BBB//[LZ956441/LZ966205]-B-3-4-4-B-5-B*7]-5-2-2-1-1-B*5
L12	[DTPWC8F31-4-2-1-6-B2/CML395//[CML445/ZM621B]-2-1-2-3-1-BB]-3-2-1-1-3-1-B*6
L13	[MAS[206/312]-23-2-1-1-B*5/[CML390/CML206]-BB-2-4-B*4]-B-5-1-4-B*4-B
L14	[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-B//EV7992/EV8449-3-2-2-2-B*9-B
L15	[P501SRc0-F2-47-3-2-1-B/[CML442/CML197//[TUXPSEQ]C1F2/P49-SR]F2-45-7-3-2-BBB]-2-1-1-1-2-BBB]-B-11-1-2-B*4-B
L16	CML395
L17	CML442
L18	P501SRc0-F2-47-3-1-1-B*5-B

Table 4.3 Pedigrees and origin of the parental lines used in the exotic x exotic EEDiallel scheme

Entry	Origin	Pedigree of EEDiallel entries
E1	Mexico sub-tropical	(43SR-123x43SR-197)-F2-B-6-2-B*4
E2	IITA	(TZMI101xTZMI501)-28-1-1-2-1-1-B*10
E3	Colombia	[(P84c3/P63C2HS161-1-3-BB-2-BB-5-1-B*4-1/P62C5HS2-1-2-2-1-1-B-4-BB-3-BB-3-1-1/CML264Q)-B]-1-B*5-1-B
E4	Mexico lowland tropical	CLWN416
E5	Mexico lowland tropical	CLWN507
E6	Kenya	ECAVL17-30-6-1-1-2-1-2-B
E7	Mexico sub-tropical	POB501c3F216-5-1-1-B*8
E8	Mexico sub-tropical	POB502c2F215-15-2-1-B*5
E9	Mexico sub-tropical	V305-87-2-2-B*4-1-B

4.2.4 Trial management

Hybrids were planted in single 4 m long row plots, 0.75 m apart, with an intra-row spacing of 0.25 m at all sites, targeting a plant population of 53 333 plants per hectare. For the managed drought sites, irrigation was withheld two weeks before anthesis irrigation for survival was resumed two weeks after anthesis. While all normal management practices were followed under random stress, randomly occurring stress factors were allowed to affect the maize naturally to represent real conditions on the farmers' fields without irrigation.

To mitigate randomly occurring pests, two routine sprays were done to prevent and control fall army worm (*S. frugiperda*) using a synthetic pyrethroid, karate (Lambda-cypermethrin) and Belt (Flubendiamide*).* African maize stem borer (*B. fusca*) was controlled using Dipterex (Trichlorfon) granules (approximately 0.1 g dropped in individual plant funnel at four weeks after planting). No supplementary irrigation was applied under random stress, whereas optimum sites received supplementary irrigation when necessary. The CIMMYT low nitrogen block has been depleted of nitrogen for more than 10 years by repeatedly growing non-leguminous crops, removal of crop residue and the non-use of nitrogenous fertilisers. The low phosphorus site has been depleted for more than seven years through the same process as for low nitrogen and the non-use of phosphorus fertilisers.

Table 4.4 Selected testing sites for the LEDII, LLDiallel and the EEDiallel trials

Site Site	Annual rainfall (mm)	GPS coordinates	Attitude (masl)	Soil type	Environmental Condition
CIMMYT Harare	820	17°43'S, 31005'E	1 480	Harare 5E series	Optimal
CIMMYT Harare	820	17°43'S, 31005'E	1 480	Harare 5E series	Low nitrogen
CIMMYT Harare	820	17°43'S, 31005'E	1 480	Harare 5E series	Low phosphorus
CIMMYT Harare	820	17°43'S, 31005'E	1 480	Harare 5E series	High density
Chiredzi	-	21°02'S, 31°58'E	433	Triangle E series	Managed drought
Chisumbanje	-	20°30'S, 33° 58'E	480	Expanding montmorillonite	Managed drought
Kadoma	800	18°32'S, 30°90'E	1155	Clays	Random stress
Rattray Arnold	865	17°40'S, 31°05'E	1369	Harare 5G2 series	Optimal

Table 4.5 Agronomic traits measured and derived for the test crosses across sites

Trait	Units
Grain yield (GY)	t ha^{-1}
Anthesis dates (AD)	Days to 50% pollen shed
Days to silking (SD)	Days to 50% protruding silk by 2-3cm
Anthesis to silking interval (ASI)	Days to 50% pollen shed
Ear aspect (EA)	Scale 1-5 (1 being big, good and disease free)
Plant height (PH)	From ground to first branch of tassel (cm)
Ear position (EPO)	Ratio EH/PH
Ears per plant (EPP)	Total number including secondary ears
Ear rot (ER)	% of rotten cobs as a proportion of total cobs
Husk cover (HC)	Scale 1-5 (1 being completely covered at the tips)
Moisture content (MOI)	% measured using a moisture meter
Texture (TEX)	Scale 1-5 (1 being flint and 5 being dent)
Stem lodging (SL)	% plants with broken stem above ground below the cob
Ear rots (ER)	Scale 1-5 (1 being clean)
Northern corn leaf blight	Scale 1-5 (1 being clean)
Grey leaf spot	Scale 1-5 (1 being clean)
Maize streak virus	Scale 1-5 (1 being clean)

4.2.5 Data collection and statistical analysis

Grain yield (GY) was recorded, together with other agronomic traits (Table 4.5). Analyses of variance (ANOVA), gene action, broad-sense heritability (H) and narrow-sense heritability (h) were calculated using the AGD-R software (Rodríguez et al., 2015). The AGD-R incorporates the formula for calculating heritability as suggested by Hallauer and Miranda (1995):

$$H = \frac{\delta_g^2}{\delta_g^2 + \delta_{g\mathrm{xe}}^2 + \delta_e^2}$$

where:

H = heritability in the broad-sense,
δ_g^2= variance component for genotype effects
δ^2_{gxe} = variance interaction of genotype and environment,
δ^2_{e} = variance component for residual effects, and

$$h = \frac{\sigma^2 sca}{\sigma^2 sca + \sigma^2 sca + \sigma^2 error}$$

Where:

h= narrow-sense heritability

$\sigma^2 gca$ = variance due to general combining ability

$\sigma^2 sca$ = variance due to specific combining ability

$\sigma^2 error$ = error variance

After the preliminary ANOVA, the data were further subjected to North Carolina Design II analysis developed by Comstock and Robinson (1952) to obtain the significance of the components of the hybrids (males, females and the male x female) and the components of the hybrids x environments interactions. The diallel analysis (Griffing, 1956) was used to obtain the GCA and SCA effects using the mathematical model adopted from Dabholkar (1992). Relative GY was obtained from across site Fieldbook analysis (Vivek et al., 2007) and used as the basis for identifying the best performing lines across environments. Relative grain yields were a measure of the deviation of that particular cross from the trial mean, which was considered as 100%. The standard deviation was used as a measure of stability across sites where the smaller the standard deviation the more stable the hybrid. Fieldbook (Vivek et al., 2007) was also used to predict and identify inbred lines with high likelihood of making good three-way and double-cross hybrids between the local and the exotic lines.

4.3 Results

4.3.1. Analysis of variance for F_1 hybrids for the LEDII and the diallel mating schemes under different stress environments

Analysis of variance for the LEDII scheme (Table 4.6) showed that the effects of site, entry, male and female were highly significant ($p<0.001$) for GY. The interaction effects of male x female, site x entry, site x male, site x female and site x male x female were also highly significant ($p<0.01$) for GY H was 97% while h was 55%. The contribution of male sum of squares (16.97%) to the entry sum of squares was only 1% more than the contribution of female sum of squares (15.98%).

Analysis of variance on a per individual site basis for the LLDiallel revealed highly significant ($p<0.01$) effects of crosses for GY in all sites. Combined analysis showed significant ($p<0.01$) entry effects for GY across sites. GCA and SCA effects were significant to highly significant at individual sites, but were not significant for combined analysis across sites. The GY interaction effects for site x entries were highly significant ($p<0.001$), while the interaction for site x GCA and site x SCA was significant ($p<0.01$) (Table 4.7). GCA/SCA ratio was below unity (less than 1) under low nitrogen and low phosphorous conditions and above unity under optimum and managed drought conditions. H ranged from 44% across sites to 81.4% for managed drought and h was lowest across sites (4.1%) and highest under managed drought (67.2%).

For the EEDiallel trial (Table 4.8), the effect of entry and SCA effects were highly significant ($p<0.001$) for GY under low nitrogen and optimal conditions. The effect of site was significant ($p<0.01$) under random stress (Table 4.8). The interaction between site x entry, site x GCA and site x SCA was significant ($p<0.01$) under optimal conditions but insignificant across sites. H increased from random stress (30.9%), managed drought (53.1%), optimal conditions (71.6%), and low nitrogen (74.7%) and was highest across sites (81.9%). Overall h was lowest under managed drought (5.1%)

and random stress (5.6%), but it increased under optimal conditions (21.6%), across all sites (27.4%) and was highest under low nitrogen conditions

Table 4.6 Analysis of variance for GY of 12 local x 18 exotic (LEDII) inbreds evaluated across eight sites

Sources of variation	DF	SS	MS
Sites	7	47.77	6.82**
Replication	8	22324.4	3720.73***
Entry	149	2540.55	17.05***
Male (GCA)	17	431.19	25.36***
Female (GCA)	11	406.03	36.91***
Male x Female (SCA)	105	1450.71	13.82***
Site x Entry	793	3224.16	4.07***
Site x Male GCA	102	470.76	4.62***
Site x Female GCA	66	486.1	7.37***
Site x Male x Female (SCA)	621	2433.46	3.92***
Residuals	925	2350.71	2.54
Male variance			0.13
Female variance			0.2
Male x female variance			0.99
Entry variance			1.27
Additive variance			5.08
Dominance variance			3.98
Site variance			0.24
Broad-sense heritability			0.97
Narrow-sense heritability			0.55

** $p \leq 0.01$, *** $p \leq 0.001$, DF DF-degrees of freedom, SS-sum of squares, MS-mean square

Table 4.7 Analysis of variance for GY of 18 local x local (LLDiallel) crosses evaluated under optimal, low nitrogen, managed drought, and low phosphorus conditions

Sources of variation	Across site DF	Across site MS	Optimal conditions DF	Optimal conditions MS	Low nitrogen DF	Low nitrogen MS	Managed drought DF	Managed drought MS	Low Phosphorus DF	Low Phosphorus MS
Stress environment	6	957.884***	3	1584.585***						
Rep(site)	7	41.968***	4	17.598*	1	62.270***	1	109.855***	1	20.615***
Cross	152	11.269 *	152	34.763***	152	33.415***	152	29.135***	152	9.173***
GCA	17	10.408 ns	17	198.257***	17	155.118***	17	210.590*	17	31.900***
SCA	135	11.557 ns	135	14.209***	135	20.360***	135	9.055***	135	6.590***
Environment x cross	912	22.131***	456	11.449***						
Environment x GCA	102	116.874***	51	38.467***						
Environment x SCA	810	10.504*	405	8.051*						
Residual	239	4.770	138	5.408	32	4.937		3.590		2.787
GCA component		0.176		6.027		4.693		6.469		0.910
SCA component		3.394		4.400		7.711		2.732		1.901
GCA-SCA ratio		0.052		1.370		0.609		2.367		0.479
Phenotypic variance		8.516		21.861		22.035		19.260		6.508
Heritability (narrow-sense)		0.041		0.551		0.426		0.672		0.280
Heritability (broad-sense)		0.440		0.753		0.776		0.814		0.572

* p≤0.05, ** p≤0.01, *** p≤0.001, DF-degrees of freedom, MS-mean square

Table 4.8 Analysis of variance for grain yield of nine exotic x exotic (EEDiallel) crosses evaluated under optimal, low nitrogen, managed drought and random stress conditions

Sources of variation	Across sites DF	Across sites MS	Optimal conditions DF	Optimal conditions MS	Low nitrogen DF	Low nitrogen MS	Managed drought DF	Managed drought MS	Random stress DF	Random stress MS
Environment	7	427.104	2	163.868	2	475.906				
Rep(site)	8	1.985**	3	0.637	3	4.351***	1	0.19	1	4.128***
Cross	35	9.914**	35	5.884***	35	7.297***	35	0.8	35	2.532
GCA	8	18.384	8	10.773	8	16.389*	8	1.064*	8	2.917*
SCA	27	11.104**	27	7.694***	27	5.369***	27	1.833	27	3.23*
Environment x Cross	245	2.321	70	2.974*	70	2.129*				
Environment x GCA	56	4.662	16	6.927	16	3.094*				
Environment x SCA	189	2.482	54	3.373*	54	2.16*				
GCA component		1.2		0.648		1.071				
SCA component		4.761		2.995		1.986		0.616		0.682
GCA-SCA ratio		0.252		0.216		0.539		0.054		0.11
Phenotypic variance		8.744		5.995		5.525		1.283		2.698
Heritability (narrow-sense)		0.274		0.216		0.388		0.051		0.056
Heritability (broad-sense)		0.819		0.716		0.747		0.531		0.309

* p≤0.05, ** p≤0.01, *** p≤0.001, DF-degrees of freedom, MS-mean square

4.3.2 Combining ability effects

4.3.2.1 GCA and SCA effects for local x exotic inbreds in LEDII crosses under different environmental conditions

Exotic inbred lines (used as males) gave both positive and negative GCA effects in the different environmental conditions (Table 4.9). Line N4 from Mexico sub-tropical breeding programme showed the largest positive GCA effects across environments. It had the largest across sites GCA effects (0.473), under optimum conditions (0.489), under low nitrogen (0.24) and under managed drought (0.57). The other male exotic lines with positive GCA effects were N3, N14, N16 and N18 under different environments. Only three local female inbred lines had significant GCA effects across sites (Table 4.9). Female line N25 had the highest positive GCA effects in all environments; 0.638 across sites, 0.583 under optimal conditions, 0.337 under low nitrogen and 0.342 under managed drought. Female lines N21, N19, N26, and N28 also displayed positive GCA effects in different environments. The highest positive and highly significant SCA effects (Table 4.10) across all stress environments and under optimal conditions were obtained from single-crosses N28 x N16 and N30 x N8. The best hybrids under low nitrogen were N29 x N3 and N19 x N3, while the best hybrid under managed drought were N27 x N2 followed by N25 x N10.

Table 4.9 General combining ability effects for grain yield of local and exotic inbreds in LEDII crosses evaluated across sites, under optimal, low nitrogen and managed drought conditions

	Across site	Across site		Optimal conditions		Low nitrogen		Managed drought	
	mean GY	GCA	GCA Rank	GCA	GCA Rank	GCA	GCA Rank	GCA	GCA Rank
Male exotic inbred lines									
N1	5.74	-0.007	11	0.001	9	0.077	6	-0.110	11
N2	5.64	-0.004	10	-0.101	11	0.078	5	0.125	5
N3	5.88	0.027	8	-0.208	15	0.190	3	0.557	2
N4	6.93	0.473	1	0.489	1	0.239	1	0.566	1
N5	6.44	0.096	6	0.159	5	0.006	7	0.050	7
N6	7.22	0.164	3	0.129	6	0.144	4	0.390	3
N7	5.76	-0.113	13	-0.127	13	0.001	8	-0.262	15
N8	5.42	-0.191	16	-0.208	16	-0.071	12	-0.289	16
N9	5.80	0.027	9	0.118	7	-0.088	15	-0.178	12
N10	6.30	0.034	7	0.074	8	-0.087	14	-0.188	13
N11	5.66	-0.079	12	-0.048	10	-0.074	13	0.037	8
N12	5.59	-0.126	15	-0.119	12	-0.187	17	-0.040	10
N13	5.66	-0.414	18	-0.493	18	-0.129	16	-0.192	14
N14	6.18	0.119	5	0.226	3	-0.061	11	-0.016	9
N15	5.13	-0.397	17	-0.410	17	-0.203	18	-0.373	18
N16	6.26	0.120	4	0.194	4	-0.026	10	0.088	6
N17	5.58	-0.113	14	-0.155	14	-0.010	9	-0.337	17
N18	6.63	0.384	2	0.480	2	0.200	2	0.172	4
Female local inbred lines									
N19	6.24	0.215	3	0.148	3	0.236	2	0.153	6
N20	5.59	-0.023	8	-0.025	8	-0.022	8	-0.100	8
N21	6.24	0.296	2	0.311	2	0.080	6	0.322	2
N22	4.88	-0.621**	12	-0.449	12	-0.393	12	-0.746	12
N23	5.30	-0.218*	10	-0.249	10	0.122	4	-0.218	10
N24	5.92	0.094	5	-0.006	7	0.081	5	0.250	4
N25	6.72	0.638**	1	0.583	1	0.337	1	0.342	1
N26	6.37	0.141	4	0.139	4	-0.191	10	0.313	3
N27	5.77	-0.026	9	-0.078	9	0.076	7	0.209	5
N28	6.17	0.018	6	0.028	5	-0.079	9	0.028	7
N29	5.82	0.013	7	-0.001	6	0.143	3	-0.382	11
N30	4.94**	-0.526**	11	-0.401	11	-0.390	11	-0.171	9

* p≤0.05, ** p≤0.01, GY-grain yield, GCA-general combining ability

Table 4.10 Specific combining ability effects for grain yield of local x exotic LEDII crosses across sites, under optimal, low nitrogen and managed drought conditions

	Across site		Optimal conditions		Low nitrogen		Managed drought	
Rank	Cross	SCA	Cross	SCA	Cross	SCA	Cross	SCA
1	N28 x N16	1.785***	N28 x N16	2.876***	N29 x N3	0.74**	N27 x N2	0.772
2	N30 x N8	1.636***	N30 x N8	2.762***	N19 x N3	0.73**	N25 x N10	0.670
3	N28 x N3	1.543***	N28 x N14	2.757***	N25 x N18	0.52	N28 x N11	0.650
4	N27 x N18	1.133**	N19 x N9	2.128***	N21 x N4	0.50	N26 x N16	0.633
5	N26 x N18	1.121**	N21 x N10	2.044***	N24 x N48	0.50	N28 x N9	0.601
6	N23 x N1	1.118**	N28 x N18	2.036***	N28 x N17	0.49	N21 x N6	0.594
7	N21 x N4	1.106**	N25 x N17	1.972***	N29 x N2	0.45	N29 x N16	0.579
8	N25 x N9	1.067**	N25 x N14	1.917**	N25 x N17	0.44	N29 x N2	0.535
9	N19 x N3	1.053**	N25 x N9	1.878**	N23 x N1	0.43	N30 x N3	0.513
10	N29 x N2	1.048**	N23 x N14	1.878**	N30 x N8	0.36	N19 x N3	0.498
11	N24 x N4	1.042**	N23 x N1	1.798**	N21 x N6	0.35	N24 x N12	0.495
12	N19 x N9	1.031**	N25 x N11	1.735**	N24 x N4	0.34	N25 x N13	0.439
13	N24 x N18	1.030**	N24 x N18	1.708**	N28 x N16	0.33	N26 x N18	0.426
14	N25 x N13	1.029**	N26 x N18	1.688**	N19 x N18	0.33	N25 x N18	0.421
15	N25 x N17	1.023	N26 x N4	1.661**	N28 x N7	0.31	N29 x N12	0.419
16	N21 x N10	1.007	N25 x N13	1.544**	N19 x N2	0.29	N25 x N14	0.384
17	N24 x N13	0.987	N27 x N18	1.531**	N21 x N15	0.29	N24 x N13	0.377
18	N28 x N18	0.959	N28 x N7	1.518**	N28 x N4	0.28	N27 x N15	0.377
19	N23 x N14	0.938	N29 x N4	1.341	N29 x N1	0.27	N29 x N1	0.375
20	N25 x N14	0.927	N24 x N4	1.339	N28 x N14	0.25	N23 x N18	0.359
129	N25 x N12	-1.570	N30 x N18	-2.244	N28 x N13	-0.42	N22 x N10	-0.723
130	N29 x N15	-1.585	N25 x N12	-2.444	N28 x N1	-0.44	N25 x N16	-0.758
131	N22 x N10	-2.069	N22 x N10	-3.277	N28 x N2	-0.45	N28 x N2	-0.759
132	N28 x N2	-2.586	N28 x N2	-3.761	N28 x N3	-0.47	N29 x N15	-0.780
133	N19 x N13	-2.888	N19 x N13	-4.983	N25 x N7	-0.49	N28 x N13	-0.794

** $p \leq 0.01$, *** $p \leq 0.001$ SCA-specific combining ability

4.3.2.2 GCA and SCA effects for local x local combinations (LLDiallel) under different growing environments

Inbreds L2, L4, L7 and L14 had highly significant GCA effects (Table 4.11) across all environments. The highest positive GCA effects across sites were shown by lines L7 (0.420), L4 (0.326) and L18 (0.172). The largest positive GCA effects for grain yield under optimal conditions were obtained by lines L4 (1.337), L7 (1.263) and L6 (1.008), respectively. Under low nitrogen conditions the largest positive GCA effects were obtained from lines L16 (3.964), L17 (3.391) and L15 (3.122). Under managed drought conditions highly significant positive GCA effects were observed for lines L15 (4.971), L16 (4.808) and L18 (3.611). Inbred lines L18 (3.422), L17 (0.683) and L16 (0.666) gave the largest positive GCA effects under low phosphorus conditions. The highest positive significant SCA effects (Table 4.12) across sites were attained by crosses L17 x L8, L18 x L1 and L15 x L6. Under optimal conditions L16 x L18, L14 x L18 and L2 x L8 produced the highest SCA. The best hybrids under low nitrogen were L3 x L18, L2 x L18 and L1 x L18 and the best hybrids under managed drought were L8 x L17, L1 x L18 and L6 x L15. Under low phosphorus, L14 x L18, L2 x L6 and L1 x L5 were the best hybrids.

Table 4.11 General combining ability effects for grain yield of 18 local inbred lines in LLDiallel crosses evaluated across eight sites

Line	Across sites GCA	Rank	Optimal conditions GCA	Rank	Low nitrogen GCA	Rank	Managed Drought GCA	Rank	Low phosphorus GCA	Rank
L1	0.086	6	0.905***	6	-1.261***	12	-1.609***	13	-0.154	9
L2	-0.434***	18	0.316	10	-1.582***	15	-2.606***	18	-0.065	8
L3	0.026	9	0.758****	8	-1.029***	10	-1.483***	12	-0.343	12
L4	0.326***	2	1.337***	1	-1.381**	13	-2.038***	15	0.301	4
L5	-0.222*	16	0.829***	7	-2.269**	17	-2.081***	16	-0.502**	15
L6	-0.032	11	1.008***	3	-1.788**	16	-1.927***	14	-0.534**	16
L7	0.420***	1	1.263***	2	-1.077**	11	-0.952***	8	-0.021	7
L8	0.134	5	0.909***	5	-1.516**	14	-1.467***	11	0.271	5
L9	0.061	7	0.947***	4	-0.901**	9	-2.129***	17	-0.354	13
L10	-0.180	15	0.400	9	-0.528	8	-1.181***	10	-1.100**	17
L11	0.160	4	0.190	12	1.291***	6	-0.697***	7	-0.279	10
L12	-0.013	10	0.234	11	0.371	7	-1.072***	9	-0.340	11
L13	0.057	8	-0.264***	13	2.363**	5	0.387	6	-1.339**	18
L14	-0.366***	17	-1.575***	15	2.366**	4	1.859***	5	-0.475**	14
L15	-0.078	13	-2.197***	17	3.122**	3	4.971***	1	0.164	6
L16	-0.036	12	-2.412***	18	3.964**	1	4.808***	2	0.666**	3
L17	-0.081	14	-2.058***	16	3.391**	2	3.606***	4	0.683**	2
L18	0.172	3	-0.590***	14	-3.535**	18	3.611***	3	3.422**	1

* p≤0.05, ** p≤0.01, *** p≤0.001, GCA- general combining ability

Table 4.12 Specific combining ability effects for grain yield of top 20 and bottom five crosses of local x local LLDiallel crosses evaluated under optimal, low nitrogen, managed drought and low phosphorous conditions

	Across sites		Optimal conditions		Low nitrogen		Managed drought		Low phosphorus	
Rank	Cross	SCA	Cross	SCA	Cross	SCA	Cross	SCA	Cross	SCA
1	L17 x L8	3.06***	L16 x L18	3.63	L3 x L18	10.10***	L8 x L17	6.37***	L14 x L18	5.17***
2	L18 x L1	2.76***	L14 x L18	2.56	L2 x L18	9.19***	L1 x L18	5.89***	L2 x L6	3.84***
3	L15 x L6	2.38***	L2 x L8	2.41	L1 x L18	9.09***	L6 x L15	4.89***	L1 x L5	3.58
4	L14 x L5	1.96	L17 x L18	2.27	L4 x L18	6.81***	L4 x L15	4.19***	L12 x L18	3.14
5	L18 x L3	1.92	L15 x L16	2.19	L1 x L13	4.92***	L12 x L16	4.08***	L3 x L10	3.03
6	L14 x L9	1.84	L16 x L17	2.08	L5 x L14	4.90***	L7 x L15	3.64***	L9 x L17	2.85**
7	L16 x L12	1.82	L3 x L10	2.07	L8 x L10	4.87***	L7 x L17	3.46***	L3 x L6	2.69**
8	L16 x L5	1.65	L6 x L9	2.04	L8 x L17	4.54***	L9 x L17	3.43***	L7 x L18	2.56**
9	L17 x L9	1.64	L1 x L4	2.02	L1 x L15	4.38***	L10 x L17	3.35**	L5 x L6	2.51**
10	L17 x L7	1.62	L15 x L18	1.97	L9 x L10	4.32***	L6 x L18	2.80**	L11 x L13	2.41**
11	L13 x L12	1.58	L5 x L7	1.86	L10 x L15	4.08***	L5 x L16	2.76**	L16 x L17	2.41**
12	L13 x L1	1.55	L7 x L8	1.85	L9 x L15	3.95***	L2 x L16	2.74**	L8 x L17	2.15
13	L16 x L3	1.50	L15 x L17	1.82	L9 x L11	3.82***	L12 x L13	2.69**	L6 x L15	2.11
14	L17 x L10	1.38	L4 x L5	1.74	L9 x L14	3.79**	L2 x L18	2.58**	L12 x L16	1.94
15	L13 x L10	1.31	L1 x L8	1.72	L7 x L17	3.65**	L5 x L14	2.55**	L12 x L13	1.93
16	L15 x L2	1.28	L4 x L10	1.57	L4 x L17	3.61**	L3 x L16	2.48**	L2 x L10	1.89
17	L13 x L5	1.25	L7 x L9	1.52	L6 x L15	3.60**	L11 x L17	2.47	L7 x L16	1.88
18	L15 x L8	1.20	L3 x L5	1.50	L7 x L16	3.59**	L3 x L15	2.36	L2 x L3	1.87
19	L11 x L2	1.19	L8 x L11	1.49	L2 x L11	3.59**	L3 x L14	2.24	L13 xL18	1.80
20	L15 x L4	1.18	L1 x L7	1.42	L8 x L14	3.54**	L10 x L18	2.21	L2 x L8	1.76
149	L16 x L15	-2.62***	L2 x L18	-2.24	L1 x L2	-5.31***	L14 x L16	-4.00***	L6 x L7	-3.69***
150	L15 x L12	-2.81***	L1 x L18	-2.29	L14 x L18	-5.58***	L15 x L18	-4.12***	L5 x L13	-4.14***
151	L13 x L5	-3.03***	L7 x L16	-2.32	L13 x L18	-6.24	L16 x L18	-4.67***	L12 x L15	-4.57***
152	L17 x L14	-3.081***	L9 x l15	-2.58	L15 x L18	-6.62	L4 x L18	-4.73***	L2 x L18	-5.84***
153	L2 x L1	-3.31***	L1 x L2	-4.33	L14 x L17	-7.11	L15 x L16	-5.79***	L3 x L17	-5.97***

* p≤0.05, ** p≤0.01, *** p≤0.001, SCA- specific combining ability

4.3.2.3 GCA and SCA effects for local x local combinations (EELLDiallel) under different growing environments

Positive, significant and highly significant (p<0.001) GCA effects (Table 4.13) were noted for some EEDiallel lines under the different stress environments. Under optimal conditions lines E9 and E1 had the largest positive GCA effects of 0.83 and 0.43, respectively. Under low nitrogen conditions the largest GCA effects for GY were obtained from lines E1 (0.849) and E2 (0.630). Under managed drought conditions E2 (0.377) and E6 (0.104) produced the largest positive GCA effects for GY and under random stress the largest positive GCA effects for GY were given by E8 (0.699) and E1 (0.529. The highest positive significant SCA effects (Table 4.14) for GY were obtained from crosses E8 x E6 (across sites), E5 x E2 (optimal conditions), E9 x E5 (low nitrogen) and E9 x E4 (managed drought). The worst performing hybrids had also the most negative SCA effects were E5 x E4 across all stress environments and E7 x E6 (across sites and under low nitrogen) and E8 x E7 under optimal conditions.

Table 4.13 General combining ability effects for grain yield of nine exotic inbreds in exotic x exotic EEDiallel crosses evaluated under optimal, low nitrogen, managed drought and random stress conditions

	Across sites		Optimal conditions		Low nitrogen		Managed drought		Random stress	
Line	GCA	Rank	GCA	Rank	GCA	Rank	GCA	Rank	GCA	Rank
E1	0.525***	1	0.43***	2	0.849***	1	0.038**	5	0.529*	2
E2	0.220***	3	0.39***	3	0.630***	2	0.377	1	-0.757**	9
E3	-0.379***	7	-0.42***	7	0.336**	3	-0.033**	8	0.035	4
E4	-0.497***	8	-0.52***	8	0.234**	4	0.072	4	-0.143	6
E5	-0.534***	9	-0.41***	6	0.203	5	-0.663	9	0.302	3
E6	-0.115	6	-0.58***	9	0.025	6	0.104	2	-0.014	5
E7	0.194***	4	0.26*	4	-0.554***	7	0.021**	6	-0.344	8
E8	0.081	5	0.02	5	-0.824***	8	0.083	3	0.699**	1
E9	0.505***	2	0.83***	1	-0.899***	9	0.000***	7	-0.306	7

* p≤0.05, ** p≤0.01, *** p≤0.001, GCA- general combining ability

Table 4.14 Specific combining ability effects for grain yield of nine exotic x exotic EEDiallel crosses evaluated under optimal, low nitrogen and managed drought conditions

	Across sites		Optimal conditions		Low nitrogen		Managed drought	
Rank	Cross	SCA	Cross	SCA	Cross	SCA	Cross	SCA
1	E8 x E6	1.145***	E5 x E2	1.550***	E9 x E5	1.395***	E9 x E4	1.651***
2	E5 x E2	1.105***	E8 x E4	1.355***	E6 x E3	1.360***	E5 x E1	1.588***
3	E7 x E1	0.864***	E7 x E3	1.263***	E7 x E1	1.131***	E9 x E6	1.314**
4	E5 x E1	0.822***	E8 x E6	1.191**	E4 x E2	1.121***	E4 x E1	1.086**
5	E6 x E3	0.814***	E8 x E5	1.071**	E9 x E4	1.107	E8 x E7	0.860
6	E9 x E4	0.761***	E5 x E1	1.027***	E8 x E6	1.082	E5 x E2	0.775
7	E8 x E5	0.656**	E9 x E1	0.932	E8 x E5	0.829	E4 x E3	0.753
8	E8 x E4	0.58**	E7 x E4	0.894	E8 x E3	0.514	E7 x E1	0.695
9	E9 x E5	0.55**	E7 x E1	0.868	E7 x E2	0.453	E6 x E5	0.598
10	E4 x E2	0.546**	E6 x E3	0.695	E4 x E1	0.394	E3 x E1	0.531
11	E7 x E3	0.497	E9 x E5	0.525	E6 x E5	0.389	E7 x E3	0.375
12	E4 x E1	0.407	E9 x E2	0.426	E7 x E5	0.333	E9 x E8	0.337
13	E4 x E3	0.258	E4 x E2	0.414	E9 x E7	0.277	E8 x E6	0.286
14	E9 x E2	0.207	E4 x E1	0.321	E5 x E2	0.274	E2 x E1	0.176
15	E8 x E3	0.156	E4 x E3	0.226	E5 x E1	0.138	E4 x E2	0.099
16	E7 x E2	0.13	E6 x E4	0.17	E6 x E1	0.096	E8 x E2	0.09
17	E6 x E4	0.13	E8 x E3	0.088	E4 x E3	0.055	E6 x E3	0.048
18	E6 x E5	0.094	E7 x E2	0.051	E6 x E4	0.034	E8 x E5	0.013
19	E7 x E5	0.064	E7 x E5	-0.019	E8 x E4	-0.016	E6 x E2	-0.006
20	E7 x E4	0.038	E9 x E4	-0.042	E9 x E3	-0.028	E9 x E2	-0.114
32	E8 x E1	-0.629	E8 x E1	-0.924**	E8 x E2	-0.693	E3 x E2	-0.683
33	E9 x E6	-0.642	E2 x E1	-1.013**	E5 x E3	-0.828	E8 x E1	-1.093**
34	E8 x E7	-0.74	E3 x E2	-1.022**	E9 x E6	-1.310***	E6 x E1	-1.177**
35	E7 x E6	-0.813	E8 x E7	-2.242***	E7 x E6	-1.575***	E9 x E1	-1.806***
36	E5 x E4	-2.719	E5 x E4	-3.339***	E5 x E4	-2.528***	E5 x E4	-2.244***

* p≤0.05, ** p≤0.01, *** p≤0.001, SCA- general combining ability

4.3.3 Mean grain yield performance of crosses

4.3.3.1 Grain yield performance of local x exotic LEDII crosses under different stress environments

The best yielding LEDII hybrids across sites (Table 4.15) were a commercial single-cross check SC727 (10.23 t ha^{-1}), followed by experimental test crosses N28 x N16 (9.22 t ha^{-1}) and N21 x N4 (8.95 t ha^{-1}) both with male parents from Mexico sub-tropical and CimZim-O and CimZim-N female parents, respectively (Table 4.16). Test crosses N21 x N1, (N1 male from Kenya) had the shortest ASI of 0.00 days while the cross N25 x N9 (male from Colombia) and N25 x N14 (male from Kenya) had the longest ASI of 3.2 days and 3.6 days, respectively. Crosses N22 x N10 was one of the few crosses with negative ASI (0.14 days).

Table 4.15 Grain yield for local x exotic LEDII crosses evaluated under optimal, low nitrogen, managed drought and random stress conditions across eight sites

		Trait performance across sites					GY performance in different environments				
Entry	Relative	Standard	AD	ASI	PH	MOI	Across site	OPT	LN	MD	RS
	GY index	deviation	Days		cm	%		(t ha^{-1})			
SC727	122.22	54	70.55	0.88	229.89	16.24	10.23	17.23	3.88	2.27	3.92
N28 x N16	128.00	37	72.33	0.55	222.61	15.37	9.22	14.32	3.70	4.16	5.79
N21 x N4	142.13	29	68.91	0.58	218.26	15.80	8.95	12.57	4.96	5.51	6.55
N28 x N14	125.46	33	70.80	1.70	221.50	16.35	8.88	14.16	3.41	5.17	2.75
N25 x N9	121.63	52	67.32	3.23	215.97	15.67	8.87	13.71	3.28	5.04	5.05
N25 x N14	123.04	23	67.68	3.61	217.44	15.97	8.77	13.84	3.23	4.82	4.03
N21 x N1	128.56	30	69.00	0.00	223.27	13.54	8.65	13.38	3.81	4.24	3.41
N25 x N17	117.37	44	69.56	2.15	218.35	15.64	8.64	13.43	4.56	2.43	3.00
N24 x N4	141.58	10	69.03	1.81	220.98	16.43	8.64	12.45	4.47	5.67	4.74
N26 x N18	125.75	30	70.61	0.98	227.15	15.61	8.60	12.92	3.11	5.81	4.55
N21 x N10	112.28	47	69.71	0.94	214.01	13.95	8.54	13.66	2.47	3.47	4.25
N27 x N18	128.43	48	67.96	1.30	207.39	14.87	8.51	12.53	3.78	4.09	6.36
PAN53	108.79	38	67.07	0.54	213.01	14.80	8.50	13.38	3.42	3.47	3.61
N24 x N18	118.21	31	68.69	1.00	204.54	15.67	8.50	12.84	4.76	3.88	2.82
30G19	110.23	49	69.13	0.83	224.38	15.47	8.48	13.66	2.70	4.98	2.13
N28 x N18	107.10	48	72.21	0.87	208.22	14.89	8.48	13.66	2.84	4.90	2.42
N25 x N10	120.54	38	67.25	2.28	215.26	15.18	8.42	12.71	3.48	5.88	3.80
N25 x N11	106.98	43	69.26	1.91	222.82	16.13	8.41	13.26	3.56	2.42	4.28
10C3271	127.35	29	65.43	0.24	216.31	14.44	8.40	12.67	3.78	6.30	3.08
N30 x N9	62.04	42	67.61	3.15	212.56	12.83	4.10	6.90	1.42	1.57	0.98
N28 x N2	55.50	23	72.89	1.57	202.89	12.04	3.27	5.09	1.68	1.51	1.51
N22 x N10	52.93	51	71.36	-0.14	219.58	13.62	3.18	5.11	1.46	0.38	1.69
N19 x N13	49.06	50	78.89	2.85	179.18	12.61	2.46	3.15	2.26	3.57	1.27
N28 x N13	43.17	55	74.84	2.76	165.74	12.36	1.41	2.25	1.39	0.20	0.75
Mean	100.00	35	69.30	1.72	215.32	14.48	6.70	10.19	2.96	3.63	3.30
LSD	19.00	10	1.69	8.33	13.06	1.68	1.69	2.69	1.85	2.57	2.79
CV			1.24	47.47	3.09	5.91	12.81	13.44	31.60	35.60	42.53
Heritability (broad-sense)			0.91	0.34	0.74	0.62	0.82	0.81	0.44	0.49	0.26

GY- grain yield, AD- anthesis date, ASI- anthesis to silking interval, PH- plant height, MOI-moisture, OPT-optimal conditions, LN-low nitrogen, MD-managed drought, RS-random stress, LSD- least significant difference, CV-coefficient of variation

Table 4.16 Origin of pollen parents and status of the local single-cross testers with the highest grain yield across sites

Rank	Cross	Origin of pollen parent	Status of local female	Across mean GY (t ha^{-1})
1	SC727	SeedCo	Check	10.26
2	N28 x N16	Mexico sub-tropical	CimZim-Old	9.22
3	N21 x N4	Mexico sub-tropical	CimZim New	8.95
4	N28 x N14	Kenya	CimZim-Old	8.88
5	N25 x N9	Colombia	CimZim New	8.87
6	N25 x N14	Kenya	CimZim New	8.77
7	N21 x N1	Kenya	CimZim New	8.65
8	N25 x N17	Mexico sub-tropical	CimZim New	8.64
9	N24 x N4	Mexico sub-tropical	CimZim New	8.64
10	N26 x N18	Mexico sub-tropical	CimZim-Old	8.60
11	N21 x N10	Mexico lowland tropical	CimZim New	8.54
12	N27 x N18	Mexico sub-tropical	CimZim-Old	8.51
13	PAN53	Pannar Seeds	Check	8.50
14	N24 x N18	Mexico sub-tropical	CimZim-New	8.50
15	30G19	Pioneer Seeds	Check	8.49
16	N28 x N18	Mexico sub-tropical	CimZim-New	8.48
17	N25 x N10	Mexico lowland tropical	CimZim-New	8.42
18	N25 x N11	Mexico lowland tropical	CimZim-New	8.41
19	10C3271	SeedCo	Check	8.40
20	N25 x N3	Kenya	CimZim-New	8.37

4.3.3.2 Grain yield performance of local x local LLDiallel crosses under different environmental conditions

The highest relative grain yield across sites (Table 4.17) for the LLDiallel was obtained by crosses L3 x L6 (132%), followed by a commercial hybrid check 10C3271 (122%), cross L4 x L14 (120%) and cross L4 x L17 (120%). There were no significant differences among the top six yielding hybrids across sites considering relative grain yield using the LSD, notwithstanding that the hybrids performed differently under the different environments.

Table 4.17 Mean grain yield of top local x local LLDiallel hybrids under optimal, low nitrogen, managed drought and low phosphorous conditions across eight sites

Cross	Relative grain yield %	Standard Deviation	Across site t ha^{-1}	Optimal conditions t ha^{-1}	Low nitrogen t ha^{-1}	Managed drought t ha^{-1}	Low phosphorus t ha^{-1}
			Top hybrids				
L3 x L6	132	89	8.91	10.9	2.84	5.67	10.23
SC727	122	30	10.12	8.38	10.65	2.96	4.56
L4 x L14	120	74	8.75	10.74	4.31	2.85	11.1
L4 x L17	120	102	8.52	10.95	4.1	3.57	8.13
L2 x L5	119	61	8.44	10.53	3.46	3.7	9.84
L8 x L17	119	105	7.7	9.12	4.09	5.01	8.32
L5 x L14	118	84	8.28	10.19	4.89	3.01	9.29
L8 x L14	118	80	8.61	11.14	3.33	3.28	9.11
L14 x L15	118	88	8.04	9.98	4.58	3.87	7.91
L11 x L17	117	75	8.34	10.72	4.09	3.66	7.79
10C3271	117	69	8.21	10.83	4.46	3.11	6.57
30G19	117	47	8.45	10.49	4.33	3.03	9.83
L10 x L16	117	86	8.12	10.18	4.31	3.22	8.6
L5 x L6	116	98	8.43	11.12	2.75	3.15	8.64
L10 x L15	116	57	8.51	10.64	5.55	2.03	9.45
L3 x L10	115	62	8.27	10.38	3.36	3.02	10.01
L1 x L11	115	94	8.82	12.23	2.84	2.91	7.12
L1 x L12	114	87	8.23	10.87	3.12	3.66	7.35
L2 x L18	114	81	8.51	11.18	3.54	2.17	9.14
L2 x L10	114	102	7.97	10.21	5.94	2.41	6.6
			Bottom hybrids				
L2 x L16	76	115	6.81	8.99	4.98	2.1	8.82
L6 x L16	73	90	6.29	8.87	0.99	0.73	6.86
L3 x L4	73	77	6.94	9.3	4.27	1.95	9.07
L2 x L9	63	71	5.79	7.55	3.87	1.61	8.07
Mean	100	86	7.56	9.77	3.28	2.02	8.42
LSD	13	21	1.93	1.34	11.38	3.05	3.89
MSe			6.73	1.84	33.44	2.4	3.91
Minimum	63	30	5.63	6.72	0.62	2.94	3.33
Maximum	132	151	9.38	12.85	5.94	5.67	12.35

LSD-least significant difference, MSe-mean square error

4.3.3.3 Grain yield performance of exotic x exotic crosses (EEDiallel) under different stress environments

Variable grain yield differences among the EEDiallel F_1 hybrids under the different stress environments showed differences as shown by the least significant differences in Table 4.18. The highest yielding hybrids were E7 x E1 (128%), followed by E1 x E9 (126%) and E6 x E8 (120%). The GY performances of the crosses were variable across all the sites.

Table 4.18 Mean grain yield of top 20 EEDiallel crosses evaluated under optimal, low nitrogen and managed drought conditions across eight sites

			Across traits traits			Across grain yield		Optimal conditions		Low nitrogen		Managed drought	
Cross	Relative GY %	Standard deviation	AD (days)	ASI	PH (cm)	GY t ha-^{1}	Rank #	GY t ha-^{1}	Rank #	GY t ha^{-1}	Rank #	GY t ha^{-1}	Rank #
SC727	159	1	71.40	2.00	276.80	11.68	2	15.61	2	4.93	3	8.49	1
E7 x E1	128	24	71.30	1.00	266.90	9.25	25	11.60	29	5.22	2	4.96	75
E1 x E9	126	14	72.40	1.80	254.00	9.36	20	13.13	6	4.00	20	6.47	24
E6 x E8	120	36	71.70	3.90	266.00	8.96	33	12.03	23	3.21	46	7.77	4
E4 x E9	116	20	71.40	1.00	262.90	8.60	39	11.08	46	3.06	54	7.05	12
E5 x E9	114	32	74.60	0.90	238.30	8.66	42	12.75	14	3.62	26	4.83	78
E8 x E1	113	31	71.10	2.20	261.50	8.17	52	10.14	67	3.78	23	7.67	5
E7 x E9	113	36	70.70	1.30	276.10	8.64	48	11.96	36	3.42	36	5.24	57
E5 x E2	113	33	74.30	1.30	272.90	8.64	41	12.40	14	2.39	86	6.65	17
E2 x E9	113	30	72.10	1.00	261.60	8.63	43	11.21	43	2.43	84	5.52	46
E4 x E7	112	37	73.00	1.50	256.80	8.42	47	10.14	71	3.00	58	6.76	14
E1 x E2	112	39	71.20	1.60	268.00	8.14	52	9.43	88	4.42	9	4.44	93
E5 x E1	111	33	73.10	0.50	243.90	8.42	44	11.50	32	2.55	77	7.04	13
E7 x E2	110	38	72.20	1.10	265.30	8.30	49	11.75	27	4.07	16	3.26	122
E8 x E2	109	33	72.20	1.80	272.70	7.86	61	9.66	84	4.40	10	4.52	89
E8 x E7	107	44	71.80	1.00	245.40	7.71	58	9.55	71	4.01	17	6.57	21
E2 x E6	106	23	72.20	2.20	265.40	7.78	61	9.62	80	3.43	35	5.35	54
E4 x E2	106	40	73.20	1.30	264.70	8.04	60	11.74	36	3.28	43	4.82	80
E8 x E3	105	29	71.30	0.70	263.90	8.15	54	11.43	36	2.26	90	5.23	58
E1 x E6	104	27	70.00	3.40	253.60	7.83	60	9.67	79	3.16	50	5.00	69
Mean	100	29	71.70	2.00	257.40	7.54	65	10.01	66	2.74	65	5.12	66
LSD (0.05)	20	10	1.30	1.50	17.90	1.01	25	2.22	32	2.33	37	2.67	38
MSe			2.70	2.20	246.90	1.83		2.53		1.38	0	0.29	
Minimum	21	1	66.60	-0.90	220.60	1.96	1	2.05	1	0.90	1	1.16	1
Maximum	159	49	76.40	5.50	278.80	11.68	128	16.54	130	6.25	129	8.49	130

GY-grain yield, AD-anthesis date, ASI-anthesis to silking interval, PH-plant height, LSD-least significant difference, MSe-mean square error

4.3.4 Grain yield prediction of inbred line performance in three-way and double-cross hybrids

LEDII predictions (Table 4.19) for three-way and double-crosses identified local lines N22, N27, N25 and N28, and exotic lines N4, N5 and N6 as the inbreds to produce the best three-way crosses while local lines N22, N28 and N29 were depicted as the best for double-crosses in conjunction with exotic lines N2, N3 and N4. Similarly, for the LLDiallel scheme, three-way hybrids L4/L8//L14, L3/L5//L6, and L2/L5//L18 were predicted to give the highest yields while double-crosses L3/L15//L10/L13, L10/L13//L15/L16 and L4/L8//L14/L17 were expected to give the highest yields (Appendix 4.1 and Appendix 4.2). For EEDiallel three-way hybrids E7/E9//E1, E1/E7//E9, E1/E2//E9 and E1/E9//E7 were expected to give the highest yields while double-crosses E1/E2//E7/E9, E1/E2//E5/E9 and E1/E5//E2/E9 were expected produce the best hybrids (Table 4.19; Appendix 4.3 and 4.4).

Table 4.19 Best predicted three-way and double-cross hybrids from LEDII, LLDiallel and the EEDiallel single-cross data generated from across eight sites

Three-way hybrid predictions				Double-cross hybrid predictions			
Entry	SX Parent 1	Parent 2	GY (t ha-1)	Entry	SX Parent 1	SX Parent 1	GY (t ha-1)
LEDII predictions (top 10 out of a possible 660 three-way hybrids and a possible 1485 double-crosses							
325	N4/N25	N24	7.97	1158	N4/N25	N6/N28	7.77
484	N6/N28	N22	7.97	1159	N6/N28	N6/N29	7.55
494	N6/N29	N22	7.89	551	N6/N29	N6/N29	7.48
385	N5/N24	N25	7.85	867	N5/N24	N6/N29	7.34
464	N6/N26	N22	7.82	1168	N6/N26	N10/N29	7.35
634	N10/N29	N22	7.69	1157	N10/N29	N6/N27	7.23
426	N5/N28	N25	7.64	549	N5/N28	N6/N28	7.12
574	N8/N28	N22	7.63	119	N8/N28	N6/N29	7.20
486	N6/N28	N25	7.57	664	N6/N28	N6/N29	7.14
328	N4/N25	N28	7.57	563	N4/N25	N9/N29	7.14
LLDiallel top 10 out of a possible 2448 three-way hybrids and a possible 9180 double-crosses							
828	L4/L8	L14	8.68	4787	L3/L15	L10/L13	8.40
548	L3/L5	L6	8.67	8860	L10/L13	L15/L16	8.32
320	L2/L5	L18	8.65	5390	L4/L8	L14/L17	8.40
995	L5/L6	L3	8.65	3831	L3/L5	L6/L13	8.49
2049	L11/L15	L1	8.65	5093	L4/L5	L6/L14	8.39
1299	L6/L13	L3	8.64	1075	L1/L10	L15L/16	8.34
170	L1/L12	L11	8.64	6316	L5/L8	L6/L14	8.26
2324	L14/L17	L4	8.63	1422	L1/L13	L11/L15	8.47
516	L2/L18	L5	8.62	1435	L1/L13	L15/L16	8.34
1381	L6/L18	L5	8.61	5149	L4/L5	L13/L14	8.26
EEDiallel top 10 out of a possible 252 three-way hybrids and a possible 378 double-crosses							
239	E7/E9	E1	9.17	20	E1/E2	E7/E9	8.76
42	E1/E7	E9	8.96	15	E1/E2	E5/E9	8.64
7	E1/E2	E9	8.89	69	E1/E5	E2/E9	8.6
55	E1/E9	E7	8.88	164	E1/E9	E5/E7	8.59
28	E1/E5	E9	8.87	62	E1/E4	E7/E9	8.59
21	E1/E4	E9	8.85	83	E1/E5	E7/E9	8.58
204	E5/E9	E1	8.69	152	E1/E9	E2/E7	8.58
12	E1/E3	E7	8.65	41	E1/E3	E7/E9	8.54
99	E2/E9	E1	8.63	161	E1/E9	E4/E7	8.54
5	E1/E2	E7	8.62	111	E1/E7	E2/E9	8.52

SX-single cross, GY-grain yield,

4.4 Discussion

The formation of new and higher levels of heterosis and the availability of new genetically diverse and stable source populations are prerequisites for successful development of superior maize hybrids (Chandel et al., 2014). Effective hybrid development is premised on the creation of new parental combinations followed by identification and selection of the best performers (Zamir, 2001). This study aimed at identifying exotic tropical inbreds that combined well with CimZim inbreds (which are the backbone of the local breeding programme), to form good hybrids for immediate commercialisation. The results of this study showed significant differences in GY among the entries, implying that the crosses were sufficiently dissimilar, and hence gainful improvements could be achieved through effective selection (Carena, 2011). On a performance per site basis, both the GCA and SCA were highly significant, suggestive of equal importance of both additive and non-additive gene actions in determining GY.

The GY results of the LEDII entries across sites showed highly significant additive variance (5.08) which was greater than dominance variance (3.98), demonstrating the preponderance of additive gene action over dominance and epistatic gene actions in the local x exotic combinations (Estakhr and Heidari, 2012). Highly significant ($p<0.01$) site x entry interactions (both male and female) indicated that the performance of these crosses was, however, affected differently by different environmental conditions. Thus predominant gene action controlling GY varied with type of stress, with additive gene action appearing to be more significant under drought stress, while non-additive gene action was more important under low nitrogen stress, consistent with other findings (Nyombayire et al., 2010; Makumbi et al., 2011). Selection under different stress environments was supported by Edmeades et al. (1997), who concluded that the probability of obtaining a hybrid that yielded 40% more than the trial mean under severe drought stress was four times higher if the inbreds were extracted from a population improved for drought tolerance.

The local germplasm must be improved simultaneously with the new and incoming germplasm, hence the inclusion of the LLDiallel in this study. The LLdiallel identified a large number of local inbreds with positive GCA effects. Such large numbers of inbred lines with positive GCA effects encourage the development of synthetic varieties (Makumbi et al., 2011). These high GCA parents can also be combined to develop improved populations, or can be used in pedigree starts to extract recombinant inbreds with different levels of tolerance to specific environmental stresses. Makumbi et al. (2011) also postulated that the existence of genetic variation amongst maize inbreds ensured good chances of obtaining high yielding hybrid combinations for specific environments. This approach has been successfully used by other researchers including Gowda et al. (2012) who investigated the magnitude of variance of GCA and SCA effects and their interaction with stress environments in wheat using the diallel scheme, and Gichuru et al. (2011) who used a half diallel to select genotypes with MSV resistance under different stress environments. The significant interactions between GCA effects and the environments confirmed the presence of variable gene action among inbreds. Significant interaction of the environment and GCA and SCA was also reported by Pswarayi and Vivek (2007) and Murtadha et al. (2018). The occurrence of such interactions led Kumar and Kumar (2015) to propose that selection based on GCA and SCA effects should be evaluated over many seasons. However, due to resource limitations, the MET approach in one season at this stage of testing is deemed sufficient for conclusive and progressive selections. Similar work by Carena (2011) used GCA and SCA to identify and characterise exotic germplasm for the production of adapted short season climate smart varieties in North Dakota, USA.

Some inbreds with medium GCA were constituents of some of the highest yielding hybrids under the different stress environments in both schemes. For example, crosses N2 x N27 and N10 x N25 in LEDII were among the best hybrids, but inbreds N2 and N10 were not among the highest GCA parents. Some of the best hybrids therefore only involved one high GCA parent, demonstrating that high heterosis could be generated between one high GCA parent and one medium GCA parent, in agreement with findings of Lay and Razdan (2017). Recently Al-Nagger et al. (2017), working on high plant density tolerance in maize, attributed the one high GCA parent phenomenon to heterobeltiosis, a term that has been proposed to describe the increased performance of the hybrid over the better parent. Large negative SCA effects were observed in some crosses, suggestive of same heterotic group combinations; a probable confirmation of the presence of sister lines. These inbreds can be further utilised as same heterotic group single-crosses for use as females in the production of three-way hybrids, or could be further investigated with more testers from the other heterotic groups.

The wide ranges in GY for the three trials under different stress environments was evidence that wide variability existed among both the local and exotic inbred lines. The complexity of

GY as a trait has continuously motivated breeders to try and unravel its genetic and physiological basis, especially under drought, the most common stress environment to the poorly resourced rain dependent farmers (Edmeades, 2013). The varying yield response patterns under different stress environments reaffirm the existence of genetic variation, hence donor genotypes for the specific stress factors (Aliu et al., 2008). Using combining ability effects under different environments, the two mating schemes used in this study managed to identify inbreds that were capable of producing hybrids with higher yields than the commercial checks under different stress environments. Both mating schemes identified different inbreds that could be used as donors for optimal, low nitrogen and low phosphorus conditions. Besides the variation in yield, the results also confirmed the presence of genetic variability in other agronomic traits such as maturity (AD) and reaction to the common diseases (results shown in appendices). The variable anthesis dates, for example, revealed that the inbreds had different genetic controls for anthesis under different stress environments (Hefny, 2010).

Across sites H and h estimates were generally high, but lower under stressful conditions. Kamutando et al. (2018) found similar results working with advanced CIMMYT inbred lines adapted to mid-altitude conditions. For the LLDiallel, H was highest under managed drought in agreement with findings by Dao et al. (2017) who used heritability and path coefficient analysis to identify traits that were correlated with GY under drought. However, for the EEDiallel, H under optimal conditions was higher than H under drought, in contrast with both Dao et al. (2017) and Makumbi et al. (2011) who reported increased H under drought stress. In addition to H analysis, the relationship between GCA and SCA was expressed as a ratio. Variable GCA/SCA ratios were observed from both mating schemes. For the LLDiallel scheme GCA/SCA ratio was greater than 1 under managed drought (2.367) and optimal conditions (1.370), revealing the preponderance of GCA over SCA effects for GY. The reverse was true under low nitrogen (0.609) and low phosphorus (0.479), exposing the preponderance of SCA over GCA effects for GY. The seemingly contradictory results were, however, indicative of dissimilar gene action controlling GY under different stress environments (Al-Naggar et al., 2017). Perhaps low GCA/SCA ratio is desirable at this advanced stage of inbred line evaluation where the primary objective is to identify the highest yielding specific hybrid combinations for commercialisation. Since the present study evaluated exotic inbreds in the local programme for the first time, initial flexible selection intensity was used to accommodate a large number of hybrids, which would be screened with more stringent selection intensity in the next stage of testing (Silvela et al., 1989).

Most ESA communities depend on maize as a single staple and their vulnerability to the risk of crop failure mainly due to heterogeneity of the environments, poor rainfall patterns and lack of irrigation is very high (Setimela et al., 2005). Due to genetic uniformity, single-cross hybrids are not suitable for most rain dependent farming communities. Three-way and double-cross hybrids and open pollinated varieties are more resilient and considered more appropriate for these harsh environments. The impracticality of field testing all the possible combinations of three-way and double-crosses hybrids that can be generated in a breeding programme led to the development of statistical prediction techniques based on single-cross diallel or LxT data (Vivek at al., 2007; Cooper et al., 2014). Interestingly, predictions for the possible best yielding combinations in this study identified inbreds N19, N21 and N25, which showed high GCA as well. Exotic inbreds N1, N2 and N3 were involved in the highest SCA effects and were also identified in the predicted possible best hybrids. Predictions enable the identification and selection of a set of best hybrid combinations from the numerous possibilities (Appendices 4.2-4.5). The effect is the massive reduction in the cost of research and the acceleration of breeding pipeline releases. The selected top predictions, however, would still undergo extensive field evaluations before commercialisation, as suggested by Cooper et al. (2014).

The use of exotic material is faced with many challenges, including photoperiod sensitivity, disease susceptibility (Mahuku et al., 2015), and weak roots and stalks (Goodman, 2005). To minimize the magnitude of these effects, Nelson and Goodman (2008) advocated for and used tropical x exotic parents that were more adapted to temperate US environments. Similarly, this study used tropical materials that were likely to be easily adaptable to local tropical conditions. The materials presented in this study therefore denote rich and diverse source populations for the generation of new CimZim-N x exotic, CimZim-O x exotic populations and new CimZim-N x CimZim-N testers. This approach is comparable to the system used at North Carolina State University (Nelson and Goodman, 2008), and also similar to work done on heterotic patterns of IITA and CIMMYT early maturing inbreds under contrasting environments by Badu-Apraku et al. (2018).

The creation of new genetic variability or new source populations was also effectively used by Rice and Tracy (2014) within modern sweet corn, by incorporating more vigorous nonsweet corn germplasm. They managed to extract crosses that significantly out-yielded even the top yielding sweet corn commercial controls. The principle of deriving more productive lines from a combination of better and diverse germplasm for GY, has found effective use in CIMMYT breeding programmes, exemplified by the creation of the highly productive CML536. This public inbred is a high yielding, disease and drought tolerant donor derived from CML442 (good adaptation but susceptible to ear rots) x CML197 (high grain quality and productivity but poor for *turcicum* and self-pollination) x exotic line *Tuxpeno* (*turcicum* resistance but no adaptation) (Magorokosho pers. comm.).

Inbreds originating from Mexico sub-tropical breeding programmes formed the best test cross hybrids under different growing environments (inbreds E1 and E5 - low nitrogen; E9 - drought) demonstrating their potential as donor parents. Kenya inbred E4 also showed its capacity as a potential donor parent for drought conditions. The results showed no significant differences in GY between the best commercial hybrid checks and the best test cross hybrids, indicating that some of the exotic germplasm have the potential to produce superior hybrid combinations with local materials. Intensification of collaboration with breeding programmes in exotic germplasm source countries, especially CIMMYT Mexico and CIMMYT Kenya, can result in the acquisition of more and better characterised germplasm for immediate use in hybrid construction and to enhance genetic variation for further breeding development.

4.5 Conclusions

This study identified local CimZim-N inbreds N21, N25 and L16; CimZim-O inbreds N19 and L4, and exotic inbreds N3, N4, N18, E1 and E9 as the best general combiners that could be used in future breeding programmes. CimZim-N inbreds were superior under optimal conditions while CimZim-O hybrids performed better under stress conditions. Single-crosses N28 x N15, N21 x N4, L3 x L6, L4 x L14, E7 x E1 and E1 x E9 were high yielding crosses which could be considered for immediate commercialisation. Local inbreds N19, N28 and N30 and exotic inbreds N3, N8 and N16 had significant positive SCA effects and can be recommended for further use with the better local lines for final hybrids. The best local x exotic crosses were made up of 73.3% CimZim-N and 26.7% CimZim-O inbreds in combination with the majority of inbred lines from Mexico and a few from Kenya, suggesting that future emphasis should be placed on acquisition of germplasm from Mexico. While CimZim-N x exotic hybrids produced highest average yields across sites, some CimZim-O x exotic hybrids were better performing in specific stress conditions. This showed that some local elite materials still have potential to produce hybrids with higher GY. The results of this study provide the basis for a bigger pre-breeding initiative that can benefit both public and private breeding programmes. Inbreds identified in the current study could be used for pedigree starts, trait introgression and production of commercial hybrids in combination with local inbred lines.

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CHAPTER 5

Strengths and limitations of exotic maize germplasm from diverse sources and opportunities for leveraging local CIMMYT Zimbabwe single-crosses

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5.0 Abstract

Limited land for expansion of crop production, the increasing demand for maize and the possibility of genetic yield stagnation have exerted increased pressure on the need to improve maize productivity. The necessity to achieve sustainable global food and nutritional security for the ever-growing human population in the presence of production stress factors and the added challenge of climate change, have created a need to generate more resilient and genetically variable maize gene pools that can be used to continuously develop crop varieties with higher yield potential and better grain quality. The objective of this study was to identify the best tropical exotic inbreds from diverse sources that can be used directly to leverage the local single-crosses to produce three-way hybrids with potential to out-perform the local commercial checks. A total of 296 elite inbreds from the CIMMYT tropical breeding programmes in Colombia, Kenya, Mexico, Zimbabwe, and IITA in Nigeria were crossed to 68 CIMMYT Zimbabwe single-crosses to produce 1 860 F_1 hybrids. The hybrids were grouped into nine sets according to the maturity groups of the female single-crosses and were evaluated across seven sites for each set alongside 10 commercial checks. Across site analysis of variance indicated highly significant ($p<0.01$) entry effects for grain yield (GY), days to anthesis (DA), ears per plant (EPP) and stalk lodging (SL) in each of the nine sets. The best single-crosses and the best inbred lines were identified on the basis of their presence as constituents of the highest yielding three-way hybrids in each set. The combination of new CIMMYT single-crosses (CimZim-N x CimZim-N) x CimZim-N inbreds produced the highest yielding three-way hybrids. The most prominent CimZim-N x CimZim-N single-crosses were SXA522 and SXB52 and the most prominent CimZim-O x CimZim-O single-crosses were SXA504, SXB503 and SXB504. Although the local inbreds provided the bulk of the top hybrids in terms of GY, a number of exotic inbreds produced equally competitive hybrids. The most prominent local inbreds used as pollen parents were CimZim-O: LA4 and LB3, and CimZim-N: LA23, LA60, LB114 and LB14. The best general combiners from the exotic inbreds were LB56, LA136 and LB81, originating from IITA, LA101 from Mexico and LB44 from Kenya. The most prominent exotic GY enhancers originated from IITA (11%)

and Kenya (4%). Of the 180 best crosses, 49.4% of the pollen parents were from heterotic group A and 31.1% from heterotic group B. The selected inbreds in this study are valuable candidates for future CIMMYT breeding programmes, usable in pedigree start-ups to generate more diverse segregating F_1 populations, and as candidates for more bi-parental crosses to produce single-crosses or in the direct creation of thee-way hybrids, and/or as sources of bulk pollen crosses, as appropriate.

5.1 Introduction

Increase in human population globally, and the changing dietary habits towards more affluent diets consisting of a larger share of animal products, vegetable oils and sugar-sweeteners by the emerging middle class population are considered to be the main drivers of the increase in maize demand (Pradhan et al., 2015). Meeting the projected crop demand for major cereals can only be achieved through increased crop productivity in the face of limited land for expanding crop production as well as the debilitating effects of climate change. The combined effects of increased crop demand, forces of biotic and abiotic stress factors and climate change have created a big research gap for plant breeders. The challenge is for breeders to produce appropriate varieties that are capable of reducing the yield gap (Ray et al., 2012; Mourice et al., 2014). Reducing the yield gap through the use of improved varieties enables farmers to use less fungicide, insecticide or water on their farms thus reducing negative impact on the environment while at the same time sustainably producing adequate food and feed.

The productivity of maize the world over is frequently threatened by common and various biotic stress factors (Bazzaz, 1996) and abiotic stress factors (Bänziger et al., 2000; Edmeades, 2013). Low input levels in poor countries (Fischer, 2015; Lassaletta et al., 2014), soil degradation (Pimentel et al., 1999), poor genetic variability and climate change (Luck et al., 2011; Ross-Ibarra et al., 2017) are some of the less mentioned factors responsible for yield stagnation and sometimes yield deterioration (Fisher, 2012; Ray et al., 2012). History has shown that serious problems can occur when the genetic base of a crop becomes too narrow and changes in the environmental pressures such as new pathogens, new insect pests or unusual environmental stresses come into play (Ray et al., 2012).

Natural genetic variability (Rasmusson and Phillips, 1997) and generated genetic variability (Bansal et al., 2014) have been exploited to date by breeders to produce the current rate of genetic gain and yield stability so far experienced in maize development. In order to maintain this genetic gain and global food security in the presence of the added challenge of climate change, there is an increasing need to exploit genetic variability from diverse sources to develop varieties with superior stress adaptation and genetic yield potential (Reynolds et al., 2016). While serious genetic stagnation has not been recorded in maize as it was in wheat (Willoughby, 2015); serious droughts (Gaffney et al., 2015), and disease and pest outbreaks (Klinkowski, 1970) which in some cases completely wiped out uniform crops, have been recorded in maize. It is contended that the magnitude of these catastrophic droughts, pest and disease outbreaks could have been minimised had there been enough inherent crop genetic variability.

Breeding with exotic germplasm involves purposeful inclusion of germplasm from external populations to generate more desired gene pools for superior variety extraction that give better yields and disease resistance. Most breeding programmes have placed greater emphasis on the utilisation of elite germplasm to curtail maize vulnerability to drought, low soil nitrogen and disease susceptibility (Ramegowda and Senthil-Kumar, 2015; Grauke et al., 2016; O'Hara et al., 2016). Few breeders have examined the use of exotic germplasm as a source of valuable genetic variability for improved GY and other agronomic traits under the current threats. Importation and exploitation of exotic germplasm contributing novel sources of variation for both quantitative and qualitative traits permit the increase of gene frequency of favourable alleles in breeding populations (Hallauer et al., 2010).

Incorporation of exotic germplasm remains one of the most important vehicles for introducing new variability in populations (Mba, 2013) and is commonly implemented through gene introgression, recurrent selection methods (Breseghello, 2013) and genomic selections (Gorjanc et al., 2016). Introgression, together with backcrossing techniques, has been used widely by breeders to introduce new, but only a few genes, into populations. Other commonly used mechanisms to generate genetic variability include hybridisation of adapted material and the use of mutagenic agents (Bansal et al., 2014). It is important to note that recurrent selection schemes imposed on populations do not create new alleles *per se*, but they do generate new genetic combinations and increase the frequency of favourable alleles (Hallauer and Darrah, 1985). In order to introduce genetic variability the choice of source parents must be based on performance *per se* and in direct comparison with adapted commercial germplasm.

Genetic yield gain has been experienced differentially in different parts of the globe, resulting in the existence of germplasm with different GY potential, even when developed from within the same latitudes. Some regions of the world, mostly the USA and other developed countries, have experienced higher rates of genetic gain than all the developing countries (Duvick, 2005). However, most of the USA germplasm is temperate and importation of these materials for direct use in local breeding programmes always meets with serious challenges of adaptation and diseases. Most of the high yielding temperate USA germplasm is also yellow (Salhuana et al., 1998) which is not the favoured colour in the ESA communities where white maize is preferred. Therefore temperate materials cannot be used directly in the tropical environments. On the contrary, tropical germplasm can easily be imported and adopted into other tropical breeding programmes with minimal challenges of adaptation and this has been the motivational basis for the current study.

Within the tropics, different regions and countries have managed to produce hybrids that have specific but different localised genetic GY potential, that are conspicuously variable from country to country and within the countries from one ecological region to another. The GY of maize hybrids on the ESA market are therefore inconsistent even within the same mega-environments. Presently, maize yields in some countries within the tropics have surpassed the 10 t ha^{-1} mark while other countries within the same tropics are still struggling to produce average yields of 7 t ha^{-1} under optimal conditions. National GY averages ranging from 0.9 to 3.5 t ha^{-1} within the SSA were reported by Masuka et al. (2017). In contrast, national averages of maize GY for USA and the developing world are currently beyond 8 t ha^{-1}, with GY potential as high as 16 t ha^{-1} (Duvick, 2005). The above national averages are clear evidence that the developing world need to develop more appropriate new varieties with enough genetic variation capable of producing better yields under the naturally heterogeneous environmental conditions.

Adoption and utilisation of maize hybrids in ESA have increased significantly over the years (Langyintuo et al., 2010) due to improving availability and reduced cost of hybrid seed production. Hybrid seed production is dependent upon controlled pollination with specified male and female parents. Controlled pollination is achieved through isolating the desired parents and de-tasseling the female to ensure that only pollinations from the designated male parent can occur. The next big challenge after isolation is nicking. Nicking is the synchronisation of anthesis of the male and the female. Pollen shedding must occur during the most receptive period of the silks of the female parent. To achieve a perfect nick, hybrid seed producers vary the planting dates through split planting of the parents. The easiest and cheapest, and hence the most preferred nick, is same day planting where the male and female parents are both planted on the same day in the same mechanical run. Same day plantings normally offer a good nick that result in perfect pollination and fertilisation and hence good yields. High yields and reduced cost of seed production stimulate the reduction in the final hybrid seed price. The direct impact is that more farmers will be able to afford hybrid seed, leading to higher adoption rates and hence higher productivity by farmers.

The motivation to use exotic tropical germplasm directly in the local CIMMYT breeding programmes emanates from the fact that along the same latitudes, day lengths and growing conditions are generally similar, and thus the germplasm is partly or wholly adapted. Hybrids produced from exotic tropical inbreds may therefore be directly usable without further genetic manipulation or with minimal refinement within the tropics. This study was based on hybrids derived from exotic inbreds that had perfect nick with local single-crosses to form three-way hybrids. The objectives of the study were to (i) identify exotic inbreds from Colombia, Kenya, Mexico and Nigeria (IITA) that give the best hybrids with perfect nick with local single-crosses (ii) to identify exotic inbreds that could be used directly to leverage the local single-crosses to produce quick-fix hybrids for immediate commercialisation (iii) to identify exotic inbreds that could be used in the long term breeding programme as donors of desirable alleles and (iv) to identify new local x local hybrids that could out-yield both the commercial checks and the new local x exotic hybrids. The local inbreds form the pillars of the local breeding programme and hence the elite materials should be improved continuously and simultaneously with the exotic materials. This study presents one of the simplest ways of creating commercial hybrids within the shortest possible time. The approach leverages on the selection and breeding already done in the places of origin of the inbreds as well as on the fact that exotic germplasm possibly contains desirable alleles that could be used to surmount local genetic yield thresholds. While leveraging the local single-crosses with exotic tropical material to produce three-way hybrids ready for commercialisation within one season, the genetic variability of the local gene pool would also be enhanced, increasing the chances of obtaining even more superior recombinants.

5.2 Materials and methods

5.2.1 Hybrid formation

A total of 296 inbred lines obtained from Colombia, IITA (Nigeria), Kenya, Mexico and Zimbabwe (Tables 5.1 and 5.2) were crossed with 68 CIMMYT-Zimbabwe (CimZim) single-cross females (Table 5.3) during the 2015/2016 season in Muzarabani in Zimbabwe (latitude $17^{o}48'$ S, longitude, $31^{o}02'$ E and altitude, 570 masl). The single-cross females included different cross combinations of old inbreds x new inbreds (CimZim-O x CimZim-N; CimZim-O x CimZim-O and CimZim-N x CimZim-N). A total of 35 single-crosses from the CIMMYT heterotic group A were crossed with 146 heterotic group B inbred lines. On the other hand, 33 single-crosses in heterotic group B were crossed with 150 inbreds from heterotic group A. Inbreds whose heterotic grouping information was not known were crossed with both sets of single-cross hybrids and appeared in both heterotic groups.

A modified top cross mating design was adopted but due to the large number of possible common parents all the crosses were hand-made. The target was to pollinate at least three female plants within each female plot with one pollen parent to generate enough seed for the trials. The crosses were made at random depending on the nick between the single-cross and the pollen parent. This implied that only pairs with a good nick were crossed. No efforts were made to make crosses from non-nicking parents. The aim was to promote male and female parent synchronisation with same day planting, thereby enhancing cheap seed production.

5.2.3 Trial sites

The hybrids were evaluated on at least four sites representing the major maize growing areas in Zimbabwe (Table 5.4).

Table 5.1 Codes, origin and heterotic groups of inbred lines crossed to local single-crosses to produce three-way hybrids

Heterotic group A inbred lines									Heterotic group B inbred lines								
Entr	Name	Origin	Entr	Name	Origin	Entr	Name	Origin	Entr	Name	Origin	Entr	Name	Origin	Entr	Name	Origin
A1	CML312	CimZim-	A51	CL114139	CimZim-	A10	CL147166	Mexico ST	B1	CML444	Cim Zim-O	B51	IITAB551	IITA	B101	TZMI1162	IITA
A2	CML442	CimZim-	A52	CL106535	CimZim-	A10	CL147167	Mexico ST	B2	CML395	CimZim-O	B52	IITAB552	IITA	B102	TZMI1163	IITA
A3	CML197	CimZim-	A53	CL131023	CimZim-	A10	CL147168	Mexico LT	B3	CML547	CimZim-O	B53	IITAB553	IITA	B103	TZMI1164	IITA
A4	CML536	CimZim-	A54	CL131019	CimZim-	A10	CL147169	Mexico LT	B4	CML543	CimZim-O	B54	IITAB554	IITA	B104	TZMI1167	IITA
A5	CML537	CimZim-	A55	CL131020	CimZim-	A10	CL147170	Mexico LT	B5	CML546	CimZim-O	B55	IITAB555	IITA	B105	TZMI1169	IITA
A6	CML538	CimZim-	A56	CL121376	CimZim-	A10	CL147171	Mexico LT	B6	CL115811	CimZim-N	B56	IITAB556	IITA	B106	TZMI1255	IITA
A7	CML539	CimZim-	A57	CL121375	CimZim-	A10	CL147172	Mexico LT	B7	CL101372	CimZim-N	B57	CL147164	Mexico ST	B107	TZMI407	IITA
A8	CL121073	CimZim-	A58	CL121136	CimZim-	A10	CL147173	Mexico LT	B8	CL121519	CimZim-N	B58	CL147165	Mexico ST	B108	TZMI407	IITA
A9	CL121074	CimZim-	A59	CL121129	CimZim-	A10	CL147174	Mexico LT	B9	CL121518	CimZim-N	B59	CL147166	Mexico ST	B109	CL107230	CimZim-
A10	CL121129	CimZim-	A60	CL121290	CimZim-	A11	CL147175	Mexico LT	B10	CL109290	CimZim-N	B60	CL147167	Mexico ST	B110	CL101431	CimZim-
A11	CL121129	CimZim-	A61	CL121358	CimZim-	A11	CL147176	Mexico LT	B11	CL121518	CimZim-N	B61	CL147168	Mexico LT	B111	CL121521	CimZim-
A12	CL121129	CimZim-	A62	CL121259	CimZim-	A11	CL147177	Mexico LT	B12	CL101361	CimZim-N	B62	CL147169	Mexico LT	B112	CL114305	CimZim-
A13	CL121130	CimZim-	A63	CL121358	CimZim-	A11	CL147178	Mexico LT	B13	CL115562	CimZim-N	B63	CL147170	Mexico LT	B113	CL114275	CimZim-
A14	CL121167	CimZim-	A64	CL121313	CimZim-	A11	CL147179	Mexico LT	B14	CL101372	CimZim-N	B64	CL147171	Mexico LT	B114	CL114306	CimZim-
A15	CL121168	CimZim-	A65	CL121280	CimZim-	A11	CL147180	Mexico LT	B15	CL121068	CimZim-N	B65	CL147172	Mexico LT	B115	CL114309	CimZim-
A16	CL121257	CimZim-	A66	CL121250	CimZim-	A11	CL147181	Mexico LT	B16	CL101215	CimZim-N	B66	CL147173	Mexico LT	B116	CL121520	CimZim-
A17	CL121073	CimZim-	A67	CL121250	CimZim-	A11	CL147182	Mexico LT	B17	CL115798	CimZim-N	B67	CL147174	Mexico LT	B117	CL121521	CimZim-
A18	CZL518	CimZim-	A68	KUA568	Kenya	A11	CL147183	Mexico LT	B18	CL101376	CimZim-N	B68	CL147175	Mexico LT	B118	CL107253	CimZim-
A19	CZL519	CimZim-	A69	KUA569	Kenya	A11	CL147184	Mexico LT	B19	CL101141	CimZim-N	B69	CL147176	Mexico LT	B119	CL121521	CimZim-
A20	CZL520	CimZim-	A70	KUA570	Kenya	A12	CL147185	Mexico LT	B20	CL115487	CimZim-N	B70	CL147177	Mexico LT	B120	CL114229	CimZim-
A21	CZL521	CimZim-	A71	KUA571	Kenya	A12	CL147186	Mexico LT	B21	CL121069	CimZim-N	B71	CL147178	Mexico LT	B121	CL114302	CimZim-
A22	CZL522	CimZim-	A72	KUA572	Kenya	A12	CL147187	Mexico LT	B22	CL121519	CimZim-N	B72	CL147179	Mexico LT	B122	CL114317	CimZim-
A23	CZL523	CimZim-	A73	KUA573	Kenya	A12	TZMI761	IITA	B23	CL121069	CimZim-N	B73	CL147180	Mexico LT	B123	CL114302	CimZim-
A24	CZL524	CimZim-	A74	KUA574	Kenya	A12	TZMI754	IITA	B24	CL101370	CimZim-N	B74	CL147181	Mexico LT	B124	CL114271	CimZim-
A25	CZL525	CimZim-	A75	KUA575	Kenya	A12	TZMI751	IITA	B25	CL101370	CimZim-N	B75	CL147182	Mexico LT	B125	CL114267	CimZim-
A26	CZL526	CimZim-	A76	KUA576	Kenya	A12	TZMI899	IITA	B26	KUB526	Kenya	B76	CL147183	Mexico LT	B126	CL114307	CimZim-
A27	CZL527	CimZim-	A77	KUA577	Kenya	A12	TZMI757	IITA	B27	KUB527	Kenya	B77	CL147184	Mexico LT	B127	CL121523	CimZim-
A28	CZL528	CimZim-	A78	KUA578	Kenya	A12	TZMI763	IITA	B28	KUB528	Kenya	B78	CL147185	Mexico LT	B128	CL114315	CimZim-
A29	CZL529	CimZim-	A79	ColA579	Colombia	A12	TZMI764	IITA	B29	KUB529	Kenya	B79	CL147186	Mexico LT	B129	CL114302	CimZim-
A30	CZL530	CimZim-	A80	ColA580	Colombia	A13	TZMI765	IITA	B30	KUB530	Kenya	B80	CL147187	Mexico LT	B130	CL114230	CimZim-
A31	CL106508	CimZim-	A81	ColA581	Colombia	A13	TZMI747	IITA	B31	KUB531	Kenya	B81	TZMI761	IITA	B131	CL121521	CimZim-
A32	CL101141	CimZim-	A82	ColA582	Colombia	A13	TZMI748	IITA	B32	KUB532	Kenya	B82	TZMI754	IITA	B132	CL107228	CimZim-
A33	CL115337	CimZim-	A83	ColA583	Colombia	A13	TZMI753	IITA	B33	KUB533	Kenya	B83	TZMI751	IITA	B133	CL107248	CimZim-
A34	CL115339	CimZim-	A84	ColA584	Colombia	A13	TZMI754	IITA	B34	KUB534	Kenya	B84	TZMI899	IITA	B134	CL121521	CimZim-
A35	CL121516	CimZim-	A85	ColA585	Colombia	A13	TZMI755	IITA	B35	KUB535	Kenya	B85	TZMI757	IITA	B135	CL121521	CimZim-
A36	CL115324	CimZim-	A86	KUA586	Kenya	A13	TZMI878	IITA	B36	KUB536	Kenya	B86	TZMI763	IITA	B136	CL114265	CimZim-
A37	CL121516	CimZim-	A87	IITAA587	IITA	A13	TZMI882	IITA	B37	CoLB537	Colombia	B87	TZMI764	IITA	B137	CL121096	CimZim-
A38	CL121517	CimZim-	A88	IITAA588	IITA	A13	TZMI886	IITA	B38	CoLB538	Colombia	B88	TZMI765	IITA	B138	CL121088	CimZim-
A39	CL115324	CimZim-	A89	IITAA589	IITA	A13	TZMI889	IITA	B39	CoLB539	Colombia	B89	TZMI747	IITA	B139	CL121226	CimZim-
A40	CL115487	CimZim-	A90	IITAA590	IITA	A14	TZMI903	IITA	B40	CoLB540	Colombia	B90	TZMI748	IITA	B140	CL121230	CimZim-
A41	CL115324	CimZim-	A91	IITAA591	IITA	A14	TZMI909	IITA	B41	CoLB541	Colombia	B91	TZMI753	IITA	B141	CL121269	CimZim-
A42	CL115268	CimZim-	A92	IITAA592	IITA	A14	TZMI1161	IITA	B42	CoLB542	Colombia	B92	TZMI754	IITA	B142	CL121388	CimZim-
A43	CL121516	CimZim-	A93	IITAA593	IITA	A14	TZMI1162	IITA	B43	CoLB543	Colombia	B93	TZMI755	IITA	B143	CL121361	CimZim-
A44	CL121517	CimZim-	A94	IITAA594	IITA	A14	TZMI1163	IITA	B44	KUB544	Kenya	B94	TZMI878	IITA	B144	CL121392	CimZim-
A45	CL115324	CimZim-	A95	IITAA595	IITA	A14	TZMI1164	IITA	B45	IITAB545	IITA	B95	TZMI882	IITA	B145	CL121193	CimZim-
A46	CL115323	CimZim-	A96	IITAA596	IITA	A14	TZMI1167	IITA	B46	IITAB546	IITA	B96	TZMI886	IITA	B146	CL121093	CimZim-
A47	CL106547	CimZim-	A97	IITAA597	IITA	A14	TZMI1169	IITA	B47	IITAB547	IITA	B97	TZMI889	IITA			
A48	CL121517	CimZim-	A98	IITAA598	IITA	A14	TZMI1255	IITA	B48	IITAB548	IITA	B98	TZMI903	IITA			
A49	CL121516	CimZim-	A99	CL147164	Mexico ST	A14	TZMI407	IITA	B49	IITAB549	IITA	B99	TZMI909	IITA			
A50	CL131027	CimZim-	A10	CL147165	Mexico ST	A15	TZMI407-	IITA	B50	IITAB550	IITA	B100	TZMI116	IITA			

Table 5.2 Codes and heterotic groups of local single-crosses (SX) used to form three-way hybrids

Heterotic group A			**Heterotic group B**		
Entry	Common Name	Cross	Entry	Common Name	Cross
SXA501	CHA16501	CimZim-O x CimZim-O	SXB501	CH14174	CimZim-O x CimZim-O
SXA502	CH102103	CimZim-O x CimZim-O	SXB502	CH14193	CimZim-O x CimZim-O
SXA503	CHA16503	CimZim-O x CimZim-O	SXB503	CHB16503	CimZim-O x CimZim-O
SXA504	CH16504	CimZim-O x CimZim-O	SXB504	CH14221	CimZim-O x CimZim-O
SXA505	CH1211	CimZim-O x CimZim-O	SXB505	CH14243	CimZim-O x CimZim-O
SXA506	CH16506	CimZim-O x CimZim-O	SXB506	CH14226	CimZim-O x CimZim-O
SXA507	CH102091	CimZim-O x CimZim-O	SXB507	CH142415	CimZim-O x CimZim-N
SXA508	CH142417	CimZim-N x CimZim-N	SXB508	CH142416	CimZim-O x CimZim-N
SXA509	CH142418	CimZim-N x CimZim-N	SXB509	CHB16509	CimZim-N x CimZim-N
SXA510	CH142419	CimZim-N x CimZim-N	SXB510	CH16510	CimZim-N x CimZim-N
SXA511	CH142420	CimZim-N x CimZim-N	SXB511	CH14187	CimZim-N x CimZim-N
SXA512	CHA512	CimZim-O x CimZim-O	SXB512	CH14197	CimZim-N x CimZim-N
SXA513	CHA513	CimZim-O x CimZim-O	SXB513	CH14163	CimZim-N x CimZim-N
SXA514	CH16514	CimZim-N x CimZim-N	SXB514	CH14166	CimZim-N x CimZim-N
SXA515	CHA514	CimZim-N x CimZim-N	SXB515	CH14174	CimZim-N x CimZim-N
SXA516	CH14187	CimZim-N x CimZim-N	SXB516	CH14221	CimZim-N x CimZim-N
SXA517	CH14197	CimZim-N x CimZim-N	SXB517	CH14243	CimZim-N x CimZim-N
SXA518	CH14163	CimZim-N x CimZim-N	SXB518	CH14226	CimZim-N x CimZim-N
SXA519	CH14166	CimZim-N x CimZim-N	SXB519	CHB16519	CimZim-N x CimZim-N
SXA520	CH14174	CimZim-N x CimZim-N	SXB520	CHB16520	CimZim-O x CimZim-N
SXA521	CH14193	CimZim-N x CimZim-N	SXB521	CHB16521	CimZim-O x CimZim-N
SXA522	CH14243	CimZim-N x CimZim-N	SXB522	CHB16522	CimZim-O x CimZim-N
SXA523	CH14252	CimZim-N x CimZim-N	SXB523	CHB16523	CimZim-O x CimZim-N
SXA524	CHA16524	CimZim-N x CimZim-N	SXB524	CHB16524	CimZim-N x CimZim-N
SXAB525	CHA16525	CimZim-N x CimZim-N	Heterotic group AB		
SXAB526	CHA165263	CimZim-N x CimZim-N	SXAB525	CHAB16525	CimZim-O x CimZim-O
SXAB527	CHAB527	CimZim-O x CimZim-O	SXAB526	CHAB16526	CimZim-O x CimZim-O
SXA528	CHAB528	CimZim-O x CimZim-O	SXAB527	CHAB16527	CimZim-O x CimZim-O
SXA529	CHAB529	CimZim-O x CimZim-O	SXAB528	CHAB16528	CimZim-O x CimZim-O
SXA530	CHAB530	CimZim-O x CimZim-O	SXAB529	CHAB16529	CimZim-O x CimZim-O
SXA531	CHAB531	CimZim-O x CimZim-O	SXAB530	CHAB16530	CimZim-O x CimZim-O
SXA532	CHAB532	CimZim-O x CimZim-O	SXAB531	CHAB16531	CimZim-O x CimZim-O
SXA533	CHAB533	CimZim-O x CimZim-O	SXAB532	CHAB16532	CimZim-O x CimZim-O
SXA534	CHAB534	CimZim-O x CimZim-O	SXAB533	CHAB16533	CimZim-O x CimZim-O
SXA535	CHAB535	CimZim-O x CimZim-O			

SXA-single-cross in heterotic group A, SXB-single-cross in heterotic group B, SXAB-single-cross in heterotic group AB, CH-CIMMYT hybrid, CimZim-O-CIMMYT Zimbabwe elite inbred line, CimZim-N-CIMMYT Zimbabwe new inbred line

5.2.2 Hybrid evaluation

A total of 1 860 hybrids, which had sufficient seed for planting on at least four sites, were selected for evaluation. Due to the large number of hybrids, they were sub-divided into nine sets with different numbers of entries, depending on the maturity of the single-cross (i.e., set 1=245; set 2=210; set 3=195; set 4=220; set 5=230; set 6=250; set 7=275; set 8=100, and set 9=135 entries). Single-cross parents with the same anthesis dates were grouped into the same set. Ten local commercial checks and five local CIMMYT checks were included in each of the nine sets (Table 5.3). Only one season was used for the selections due to the challenges in the production of enough seed (Sprague and Eberhart, 1977). The hybrids were evaluated during the 2016 season under managed drought (Table 5.4) as well as during the 2016/2017 summer season. The alpha (0.1) lattice design was used with two replications on each site.

Table 5.3 Local commercial and local CIMMYT checks used in all the sets

Hybrid	Maturity	Source
Local commercial checks		
SC301	Ultra-early	Seed Co
SC403	Early	Seed Co
SC419	Early	Seed Co
SC513	Medium	Seed Co
SC643	Medium	Seed Co
PAN53	Medium	Pannar
PAN7M-81	Medium	Pannar
PHB30G19	Medium	Pioneer
SC727	Late	Seed Co
10C3271	Late	Seed Co
Local CIMMYT checks		
CZH131001	Medium	CIMMYT
CZH131013	Medium	CIMMYT
CZH141028	Medium	CIMMYT
CZH131006	Medium	CIMMYT
CZH131007	Late	CIMMYT

Table 5.4 Sites for the evaluation of the three-way crosses from leveraged single-crosses

Site	Agro-ecology	Mean annual rainfall (mm)	Coordinates	Altitude (masl)	Soil type	Environment
Chiredzi	V	-	21°02’S, 31°58’E	433	Triangle E series	Managed drought
Chisumbanje	V	-	20^{o}30’S, 33^{o}58’E	480	Expanding montmorillonite	Managed drought
Kadoma-RS	III	800	18°32’S, 30°90’E	1155	Clays	Random stress
CIMMYT Harare-OPT	IIa	820	17°43’S, 31^{0}05’E	1 480	Harare 5E series	Optimal
CIMMYT Harare-LN	IIa	820	17°43’S, 31^{0}05’E	1 480	Harare 5E series	Low nitrogen
CIMMYT Harare-LP	IIa	820	17°43’S, 31^{0}05’E	1 480	Harare 5E series	Low phosphorus
CIMMYT Harare-HD	IIa	820	17°43’S, 31^{0}05’E	1 480	Harare 5E series	High density

OPT-optimal conditions, LN-low nitrogen, LP-low phosphorus, HD-high dnsity

5.2.4 Trial management and data collection

Hybrids were planted in single 4 m row plots, 0.75 m apart with an intra-row spacing of 0.25 m at all sites. Two peeps were planted per each planting station and thinned out at 5 to 7 leaf stage targeting 17 plants per single row for the optimal plant density of 53 333 plants ha^{-1}, and 21 plants per row for the high density population of 80 000 plants ha^{-1}. For the managed drought sites, irrigation water was withheld two weeks before anthesis and only enough irrigation for crop survival was given two weeks after anthesis. Recommended agronomic practices were used at each trial site. A general recommended basal fertiliser rate of 400 kg ha^{-1} (8%N:14%P:7%K and 7.5%S) and a top dressing rate of 300 kg ha^{-1} ammonium nitrate (34.5%N) was applied.

The same management recommendations as in Chapters 3 and 4 were used for these trials (see Section 3.2.5 for details). Where herbicides were not used, hand weeding was done to keep all fields weed free during the active growth of the crop. Diseases were also not scored at Chiredzi and Chisumbanje as diseases do not manifest during the dry season (Bänziger et al., 2000). The agronomic traits recorded were as listed in Table 3.2 (see Chapter 3 for details). Due to the large trials, not all trials were successful on all the sites and only sites with complete sets of trials were considered for inclusion in data analysis and this report.

5.2.5 Data analysis

Combined ANOVA for each set was performed using the *aov* function in the Agricolae R package (De Mendiburu and Simon, 2015). Best Linear Unbiased Predictors (BLUPs) and broad-sense heritability (H) or repeatability were calculated for each trait in the different sets on both individual sites and across sites, using the Multi-environment trial analysis with R for windows (META-R) version 5.0 (Alvarado et al., 2015). Also see section 4.2.5 for the incorporated formula used for calculation of H. Mean separations were done using the Tukey's Honestly Significant Difference test (HSD test) function in the Agricolae R package (R Foundation for Statistical Computing, 2017). Phenotypic data for each set were also analysed using the residual maximum likelihood procedure in Fieldbook (Vivek et al., 2007) and to obtain relative grain yield rankings and standard deviations.

5.3 Results

5.3.1 Analysis of variance

Highly significant ($p<0.01$) entry effects and site effects were recorded for GY and for most for the selected traits (Table 5.5). The interaction effects of entry x site were also highly significant ($p<0.001$) for GY at all sites and in all sets. The GY and average trait performance across sites are given in Appendix 5.1 to 5.9.

Table 5.5a Analysis of variance for yield and selected traits in sets 1-4

Source of variation	Degrees of freedom	Grain yield	Anthesis date	Anthesis-silking interval	Plant height	Ear height	Ears per plant	Stem lodging	Texture	Moisture	Ear aspect	Ear rots
Response SET1												
Site	3	194.65***	43049.2	1269.54	41245***	15759.6***	0	132.83***	461.02 1***	173187***	47.217 1***	177037***
Replication	1	1.81	121125.2	122.28	109	528.9	0.49	0.56	0.2	127	6.48	7040**
Entry	244	9.43**	123405.6	123.39	729	760.2**	0.29**	95.88	4.08***	546	3.967	934
Block (Replication)	2	29.01	122976.4	123.189	13570***	3063.7**	0.02	25.72	1.89	2576	41.368***	785
Entry x Site	244	2.38**	123373.8	1234.03	301	275.1	0.01	89.19	0.96	307	1.696	840
Block (Replication x Site)	2	25.28**	123003	1240.67	377	441.9	0.07	553.19**	4.24	786	2.016	3967**
Response SET2												
Site	5	4050.81***	32140.5***	563.70 ***	302125.07***	11005.75***	0.29*	113.85***	237.239***	6 3352233***	68.455***	169015***
Replication	1	41.90***	315.3***	31.7**	8573	239	0.046	5.29*	4.08***	3 19483***	0.15	460
Entry	209	5.75***	42.2***	8.65***	95531***	83054	0.13	1.06	2.06***	5 1830**	1.33**	710
Block (Replication)	82	3.94***	11.1***	5.11***	79248*	23437	0.09	1.54***	1.132	8 1357	1.35*	752
Entry x Site	1045	2.81***	7.4***	4.57**	11235***	73440*	0.11	1.19**	0.946	7 1441	1.12*	764*
Block (Replication x Site)	415	3.75***	8.3***	3.74***	33279***	13253	0.12	1.14**	0.991	7 1822***	1.21**	622
Response SET3												
Site	4	3042.85 ***	367.31 ***	1.45	72577.55 ***	888.12 ***	56.87 ***	119.37 ***	1709.8937 ***	230.6152 ***	2743.7099 ***	246.79 ***
Replication	1	1.97	0.19	0.94	7810.89 **	92.66	22.83	0.37	5.9271 *	16.2822 ***	0.9613	6.0224 0 *
Entry	194	4.23 ***	1.34 ***	1.38 **	292.45 ***	60.85	92.4112 ***	1.52 ***	4.2698 ***	1.447 ***	2.206 ***	0.8264 0
Block (Replication)	76	1.78 ***	1.52 **	1.42 *	682.71 ***	0.86	81.2652	1.23	2.7484 ***	2.5158 ***	2.8347 ***	1.1809 0
Entry x Site	773	2.06 ***	1.32 ***	1.29 ***	691.44 ***	11	81.3588 ***	1.44 ***	2.1076 ***	1.4861 ***	1.9323 ***	0.9501 0
Block (Replication x Site)	298	1.63 ***	0.95	1.03	131.33 **	11.05	1.0964	1.27 ***	2.6563 ***	2.1586 ***	1.6362 ***	1.0600 0
Response SET 4												
Site	4	2567.2967***	446.38***	11.37 ***	397.3***	185.1531***	50.6074***	3782.61***	605.6343 ***	542.24***	1983.4725***	2567.297
Replication	1	0.25	0.32	0.34	44.83***	0.6951	10.8218**	15.89***	27.9283***	12.14 ***	6.2171*	0.2419
Entry	219	3.07***	2.037***	1.36**	1.90***	1.2823*	1.3918 ***	5.43***	3.9773***	3.71***	1.8412***	3.0679
Block (Replication)	86	3.65***	2.077***	1.99 ***	2.03***	1.5183**	1.0915	12.13***	2.3802***	3.05***	3.5879***	3.6477
Entry x Site	876	1.77***	1.38***	1.15	1.48***	1.1866**	1.1403 *	4.99***	1.4980 ***	3.48 ***	1.6133***	1.7678
Block (Replication x Site)	346	1.74***	1.74 ***	1.67 ***	1.86***	1.2659**	1.1327	6.49***	1.6769 ***	1.94 ***	1.531***	1.7436

* p≤0.05, ** p≤0.01, *** p≤0.001,

Table 5.5b Analysis of variance for yield and selected traits in sets 5-9

Source of variation	Degrees of freedom	Grain yield	Anthesis date	Anthesis-silking interval	Plant height	Ear height	Ears per plant	Stem lodging	Texture	Moisture	Ear aspect	Ear rots
Response: SET 5												
Site	3	6078.39 ***	46069.49 ***	42.064 ***	476.12 ***	847.16 ***	215.03 ***	957.35***	629.26 ***	295.80 ***	82.62 ***	37903***
Replication	1	15.46 ***	0.12	0.58	0.26	0.01	0.46	110.66	0.09	61.01 ***	10.99**	210
Entry	229	4.10 ***	12.99 ***	1.99 ***	1.52 ***	1.30 **	2.19 ***	58.27**	2.45 ***	1.53 ***	1.05	440***
Block (Replication)	90	5.52 ***	3.07 ***	1.37*	3.00 ***	1.29 *	1.33 *	68.47***	2.78 ***	1.72 ***	1.45	350**
Entry x Site	687	2.22 ***	1.89 ***	1.26 *	1.67 ***	1.1	0.97	47.2	1.72 ***	1.46 ***	0.95	391***
Block (Replication x Site)	273	3.56 ***	1.98 ***	1.22	1.86 ***	1.32 **	1.11	60.55**	1.59 ***	1.89 ***	1.12	381***
Response SET 6												
Site	3	5143 ***	9636.00 ***	28.64***	874854***	308191***	0.219***	11793.0***	135.29***	3039.33***	147.58***	2450.85***
Replication	1	31.7 ***	1359	10.96*	865***	366	0.040**	530.7***	0.03*	24.44	1.25.	295.88***
Entry	249	5.2 ***	1202	3.16**	820***	753***	0.012***	52.1*	1.22	17.81	0.53***	32.25***
Block (Replication)	98	3.9 ***	1240	2.6	827***	267	0.004	62.1**	0.92	18.47	0.51*	23.19
Entry x Site	747	3.2 ***	1206	2.72	363***	299***	0.006*	56.7***	0.92	17.98	0.42.	28.23**
Block (Replication x Site)	297	2.7 ***	1192	3	533***	371***	0.005.	57**	0.81	16.39	0.4	27.55*
Response: SET 7												
Site	2	12210.1***	123077***	116.51	1681075***	462328***	0.03*	957.35***	73.01***	4048.9***	1093.88*	37903***
Replication	1	0.8	385***	37.83	1709*	1134*	0.02	110.66	0.01	0.12	16.45	210
Entry	274	4.7***	29***	76.89	758***	944***	3.39***	58.27**	0.82	9.73	3.27**	440***
Block (Replication)	108	3.2***	9***	77.36	612***	441***	0.55	68.47***	0.65	10.51	4.26	350**
Entry x Site	548	3***	5*	74.34	363*	320	3.35	47.2	0.75	9.71	2.18*	391***
Block (Replication x Site)	218	2.1*	6***	69.52	387*	280	1.22	60.55*	0.59	9.52	2.79	381***
ResponseSET8												
Site	1	285.24***	27152.82***	0.85.	58.5567***	10.72 **	154.05***	-	173.97***	2081.15***	124.88*	6.59*
Replication	1	24.24***	11.35**	0.60.	15.6932***	16.07 ***	12.39	-	221.38***	1.02	16.606*	13.54***
Entry	99	2.07***	11.46***	1.83 ***	2.2190***	3.18.	61.96***	-	5.45***	2.42***	1.584***	1.41*
Block (Replication)	38	1.95***	3.08***	1.13 0.	1.7368*	1.46.	0.97	-	2.78***	1.38*	2.197	2.40 ***
Entry x Site	99	1.64***	1.49*	1.10.	1.2140 0.	1.35.	71.12	-	1.37*	1.29*	1.437	0.96
Block (Replication x Site)	39	1.34	2.40***	0.988.	1.7532*	1.12	71.08	-	3.20***	1.11	1.686	1.75*
Response: SET 9												
Site	2	5086.12***	39 253***	8.07*	872971***	315392***	0.320***	154.29	96.64***	3096.13***	189.42***	716.71***
Replication	1	18.43**	4	2.96	7218***	1070*	0.001	113.24*	1.59**	28.25***	0.01	552.64**
Entry e	134	7.72***	36.10***	3.49***	888***	774***	0.011***	107.89	1.01***	2.81***	0.62***	107.61***
Block (Replication)	52	3.81***	6.00***	2.72	736***	502***	0.006***	82.01	0.32***	3.03***	0.77***	88.86*
Entry x Site	267	3.20***	5.00***	2.01	297***	203	0.005*	143.88**	0.28***	1.76*	0.43*	81.02*
Block (Replication x Site)	106	4.40***	5.00***	1.78	516**	251*	0.005*	83.51	0.22*	2.83***	0.83***	85.05*

* $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$,

5.3.2 Grouping test cross hybrids by average anthesis dates

All sets with average anthesis dates across sites of 60 days and below were considered as early maturing, and these included set 1 (57 days) and set 3 (59 days). Sets with average anthesis dates between 61 and 66 days were grouped in the intermediate maturing cluster and these were set 2 (65 days), set 4 (66 days), set 6 (66 days) and set 7 (65 days). Lastly, sets with average anthesis dates above 66 days were considered as late maturing hybrids and these included set 5 (67 days), set 8 (67 days) and set 9 (74 days). Within each set, the anthesis dates showed significant variability, with earliness and lateness being evident from the different crosses in different sets (Table 5.6).

Table 5.6 Mean anthesis dates of all nine sets and their heritability, grouped according to maturity

	Anthesis dates (AD)								
	Early sets		Intermediate sets				Late sets		
Statistic for AD	1	3	2	4	6	7	5	8	9
Minimum	48.62	55.66	58.00	60.00	58.25	53.09	58.52	58.67	65.90
Maximum	62.68	64.05	70.88	79.00	72.50	74.00	75.69	74.22	84.07
Mean AD	56.97	59.97	64.98	66.28	66.43	66.20	67.01	67.10	74.05
LSD	2.55	2.83	3.52	7.44	4.80	3.22	3.10	2.70	3.17
CV	2.28	2.40	2.76	5.71	7.08	2.47	2.35	2.03	2.17
Heritability (broad-sense)	0.82	0.31	0.44	0.67	0.37	0.82	0.86	0.89	0.86

5.3.3 Grain yield and other traits performance of the early maturing hybrids (<60 days)

GY for set 1 ranged from 2.69 t ha^{-1} to 9.98 t ha^{-1} with a mean of 6.19 t ha^{-1}. GY for set 3 ranged from 2.24 t ha^{-1} to 8.47 t ha^{-1} with a mean of 5.36 t ha^{-1} (Table 5.7). The best hybrids in terms of GY across sites for set 1 were SC727 (9.98 t ha^{-1}) (a commercial, single-cross check hybrid) followed by

DJH161178 (8.75 t ha^{-1}) (a cross between an IITA pollen parent, LA136, with SXB509). The top GY performing hybrids in set 3 were SC727 (8.47 t ha^{-1}) followed by DJH153523 (7.96 t ha^{-1}) and DJH153564 (7.87 t ha^{-1}), both with CimZim pollen parents. There was no significant difference in GY performance between SC727 and DJH153523. The exotic pollen parents that made the best hybrids in set 1 were A136, A137 and A147 while the best local pollen parents were A139, B109 and B139. Within the early maturing group, the best performing 100% local hybrids and the best performing 50% exotic hybrids in terms of GY were compared with the best performing local commercial checks in Tables 5.7, Appendices 5.1 and 5.3.

Table 5.7 Grain yield and agronomic traits for the best early maturity hybrids averaged across all sites

	Hybrid	GY	GY Rank	Anthesis dates	Plant height	Ear aspect	Stem lodging	Grey Leaf Spot	Turcicum
SET1									
Best local x local hybrids	DJH152381	8.27	4	55.73	202.65	2.72	4.74	2.5	2.5
	DJH152266	8.13	5	55.72	207.49	2.38	0.82	2.38	2.27
	DJH152418	7.97	7	59.75	208.94	2.84	10.93	1.88	2.36
	DJH152099	7.96	8	55.92	203.45	2.75	2.94	1.62	2.36
	DJH16183	7.63	12	55.93	200.62	3.07	1.31	1.63	2.01
Best local x exotic hybrids	DJH161178	8.75	2	58.52	223.63	2.63	3.26	1.12	2.17
	DJH16179	7.72	11	60.32	216.88	3.2	1.42	1.87	2.6
	DJH152301	7.63	13	58.36	203.86	2.67	7.71	1.43	2.14
	DJH152404	7.51	18	59.79	194.14	2.89	2.45	1.75	2.24
Best commercial checks	SC727	9.98	1	62.68	223.69	2.16	9.95	1.37	2.05
	PAN7M-81	8.49	3	59.72	211.23	2.77	0.84	1.37	2.78
	SC643	8.09	6	56.72	216.69	2.89	1.74	1.51	2.22
	PAN53	7.89	9	58.85	201.5	2.66	3.18	1.75	2.18
	10C3271	7.8	10	55.56	205.71	2.89	6.62	3	2.76
Grand mean		6.19		56.97	202.57	2.88	3.2	1.9	2.3
LSD		1.41		2.55	16.73	0.65	9.89	1.5	0.52
CV (%)		11.64		2.28	4.21	11.41	156.8	40.09	11.43
Heritability (broad-sense)		0.75		0.82	0.5	0.35	0.26	0.39	0.18
SET 3									
Best local by local hybrids	DJH153523	7.96	2	61.91	199.99	2.34	2.52	1.38	1.48
	DJH153564	7.87	3	60.23	196.73	1.92	0.12	1.21	1.64
	CZH141028	7.56	5	61	211.26	2.05	0.95	1.21	1.56
	DJH153122	7.39	6	57.39	188.25	2.35	4.21	1.21	1.56
	DJH153275	7.36	7	59.36	200.73	2.05	5.4	1.38	1.64
Best local x exotic hybrids	DJH153547	7.04	9	60.37	197.71	2.53	2.05	1.29	1.56
	DJH153084	6.93	12	60.72	195.14	2.34	6.68	1.29	1.64
	DJH153142	6.85	18	61.36	190.51	2.54	0.63	1.13	1.73
	DJH153107	6.79	19	58.54	182.88	2.35	1.88	1.21	1.64
Best commercial checks	SC727	8.47	1	64.05	212.14	2.28	0.4	1.46	1.81
	PAN7M-81	7.58	4	61.98	212.07	2.15	1.69	1.46	1.81
	SC643	6.92	13	59.79	206.32	2.09	2.13	1.29	1.73
	PAN53	6.79	20	61.09	198.59	2.15	2.29	1.79	1.64
Mean		5.46		59.97	195.28	2.36	3.96	1.37	1.57
LSD		2.34		2.83	23.07	0.74	12.01	0.62	0.61
CV		21.74		2.4	6.01	16.02	154.2	23.01	19.63
Heritability (broad-sense)		0.28		0.31	0.29	0.12	0.32	0.22	0.53

GY-grain yield, LSD-least significant difference, CV-coefficient of variation

5.3.4 Grain yield and other trait performance of the intermediate maturity hybrids (60-66 days)

Grain yield performance for set 2 ranged from 3.92 t ha^{-1} to 9.67 t ha^{-1} (Appendix 5.2), with a mean of 6.80 t ha^{-1} The best 50% exotic hybrids in set 2 were DJH162087 and DJH152780 with exotic parents LA145 and LA150, respectively, from IITA. GY performance for set 4 ranged from 1.5 t ha^{-1} to 8.00 t ha^{-1} with a mean of 4.35 t ha^{-1} (Appendix 5.4). The best hybrids with exotic parents in set 4 were DJH152183 and DJH152221 with exotic parents LA136 and LA147, respectively, both from IITA. For set 6, GY performance ranged from 2.89 t ha^{-1} to 9.66 t ha^{-1} with a mean of 6.76 t ha^{-1} (Appendix 5.6). DJH166146 with exotic parent A119 and DJH166015 with exotic parent A137 proved to be the best GY performers in set 6. Lastly, GY performance for set 7 ranged from 2.49 t ha^{-1} to 8.26 t ha^{-1} with a mean of 5.37 t ha^{-1} (Appendix 5.7). DJH167209 and DJH167207 with exotic parent A101 and B82, respectively, were distinguished as the most superior entries.

Commercial hybrids ranked first in terms of GY in all the intermediate maturity sets except in set 4 where the experimental hybrid DJH152318 with a local pollen parent B15 gave the highest overall mean GY (Table 5.8).

Table 5.8a Grain yield and agronomic traits for the best intermediate maturity hybrids averaged across all sites for sets 2 and 4

SET 2	Name	GY	GY Rank	Anthesis dates	Plant height	Moisture	Ear aspect	Stem lodging	Texture	Turcicum
Best local x local hybrids	CZH141028	8.68	2	65.71	237.71	16.05	2.88	2.54	2.65	1.00
	CH124294	8.39	5	63.82	224.39	15.99	2.38	4.18	2.77	1.12
	DJH152994	8.23	6	65.96	212.85	15.85	2.88	2.18	2.69	0.97
	DJH153000	8.18	7	65.65	219.20	16.40	2.60	4.30	2.49	1.12
	CZH131007	8.18	8	67.55	214.53	16.90	3.06	1.64	5.70	1.13
Best local x exotic hybrids	DJH162087	8.13	9	66.44	209.27	16.64	2.74	5.26	2.21	1.13
	DJH152780	7.86	23	66.89	207.74	16.44	3.00	1.37	3.07	1.13
	DJH152779	7.74	28	66.64	213.27	16.86	2.49	1.72	2.76	1.25
	DJH152789	7.74	29	65.56	222.25	16.79	2.63	1.50	2.51	0.97
Best commercial checks	SC727	9.67	1	70.89	234.25	16.71	2.66	3.89	3.53	1.25
	10C3271	8.47	3	63.05	233.28	16.36	2.44	3.95	2.97	1.00
	PAN7M-81	8.4	4	67.28	240.04	15.55	2.50	5.77	2.88	1.38
	SC643	7.96	14	65.55	224.51	16.58	2.44	2.19	2.46	1.13
Mean		6.8		64.98	216.58	16.32	2.82	2.65	2.73	1.14
LSD		1.38		3.52	83.78	1.38	0.86	6.26	0.81	0.43
CV		10.4		2.76	19.70	4.31	15.46	0.00	0.00	9.10
Heritability (broad-sense)		0.51		0.44	0.06	0.11	0.08	0.08	0.41	0.00
SET 4										
Best local x local hybrids	DJH152318	8.00	1	65.90	185.40	15.70	2.60	5.80	2.50	1.50
	DJH152313	6.30	7	65.30	206.90	16.80	2.60	3.10	2.60	1.50
	SC608	5.90	10	64.60	196.70	16.50	3.00	1.20	3.10	1.70
	DJH152231	5.90	12	64.00	208.00	15.90	2.20	16.80	2.40	1.00
	DJH152206	5.80	13	66.80	206.40	17.10	2.70	0.10	2.60	1.50
Best local x exotic hybrids	DJH152183	7.00	3	67.00	206.00	18.00	2.60	10.70	2.30	1.30
	DJH152221	6.70	4	67.50	207.40	18.20	2.20	3.10	1.70	1.60
	DJH152181	6.50	5	65.80	201.00	17.50	2.80	20.00	2.20	1.50
	DJH152241	6.10	8	67.60	206.70	17.60	2.70	-0.10	2.50	1.50
	DJH152329	6.00	9	68.10	201.20	17.50	2.40	5.70	2.60	1.20
Best commercial checks	PAN7M-81	7.50	2	65.90	214.90	18.10	2.30	2.70	2.80	1.50
	SC419	6.30	6	62.80	203.00	16.80	2.70	6.50	2.60	2.00
	SC727	5.80	16	68.90	213.50	18.00	2.50	1.60	2.70	1.70
Mean		4.35		66.28	196.90	16.47	2.75	5.41	2.28	1.45
LSD		2.22		7.44	18.62	2.90	1.48	15.49	0.55	0.66
CV		25.90		5.71	4.82	8.95	27.46	145.40	12.28	22.80
Heritability (broad-sense)		0.34		0.00	0.37	0.06	0.03	0.02	0.49	0.21

GY-grain yield, LSD-least significant difference, CV-coefficient of variation

Table 5.8b Grain yield and agronomic traits for the best intermediate maturity hybrids averaged across all sites for sets 6 and 7

SET 6	Name	GY	GY rank	Anthesis dates	Plant height	Moisture	Ear aspect	Stem lodging	Texture	Turcicum
Best local x local hybrids	DJH166025	8.80	4	68.25	217.30	14.43	2.50	2.55	2.39	1.50
	DJH166043	8.68	5	69.50	212.18	14.17	2.38	1.74	2.57	1.49
	DJH166041	8.66	6	65.00	213.72	14.05	2.50	3.67	2.70	1.50
	DJH166238	8.61	7	66.25	215.00	14.32	2.00	0.73	2.64	1.50
Best local x exotic hybrids	DJH166015	8.18	17	68.75	226.75	13.86	2.57	1.98	2.75	1.51
	DJH166164	8.15	18	69.25	217.20	13.92	2.21	0.97	2.00	1.49
	DJH166146	8.20	14	66.25	209.27	14.06	2.06	3.80	2.68	1.50
	DJH166150	7.99	23	70.50	208.06	14.01	2.37	6.71	2.44	1.51
	DJH166018	7.95	26	67.50	208.40	14.06	2.39	0.06	2.63	1.50
Best commercial checks	PAN7M-81	9.66	1	67.25	232.15	13.93	2.27	4.25	2.82	1.75
	SC727	9.66	2	70.00	225.35	13.60	2.19	11.07	3.00	1.75
	10C3271	8.13	19	67.00	204.73	14.23	2.38	10.99	2.88	2.00
Mean		6.76		66.43	206.33	13.60	2.49	3.74	2.80	1.60
LSD		2.02		48.53	17.59	4.21	0.64	8.64	0.95	0.37
CV		15.20		37.09	4.34	15.75	13.15	117.40	17.24	11.60
Heritability (broad-sense)		0.52		0.14	0.56	0.00	0.20	0.00	0.24	0.26
SET 7										
Best local x local hybrids	DJH167263	7.62	2	65.89	221.11	14.39	135.00	0.21	2.10	
	DJH167265	7.42	3	67.72	200.74	13.67	107.60	0.34	3.26	
	DJH167219	7.20	5	71.30	213.71	13.81	130.80	3.46	2.14	
	DJH167170	6.97	8	66.01	200.21	13.38	101.50	1.30	2.31	
	DJH167164	6.96	9	65.17	199.03	13.85	101.70	0.22	2.48	
Best local x exotic hybrids	DJH167229	7.03	6	70.44	202.04	13.85	124.90	1.90	2.80	
	DJH167207	6.58	18	70.81	206.52	13.87	135.00	0.15	2.68	
	DJH167203	6.87	10	70.08	200.64	14.64	119.50	3.69	2.84	
	DJH167053	6.43	26	63.09	182.29	13.18	97.31	0.33	2.38	
Best commercial checks	SC635	8.26	1	63.91	190.28	11.46	101.90	5.06	2.76	
	PAN7M-81	7.34	4	66.07	217.04	13.38	130.20	6.01	2.79	
	SC727	6.97	7	71.26	198.27	12.82	116.70	6.00	3.52	
Mean		5.37		66.20	193.00	13.30	100.80	2.27	2.69	
LSD		2.04		3.22	22.41	3.61	20.55	8.00	0.99	
CV		19.40		2.47	5.91	13.80	10.38	179.60	18.82	
Heritability (broad-sense)		0.31		0.83	0.47	0.00	0.66	0.11	0.70	

GY-grain yield, LSD-least significant difference, CV-coefficient of variation

5.3.5 Grain yield performance of the late maturity hybrids (>66 days)

Mean GY for set 5 ranged from 3.35 t ha^{-1} to 8.23 t ha^{-1} with a mean of 6.18 t ha^{-1} (Appendix 5.5). Mean GY for set 8 ranged from 2.43 t ha^{-1} to 9.48 t ha^{-1} (Appendix 5.8) and mean GY for set 9 ranged from 3.76 t ha^{-1} to 11.39 t ha^{-1} (Appendix 5.9). The hybrids with the highest average GY across all sites in set 5 were DJH152580 with CimZim-N pollen parent B14, and DJH152372 with exotic pollen parent B56 from IITA. In set 8 the best hybrids were DJH168087 with CimZim-N pollen parent B114 and DJH168058 with exotic pollen parent B81 from IITA, and in set 9 the best hybrids were CZH141028 with CimZim-N pollen parent B114 and DJH152203 with CimZim-N pollen parent A60 (Table 5.12).

5.3.6 Most predominant single-crosses, exotic inbred lines and their heterotic groups for all sets

The most predominant leveraged single-crosses were the CimZim-O x CimZim-O crosses making up 60% of the top 20 hybrids in all trials, followed by CimZim-N x CimZim-N single-crosses making up 33% and lastly, the CimZim-O x CimZim-N combinations contributing approximately 7% of the top performing hybrids (Table 5.10). The most prominent exotic inbreds producing the highest yielding hybrids were sourced from IITA as compared to the inbreds sourced from Colombia, Kenya and Mexico (Table 5.11).

Table 5.9a Grain yield and agronomic traits for the best late maturity hybrids averaged across all sites for set 5

	Hybrid	GY	GY rank	Anthesis date	Plant height	Moisture	Texture	Stem lodging	MSV	Turcicum
A SET 5										
Best local x local hybrid	DJH152580	8.17	3	69.06	219.84	15.67	3.12	5.82	1.02	1.75
	DJH152535	7.81	7	67.42	215.32	15.69	3.13	19.63	1.04	2.00
	DJH152670	7.67	9	69.80	217.44	14.25	2.80	1.94	1.00	1.50
	DJH165001	7.51	12	62.54	213.56	13.85	3.11	14.45	1.01	1.50
	DJH152468	7.50	13	64.78	201.46	16.28	2.18	0.22	1.00	1.50
Best local by exotic Hybrid	DJH152552	7.96	5	70.80	212.09	15.35	2.35	1.05	0.98	1.75
	DJH165021	7.89	6	69.78	218.42	12.29	2.81	2.21	1.25	2.00
	DJH152372	7.73	8	70.38	200.06	15.97	2.93	0.15	1.00	1.75
	DJH152654	7.52	11	68.37	197.87	15.26	2.75	0.03	1.00	1.50
	DJH152656	7.47	14	66.41	209.59	15.19	2.82	0.08	1.00	1.75
	DJH152650	7.45	15	68.43	199.57	15.89	2.51	0.67	1.00	1.75
Best commercial checks	DJH152483	7.41	16	68.43	197.34	16.37	2.44	4.47	1.00	1.75
	PAN7M-81	8.23	1	67.31	209.20	15.86	2.69	4.09	0.98	2.00
	PAN53	8.19	2	65.83	209.82	15.50	2.87	2.67	1.00	1.75
	SC643	7.99	4	73.56	224.78	14.77	3.05	1.51	1.00	1.50
	SC727	7.64	10	67.23	207.31	14.59	2.75	12.08	1.25	1.50
Mean		6.18		1.27	1.23	12.04	1.27	2.76	1.62	1.62
LSD		1.64		2.64	0.61	5.53	0.66	1.49	0.39	0.39
CV		13.47		105.63	24.96	23.39	26.37	27.58	12.25	12.25
Heritability (broad-sense)		0.58		0.35	0.24	0.27	0.46	0.05	0.16	0.16

GY-grain yield, LSD-least significant difference, CV-coefficient of variation

Table 5.9b Grain yield and agronomic traits for the best late maturity hybrids averaged across all sites for sets 8 and 9

	Hybrid	GY	GY rank	Anthesis date	Plant height	Moisture	Texture	Stem lodging	MSV	Turcicum
B SET 8										
Best local x local hybrids	DJH168087	8.17	2	69.06	219.84	15.67	3.12	5.82	1.02	1.75
	DJH168090	7.81	8	67.42	215.32	15.69	3.13	19.63	1.04	2.00
	DJH168022	7.67	10	69.80	217.44	14.25	2.80	1.94	1.00	1.50
	DJH168068	7.51	11	62.54	213.56	13.85	3.11	14.45	1.01	1.50
	DJH168043	7.50	12	64.78	201.46	16.28	2.18	0.22	1.00	1.50
Best local by exotic	DJH168063	7.96	3	70.80	212.09	15.35	2.35	1.05	0.98	1.75
hybrid	DJH168058	7.89	7	69.78	218.42	12.29	2.81	2.21	1.25	2.00
	DJH168012	7.73	20	70.38	200.06	15.97	2.93	0.15	1.00	1.75
	DJH168046	7.52	23	68.37	197.87	15.26	2.75	0.03	1.00	1.50
Best commercial	SC727	8.23	1	67.31	209.20	15.86	2.69	4.09	0.98	2.00
checks	10C3271	8.19	4	65.83	209.82	15.50	2.87	2.67	1.00	1.75
	PAN7M-81	7.99	5	73.56	224.78	14.77	3.05	1.51	1.00	1.50
	SC643	7.64	9	67.23	207.31	14.59	2.75	12.08	1.25	1.50
Mean		6.18		67.01	201.91	14.54	2.76	8.18	1.02	1.62
LSD		1.64		3.10	17.52	2.23	1.49	21.11	0.17	0.39
CV		13.47		2.35	4.42	7.81	27.58	130.01	8.61	12.25
Heritability (broad-sense)		0.58		0.86	0.59	0.20	0.05	0.59	0.32	0.16
C SET 9										
Best local x local	CZH141028	10.73	2	73.50	217.76	14.53	2.83	0.00	1.00	1.75
Hybrid	DJH152203	10.34	3	75.60	211.58	15.50	2.97	0.00	1.46	1.75
	DJH151818	9.38	5	76.94	202.22	13.87	2.83	0.00	1.75	1.50
	DJH153479	9.24	6	79.86	207.34	12.76	2.59	0.00	1.26	1.50
	DJH152916	8.90	8	71.81	193.18	13.84	3.41	0.00	1.01	1.50
Best local by exotic hybrids	DJH16024	7.99	20	72.63	187.88	13.83	3.03	0.00	0.98	1.50
Hybrid	CH1126	7.83	23	76.93	199.28	13.49	2.72	4.17	1.48	1.75
	DJH16020	7.24	24	74.53	183.92	13.78	3.08	3.85	1.50	1.50
	DJH16021	7.23	25	73.09	192.41	14.26	2.72	0.00	0.97	1.50
Best commercial	SC727	11.39	1	78.50	208.52	14.41	3.78	0.00	1.27	1.50
Checks	SC643	9.53	4	71.59	192.62	14.25	3.06	0.00	1.27	1.50
	PAN7M-81	9.10	7	73.98	200.17	13.09	3.35	0.00	1.75	1.75
Mean		6.61		74.05	190.34	13.47	2.83	3.19	1.44	1.61
LSD		2.45		3.17	19.32	1.49	0.61	18.56	0.53	0.40
CV		18.74		2.17	5.16	5.60	11.02	292.81	18.68	12.59
Heritability (broad-sense)		0.63		0.86	0.62	0.39	0.72	0.18	0.74	0.04

GY-grain yield, LSD-least significant difference, CV-coefficient of variation

Table 5.10 Most prominent single-crosses and derived hybrids, excluding commercial checks for all the sets

Set	GY t ha^{-1}	SX female	Status of SX female	Pollen parent	Source of pollen parent	Final hybrid
Set 1	8.75	SXB509	CimZim-N x CimZim-N	A136	IITA	DJH161178
Set 1	8.27	SXA514	CimZim-N x CimZim-N	A60	CimZim-N	DJH152381
Set 1	8.13	SXA536	CimZim-N x CimZim-N	B109	CimZim-N	DJH152266
Set 1	7.97	SXA537	CimZim-N x CimZim-N	B139	CimZim-N	DJH152418
Set 1	7.96	SXA538	CimZim-N x CimZim-N	B127	CimZim-N	DJH152099
Set 2	8.68	SXB503	CimZim-O x CimZim-O	B114	CimZim-N	CZH141028
Set 2	8.39	SXAB530	CimZim-O x CimZim-O	B110	CimZim-N	CH124294
Set 2	8.23	SXB506	CimZim-O x CimZim-N	A30	CimZim-N	DJH152994
Set 2	8.18	SXB506	CimZim-O x CimZim-N	A43	CimZim-N	DJH153000
Set 2	8.18	SXB504	CimZim-O x CimZim-O	A60	CimZim-N	CZH131007
Set 3	7.96	SXAB537	CimZim-O x CimZim-O	A4	CimZim-O	DJH153523
Set 3	7.87	SXAB531	CimZim-O x CimZim-O	A49	CimZim-N	DJH153564
Set 3	7.56	SXB503	CimZim-O x CimZim-O	B114	CimZim-N	CZH141028
Set 3	7.39	SXB18	CimZim-N x CimZim-N	A23	CimZim-N	DJH153122
Set 3	7.36	SXA522	CimZim-N x CimZim-N	A23	CimZim-N	DJH153275
Set 4	8.00	SXA522	CimZim-N x CimZim-N	B15	CimZim-N	DJH152318
Set 4	7.00	SXA504	CimZim-O x CimZim-O	B94	IITA	DJH152183
Set 4	6.70	SXA505	CimZim-O x CimZim-O	B105	IITA	DJH152221
Set 4	6.50	SXA504	CimZim-O x CimZim-O	B87	IITA	DJH152181
Set 4	6.10	CH102091	CimZim-O x CimZim-O	B3	CimZim-O	DJH152313
Set 5	8.17	SXB521	CimZim-N x CimZim-N	B14	CimZim-N	DJH152580
Set 5	7.96	SXB515	CimZim-N x CimZim-N	B56	IITA	DJH152552
Set 5	7.89	SXA525	CimZim-N x CimZim-N	B56	IITA	DJH165021
Set 5	7.81	SXB515	CimZim-N x CimZim-N	B14	CimZim-N	DJH152535
Set 5	7.73	SXB521	CimZim-N x CimZim-N	B56	IITA	DJH152372
Set 6	9.02	SXB531	CimZim-O x CimZim-O	B127	CimZim-N	DJH166030
Set 6	8.80	SXB531	CimZim-O x CimZim-O	B21	CimZim-N	DJH166025
Set 6	8.68	SXB501	CimZim-O x CimZim-O	A60	CimZim-N	DJH166043
Set 6	8.66	SXB501	CimZim-O x CimZim-O	A23	CimZim-N	DJH166041
Set 6	8.61	SXB504	CimZim-O x CimZim-O	A60	CimZim-N	DJH166238
Set 7	7.62	SXB503	CimZim-O x CimZim-O	B114	CimZim-N	DJH167263
Set 7	7.42	SXB504	CimZim-O x CimZim-O	A60	CimZim-N	DJH167265
Set 7	7.20	SXB526	CimZim-O x CimZim-O	A42	CimZim-N	DJH167219
Set 7	7.03	SXB526	CimZim-O x CimZim-O	A101	Mexico LT	DJH167229
Set 7	6.97	SXB517	CimZim-O x CimZim-N	A62	CimZim-N	DJH167170
Set 8	8.61	SXB503	CimZim-O x CimZim-O	B114	CimZim-N	DJH168087
Set 8	8.59	SXB523	CimZim-O x CimZim-O	B81	IITA	DJH168058
Set 8	8.27	SXB524	CimZim-N x CimZim-N	A5	CimZim-N	DJH168090
Set 8	7.78	SXB526	CimZim-O x CimZim-O	B84	IITA	DJH168012
Set 8	7.71	SXB531	CimZim-O x CimZim-O	B44	CimZim-N	DJH168022
Set 9	10.73	SXB503	CimZim-O x CimZim-O	B114	CimZim-N	CZH141028
Set 9	10.34	SXA506	CimZim-O x CimZim-O	A60	CimZim-N	DJH152203
Set 9	9.38	SXB526	CimZim-O x CimZim-O	A4	CimZim-O	DJH151818
Set 9	9.24	SXB526	CimZim-O x CimZim-O	A45	CimZim-N	DJH153479
Set 9	8.90	SXB526	CimZim-O x CimZim-O	A28	CimZim-N	DJH152916

GY-grain yield, SX-single cross, CIMZim-O-CIMMYT Zimbbawe elite, CIMZim-N-CIMMYT Zimbabwe new

Table 5.11 Sources of the best exotic inbred lines used to leverage local single-crosses

Set	GY	Entry	Final Hybrid	Source of pollen	Exotic pollen parent
Set	8.7	A136	DJH161178	IITA	TZMI878
Set	7.7	A137	DJH16179	IITA	TZMI882
Set	7.6	A147	DJH152301	IITA	TZMI1169
Set	7.5	A149	DJH152404	IITA	TZMI407
Set	8.1	A145	DJH162087	IITA	TZMI1164
Set	7.8	A150	DJH152780	IITA	TZMI407-Short
Set	7.7	A147	DJH152779	IITA	TZMI1169
Set	7.7	B145	DJH152789	Colombia	(CH102641)-B-15-2-1-B-B
Set	7.0	A076	DJH153547	Kenya	ECAVL17-42-5-1-5-2-1-1-BB
Set	6.9	B141	DJH153084	Colombia	[DTPWC8F31-4-2-1-6-
Set	6.8	A85	DJH153142	Colombia	[CML312xCML363]-BB-1-B*7-
Set	6.7	A71	DJH153107	Kenya	((KU1403x1368)-7-2-1-1-
Set	7.0	A136	DJH152183	IITA	TZMI878
Set	6.7	A147	DJH152221	IITA	TZMI1169
Set	6.5	B87	DJH152181	IITA	TZMI764
Set	6.1	B95	DJH152241	IITA	TZMI882
Set	6.0	B95	DJH152329	IITA	TZMI882
Set	7.9	A98	DJH152552	IITA	TZMI407-Short-B*4
Set	7.8	A98	DJH165021	IITA	TZMI407-Short-B*4
Set	7.7	B56	DJH152372	IITA	TZMI407-Short-B*4
Set	7.5	B134	DJH152654	IIAT	TZMI754
Set	7.4	A137	DJH152656	IIAT	TZMI882
Set	7.4	A98	DJH152650	IIAT	TZMI407-Short-B*4
Set	8.1	A137	DJH166015	IITA	TZMI882
Set	8.1	A47	DJH166164	Kenya	[[KILIMA(ST94)-
Set	8.2	A119	DJH166146	Mexico	CLWN509
Set	7.9	A131	DJH166150	IITA	TZMI747
Set	7.0	A101	DJH167229	Mexico	POB502c2F215-15-2-1-B*5
Set	6.5	B82	DJH167207	IITA	TZMI754
Set	6.8	A86	DJH167203	Kenya	ECAVL17-30-6-1-1-2-1-2-B
Set	6.4	B88	DJH167053	IITA	TZMI765
Set	8.5	A123	DJH152916	IITA	TZMI761
Set	7.7	A126	DJH168012	IITA	TZMI899
Set	7.7	B44	DJH168022	Kenya	ECAVL17-30-6-1-1-2-1-2-B
Set	7.4	A52	DJH168068	Mexico	CIMCALI8843/S9243-BB-#-B-5-
Set	6.9	A71	DJH168046	Kenya	((KU1403x1368)-7-2-1-1-
Set	7.9	B100	DJH16024	IITA	TZMI1161
Set	7.8	A47	CH1126	Mexico	[[KILIMA(ST94)-
Set	7.2	B44	DJH16020	Kenya	ECAVL17-30-6-1-1-2-1-2-B
Set	7.2	B53	DJH16021	IITA	TZMI407-SxMO17LPA-16-2-

GY-grain yield

5.4 Discussion

The possibility of genetic gain stagnation (Ray et al., 2012; Fisher, 2012) is a real threat to maize breeding. This challenge is conceivably caused by lack of genetic variability within the elite gene pools, and can be addressed, for example, by introducing new genes from other sources (Groot, 2012). This study used exotic tropical inbreds from other tropical breeding programmes to introduce new genes into CimZim single-crosses and to identify the resulting best three-way hybrid combinations. This study was based on the hypothesis that favourable alleles, such as those coding for higher GY, disease and insect pest resistance, as well as those coding for abiotic stress tolerance such as drought, were present in exotic populations. The frequency and variability of these alleles can only be revealed by systematically combining them with elite materials for evaluation. Inbreds from other breeding programmes are considered ready to use materials and would enable a significant reduction in the turnaround time for hybrid release cycle.

The GY performances of the test hybrids were used to infer the usability of the component inbreds in the short term breeding programmes. These results were further used to identify inbreds that carry special alleles conferring tolerance to different stress environments. The availability of such desirable alleles in different inbreds can be used in the long term to generate genetic variability for accelerated genetic gains. The increasing importance of GY under varied environments and the increasing frequency of new strains of diseases in ESA require the constant upgrading of the local gene pools (Wang et al., 2014). This upgrading process is essential for the purpose of introducing and increasing the frequency of alleles that can confer resistance or tolerance to stress. The diverse genetic backgrounds of the germplasm was responsible for the variable mean GY performance and variable disease reaction among the different sets of hybrids under different stress environments as observed.

The results, therefore, confirm that desirable alleles were present in the exotic germplasm even for various other traits. For example; the diverse range of anthesuis dates revealed that the exotic materials were capable of introducing variation to the anthesis dates. Breeding for high yields should always be accompanied by subsidiary objectives related to other important and better agronomic and qualitative traits (Lee and Tracy, 2009).

Several factors have to be considered when choosing the parental lines for commercial hybrid development. Commercial inbreds suitable for use as pollen parents should be as tall as, or taller than the female parents for effective pollination to occur under isolation, and should provide a good nick (flower at the same time) with the targeted female. The current study was designed in such a way that only those single-crosses with a natural nick with the exotic pollen parents were used. The importance of selecting female and male parents that nick has been explained in other studies (Mandal, 2014; MacRobert et al., 2014).

Ideally, the male plants should begin shedding pollen when the first female silks begin appearing and they should shed pollen for as long as it takes for all the female silks to emerge. More often parental combinations with a perfect nick will result in relatively higher productivity and hence cheaper hybrid seed production. Since the parental combinations for this study were selected from the same day plantings, the hybrids which showed superior performance for GY and the other agronomic traits would be offered for commercialisation as cheaper options (Lauer and Stanger, 2018). Selection for synchronisation under optimal conditions or under mild stress is considered adequate, since most of the seed production is done under irrigation (MacRobert et al., 2014). Seed producibility studies for the top hybrids can confirm the cheapest options for production.

The potential seed output is any production system is determined by the type of seed being produced and the parental choices made. Traditionally, three-way hybrid development programmes involve the formation of the single-crosses first and then crossing them with the final pollen parents. The single-cross is normally formed from the same heterotic group inbreds and is used as the female in both three-way and double-cross hybrids for high seed yields. In fact, double-cross hybrids seed is the cheapest while single-cross hybrid seed is the most expensive, due to the differences in parental productivity of the female parent. Three-way hybrids are the most common in ESA, while single-cross hybrids are most common in developed seed markets (MacRobert et al., 2014). One way of ensuring the availability of affordable hybrid seed for poorer regions such as ESA, is the adoption of less expensive production techniques through minimizing field operations, early planting date, appropriate parental selection, as well as adherence to rigorous cultural practices that ensure purity and uniformity of the seed.

The results showed that the highest yielding three-way crosses were made from CimZim-N x CimZim-N single-crosses, demonstrating the superiority of new over old germplasm. However the old (CimZim-O x CimZim-O) single-crosses had the highest frequency in the best hybrids, making up 53% of the top yielding hybrids, followed by CimZim-N x CimZim-N single-crosses (22%) and CimZim-N x CimZim-O single-crosses (5%). The target of pipeline breeding is to continuously produce new single-crosses that can be used in combination with new inbreds to generate continuous higher levels of heterosis and genetic gain.

The expectation is that new inbreds will perform better than old inbreds and the old inbreds will be gradually and eventually phased out as they become less productive and more susceptible to new diseases. This prospect is confirmed by the performance of CimZim-N hybrids which were the highest yielding group though fewer in numbers than the CimZim-O hybrids. Interestingly however, the appearance of many CimZim-O derived single-crosses among the best hybrids show that the old inbreds were still producing competitive hybrids. Another noteworthy result was that some competitive three-way hybrids with all parents originating from the same heterotic group (7.2% in heterotic group A and 11.1% in heterotic group B) were also produced. This phenomenon provides greater opportunities for selecting more diverse female single-crosses for the production of higher yielding three-way and double-cross hybrids, although further testing will be required to confirm the heterotic groupings.

Overall, germplasm from IITA showed more promise than germplasm from Colombia, Kenya and Mexico for leveraging local single-crosses. IITA was the only source outside the CIMMYT breeding programmes. According to Bankole et al. (2017), IITA has improved their bi-parental maize population selections through Marker Assisted Recurrent Selections (MARS) using single nucleotide polymorphism (SNP) markers to enhance GY and other traits under drought stress and well-watered conditions. In addition the parents used to develop these bi-parental crosses were elite drought tolerant maize inbreds (Edmeades et al., 1997). The methods of population development at IITA are distinctly different from the largely pedigree method used at CIMMYT, hence the high heterosis.

The generation of such high heterosis between germplasm from different breeding programmes has also been reported in China. While recognising the challenges of incorporating diversity into Chinese elite maize breeding pools from exotic germplasm, Fan et al. (2014) acknowledged the great heterotic differences that exist between CIMMYT tropical maize germplasm and temperate maize germplasm from China and the USA. Similar findings by Yong et al. (2013) showed that a 1% increase in the genetic contribution of exotic germplasm from CGIAR and the USA increased maize GY in China by 0.025 and 0.01 t ha^{-1}, respectively. Lu et al. (2011) also reported that exotic germplasm from other breeding programmes has introduced lower ear height, earlier maturity, high harvest index and drought tolerance in Chinese maize, resulting in a gradual increase in plant population density and grain yield.

5.5 Conclusions

The outstanding (local x local) x local hybrids were DJH141028 in set 2, DJH153523 in set 3, DJH152318 in set 4, DJH152580 in set 5, DJH166030 in set 6, DJH167263 in set 7 and DJH168087 in set 8. The top performing (local x local) x exotic hybrids were DJH161178 in set 1, DJH152183 in set 4, DJH152552 in set 5 and DJH168068 in set 8. These and other good three-way hybrids that performed well in each of the nine sets may be considered for evaluation for direct commercialisation. CimZim-O inbreds that showed superior performance in three-way hybrid combinations were A4, B3 and A5. CimZim-N inbred lines with superior performance were A60, A23, A26, B14 and B114. While CimZim-N crosses produced the topmost yielding hybrids, more CimZim-O crosses than CimZim-N crosses were found in the top hundred hybrids. The generally good performance of more CimZim-O inbreds is the most probable reason why breeders are reluctant to adopt exotic germplasm wholesale. Germplasm from IITA produced better hybrids than germplasm from Colombia, Kenya and Mexico, indicating the existence of high heterosis between CIMMYT and IITA germplasm. The high heterosis is possibly the result of the genetic differences and breeding methodologies deployed by the two organisations. Generally this study provides positive preliminary results pointing to the need for a bigger and more comprehensive utilisation of a wider range of exotic tropical germplasm by the local breeding programmes. Short and long term breeding goals would be easier to achieve if breeders have access to comprehensive data sets of exotic germplasm.

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CHAPTER 6

General discussion, conclusions and recommendations

6.1 Introduction

Maize breeders play an important role in feeding the future by generating varieties that are adaptable, stress tolerant, easy to produce and affordable. In commercial seed production, the seed yield output of any hybrid is determined by the inherent genetic potential of the parents and the type of seed being produced (whether single-cross sot three-way cross). The role of breeding is to make competitive parental choices that will give the highest possible genetic yield potential and the lowest possible seed production cost (Badu-Apraku et al., 2017).

The major cost components which can reduce or enhance the yield potential in the production of high quality hybrid maize seed include irrigation, planting operations (split or same day planting), weed and pest control as well as seed processing costs (Lauer and Stanger, 2018). The production cost determines the eventual selling price, which critically affects the adoption rates by farmers. In order to maximise adoption and improve productivity of maize, the breeder should use a mix of technologies that will enable the production of affordable hybrid seed. The use and inclusion of exotic maize germplasm is one such technology that will result in the production of high yielding and inexpensive hybrid seed, leading to higher adoption rates and increased productivity by small scale poorly resourced farmers. As confirmed by the results from this study, temperate and tropical exotic maize inbreds harbour a diversity of alleles that are capable of enhancing genetic gain and grain yield potential, and conferring better agronomic traits to the local maize germplasm.

6.2 Closing the research gap

Agriculture in the 21st century has to produce more food to feed the growing human population. The world population is expected to grow by 2.3 billion people between 2009 and 2050 (Shiferaw et al., 2011). SSA's population is predicted to grow the fastest (+114%) and slowest in east and Southeast Asia (+13%)(FAO, 2009). There must be significant increases in the production of several key commodities, including maize, in order to meet the projected demand. Annual cereal production, for instance, has to grow by almost one billion tons by 2050 (FAOSTAT, 2017) to be able to feed the anticipated ten billion people. Since the bigger portion of the population in SSA depends on maize as a single staple, maize production in these countries needs to almost double (Shiferaw et al., 2011) to be able to feed the increased population as well as produce large quantities of biofeed stock for a potentially huge bioenergy market.

For maize breeders, the inflexibility of using only elite material is now being undermined by the realistic expectations to produce larger quantities of maize, in the face of possible genetic gain and yield deterioration (Ray et al., 2012). Current maize germplasm pools of elite material may now require a genetic boost from external germplasm, primarily from exotic populations in order to introduce new alleles and generate variability that will enable the formation of new and superior parental combinations. The easiest sources of exotic novel genes for immediate deployment in maize breeding programmes reside in inbreds and hybrids from other breeding programmes. These have already been used successfully in their places of origin and thus may be readily available for immediate deployment, notwithstanding the challenges of adaptation. The use of exotic maize inbreds and hybrids has the dual benefits of increasing the genetic variability of the local populations, as well as accelerating the rate of possible hybrid commercialisation as compared to the conventional pedigree method. This viewpoint is premised on the possible benefits of leveraging current research on advances that have already been undertaken by other breeders with other breeding organisations across the world. Novel alleles from exotic populations to complement the elite gene pools should be gradually and systematically considered on a long-term basis as an *ex-ante* measure against the uncertainty of future inadequacy of maize as a staple, using the available simple mating techniques such as diallel and the North Carolina designs.

6.3 Objectives of this study

The overall purpose of the study was to identify beneficial inbreds from both temperate germplasm in Chapter 3, and exotic tropical germplasm in Chapter 4 and 5, for inclusion in the CIMMYT-Zimbabwe breeding programme. This strategy could be considered as an easier method of creating commercial hybrids within the shortest possible time. The underlying hypothesis was that both exotic temperate germplasm and exotic tropical germplasm possess favourable alleles that could be easily transferred to leverage the CIMMYT-Zimbabwe maize germplasm to produce superior hybrid combinations. Parental choices in hybrid seed production and the types of hybrids being produced takes centre stage and have a direct bearing on the overall production cost and productivity of the seed.

6.4 Summary of the main research findings

Diverse opportunities for exploiting both the exotic temperate and exotic tropical germplasm to close the yield gaps are available, but are currently minimally exploited. Even in the developed world and advanced breeding programmes, the use of exotic germplasm is still equally limited (Goodman, 1999). Nonetheless, realistic possibilities exist where specialised genotypes with special adaptation to specific growing environments can be selected from local x exotic populations. Additionally, generalised genotypes with moderate suitability in most growing environments and genotypes with phenotypic plasticity, where environmental signals interact with the genotype and stimulate the production of alternative phenotypes, can also be selected from the wide range of possibilities (Fritsche-Neto and DoValem, 2012).

The results showed the existence of distinct genetic variability, high trait heritability as well as an inconsistent degree of trait inter-relationships and trait correlations with GY. Although temperate inbreds cannot be used directly to produce final hybrids for immediate commercialisation due to adaptation challenges, the GY results and the trait performance indicators of the local x temperate test crosses, showed that temperate germplasm can be a useful source of favourable traits for introgression into tropical adapted germplasm. Of the exotic tropical materials, IITA and Mexico sub-tropical materials showed the greatest heterosis with CIMMYT-Zimbabwe materials, suggesting that more effort can be channelled towards IITA and CIMMYT Mexico breeder involvement as well as more material inclusion to capitalise on the identified unique heterosis (Abera et al., 2016). Different breeding techniques and different breeding strategies used by IITA and CIMMYT have possibly resulted in the identified high heterosis between materials from the two organisations.

Several inbreds that performed well under contrasting growing environments can be considered as donors for specific alleles useful for pedigree starts, introgression of specific traits and for direct use in combination with local materials to produce more productive hybrids. The identified hybrids and the component inbred lines provide a rich basis to launch future and expanded breeding programmes with greater inherent genetic variability.

Short and long term breeding goals would be easier to achieve if breeders had access to comprehensive data sets of exotic germplasm from both private (ex-

PVP) and public institutions. This study provided encouraging preliminary data with indications that can be utilised for greater and more comprehensive breeding programmes exploiting temperate and exotic tropical germplasm.

6.5 Discussion of general implications of the results

The success of maize as a crop has been attributed more to improvement in productivity rather than agronomic advances and is subsumed in the general and steady growth in genetic gain. However, the current rates of genetic gain and the production levels are considered insufficient in view of rapid human population growth and global environmental changes. The impending yield stagnation, and in some cases possible yield deterioration, poses the greatest threat to future food and nutrition security. The need to generate genetic pools that have the capacity to sustainably produce hybrid varieties that can keep up pace with the growing maize demand in the presence of known and anticipated biophysical and socio-economic production challenges, remain a well-known reality.

While it is considered a sophisticated technology, the use of maize hybrids by subsistence and smallholder farmers is on the increase and it is one of the easiest technological interventions that can critically help transform these poor farmers to viable commercial farmer status. Furthermore this technology remains one of the most practical forms of intervention which is however currently marginally utilised. The cost of hybrid seed production has a direct bearing on the affordability, which in turn is positively correlated with the adoption and utilisation of the hybrid seed. Therefore, there is need to devise ways of producing and availing affordable high yielding adaptable germplasm (Carena et al., 2010), in order to expedite the ease of adoption by poorly resourced farmers.

Faster and cheaper techniques to improving the turnaround times for maize hybrid variety development and release are required to augment the options currently available to farmers. These shorter cycle techniques will result in faster inbred line extraction, faster hybrid creation and evaluation, as well as faster hybrid release. Many farmers in SSA, for example, still plant about 6.7 million hectares of recycled maize seed and open pollinated varieties due to the high cost of hybrid seed (Ray et al., 2012), a practice which has relegated them to perpetual poverty cycles. The obligation to improving the uptake and use of hybrid maize seed in order to break the perpetual poverty cycles and preclude the pending catastrophic food shortage therefore partly lies with the modern maize breeders.

Over the years, maize breeders have been credited with successfully increasing crop performance through the exploitation of genetic variability in crops. However, the presently achieved and reported annual yield increases are not sufficient when juxtaposed with the projected human population growth requirements and the pressures exerted by the current and expected global environmental changes (Al-Naggar et al., 2016). While the utilisation of exotic germplasm is essential in creating genetic variability, several breeding steps and procedures are required to identify, manage and sustainably exploit this useful variability. Well managed, exotic germplasm can easily rejuvenate and broaden the genetic base of the current maize germplasm as well as produce more breeding choices.

6.6 Conclusions

The key findings in this study were centred on the improvement and broadening of the CIMMYT maize germplasm base using exotic well-established inbreds from diverse sources. This study provided an opportunity for identifying useful exotic tropical inbreds and selecting the best inbred combinations for further testing under different stress conditions and eventual release to seed companies for commercialisation (Badu-Apraku et al., 2018).

Overall results showed significant variations in combining abilities for GY and other agronomic traits of the inbreds as shown by the interactions of GCA with different growing environments such as manged drought, low nitrogen, low phosphorus, high plant density and optimal conditions across sites. The objective of increasing genetic variability in elite gene pools using exotic germplasm will result in the introduction of new alleles, generation of new heterotic combinations with enhanced agronomic performance, and improved rates of genetic gain and ultimate reduction in the existing yield gaps in maize production. The enhanced yield performance from exotic germplasm augment overall maize hybrid yield performance and makes them more appropriate and easier to adopt by the farmers ensuring future global food security in the process.

Poorly resourced maize dependent communities in the developing countries are prone to larger yield gaps in their predominantly rain-fed conditions, allowing breeding with exotic germplasm to play a major role in closing these gaps by providing appropriate and competitive varieties. The identified research gaps, together with the existing yield gaps, present extensive opportunities for gap closing technologies such as hybrid seed development and utilisation. It is rationally hereby acknowledged that no single step alone or single technology alone could independently provide adequate solutions for closing the yield gaps.

6.7 Future perspectives for closing the research and yield gaps

At the heart of the Agenda for Sustainable Development of the United Nations are the 17 Sustainable Development Goals (SDGs) (FAO, 2015). The goals are broad based and interdependent and they aim to create a better world by

2030. These goals have the power to end poverty, fight inequality and stop climate change. More than any other sector, agriculture appears to be the most common thread which holds most of the SDGs together especially in all agriculture dependent countries.

Agricultural productivity remains key to ending poverty and other deprivations in most developing countries. The adoption and use of new hybrids by all farmers may be one of the easiest possibilities that could contribute to the reduction and alleviation of the poverty trap and extreme hunger. The poor agriculture dependent communities are largely vulnerable to the changing weather conditions, new pests and diseases. Crop genetic vulnerability to these new biotic and abiotic stresses (Warburton et al., 2008) could be reduced by the incorporation of exotic germplasm into elite material, that effectively broadens the genetic base. The current study can be extrapolated and expanded, and can be complemented with other modern and advanced technologies. Faster plant breeding techniques such as the doubled haploid technology, genomics and other molecular technologies, as well as genetic prediction and modelling methodologies, can also be integrated to speed up the breeding process (Wang et al., 2017).

Regrettably, the substantial investment required to sufficiently generate genetic variability among crops has always been debilitating, especially to poorly resourced and developing breeding programmes (Guimaraes et al., 2006). This study has however, exposed some realistic possibilities and opportunities that can be engendered by the use of exotic germplasm. Carefully identified exotic tropical and temperate inbreds can be used in combination with elite local germplasm to generate new maize hybrids and set new grain yield thresholds that can contribute in the fight against hunger and extreme poverty. The current findings can further be used by the wider research community for future studies and possible commercial applications.

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Appendix 3.1 Grain yield and agronomic traits for temperate test cross hybrids across sites

Entry	Tester	Male	GY	MOI	AD	ASI	PH	EH	EPP	ER	HC	SL	EA	TEX
1	SXTB	PHJ40	5.59	17.37	61.69	1.86	177.46	84.65	0.85	20.51	13.96	4.11	3.67	3.92
2	SXTB	PHAA0	4.16	14.40	60.44	0.87	184.27	85.74	0.87	22.24	11.72	0.29	3.85	3.95
3	SXTB	PHTE4	4.98	13.96	59.51	0.93	185.63	85.64	0.90	22.62	14.16	5.96	3.78	3.84
4	SXTB	PHEM9	4.36	15.68	61.11	0.79	179.21	83.72	0.86	16.39	10.10	-0.13	3.87	3.76
5	SXTB	AQA3	4.26	13.48	60.06	0.79	181.19	91.79	0.86	20.24	2.79	3.60	4.26	4.55
6	SXTB	LH223	4.61	13.67	61.23	1.08	174.27	94.38	0.93	17.40	3.81	7.98	4.01	4.33
7	SXTB	PHT69	3.91	13.64	61.44	0.86	187.85	93.59	0.77	22.47	5.75	6.57	3.85	4.17
8	SXTB	MQ305	3.34	13.60	62.38	0.79	180.60	87.99	0.90	25.82	9.24	3.27	3.97	4.19
9	SXTB	PHN66	4.80	15.11	62.33	1.14	187.97	91.49	0.81	21.59	6.09	9.26	3.90	4.11
10	SXTB	FBLA	4.54	14.10	58.70	1.86	190.18	88.49	0.89	24.57	12.13	0.18	3.92	4.25
11	SXTB	PHW51	4.91	15.55	65.67	0.30	191.12	92.16	0.90	14.73	7.94	8.16	3.56	3.78
12	SXTB	PHV07	5.33	17.90	68.53	0.51	195.53	107.67	0.92	8.83	3.43	10.00	3.08	2.55
13	SXTB	RS710	2.82	13.27	58.73	1.50	166.96	72.81	0.83	23.41	1.85	0.33	4.07	3.69
14	SXTB	1538	4.36	14.37	63.48	0.79	184.52	86.58	0.89	18.27	4.47	3.99	3.78	4.21
15	SXTB	HB8229	6.06	16.82	65.85	0.51	183.89	95.38	0.88	18.16	12.95	8.92	3.65	3.76
16	SXTB	FBHJ	3.75	14.82	62.57	1.65	200.32	89.31	0.90	18.79	12.14	0.78	4.89	4.06
17	SXTB	BO9	4.47	14.91	62.91	0.86	188.93	97.66	0.79	22.66	6.44	8.69	3.55	3.48
18	SXTB	PHHB4	5.03	16.34	66.52	1.01	192.55	86.62	0.93	17.92	1.77	-0.68	3.74	3.74
19	SXTB	PHEG9	5.22	16.05	66.13	0.85	199.55	100.40	1.00	12.93	8.25	2.95	3.70	3.94
20	SXTB	PHBB3	4.21	15.36	65.46	1.15	193.08	93.54	0.90	12.08	2.63	6.20	3.81	4.01
21	SXTB	PHMK0	4.69	15.76	64.37	1.15	195.87	95.34	0.85	8.99	8.23	-0.64	3.50	4.02
22	SXTB	PHEW7	3.65	13.96	62.17	1.09	185.03	85.32	0.84	14.56	10.25	-0.13	3.73	3.96
23	SXTB	PHVA9	4.71	14.24	61.50	0.93	196.35	89.72	0.87	9.16	5.78	3.28	3.64	4.11
24	SXTB	PHT47	3.45	14.67	64.53	1.79	189.41	89.01	0.85	19.91	8.79	6.33	3.57	3.54
25	SXTB	PHP85	4.65	15.49	66.32	1.29	198.30	98.53	0.97	13.57	8.95	13.38	3.53	3.96
26	SXTB	PHW20	4.10	14.42	62.19	0.57	190.13	96.18	0.86	15.25	7.11	0.40	3.76	3.87
27	SXTB	PHV37	4.71	15.61	61.46	1.30	185.45	92.30	0.79	17.54	8.64	2.63	3.60	3.91
28	SXTB	PHT55	4.15	15.71	67.22	0.86	192.03	95.77	0.90	12.81	7.59	-0.24	3.55	3.51
29	SXTB	807	3.69	13.89	60.74	1.22	181.64	91.11	0.80	26.66	9.04	6.18	4.00	3.94
30	SXTB	778	3.35	14.44	61.59	0.43	166.84	78.56	0.85	29.27	12.50	6.01	4.07	4.04
31	SXTB	4676A	4.79	14.96	60.75	0.74	185.01	85.64	0.79	24.79	2.01	2.98	4.01	3.75
32	SXTB	6103	4.78	15.28	65.37	1.01	187.24	91.96	0.88	25.71	6.33	5.72	3.83	3.93
33	SXTB	FAPW	4.70	15.55	62.73	22.43	181.96	87.88	0.79	21.55	7.05	-0.40	4.02	3.97
34	SXTB	FBLL	4.87	14.76	64.67	0.65	198.69	98.64	0.94	17.82	4.18	3.19	3.84	4.14
35	SXTB	LH132	4.25	15.61	64.52	1.07	192.71	91.98	0.85	16.54	5.63	17.11	3.66	3.9
36	SXTB	LH208	4.36	14.95	65.86	1.07	190.63	91.18	0.83	15.68	5.38	0.21	3.57	4.19
37	SXTB	LH202	4.62	15.79	62.63	0.94	185.77	96.69	0.83	18.15	18.08	7.56	3.87	4.2
38	SXTB	LH196	4.27	15.56	62.99	0.72	192.28	86.73	0.82	16.49	3.87	11.22	4.02	4.35
40	SXTB	LH195	4.84	16.06	66.89	0.71	184.95	89.63	0.88	15.39	4.62	0.22	3.66	3.89
41	SXTB	87916W	4.31	16.06	64.41	0.72	198.93	101.11	0.89	11.54	7.88	6.37	3.81	3.68
42	SXTB	H8431	4.84	14.38	61.26	0.86	192.85	93.43	0.86	13.13	12.09	0.32	3.72	3.93
43	SXTB	LH198	5.63	17.25	64.22	1.09	175.94	85.07	0.89	6.07	6.31	16.33	3.46	3.81
44	SXTB	PHJR5	4.03	14.48	61.39	1.64	188.67	88.99	0.85	14.71	12.96	8.94	3.91	4.05
45	SXTB	SC403	4.30	15.73	63.60	0.57	188.86	83.37	0.80	40.44	13.35	-0.06	3.91	3.91
46	SXTB	LH224	4.57	14.19	64.56	0.58	194.57	94.64	0.89	20.41	4.50	7.57	3.79	4.1
47	SXTB	PHPR5	5.38	16.24	64.36	1.42	191.41	89.33	0.86	14.23	8.35	0.38	3.44	3.45
48	SXTB	CS405	3.43	14.63	60.18	0.72	185.16	78.29	0.90	17.83	8.99	11.69	3.94	4.02
49	SXTB	ICI893	3.57	14.44	65.15	0.80	187.07	91.07	0.89	18.14	6.25	6.04	3.80	4.04
50	SXTB	LH222	4.43	13.94	60.42	1.66	188.92	87.57	0.89	15.52	7.13	0.35	3.75	4.22
51	SXTB	LH199	5.38	16.07	64.40	0.79	187.54	87.79	0.80	13.41	6.31	-0.23	3.30	3.57
52	SXTB	LH197	4.85	16.13	65.06	1.02	197.69	99.44	0.83	13.85	5.32	9.54	3.65	3.97
53	SXTB	F118	4.59	16.18	65.40	0.85	194.59	99.88	0.86	11.18	3.39	5.27	3.59	4.04
54	SXTB	LH209	4.22	14.32	62.83	1.58	196.75	89.75	0.80	20.13	5.53	-0.44	3.95	4.19
55	SXTB	NL001	4.05	14.08	63.17	0.72	188.92	94.64	0.88	13.36	6.25	12.75	4.03	4.36
56	SXTB	6F629	4.02	14.44	63.26	1.07	182.16	93.72	0.86	12.46	10.51	0.03	3.91	4.28
57	SXTB	LH193	3.76	15.38	64.72	0.80	180.37	84.40	0.86	14.15	8.43	5.85	3.38	3.81
58	SXTB	LH192	4.79	14.56	65.71	0.79	189.83	91.74	0.83	16.34	15.08	-0.06	3.93	4.18
59	SXTB	LH191	4.08	16.04	64.96	1.29	180.39	87.47	0.87	16.26	2.83	3.95	3.80	4.13
60	SXTB	LH190	5.57	15.72	66.18	1.28	208.61	105.27	0.94	12.75	7.41	3.09	3.64	3.95
61	SXTB	LH220Ht	4.22	15.26	61.54	1.30	180.22	82.68	0.81	18.80	2.74	9.70	3.63	3.9
62	SXTB	LH206	4.71	13.98	63.51	1.09	186.13	86.54	0.89	10.66	5.34	17.25	3.64	3.85
63	SXTB	LH204	4.26	14.67	63.28	1.01	189.99	90.05	0.85	18.53	6.94	2.16	3.59	4.04
64	SXTB	PHJ70	4.91	15.91	65.99	0.07	199.69	95.90	0.80	20.75	14.05	4.44	3.93	4.14
65	SXTB	4N506	5.13	15.42	64.73	0.93	205.42	108.02	0.85	15.14	11.41	8.92	3.73	4.03
66	SXTB	W8555	4.98	15.89	65.88	0.78	210.52	100.95	0.90	13.15	4.56	2.99	3.43	4.05
67	SXTB	CR14	3.30	13.97	61.37	0.36	182.08	91.37	0.84	12.67	2.38	9.02	4.00	4.2
68	SXTB	2369	5.26	16.49	66.18	0.79	202.27	106.08	0.85	16.94	8.47	0.19	3.68	3.96
69	SXTB	S8324	3.45	14.75	61.91	1.29	187.74	82.18	0.84	16.38	3.67	0.91	3.98	4
70	SXTB	LH149	4.17	14.17	59.62	1.07	191.05	94.32	0.86	20.14	11.94	11.69	3.93	4.23
71	SXTB	W8304	5.97	15.94	66.93	0.43	199.90	104.89	0.92	12.17	6.42	3.17	3.74	4.14
72	SXTB	793	4.58	14.45	62.71	0.86	189.39	95.35	0.88	16.92	9.41	2.91	3.72	4.06
73	SXTB	790	4.30	14.99	63.92	1.14	201.07	102.89	0.85	12.77	4.06	0.48	3.45	4.02
74	SXTB	PB80	4.76	15.49	66.12	1.14	193.75	99.95	0.81	12.22	7.06	0.21	3.74	3.88
75	SXTB	PHG86	4.66	15.77	65.34	0.29	192.82	100.95	0.89	17.53	4.46	-0.24	3.46	3.72

Entry	Tester	Male	GY	MOI	AD	ASI	PH	EH	EPP	ER	HC	SL	EA	TEX
76	SXTB	LH146Ht	4.67	14.68	60.87	1.51	191.09	96.34	0.88	17.05	1.88	5.99	3.86	4.24
77	SXTB	794	4.72	14.64	61.92	0.86	186.53	91.59	0.92	13.41	11.33	0.01	4.05	4.47
78	SXTB	764	4.51	14.70	64.23	0.86	182.90	89.53	0.87	16.97	5.17	9.48	4.01	4.06
79	SXTB	78002A	3.55	13.74	65.66	0.64	186.88	97.57	0.80	35.60	5.40	-0.03	3.74	3.83
80	SXTB	78010	5.15	15.10	61.23	1.36	182.51	93.80	0.84	13.02	3.40	6.25	3.94	4.13
81	SXTB	SC708	4.64	15.28	70.85	-0.50	220.02	122.48	0.87	22.63	1.51	23.16	3.37	3.19
82	SXTB	PHW52	4.37	15.43	65.37	1.16	193.02	94.22	0.94	7.50	4.88	0.19	3.44	3.7
83	SXTB	OS602	3.50	13.14	61.50	1.15	187.22	92.37	0.86	20.73	4.42	0.33	4.17	4.27
84	SXTB	PHVJ4	5.06	13.57	60.12	1.36	192.42	89.27	0.91	21.89	17.41	-0.11	3.70	4.23
85	SXTB	PHG71	4.41	14.39	63.92	0.73	188.35	95.64	0.88	13.50	9.41	3.36	3.56	3.97
86	SXTB	PHRE1	5.05	14.28	58.65	1.35	193.15	96.10	0.88	20.43	10.08	6.46	3.92	4.09
87	SXTB	PHBW8	2.58	14.07	61.79	0.71	189.40	87.24	0.74	29.73	3.61	3.20	4.04	4.13
88	SXTB	PHT11	4.54	16.29	64.95	0.72	193.68	92.27	0.95	17.76	4.87	6.06	3.84	3.83
89	SXTB	PHHV4	4.11	14.36	64.58	0.50	195.06	98.38	0.94	11.71	3.84	2.87	3.75	4.01
90	SXTB	L155	4.15	15.79	63.32	0.57	182.65	86.71	0.81	26.23	5.16	6.17	3.98	4.27
91	SXTB	PHR61	5.02	15.88	65.27	0.93	201.27	96.90	0.84	11.68	5.18	5.58	3.45	3.62
92	SXTB	PHP02	4.30	14.42	62.41	1.15	182.82	87.93	0.85	23.57	11.11	6.99	4.06	4.24
93	SXTB	3IIH6	3.94	13.41	63.69	0.43	182.24	90.90	0.83	21.36	3.94	6.76	3.87	4.38
94	SXTB	PHR25	2.97	13.54	56.99	1.64	179.72	87.11	0.80	31.23	4.06	5.92	4.09	4.42
95	SXTB	PHTD5	3.70	13.29	60.36	0.88	184.90	90.22	0.88	24.90	13.19	0.00	4.15	4.26
96	SXTB	PHN82	4.09	14.95	65.59	-0.20	177.34	88.67	0.89	16.29	4.74	8.81	3.84	4.05
97	SXTB	PHN18	3.91	15.52	63.81	1.21	190.47	92.99	0.89	9.61	2.52	6.72	3.56	3.59
98	SXTB	IBC2	4.04	13.60	61.26	0.71	178.35	91.11	0.81	23.31	13.28	-0.24	3.89	4.16
99	SXTB	PHG29	3.76	14.70	63.95	0.50	181.39	91.52	0.85	29.65	9.52	5.99	4.10	4.3
100	SXTB	PHJ90	4.48	14.79	63.25	0.44	188.34	91.26	0.85	18.04	9.14	0.24	3.73	4.14
101	SXTB	PHM10	4.30	14.92	64.61	0.43	184.50	91.41	0.84	26.11	8.81	1.02	4.11	4.25
102	SXTB	PHW53	4.77	14.87	64.39	-0.14	185.54	89.64	0.87	15.95	8.46	21.35	4.05	4.31
103	SXTB	PHV57	3.97	14.55	61.91	0.86	170.77	87.31	0.82	22.94	2.04	9.32	3.72	3.92
104	SXTB	207	3.87	13.27	62.25	0.78	179.09	80.56	0.86	21.39	9.94	7.75	4.19	4.4
105	SXTB	PHKE6	4.50	14.57	62.66	0.93	184.57	87.25	0.84	21.30	14.69	15.77	3.65	4.17
106	SXTB	PHFA5	3.96	15.42	57.82	0.87	182.53	83.93	0.81	18.22	2.80	2.92	3.79	3.67
107	SXTB	PHAW6	4.34	14.96	65.42	0.50	179.19	92.34	0.88	17.54	8.14	0.78	3.75	4.12
108	SXTB	3IJI1	3.82	13.99	60.74	0.80	180.53	84.21	0.89	14.05	7.11	9.95	3.87	4.16
109	SXTB	91IFC2	3.84	13.73	61.07	1.36	181.65	86.23	0.84	20.53	4.39	15.70	4.08	4.27
110	SXTB	PHTM9	3.53	13.79	58.39	1.30	188.22	83.09	0.82	13.29	6.72	-0.98	4.19	4.05
111	SXTB	PHR31	3.61	15.12	64.10	0.58	187.16	88.54	0.88	19.02	10.11	12.55	4.17	4.25
112	SXTB	PHK74	3.72	13.34	61.52	0.95	191.79	95.44	0.87	24.62	5.75	3.89	4.05	4
113	SXTB	PHGW7	4.36	13.19	60.92	1.14	193.93	86.97	0.87	18.44	7.53	16.19	4.16	4.03
114	SXTB	83IBI3	4.29	14.04	60.83	1.65	182.13	87.06	0.86	25.58	8.77	0.08	3.87	4.36
115	SXTB	PHJ89	4.51	13.60	59.16	1.21	186.70	82.80	0.81	15.53	13.74	3.00	3.80	4.05
116	SXTB	PHW86	3.42	13.73	61.80	0.58	178.41	84.34	0.81	17.37	5.88	6.23	3.89	4.41
117	SXTB	PHW06	2.63	13.30	59.30	0.52	183.98	81.91	0.84	17.53	11.50	-0.64	3.98	3.89
118	SXTB	PHP76	3.68	15.00	63.37	0.93	184.30	91.32	0.84	18.32	9.74	3.22	3.98	3.88
119	SXTB	PHK46	4.44	16.98	66.45	0.57	194.94	96.39	0.84	18.65	9.80	-0.18	3.70	3.65
120	SXTB	PHJ65	4.76	16.49	65.92	1.22	191.03	88.52	0.83	17.09	12.87	16.77	3.89	3.75
121	SXTB	PHW43	3.46	14.72	63.90	0.28	184.26	84.55	0.78	12.58	6.57	7.28	3.77	4.12
122	SXTB	PHT22	3.07	15.37	65.55	0.15	180.54	89.31	0.81	14.74	3.61	-0.19	4.09	4.13
123	SXTB	PHR63	4.28	15.77	65.48	0.71	190.12	94.04	0.87	13.09	4.49	0.37	3.85	3.96
124	SXTB	PHR62	4.39	15.57	65.08	0.65	193.18	100.70	0.93	19.36	9.46	0.04	3.66	3.83
125	SXTB	PHP60	3.44	16.01	64.49	1.02	188.10	90.38	0.71	16.09	1.91	9.02	3.43	3.8
126	SXTB	PHP55	5.06	15.12	63.87	0.51	191.67	92.16	0.85	22.35	12.10	0.05	3.80	4.39
127	SXTB	PHN73	5.00	15.37	61.10	0.93	191.04	90.25	0.83	14.90	6.00	-0.53	3.75	3.81
129	SXTB	PHM57	3.76	15.28	66.44	0.66	191.49	94.48	0.93	11.23	7.81	10.48	3.87	3.96
130	SXTB	PHJ75	3.60	13.19	59.02	1.58	177.50	80.45	0.89	24.71	14.83	8.66	3.93	4.31
131	SXTB	PHJ33	5.17	15.23	63.60	0.72	184.83	92.35	0.91	18.28	6.45	10.73	3.87	4.48
132	SXTB	PHJ31	4.72	16.61	67.14	0.30	193.40	98.67	0.89	16.80	5.90	0.08	3.58	3.86
133	SXTB	PHW79	3.65	14.80	66.88	-0.07	194.78	99.16	0.84	18.01	3.26	2.76	3.87	3.82
134	SXTB	PHN47	5.29	16.36	68.47	0.23	193.39	99.26	0.90	11.15	-0.62	-0.24	3.91	4.04
135	SXTB	IBB14	3.26	14.13	61.65	1.59	180.61	92.54	0.80	23.53	5.41	23.13	3.88	4.29
136	SXTB	PHW65	3.94	14.96	65.12	0.63	186.94	94.13	0.87	12.09	6.14	3.14	3.46	3.84
137	SXTB	PHV63	4.96	15.00	64.33	1.79	192.70	95.14	0.83	13.00	5.24	3.35	3.71	3.98
138	SXTB	PHT77	5.18	15.46	61.42	1.07	190.77	88.06	0.88	18.35	17.40	3.55	3.99	4.23
139	SXTB	PHN11	3.83	14.48	62.58	0.50	185.84	87.58	0.83	35.71	17.86	6.38	4.02	4.23
140	SXTB	PHK42	3.75	13.83	62.11	0.92	179.66	90.35	0.85	27.28	11.64	0.50	4.17	4.25
141	SXTB	PHV78	4.68	15.97	67.01	0.43	194.03	99.69	0.89	14.28	4.95	26.62	3.88	4.29
142	SXTB	IBB15	3.51	13.84	62.35	1.00	183.09	88.29	0.80	24.07	15.63	-0.15	4.26	4.64
143	SXTB	PHR36	4.27	16.08	64.11	0.86	185.80	90.46	0.93	18.71	16.81	20.47	3.93	4.15
144	SXTB	PHG72	3.65	13.63	60.79	1.30	170.72	84.32	0.84	21.36	8.96	-0.23	3.92	4.2
145	SXTB	PHZ51	4.98	14.77	63.97	0.72	194.10	96.00	0.83	24.71	5.40	2.87	4.10	4.26
146	SXTB	PHG84	4.30	16.29	65.82	0.36	189.24	89.87	0.84	15.89	7.42	0.08	3.63	3.66
147	SXTB	PHG83	4.99	14.94	63.58	0.43	182.24	88.37	0.87	25.16	16.05	0.01	4.02	4.4
148	SXTB	IB014	4.24	14.84	63.55	0.57	185.71	89.32	0.87	18.83	3.81	6.31	4.10	4.23
149	SXTB	G80	5.15	15.39	58.65	1.23	188.42	90.22	0.76	27.76	9.28	2.45	4.06	4.16
150	SXTB	PHN29	4.03	13.79	64.40	1.01	197.71	91.44	0.83	25.66	11.74	16.55	3.83	4.08
151	SXTB	IB02	3.72	13.68	60.84	1.29	184.05	80.95	0.86	18.84	8.97	10.92	4.06	4.47
152	SXTB	PHR47	4.96	14.78	61.61	1.65	199.94	95.56	0.82	19.82	6.47	9.39	3.92	4.31
153	SXTB	8M129	3.98	14.56	63.13	0.42	189.69	87.34	0.78	14.60	11.96	-0.23	3.69	4.4
154	SXTB	LH216	4.94	15.55	63.00	1.29	193.53	94.18	0.91	18.25	5.07	11.00	3.42	3.72
155	SXTB	LH59	5.10	16.04	63.90	2.28	192.83	90.08	0.83	21.33	3.16	-0.50	3.90	4.08
156	SXTB	LH210	5.41	16.26	63.87	1.07	189.62	90.86	0.87	10.51	4.40	0.05	3.51	3.94
157	SXTB	78551S	3.41	13.67	64.02	0.85	196.87	87.51	0.89	15.17	3.99	7.36	3.76	4.06
158	SXTB	LH181	5.17	15.70	62.19	1.52	187.07	86.11	0.82	21.21	0.47	0.22	3.44	3.86
159	SXTB	LH183	4.44	15.44	61.54	1.22	190.56	94.60	0.83	14.12	9.09	10.61	3.47	3.66
160	SXTB	LH217	4.90	15.00	64.23	0.44	191.58	89.48	0.83	23.09	8.56	-0.68	3.43	3.65
161	SXTB	LH215	4.68	14.93	63.69	0.42	193.30	91.58	0.86	18.20	6.20	12.82	3.58	4.06

Entry	Tester	Male	GY	MOI	AD	ASI	PH	EH	EPP	ER	HC	SL	EA	TEX
162	SXTB	Lp215D	4.36	15.28	60.39	1.51	189.41	93.65	0.84	18.27	5.52	-0.46	3.58	3.68
164	SXTA	LH162	2.74	13.01	57.30	1.15	163.37	71.99	0.85	19.00	9.39	6.03	4.18	4.04
165	SXTA	LH160	2.75	12.98	58.78	2.07	178.41	74.24	0.86	23.77	5.61	0.47	4.07	3.71
166	SXTA	E8501	4.27	15.07	63.06	0.79	182.51	84.46	0.82	19.70	0.29	18.59	3.85	4.11
167	SXTA	S8326	3.44	14.23	60.28	1.01	179.25	91.31	0.88	25.05	14.69	0.59	4.07	4.3
168	SXTA	LH65	4.52	14.67	61.53	1.00	180.28	86.08	0.86	28.50	8.25	2.84	3.88	3.89
169	SXTA	740	4.09	13.76	61.86	1.07	180.31	85.85	0.88	19.75	10.56	12.41	3.78	4.13
170	SXTA	MBPM	5.14	14.98	61.61	1.29	199.18	87.60	0.87	16.22	7.10	0.22	3.90	4.23
171	SXTA	LH61	3.28	13.67	61.01	1.31	171.68	79.41	0.85	27.12	11.06	7.45	3.94	3.82
172	SXTA	LH60	4.67	16.11	62.46	0.72	182.12	85.82	0.85	22.13	9.80	6.72	3.78	4.06
173	SXTA	LH52	3.93	13.45	60.11	1.43	178.63	84.78	0.88	26.67	15.30	6.87	3.85	3.86
174	SXTA	LH57	3.18	14.10	59.53	1.79	174.49	74.30	0.85	26.21	11.35	2.98	3.72	4.15
175	SXTA	LH54	4.28	14.35	59.69	1.28	186.77	81.17	0.85	17.60	8.84	6.46	4.14	4.11
176	SXTA	MBNA	4.73	15.18	59.35	1.23	172.79	68.97	0.86	26.50	9.56	7.09	4.00	3.96
177	SXTA	MM501D	5.04	14.53	60.66	1.50	180.96	75.79	0.88	11.93	6.48	15.29	3.74	3.73
178	SXTA	MM402A	5.28	14.85	63.05	1.37	191.09	79.99	0.75	19.16	7.15	0.20	3.96	4.34
179	SXTA	MBWZ	5.04	15.08	61.33	0.35	183.27	87.30	0.89	19.10	8.13	8.88	3.92	4.21
180	SXTA	LH159	6.42	17.22	63.84	0.65	188.83	85.38	0.84	18.37	2.24	-0.24	3.20	3.5
181	SXTA	CS608	3.52	13.38	58.14	1.38	174.38	73.62	0.83	23.17	13.31	6.41	4.07	4.09
182	SXTA	PHT73	1.98	13.17	57.29	0.22	166.31	63.28	0.78	28.66	7.16	6.78	4.15	4.02
183	SXTA	PHGV6	3.78	15.44	65.31	0.50	187.21	89.98	0.84	17.79	2.36	0.49	3.49	3.98
184	SXTA	OQ101	2.10	12.97	54.74	1.28	163.14	68.57	0.76	23.16	10.20	6.20	3.98	3.92
185	SXTA	LH164	3.41	12.65	59.94	0.94	176.73	80.48	0.78	31.69	17.51	17.81	4.47	4.22
186	SXTA	LIBC4	3.56	13.13	60.72	0.85	173.00	76.73	0.88	16.01	8.87	-0.05	4.33	4.53
187	SXTA	MBUB	4.92	15.87	62.45	1.50	178.09	71.24	0.80	19.03	4.49	11.83	3.67	3.98
188	SXTA	MBSJ	3.36	13.61	61.45	0.50	181.99	74.77	1.14	20.01	7.12	6.42	3.95	3.85
189	SXTA	29MIBZ2	3.84	14.37	60.53	0.87	175.84	87.36	0.85	15.29	8.22	6.26	3.77	4.24
190	SXTA	PHM81	2.40	12.59	57.12	1.22	170.62	67.92	0.78	25.61	8.79	2.49	4.05	3.99
191	SXTA	6M502A	4.68	15.11	62.33	0.86	170.58	72.10	0.86	18.02	13.47	-0.28	3.47	3.69
192	SXTA	LH163	2.68	12.19	59.42	0.79	169.44	73.18	0.77	27.53	12.83	6.86	4.21	4.21
193	SXTA	WIL903	4.71	15.74	63.87	0.95	178.19	82.50	0.79	23.63	5.58	2.66	3.59	3.87
194	SXTA	WIL901	4.79	16.82	64.00	0.94	194.75	101.54	0.85	22.46	5.22	20.88	3.97	4.02
195	SXTA	WIL900	5.20	16.65	63.99	0.93	189.57	89.79	0.82	18.03	8.56	9.13	3.49	3.73
196	SXTA	PHM49	4.45	14.37	63.78	0.23	179.75	81.84	0.90	13.52	10.21	0.21	3.84	4.34
197	SXTA	2MA22	3.25	13.45	61.06	1.08	172.82	66.65	0.83	31.65	16.50	0.23	3.90	4.11
198	SXTA	6M502	4.75	15.35	63.08	1.21	183.64	87.70	0.90	20.00	13.78	4.80	3.46	4.21
199	SXTA	11430	3.07	13.34	61.55	1.44	176.86	77.82	0.86	31.25	23.21	6.13	3.89	4.09
200	SXTA	787	3.97	16.61	64.39	0.30	191.12	89.80	0.85	13.26	15.01	14.52	3.60	3.76
201	SXTA	78371A	4.45	15.75	61.80	1.71	190.53	80.53	0.80	25.61	13.53	4.17	3.78	4.19
202	SXTA	LH85	2.08	13.17	57.92	1.57	165.29	68.14	0.79	16.01	13.36	2.72	4.06	4.16
203	SXTA	LH123HT	5.55	16.44	61.95	1.36	191.26	87.74	0.89	25.93	10.91	13.69	3.95	4.03
204	SXTA	PHG47	3.83	13.35	61.33	0.51	184.07	76.86	0.85	21.61	19.31	-0.12	3.96	4.05
205	SXTA	LH212Ht	5.11	15.74	61.20	1.35	186.33	88.40	0.79	18.72	6.99	0.03	3.68	3.95
206	SXTA	PHK76	4.59	14.78	60.50	1.37	175.99	79.74	0.83	25.93	8.75	0.95	3.48	3.77
207	SXTA	PHRD6	4.89	13.83	59.24	1.29	179.16	77.79	0.84	19.26	12.02	3.34	3.62	3.91
208	SXTA	ICI581	3.89	13.61	61.53	0.66	174.46	74.26	0.83	16.54	11.21	-0.54	3.88	3.67
209	SXTA	PHR30	2.30	11.39	59.34	0.93	171.49	70.00	0.77	12.77	9.66	0.49	3.82	3.86
210	SXTA	LH127	3.58	13.89	59.76	1.09	174.90	75.19	0.85	21.12	9.88	3.09	3.97	3.89
212	SXTA	LH156	3.65	13.62	59.48	1.15	176.80	74.16	0.94	22.25	10.26	-0.24	3.86	3.9
213	SXTA	LH93	3.84	14.23	61.99	0.58	181.34	85.28	0.88	11.31	7.55	12.02	4.04	4.33
214	SXTA	LH82	3.65	14.05	59.43	1.07	166.15	68.48	0.84	20.28	14.97	6.71	4.33	4.26
215	SXTA	LH172	3.73	13.82	60.55	1.14	165.82	77.85	0.88	34.24	14.63	-0.23	3.94	3.98
216	SXTA	LH166	3.38	13.27	59.87	1.56	176.93	74.86	0.84	17.70	6.95	-0.24	4.20	4.3
217	SXTA	LH167	3.52	14.14	58.75	1.43	172.80	69.93	0.80	19.72	16.46	12.31	3.62	3.73
218	SXTA	LH165	3.40	13.57	58.23	1.00	160.08	79.41	0.86	19.65	13.26	2.70	3.98	4.26
219	SXTA	LH184	4.98	14.07	59.91	1.00	182.55	83.94	0.88	25.38	5.32	3.44	4.22	4.61
220	SXTA	LH214	5.59	15.47	62.41	1.57	187.12	84.92	0.87	27.49	10.10	2.79	4.10	4.06
221	SXTA	LH213	5.53	16.70	62.64	1.51	192.77	84.00	0.88	34.50	5.75	2.91	3.89	4.1
222	SXTA	LH284	4.32	14.98	60.31	1.15	170.66	77.50	0.86	26.70	13.12	0.32	4.05	4.39
223	SXTA	PHR03	4.05	14.34	64.71	0.64	191.04	82.69	1.00	19.93	10.17	2.89	3.78	4.1
224	SXTA	PHN46	4.43	14.15	61.90	0.87	184.03	90.06	0.83	16.95	6.17	4.08	3.74	4.23
225	SXTA	PHR55	4.04	14.45	64.34	0.21	180.01	83.41	0.89	19.71	12.98	0.52	3.82	4.01
226	SXTA	PHBA6	4.60	13.08	60.33	0.79	190.93	82.86	0.85	27.56	16.17	-0.16	3.91	3.92
227	SXTAB	PHK56	4.13	13.46	60.13	1.14	167.92	69.61	0.86	22.90	9.51	0.29	4.06	4.13
228	SXTAB	899	3.62	12.96	63.85	0.71	196.76	97.87	0.90	11.12	12.05	15.45	3.72	3.96
229	SXTAB	PHN41	4.44	16.62	63.36	0.57	195.76	102.42	0.86	9.95	1.14	10.10	3.36	3.51
230	SXTAB	PHHH9	4.05	15.51	65.35	0.78	186.84	93.40	0.80	9.40	2.81	6.28	3.35	3.71
231	SXTAB	904	4.00	13.62	59.45	0.80	185.79	80.43	0.93	12.24	6.33	12.81	4.15	3.84
232	SXTAB	OQ403	2.99	13.64	60.54	0.94	181.27	86.95	0.86	13.36	10.44	6.40	4.04	4.03
233	SXTAB	CZH131007	7.44	20.95	68.50	0.35	196.36	106.74	0.91	13.46	12.54	11.18	3.47	3.49
234	SXTAB	ICI193	3.85	13.20	61.60	1.14	190.89	90.44	0.86	21.75	8.36	-0.41	3.80	4.1
235	SXTAB	912	3.97	13.46	60.55	1.15	183.07	77.85	0.84	16.46	9.23	5.86	4.01	4.11
236	SXTAB	911	3.98	14.12	62.72	0.87	182.99	85.34	0.84	13.90	14.53	4.11	3.55	3.75
237	SXTAB	PHW30	3.98	15.51	63.66	1.29	193.33	89.95	0.92	17.93	2.69	4.84	3.68	3.64
238	SXTAB	PHR58	5.46	16.42	64.55	0.85	200.50	97.31	0.88	15.88	10.83	10.50	3.75	3.87
239	SXTAB	PHK93	4.32	16.57	66.75	0.57	200.55	99.50	0.84	17.69	4.31	12.44	3.37	3.58
240	SXTAB	PHK35	4.96	16.23	62.97	0.79	190.55	95.24	0.86	13.85	8.30	6.12	3.47	3.9
241	SXTAB	L139	3.68	13.47	60.81	1.00	179.94	82.87	0.82	25.61	22.56	0.38	4.05	4
242	SXTAB	L135	3.53	13.85	61.51	0.44	184.50	92.46	0.85	14.89	6.87	11.50	3.81	4.09
243	SXTAB	L127	3.39	14.77	60.76	0.79	182.09	85.33	0.90	16.20	14.70	0.14	3.84	4.06
244	SXTAB	PHT60	3.62	14.54	63.20	1.15	183.60	85.60	0.84	15.86	8.59	6.43	3.62	3.93
245	SXTAB	PHKM5	2.08	13.31	55.02	1.02	157.98	69.78	0.80	14.74	3.44	9.35	4.00	3.84
246	SXTAB	PHV53	3.87	15.37	66.76	0.93	187.27	90.64	0.86	18.58	3.41	-0.36	3.67	3.73
247	SXTAB	ICI740	4.02	14.49	63.48	0.79	191.99	95.47	0.88	17.77	5.73	5.19	3.80	3.8
248	SXTAB	ICI441	4.89	15.10	63.15	0.86	185.63	93.25	0.87	16.38	10.05	14.15	3.81	3.78

Entry	Tester	Male	GY	MOI	AD	ASI	PH	EH	EPP	ER	HC	SL	EA	TEX
249	SXTAB	J8606	3.67	15.47	65.91	0.29	197.18	94.29	0.94	21.38	3.79	0.08	4.02	4.26
250	SXTAB	WIL500	4.98	16.65	64.16	0.86	184.89	88.10	0.79	17.01	8.17	0.65	3.60	3.54
39	CC	PHB30G19	5.53	19.78	67.76	0.15	206.39	107.22	0.82	22.85	2.79	16.65	3.27	3.17
128	CC	SC637	5.47	20.14	68.40	0.93	208.52	110.05	0.74	20.16	3.72	5.30	3.45	3.28
163	CC	CZH131001	7.84	19.51	65.74	0.07	200.24	96.19	0.83	12.93	13.06	0.25	2.73	2.9
211	CC	CZH131006	7.02	20.46	68.45	0.50	198.26	104.14	0.90	12.23	13.00	0.55	3.10	3.47
251	CC	CZH1257	6.32	17.27	61.82	1.65	195.37	74.34	0.76	16.27	28.81	-0.64	3.27	3.87
252	CC	CZH1258	6.93	19.43	64.74	0.59	196.05	96.44	0.82	10.69	15.30	2.53	3.44	3.54
253	CC	CZH0616	4.67	19.00	66.96	0.42	192.70	98.72	0.92	15.02	2.46	-0.33	3.47	3.47
254	CC	CZH0837	6.51	18.68	66.16	0.37	190.38	97.00	0.77	16.53	11.94	2.71	3.02	3.11
255	CC	CZH131011	7.86	21.76	66.63	0.52	198.73	95.70	0.81	14.06	10.37	14.37	2.98	3.24
256	CC	CZH131013	7.44	20.37	67.82	0.51	205.95	103.36	0.94	15.27	2.30	26.50	3.48	3.54
257	CC	PAN413	4.13	19.04	68.02	0.64	177.55	90.79	0.82	17.85	9.59	19.97	3.81	4.11
258	CC	PAN53	6.39	20.54	68.94	0.66	203.85	102.35	0.85	14.86	3.54	11.01	3.28	3.42
259	CC	SC513	3.91	16.91	68.43	0.64	187.02	93.97	0.80	25.76	7.85	12.58	3.80	3.63
260	CC	SC727	7.83	21.37	67.14	0.79	221.90	120.34	0.88	14.41	9.86	6.14	3.42	3.6
Mean			4.36	15.05	62.87	1.08	186.66	88.91	0.86	18.83	8.41	5.45	3.80	3.98
LSD			0.96	1.60	2.25	5.35	10.41	8.89	0.13	11.34	11.46	14.89	0.49	0.4
CV			11.18	5.43	1.82	52.79	2.84	5.10	7.89	30.67	69.42	137.65	6.53	5.11
Heritability			0.87	0.87	0.91	0.12	0.86	0.88	0.03	0.48	0.16	0.15	0.59	0.76

SXTA=Single-cross tester A, SXTB-Single-cross tester B, and SXTAB=Single-cross tester AB,

GY-grain yield, MOI-moisture, AD-anthesis date, Anthesis-silking interval, PH-plant height, EH-ear height, EPP-ears per plant, ER-ear rots, HC-husk cover, SL-stem lodging , EA-ear aspect, TEX-texture, CC- commercial check

Appendix 4.1 Grain yield and agronomic trait predictions for the highest yielding top 300 and bottom 10 of 2448 hybrids of the LLdiallel three-way crosses

Entry	Parent 1	Parent 2	GY	AD	PH	EH	SL	SEN	ER	GLS	TURC	HC	TEX
828	4/8	14	8.68	74.13	227.0	114.1	1.27	4.38	7.65	1.70	2.13	2.77	2.73
548	3/5	6	8.67	76.14	220.3	113.8	14.68	5.38	6.63	1.45	2.29	9.91	3.00
320	2/5	18	8.65	73.02	226.8	111.5	6.29	5.01	6.88	1.41	1.81	27.06	2.39
995	5/6	3	8.65	75.31	222.1	111.9	16.96	4.95	5.07	1.39	2.26	1.54	3.16
2049	11/15	1	8.65	76.62	228.0	121.4	9.00	5.28	6.77	1.43	2.13	12.46	2.61
1299	6/13	3	8.64	75.11	217.8	110.7	13.34	5.13	5.14	1.75	2.15	1.86	2.93
170	1/12	11	8.64	76.10	233.2	124.9	10.55	5.79	6.16	1.39	2.16	6.99	2.64
2324	14/17	4	8.63	73.64	222.3	113.9	1.98	4.63	7.29	1.77	2.24	3.29	3.18
516	2/18	5	8.62	73.33	221.3	109.6	9.95	4.80	9.89	1.48	1.94	25.56	2.71
1381	6/18	5	8.61	74.13	223.3	115.5	6.48	5.53	9.33	1.31	2.02	9.36	2.55
234	1/16	11	8.59	75.26	234.8	127.2	9.54	5.40	6.02	1.61	2.03	8.78	2.41
756	3/18	5	8.59	73.31	225.1	113.6	8.76	5.10	7.77	1.24	2.00	0.99	2.71
1251	6/10	3	8.59	75.13	220.9	114.7	11.84	5.49	7.74	1.32	2.32	4.24	3.25
250	1/17	11	8.58	76.11	233.5	125.3	7.87	5.14	6.06	1.51	1.98	7.96	2.69
9	1/2	11	8.58	76.30	230.0	124.5	6.12	5.55	5.41	1.48	2.20	14.03	2.52
973	4/17	14	8.56	74.25	231.8	114.8	0.55	4.60	8.89	1.77	2.12	2.45	3.14
677	3/13	6	8.55	76.30	214.3	107.0	12.85	5.49	4.24	1.58	2.24	2.25	2.78
757	3/18	6	8.55	75.79	216.5	109.5	11.58	5.01	3.60	1.58	2.31	2.70	2.96
2341	14/18	5	8.53	74.46	220.9	105.7	4.06	4.99	8.54	1.30	1.99	2.54	2.68
2065	11/16	1	8.53	75.77	231.4	123.0	10.14	5.02	4.92	1.46	2.16	14.44	2.65
2001	11/12	1	8.53	75.23	227.0	120.7	8.34	5.43	3.48	1.17	2.06	4.96	2.46
780	4/5	14	8.51	75.44	224.0	108.0	1.87	4.72	9.40	1.57	2.19	3.13	2.95
2277	13/18	5	8.51	73.80	224.6	111.6	3.34	5.38	9.88	1.40	2.07	2.80	2.52
2081	11/17	1	8.51	75.97	232.0	122.2	6.32	5.17	9.70	1.41	2.07	10.46	2.69
532	3/4	6	8.51	76.22	220.9	111.5	16.94	4.79	4.25	1.44	2.28	1.97	3.29
141	1/10	15	8.49	75.99	224.5	112.1	3.77	5.21	9.11	1.38	2.09	10.34	2.68
186	1/13	11	8.49	76.05	219.2	116.7	6.01	6.14	4.03	1.74	2.02	6.43	2.46
1008	5/6	18	8.49	73.78	219.5	111.3	3.38	5.16	6.30	1.44	2.04	2.15	2.51
1709	8/17	14	8.49	74.32	232.6	112.8	1.29	4.36	6.40	1.69	2.04	2.84	2.82
1186	5/18	2	8.48	74.26	228.2	109.6	11.31	4.64	8.35	1.64	1.95	51.42	2.59
1917	10/13	15	8.48	74.91	227.0	111.4	1.60	5.23	8.12	1.61	2.05	2.42	2.43
20	1/3	6	8.47	76.12	219.5	111.8	14.68	5.19	7.03	1.58	2.24	11.75	3.19
980	4/18	5	8.46	73.59	223.6	108.8	5.83	5.18	7.77	1.37	1.96	1.24	2.66
189	1/13	15	8.45	75.83	225.1	114.4	4.32	4.98	9.09	1.83	2.17	6.68	2.48
1036	5/8	14	8.45	75.51	224.9	106.0	2.61	4.48	6.92	1.49	2.11	3.52	2.63
860	4/10	14	8.45	73.75	228.9	115.0	0.65	5.09	8.87	1.77	2.19	2.58	3.08
927	4/14	17	8.44	73.83	228.0	112.6	2.00	4.62	6.04	1.76	2.15	3.36	3.27
324	2/6	5	8.44	75.38	224.7	113.7	11.51	5.16	10.81	1.54	2.16	33.72	2.76
322	2/6	3	8.43	76.47	211.6	107.5	13.65	5.13	7.00	1.47	2.29	5.67	3.09
1124	5/14	4	8.43	74.57	226.7	111.1	3.63	4.90	8.63	1.63	2.17	1.82	2.93
1265	6/11	1	8.43	76.24	229.2	121.7	9.78	5.56	7.25	1.44	2.09	15.76	2.73
879	4/11	17	8.43	74.56	226.0	117.4	3.83	4.66	6.54	1.76	2.09	4.90	3.10
57	1/5	11	8.43	76.70	228.1	128.2	7.59	5.45	7.40	1.43	2.15	9.54	2.69
1316	6/14	4	8.43	75.20	226.9	115.6	6.55	4.66	7.81	1.56	2.22	2.00	3.11
2098	11/18	2	8.42	75.12	230.1	116.5	4.20	5.16	6.35	1.64	2.09	35.33	2.41
275	2/3	5	8.42	74.55	226.4	111.8	13.79	4.73	9.24	1.48	2.14	25.34	2.91
957	4/16	14	8.42	74.30	228.8	118.6	3.46	4.74	8.24	1.70	2.09	4.89	3.01
709	3/15	6	8.42	75.17	218.5	110.1	15.09	5.10	7.60	1.39	2.22	1.46	2.94
1454	7/11	16	8.41	74.14	240.1	123.1	4.89	5.52	5.54	1.76	2.21	3.82	2.59
2101	11/18	5	8.41	74.57	221.4	120.1	4.30	5.23	9.87	1.43	2.03	4.98	2.71
564	3/6	5	8.41	75.35	228.4	117.7	10.32	5.46	8.69	1.31	2.22	9.15	2.75
716	3/15	13	8.41	74.44	224.5	113.6	3.77	5.19	7.68	2.01	2.04	0.09	2.34
2171	12/16	11	8.41	75.04	234.5	124.5	8.58	5.58	8.72	1.74	2.14	5.45	2.57
2187	12/17	11	8.40	75.89	233.2	122.6	6.92	5.32	8.75	1.64	2.09	4.63	2.85
426	2/12	11	8.39	76.08	229.7	121.8	5.17	5.72	8.10	1.61	2.32	10.70	2.68
941	4/15	14	8.39	75.45	218.3	112.4	3.08	4.73	8.78	1.49	2.12	1.70	2.89
1074	5/11	2	8.39	75.43	224.6	114.6	7.86	4.96	9.36	1.71	2.22	33.83	2.74
713	3/15	10	8.39	74.61	227.1	115.3	1.71	5.79	10.30	1.13	2.13	6.13	2.86
1107	5/13	3	8.39	74.33	225.8	114.6	8.99	5.21	7.20	1.60	2.07	1.09	2.68
1596	8/10	14	8.38	73.82	229.7	113.0	1.38	4.85	6.38	1.69	2.11	2.97	2.76
1283	6/12	3	8.38	75.94	217.3	112.1	14.48	4.98	3.98	1.48	2.32	0.88	3.19
1873	10/11	1	8.37	75.59	228.4	115.2	7.49	5.60	6.02	1.24	2.09	30.46	2.69
815	4/7	17	8.37	73.10	226.4	112.1	2.44	5.01	4.83	1.83	2.32	5.81	3.19
452	2/14	5	8.36	75.70	222.3	103.8	9.09	4.62	10.02	1.54	2.13	26.90	2.88
865	4/11	1	8.36	76.25	230.0	119.9	12.69	5.24	5.74	1.29	2.05	9.03	2.72
1363	6/17	3	8.36	74.93	214.9	106.5	11.79	4.84	4.42	1.59	2.12	3.74	3.21
47	1/4	17	8.36	74.42	224.5	114.2	2.28	4.69	10.18	1.66	2.18	7.41	3.10
2411	16/17	11	8.35	75.05	234.8	124.9	5.90	4.94	8.62	1.86	1.97	6.43	2.62
1317	6/14	5	8.35	76.51	224.3	109.8	5.62	5.35	9.46	1.37	2.21	10.70	2.72
2047	11/14	17	8.35	75.17	235.5	118.2	2.41	4.63	8.14	1.76	1.98	4.06	3.07
2353	15/16	1	8.35	76.06	225.9	116.6	7.64	4.69	8.23	1.64	2.24	16.58	2.77
490	2/16	11	8.35	75.24	231.3	124.1	4.16	5.34	7.97	1.83	2.19	12.49	2.45
1693	8/16	14	8.35	74.37	229.7	116.6	4.19	4.51	5.75	1.62	2.01	5.29	2.69
94	1/7	16	8.35	74.65	236.6	118.9	5.50	5.14	4.44	1.61	2.33	9.48	2.83
1557	7/18	5	8.35	73.00	230.3	111.4	7.06	4.97	8.83	1.29	1.94	20.95	2.56
2145	12/15	1	8.35	75.53	221.5	114.4	5.83	5.10	6.79	1.35	2.15	7.10	2.58
336	2/6	18	8.35	74.72	226.4	111.3	4.75	5.00	4.76	1.60	2.05	28.01	2.39
1796	9/14	4	8.35	75.29	228.1	115.8	4.37	4.59	7.09	1.73	2.17	2.09	2.86
506	2/17	11	8.34	76.09	230.0	122.2	2.49	5.08	8.00	1.73	2.14	11.67	2.73
1315	6/14	3	8.34	75.93	209.4	108.4	11.05	5.10	4.56	1.59	2.18	7.48	3.35
2407	16/17	7	8.34	73.53	239.2	115.9	1.83	5.61	3.86	1.72	2.39	3.90	2.96
154	1/11	12	8.34	75.01	226.7	118.0	7.38	5.60	6.18	1.30	2.18	1.63	2.62
1486	7/13	16	8.34	74.90	231.0	116.5	4.25	5.61	4.42	1.69	2.15	1.04	2.69
436	2/13	5	8.34	75.04	226.0	109.7	8.37	5.01	11.36	1.63	2.21	27.16	2.73
692	3/14	5	8.33	75.68	226.0	107.9	7.91	4.92	7.90	1.30	2.18	2.33	2.88
1148	5/15	13	8.33	75.13	228.4	112.7	1.96	5.30	9.73	1.80	2.23	1.59	2.38
2369	15/17	1	8.33	76.26	226.5	115.9	3.81	4.85	13.00	1.58	2.15	12.60	2.81
1059	5/10	3	8.33	74.35	228.9	118.6	7.48	5.57	9.79	1.17	2.24	3.47	3.00
645	3/11	6	8.33	76.13	225.9	120.5	11.79	5.78	4.31	1.45	2.31	2.39	3.03
105	1/8	11	8.33	76.39	229.2	120.3	7.26	5.44	2.93	1.68	2.06	6.16	2.26
1301	6/13	5	8.33	75.85	227.9	115.7	4.90	5.74	10.80	1.46	2.29	10.96	2.57
2298	14/15	10	8.33	74.25	229.0	111.5	0.91	5.51	7.87	1.46	2.07	4.43	2.88
1677	8/15	14	8.33	75.52	219.2	110.4	3.81	4.49	6.29	1.41	2.03	2.10	2.57
1907	10/13	3	8.33	74.15	224.6	117.4	3.87	5.75	9.87	1.53	2.12	3.80	2.77
2365	15/16	13	8.32	75.23	222.8	113.6	4.22	5.19	7.22	1.95	2.02	0.23	2.38
195	1/14	4	8.32	75.12	226.3	114.1	7.20	4.75	9.08	1.55	2.14	5.05	3.00
1181	5/17	14	8.32	75.63	229.7	106.7	1.89	4.70	8.15	1.56	2.10	3.21	3.04
2362	15/16	10	8.32	74.91	227.6	114.3	0.78	5.78	7.31	1.16	2.15	2.56	2.67
1172	5/17	4	8.32	74.16	222.9	109.0	5.08	4.91	5.78	1.62	2.19	2.74	3.06

Entry	Parent 1	Parent 2	GY	AD	PH	EH	SL	SEN	ER	GLS	TURC	HC	TEX
1340	6/15	13	8.32	75.64	221.1	109.9	3.27	5.55	6.78	1.85	2.13	0.48	2.18
1924	10/14	4	8.31	74.33	222.6	113.4	9.03	4.97	8.66	1.45	2.23	5.22	3.07
1109	5/13	6	8.31	76.35	220.6	112.8	6.22	5.99	7.85	1.50	2.19	9.86	2.37
1364	6/17	4	8.31	74.79	223.2	113.5	8.00	4.68	4.97	1.55	2.24	2.92	3.24
676	3/13	5	8.31	75.02	229.7	113.7	7.19	5.31	9.24	1.39	2.27	2.59	2.72
1189	5/18	6	8.31	75.83	222.8	115.4	4.94	5.52	7.22	1.50	2.26	10.31	2.56
1513	7/15	10	8.30	74.10	227.4	111.6	0.40	5.62	7.52	1.13	2.14	12.19	2.77
597	3/8	6	8.30	75.88	218.8	108.4	12.84	4.89	2.95	1.53	2.38	2.09	2.92
555	3/5	13	8.30	74.82	225.3	112.6	3.57	5.49	9.32	1.75	2.15	2.91	2.50
158	1/11	16	8.30	74.70	232.7	122.5	8.17	4.81	7.48	1.82	2.14	12.91	2.57
2123	12/13	11	8.30	75.83	219.0	114.0	5.06	6.32	6.73	1.88	2.13	3.10	2.61
581	3/7	6	8.30	73.96	217.8	103.5	11.88	5.17	3.28	1.36	2.27	1.25	3.07
732	3/16	13	8.30	74.92	219.7	113.5	5.83	5.38	6.81	1.90	1.93	1.56	2.50
2060	11/15	13	8.30	75.27	216.3	109.7	1.34	5.84	6.34	2.15	2.06	0.66	2.33
1438	7/10	16	8.29	74.43	236.5	119.4	1.36	5.98	4.49	1.36	2.36	-0.29	2.78
1503	7/14	17	8.29	73.70	235.9	112.9	1.01	4.98	6.42	1.83	2.20	4.97	3.15
2030	11/13	16	8.29	74.95	227.0	120.1	6.92	5.29	7.46	1.90	1.96	4.47	2.44
73	1/6	11	8.29	76.25	235.6	130.4	6.89	6.15	4.54	1.31	2.16	6.40	2.57
571	3/6	13	8.29	75.32	218.0	109.8	4.89	5.74	6.37	1.80	2.05	1.81	2.30
784	4/5	18	8.28	73.95	226.0	117.4	3.96	4.98	6.67	1.32	1.96	11.83	2.60
291	2/4	5	8.28	74.83	225.0	106.9	10.85	4.81	9.25	1.60	2.10	25.59	2.86
1203	6/7	3	8.28	75.74	219.9	112.2	15.19	4.91	4.64	1.56	2.13	4.55	3.03
629	3/10	6	8.28	74.55	222.3	110.7	14.72	5.43	5.60	1.29	2.16	7.70	2.95
1455	7/11	17	8.28	74.43	233.9	117.7	2.84	5.02	6.93	1.83	2.15	6.51	2.98
1959	10/16	7	8.28	73.62	236.2	116.8	0.98	5.82	4.70	1.33	2.36	9.34	2.87
207	1/14	17	8.28	75.02	234.0	115.1	0.85	4.66	11.78	1.66	2.06	6.57	3.06
1933	10/14	15	8.28	75.95	218.5	108.9	3.34	5.15	7.78	1.18	1.99	3.56	2.68
788	4/6	5	8.27	75.63	227.0	112.9	7.39	5.53	8.69	1.43	2.18	9.40	2.70
2212	13/14	4	8.27	74.97	229.0	115.5	10.83	5.14	15.38	1.88	2.16	3.46	2.87
1502	7/14	16	8.27	74.31	237.8	120.3	4.30	5.36	4.42	1.59	2.19	3.90	2.90
159	1/11	17	8.27	75.75	232.0	119.8	2.68	4.71	12.29	1.66	2.01	8.11	2.89
772	4/5	6	8.27	76.26	227.2	117.4	10.31	5.30	7.87	1.36	2.23	9.58	2.89
651	3/11	13	8.27	74.96	213.2	109.6	2.95	6.03	5.93	2.10	1.97	1.98	2.45
2340	14/18	4	8.26	74.93	229.1	119.7	1.77	4.71	7.53	1.59	2.16	12.41	2.87
540	3/4	14	8.26	74.91	215.4	112.5	0.66	4.97	8.12	1.71	2.12	7.52	3.17
2251	13/16	11	8.26	74.99	220.5	116.3	4.04	5.94	6.59	2.10	2.00	4.90	2.38
531	3/4	5	8.26	74.81	228.7	111.0	9.67	5.11	7.12	1.36	2.16	1.02	2.86
1136	5/14	18	8.25	73.74	227.3	115.1	3.55	5.23	7.31	1.60	2.06	1.13	2.57
205	1/14	15	8.25	76.87	216.5	111.8	6.06	4.90	8.75	1.40	2.12	7.81	2.73
2027	11/13	12	8.25	74.37	223.3	114.7	6.09	6.02	6.58	1.55	2.06	2.17	2.58
1329	6/15	1	8.25	76.53	223.7	115.4	7.27	5.23	10.56	1.61	2.18	17.90	2.85
300	2/4	14	8.25	74.44	219.9	111.2	0.79	4.76	7.95	1.59	2.13	9.04	2.90
2213	13/14	5	8.25	76.17	225.6	105.8	2.49	5.20	10.01	1.45	2.26	4.15	2.69
1981	10/17	14	8.25	73.94	234.5	113.7	0.67	5.07	7.61	1.76	2.10	2.65	3.18
2156	12/15	13	8.25	73.80	220.6	110.4	2.37	5.54	6.20	1.82	1.99	-0.27	2.29
2267	13/17	11	8.25	75.84	219.2	114.3	2.38	5.68	6.62	2.00	1.96	4.08	2.66
442	2/13	11	8.25	76.03	215.7	113.6	0.63	6.08	5.97	1.97	2.18	10.14	2.49
1886	10/11	16	8.24	74.49	232.5	123.1	4.04	5.65	7.53	1.56	2.17	3.14	2.52
473	2/15	10	8.24	75.30	232.4	116.3	10.32	5.67	9.44	1.34	1.94	30.49	2.69
1986	10/18	2	8.24	74.75	236.0	117.4	13.63	5.36	8.04	1.55	1.87	53.91	2.51
1098	5/12	11	8.24	76.47	227.9	125.5	6.63	5.63	10.09	1.57	2.27	6.21	2.85
2221	13/14	15	8.24	75.80	219.0	111.2	3.89	4.92	7.76	1.63	2.07	-0.10	2.47
1152	5/15	18	8.24	75.04	219.0	110.4	4.53	4.99	8.23	1.30	1.87	0.39	2.47
404	2/11	5	8.24	75.82	222.7	118.2	9.32	4.86	11.35	1.66	2.17	29.34	2.91
1040	5/8	18	8.24	72.97	226.9	115.3	8.95	4.93	8.29	1.48	1.88	0.83	2.28
202	1/14	11	8.24	76.48	236.9	125.7	6.01	5.33	5.18	1.44	2.06	6.32	2.54
754	3/18	2	8.24	75.40	221.4	109.3	6.83	5.12	8.16	1.49	2.03	30.98	2.53
52	1/5	6	8.23	76.17	225.8	117.7	8.05	5.70	10.64	1.50	2.19	19.36	2.78
989	4/18	14	8.23	74.72	230.4	117.4	1.35	4.95	8.17	1.86	2.27	1.71	2.84
2161	12/16	1	8.23	74.67	224.8	116.0	6.97	4.84	4.94	1.38	2.17	9.08	2.62
1844	9/17	4	8.23	74.87	224.3	113.7	5.82	4.60	4.25	1.72	2.20	3.01	2.99
1269	6/11	5	8.23	76.62	224.7	124.2	5.86	5.59	10.79	1.49	2.25	13.14	2.75
844	4/9	14	8.23	74.68	221.1	109.9	0.96	4.77	8.65	1.98	2.22	2.03	2.83
2046	11/14	16	8.23	74.37	233.8	123.9	6.98	5.03	7.46	1.79	2.00	7.33	2.65
266	1/18	11	8.22	76.82	236.3	128.0	7.55	5.28	4.74	1.73	2.04	6.64	2.34
190	1/13	16	8.22	75.46	223.6	115.8	7.53	4.90	6.36	1.75	2.08	10.13	2.67
2414	16/17	14	8.22	74.49	234.5	117.2	3.48	4.73	6.98	1.69	2.00	4.97	3.10
2040	11/14	8	8.22	75.33	226.3	112.5	2.51	4.71	3.78	1.87	2.06	2.58	2.22
1261	6/10	15	8.22	74.65	224.7	110.7	4.96	5.40	10.16	1.20	2.03	3.35	2.55
667	3/12	13	8.22	73.49	217.6	110.3	3.98	5.73	5.79	1.76	1.90	1.06	2.41
1164	5/16	13	8.22	75.61	223.6	112.6	4.02	5.48	8.85	1.69	2.12	3.05	2.54
217	1/15	10	8.22	74.95	224.8	105.9	2.26	5.52	8.36	1.19	2.04	28.35	2.77
2401	16/17	1	8.22	75.41	229.9	117.5	4.95	4.58	11.15	1.62	2.18	14.59	2.85
644	3/11	5	8.21	75.80	226.5	122.3	8.14	5.16	9.23	1.43	2.23	4.76	2.91
2177	12/17	1	8.21	74.87	225.5	115.2	3.15	4.99	9.71	1.33	2.09	5.11	2.66
1379	6/18	3	8.21	75.87	217.6	113.0	14.84	4.81	4.45	1.58	2.19	3.19	3.08
1003	5/6	13	8.21	76.01	221.9	108.9	3.08	5.85	8.41	1.59	2.24	3.30	2.34
1068	5/10	14	8.21	75.14	226.8	106.9	1.98	5.19	8.13	1.56	2.17	3.33	2.98
1058	5/10	2	8.21	75.06	230.5	115.5	17.28	5.16	11.05	1.62	2.00	52.41	2.83
1088	5/11	18	8.21	74.70	229.5	119.9	4.26	5.06	7.22	1.73	1.91	2.08	2.35
697	3/14	10	8.21	73.80	229.7	117.6	1.56	5.83	10.03	1.43	2.23	4.48	3.10
243	1/17	4	8.21	74.70	222.5	111.9	8.65	4.76	6.23	1.54	2.16	5.97	3.13
95	1/7	17	8.20	74.29	232.4	114.5	1.29	5.05	10.57	1.73	2.23	9.01	2.98
546	3/5	2	8.20	75.71	216.0	107.4	10.48	4.91	11.17	1.56	2.16	29.48	2.85
1356	6/16	13	8.20	76.11	216.2	109.7	5.34	5.74	5.90	1.73	2.02	1.95	2.34
2382	15/17	14	8.20	75.64	224.0	111.0	3.10	4.72	7.52	1.48	2.03	1.78	2.98
2017	11/13	1	8.20	76.38	226.3	111.9	6.49	5.93	5.54	1.37	1.97	7.55	2.43
876	4/11	14	8.20	75.34	233.2	119.9	0.52	4.83	8.52	1.70	2.14	2.35	2.82
916	4/14	5	8.20	75.96	224.6	103.0	4.97	5.00	7.90	1.43	2.15	2.58	2.82
1989	10/18	5	8.20	74.41	226.2	113.6	3.19	5.69	11.30	1.25	2.01	1.36	2.72
1162	5/16	11	8.20	75.63	229.4	127.8	5.62	5.25	9.96	1.79	2.14	8.00	2.62
77	1/6	15	8.20	75.58	222.8	113.7	7.68	5.15	11.13	1.43	2.16	7.61	2.60
729	3/16	10	8.20	74.47	228.3	120.4	1.44	6.11	9.47	1.14	2.31	2.60	2.90
1972	10/17	4	8.20	73.91	218.8	111.2	10.48	4.98	5.82	1.44	2.26	6.14	3.20
937	4/15	10	8.20	74.83	222.7	109.9	9.29	5.39	7.67	1.14	2.10	7.08	2.86
1937	10/15	1	8.19	75.88	222.9	108.9	4.98	5.27	9.32	1.42	2.17	32.61	2.82
604	3/8	14	8.19	74.98	216.3	110.5	1.40	4.73	5.63	1.63	2.03	7.91	2.85
1083	5/11	13	8.19	75.65	217.1	108.7	1.14	6.13	7.98	1.89	2.17	3.48	2.48
2278	13/18	6	8.19	76.00	216.8	108.6	3.12	5.63	4.82	1.63	2.21	2.65	2.33
1178	5/17	11	8.19	76.48	228.1	125.9	3.96	4.99	9.99	1.69	2.09	7.18	2.90
364	2/8	14	8.19	74.51	220.8	109.2	1.52	4.52	5.46	1.51	2.04	9.43	2.58
313	2/5	11	8.19	76.67	224.6	125.1	2.21	5.39	9.34	1.66	2.31	13.25	2.73
1158	5/16	7	8.18	74.01	242.3	115.4	5.71	5.31	5.87	1.45	2.24	20.54	2.73
584	3/7	10	8.18	73.66	228.1	117.7	1.06	5.95	9.68	1.10	2.31	12.23	2.99
1309	6/13	15	8.18	74.50	225.3	113.0	5.51	5.17	10.14	1.66	2.11	-0.31	2.34
2076	11/16	13	8.18	75.74	211.5	109.6	3.40	6.03	5.47	2.03	1.95	2.12	2.49
1165	5/16	14	8.18	75.69	226.7	110.5	4.79	4.84	7.50	1.49	2.08	5.65	2.90

Entry	Parent 1	Parent 2	GY	AD	PH	EH	SL	SEN	ER	GLS	TURC	HC	TEX
929	4/15	1	8.18	76.55	224.6	113.6	10.18	4.92	9.05	1.46	2.14	11.17	2.84
142	1/10	16	8.18	74.99	229.1	118.8	4.64	5.27	6.42	1.42	2.30	8.80	2.76
1141	5/15	6	8.18	75.21	224.8	115.9	8.45	5.61	11.22	1.31	2.17	9.07	2.53
306	2/5	3	8.18	75.69	219.7	111.4	9.30	5.21	9.05	1.32	2.22	4.90	2.85
1347	6/16	3	8.18	76.29	215.8	111.8	18.89	5.14	5.10	1.55	2.29	6.89	3.09
340	2/7	5	8.18	74.25	231.7	109.6	12.08	4.60	10.30	1.53	2.08	45.30	2.77
2292	14/15	4	8.17	75.41	225.2	115.8	6.47	4.74	8.19	1.62	2.02	2.13	3.02
900	4/13	5	8.17	75.30	228.3	108.9	4.25	5.39	9.24	1.52	2.23	2.84	2.67
1275	6/11	13	8.17	76.15	209.8	105.9	2.46	6.39	5.03	1.93	2.07	2.37	2.29
434	2/13	3	8.17	75.49	215.4	110.3	5.69	5.38	9.13	1.68	2.10	5.23	2.62
1205	6/7	5	8.17	75.05	233.6	115.5	8.62	5.33	9.74	1.36	2.16	29.11	2.61
1104	5/12	18	8.17	72.26	220.5	112.6	4.59	5.13	6.18	1.44	1.89	1.30	2.51
1918	10/13	16	8.17	75.24	223.4	116.4	3.39	5.74	6.41	1.50	2.12	0.36	2.62
1725	8/18	14	8.17	74.79	231.3	115.4	2.09	4.72	5.69	1.78	2.18	2.11	2.52
303	2/4	17	8.16	74.60	222.8	112.8	4.82	4.46	5.36	1.64	2.16	12.33	3.19
543	3/4	17	8.16	73.50	217.2	108.4	2.85	4.73	5.13	1.71	2.08	4.69	3.16
206	1/14	16	8.16	74.88	230.4	119.6	7.58	4.65	6.35	1.65	2.12	12.99	2.89
1267	6/11	3	8.16	77.77	223.1	112.6	13.11	4.99	6.71	1.66	2.20	2.17	3.04
2434	17/18	2	8.16	74.96	230.3	112.7	6.93	4.56	5.81	1.54	1.94	36.69	2.68
1580	8/9	14	8.16	74.75	222.0	107.9	1.70	4.53	6.16	1.90	2.13	2.42	2.52
1319	6/14	8	8.16	74.93	225.7	110.4	3.19	4.53	4.03	1.58	2.23	2.52	2.42
1149	5/15	14	8.16	76.84	216.2	104.3	4.41	4.83	8.04	1.28	2.10	2.46	2.78
2260	13/17	4	8.16	74.55	225.2	113.4	12.27	5.16	12.53	1.87	2.18	4.37	3.00
2328	14/17	8	8.16	75.46	225.1	113.6	2.87	4.14	10.16	1.89	1.98	1.99	2.69
1874	10/11	2	8.16	75.91	232.4	122.4	10.17	5.69	9.04	1.61	2.14	36.32	2.65
1975	10/17	7	8.16	73.06	231.4	113.2	0.60	5.58	6.05	1.50	2.35	12.86	2.98
1601	8/11	1	8.15	77.36	231.5	117.5	8.13	5.21	5.41	1.52	2.13	16.38	2.33
2037	11/14	5	8.15	76.95	222.3	114.3	3.44	5.06	10.00	1.49	2.22	6.32	2.87
560	3/5	18	8.15	73.87	220.5	114.7	6.64	4.96	7.14	1.44	1.92	2.64	2.63
642	3/11	2	8.15	76.56	217.9	114.2	3.37	5.44	9.16	1.55	2.30	13.39	2.67
580	3/7	5	8.15	74.23	235.4	113.6	10.90	4.90	8.18	1.29	2.14	20.73	2.76
2222	13/14	16	8.15	75.12	224.8	117.2	6.33	5.12	6.34	1.73	1.94	4.55	2.75
901	4/13	6	8.15	76.43	221.2	110.6	8.49	5.41	5.48	1.49	2.18	1.92	2.66
2344	14/18	8	8.15	74.02	230.8	115.6	7.49	4.42	6.67	1.66	2.00	1.81	2.23
650	3/11	12	8.15	75.84	226.7	119.2	8.62	5.53	6.90	1.48	2.28	1.55	2.88
2436	17/18	4	8.14	74.52	225.3	117.5	3.22	4.72	4.68	1.58	2.19	13.33	3.00
981	4/18	6	8.14	75.92	223.4	113.1	7.21	4.93	4.84	1.49	2.25	2.37	2.85
187	1/13	12	8.14	73.50	217.1	110.5	3.88	5.67	3.90	1.33	1.97	0.15	2.40
1099	5/12	13	8.14	74.18	221.5	109.4	2.17	5.84	7.83	1.56	2.09	2.55	2.45
304	2/4	18	8.14	74.88	232.8	117.4	5.33	4.82	5.13	1.48	1.97	37.69	2.48
1626	8/12	11	8.14	76.17	228.9	117.5	6.30	5.62	5.63	1.82	2.17	2.83	2.42
1345	6/16	1	8.14	75.68	227.1	117.0	8.42	4.97	8.71	1.65	2.20	19.88	2.89
2172	12/16	13	8.14	74.28	215.8	110.3	4.43	5.73	5.32	1.70	1.88	1.20	2.45
2338	14/18	2	8.13	74.39	223.7	108.9	4.35	4.87	5.55	1.49	1.93	34.31	2.51
1281	6/12	1	8.13	75.15	222.7	114.8	6.61	5.37	7.27	1.35	2.11	10.40	2.70
2097	11/18	1	8.13	76.14	225.7	119.5	13.81	5.00	5.94	1.40	2.11	12.73	2.69
2314	14/16	10	8.13	74.11	230.3	116.7	0.63	5.83	7.04	1.46	2.25	0.90	2.91
1741	9/10	15	8.13	75.83	220.4	106.0	0.33	5.20	6.30	1.28	2.11	2.83	2.42
1612	8/11	14	8.13	75.41	234.1	117.9	1.26	4.60	6.03	1.62	2.06	2.74	2.50
280	2/3	10	8.12	74.85	233.0	122.4	10.98	6.00	11.60	1.31	2.11	30.54	2.92
25	1/3	11	8.12	77.89	232.9	122.4	8.21	5.36	6.93	1.52	2.06	6.18	2.58
940	4/15	13	8.12	75.32	229.7	114.3	11.64	5.33	14.35	2.02	2.12	1.66	2.46
1091	5/12	3	8.12	75.16	225.3	116.0	10.13	5.06	6.03	1.34	2.24	0.11	2.94
1497	7/14	10	8.12	73.29	230.0	114.0	0.25	5.67	7.24	1.43	2.24	10.54	3.01
1361	6/17	1	8.12	75.88	227.7	116.2	4.59	5.12	13.48	1.59	2.12	15.91	2.93
386	2/10	3	8.12	75.51	218.5	114.2	4.18	5.75	11.72	1.26	2.27	7.60	2.93
64	1/5	18	8.12	74.02	218.9	111.4	10.51	4.78	8.41	1.40	1.98	8.17	2.70
181	1/13	6	8.12	76.33	219.7	110.9	6.23	5.80	8.25	1.63	2.14	11.70	2.56
1965	10/16	14	8.11	73.99	231.6	117.5	3.57	5.21	6.97	1.69	2.07	5.09	3.04
2115	12/13	3	8.11	74.96	221.0	114.8	6.52	5.24	6.11	1.69	2.12	0.43	2.72
464	2/14	18	8.11	74.67	234.2	115.1	4.91	5.07	5.78	1.76	2.07	26.99	2.45
2033	11/14	1	8.11	76.64	229.6	113.4	10.44	5.74	4.27	1.52	2.16	12.96	2.45
261	1/18	6	8.11	75.82	222.0	113.4	4.95	5.33	7.61	1.63	2.21	12.15	2.74
996	5/6	4	8.11	75.72	227.5	110.6	9.66	4.95	6.31	1.41	2.17	1.45	2.99
831	4/8	17	8.11	74.97	220.4	113.5	3.58	4.39	9.80	1.96	2.09	2.51	3.14
1529	7/16	10	8.11	73.96	228.6	116.7	0.13	5.95	6.68	1.13	2.32	8.66	2.80
125	1/9	15	8.11	76.75	218.5	109.0	3.05	4.95	7.26	1.50	2.24	7.09	2.47
137	1/10	11	8.11	75.71	232.1	128.2	5.68	5.84	4.13	1.32	1.97	19.89	2.60
2011	11/12	13	8.11	74.32	209.3	106.4	1.55	6.38	4.45	1.90	1.92	1.62	2.40
1934	10/14	16	8.10	74.66	230.2	120.2	3.45	5.49	6.41	1.39	2.15	3.22	2.83
1745	9/11	1	8.10	75.45	226.3	114.8	5.62	5.08	4.51	1.27	2.12	25.15	2.28
1122	5/14	2	8.10	74.70	218.2	107.0	8.00	4.67	8.56	1.56	2.06	32.81	2.83
1171	5/17	3	8.10	74.15	223.0	110.4	7.44	4.92	6.48	1.44	2.05	2.97	2.96
1290	6/12	11	8.10	76.02	235.3	127.6	5.93	6.32	7.23	1.44	2.27	3.06	2.73
1998	10/18	15	8.10	76.52	222.2	109.2	2.60	5.13	8.10	1.25	1.95	2.83	2.53
1690	8/16	11	8.10	75.33	230.4	119.8	5.29	5.23	5.49	2.04	2.04	4.62	2.19
2234	13/15	10	8.10	74.92	233.1	110.8	2.77	5.79	7.08	1.19	2.07	7.70	2.64
480	2/15	18	8.10	75.97	225.8	110.4	5.90	4.82	6.70	1.46	1.88	26.25	2.35
368	2/8	18	8.10	73.90	233.7	115.3	10.32	4.77	6.76	1.64	1.89	26.69	2.16
959	4/16	17	8.10	74.60	228.1	118.1	3.46	4.81	7.55	1.85	2.08	1.65	2.97
2259	13/17	3	8.10	73.95	218.6	109.3	3.83	5.10	6.55	1.80	1.93	3.29	2.74
1789	9/13	15	8.09	75.67	221.0	108.3	0.88	4.97	6.27	1.73	2.20	-0.83	2.21
24	1/3	10	8.09	74.51	225.5	112.0	2.92	5.85	10.51	1.17	2.21	28.39	2.99
1114	5/13	11	8.09	76.42	213.9	117.3	2.10	5.99	7.96	1.92	2.13	5.65	2.67
1493	7/14	5	8.09	75.38	231.3	105.6	6.20	4.80	8.96	1.35	2.13	22.29	2.73
1077	5/11	6	8.09	76.17	232.2	126.3	5.16	6.28	7.93	1.37	2.26	10.00	2.63
1949	10/15	14	8.09	75.14	221.1	111.3	3.19	5.20	7.51	1.48	2.09	1.90	2.92
539	3/4	13	8.09	75.00	226.7	114.2	13.25	5.53	13.94	1.97	2.03	2.98	2.58
1706	8/17	11	8.09	76.18	229.2	117.9	3.63	4.97	5.53	1.94	1.99	3.80	2.46
361	2/8	11	8.09	76.37	225.7	117.1	1.88	5.38	4.88	1.91	2.22	9.87	2.29
463	2/14	17	8.09	75.20	232.2	113.6	3.39	4.44	6.96	1.64	2.04	11.49	3.16
1202	6/7	2	6.25	76.33	225.2	111.1	11.70	5.79	7.86	1.71	2.03	34.28	2.47
1102	5/12	16	6.24	75.20	219.7	107.5	2.70	5.65	6.80	1.67	2.11	2.23	2.69
1355	6/16	12	6.24	76.14	222.3	112.1	2.30	5.60	5.66	1.43	2.14	0.10	2.84
1294	6/12	16	6.21	76.13	220.1	117.7	15.07	5.47	5.17	1.58	2.08	0.08	2.70
424	2/12	9	6.20	75.25	215.6	104.2	1.23	5.82	4.09	1.49	2.26	3.33	2.19
343	2/7	9	6.16	75.52	223.4	101.5	2.81	5.65	5.54	1.71	2.39	2.67	2.30
834	4/9	2	6.10	75.84	214.7	111.2	5.68	5.16	4.92	1.39	1.99	8.04	2.56
1234	6/9	2	6.08	76.56	220.1	109.9	2.47	5.51	6.32	1.59	2.18	18.73	2.29
504	2/17	9	6.01	75.00	218.0	107.5	1.81	5.55	5.79	2.09	2.13	3.37	2.47
1410	7/9	2	5.95	75.32	221.4	107.2	10.76	5.80	6.22	1.74	2.06	21.45	2.37

AD-anthesis date, Anthesis-silking interval, PH-plant height, EH-ear height, , SL-stem lodging, SEN-senescence, ER-ear rots, GLS-grey leaf spot, TURC- turcicum, HC-husk cover, TEX-texture.

Appendix 4.2 Grain yield and agronomic trait predictions for the highest yielding top 300 and bottom 10 of 9180 hybrids of the LLdiallel double-crosses

Entry	Parent 1	Parent 2	GY	MOI	AD	PH	EH	SL	ER	TURC	HC	TEX
5008	3/18	5/6	8.57	14.44	74.55	220.80	111.58	10.17	5.68	2.15	1.84	2.84
3831	3/5	6/13	8.49	14.47	75.48	222.84	113.19	9.12	7.97	2.22	6.41	2.75
1422	1/13	11/15	8.47	14.93	75.94	222.15	115.55	5.17	6.56	2.10	6.56	2.47
2357	2/6	3/5	8.44	14.14	75.92	218.15	110.58	12.58	8.90	2.22	19.69	2.93
4553	3/13	5/6	8.43	14.12	75.66	222.00	110.37	10.02	6.74	2.25	2.42	2.75
2334	2/5	11/18	8.42	14.66	74.84	225.72	118.28	4.25	8.11	2.06	20.15	2.56
2264	2/5	3/18	8.41	14.49	74.35	223.25	111.45	7.80	7.96	2.01	15.98	2.62
4753	3/15	6/13	8.41	15.38	74.81	221.52	111.85	9.43	7.64	2.13	0.78	2.64
3836	3/5	6/18	8.41	14.81	75.00	220.44	114.26	10.66	6.89	2.11	6.27	2.82
4750	3/15	6/10	8.40	15.18	74.89	222.80	112.69	8.40	8.95	2.17	3.80	2.90
4787	3/15	10/13	8.40	15.50	74.53	225.79	114.44	2.74	8.99	2.09	3.11	2.60
5157	4/5	14/18	8.40	15.10	74.70	225.00	112.69	2.92	8.04	2.07	7.48	2.77
5390	4/8	14/17	8.40	15.12	74.55	223.70	113.79	2.43	8.73	2.11	2.64	2.93
1836	1/17	4/11	8.39	15.07	75.41	228.02	118.62	8.26	6.14	2.07	6.96	2.91
2394	2/6	5/18	8.39	14.55	75.05	225.50	112.50	8.13	7.79	2.11	30.86	2.58
2369	2/6	3/18	8.39	14.25	75.60	219.00	109.41	9.20	5.88	2.17	16.84	2.74
5093	4/5	6/14	8.39	14.97	75.85	225.59	112.68	6.09	8.64	2.21	6.35	2.92
3741	3/4	6/14	8.38	14.25	75.57	218.17	112.00	8.80	6.19	2.20	4.74	3.23
3721	3/4	5/6	8.38	13.92	75.51	224.82	111.24	13.31	5.69	2.22	1.50	3.07
1423	1/13	11/16	8.36	14.49	75.75	221.41	116.27	6.77	5.19	2.05	8.28	2.57
6233	5/6	13/18	8.35	14.88	74.90	220.70	110.08	3.23	7.35	2.14	2.73	2.43
3922	3/6	5/13	8.35	14.48	75.34	223.20	113.74	7.61	7.53	2.13	5.48	2.53
3832	3/5	6/14	8.35	14.52	76.22	216.83	109.07	8.34	7.01	2.19	9.09	3.03
7873	7/11	16/17	8.35	15.06	74.29	236.98	120.40	3.87	6.24	2.18	5.16	2.79
6108	4/18	5/14	8.34	15.00	74.16	227.02	113.10	3.59	7.97	2.11	1.47	2.75
6369	5/8	14/18	8.34	14.98	74.24	225.88	110.63	5.78	7.60	2.00	2.18	2.45
1435	1/13	15/16	8.34	15.33	75.65	224.32	115.11	5.93	7.72	2.13	8.41	2.57
1075	1/10	15/16	8.34	15.07	75.49	226.77	115.48	4.21	7.77	2.19	9.57	2.72
2349	2/5	14/18	8.33	14.94	74.42	222.30	107.28	4.21	7.05	1.96	18.43	2.59
3744	3/4	6/17	8.33	14.42	74.86	219.03	109.97	9.90	4.69	2.18	3.33	3.23
407	1/5	6/11	8.33	14.93	76.43	226.95	122.94	7.82	9.02	2.17	14.45	2.74
8860	10/13	15/16	8.32	15.76	75.07	225.20	113.93	2.50	7.26	2.08	1.39	2.53
1183	1/11	12/16	8.32	15.13	74.86	229.68	120.25	7.78	6.83	2.16	7.27	2.59
5798	4/14	5/17	8.32	14.59	74.90	226.30	107.81	3.49	6.97	2.15	2.97	3.05
1420	1/13	11/12	8.32	15.13	74.77	218.15	113.59	4.94	3.96	1.99	3.29	2.43
5624	4/11	14/17	8.31	15.07	74.95	229.60	118.62	2.18	7.53	2.12	3.62	2.96
1773	1/16	10/11	8.31	14.68	75.04	230.43	119.14	5.77	6.77	2.13	16.80	2.61
1184	1/11	12/17	8.30	14.84	75.38	229.35	118.91	5.03	9.23	2.09	4.87	2.75
3828	3/5	6/10	8.30	14.51	75.79	225.20	116.20	8.29	9.98	2.27	6.88	3.01
1379	1/13	6/11	8.30	14.40	76.19	219.49	113.79	6.12	6.14	2.08	9.07	2.51
3648	2/18	5/11	8.30	14.65	75.06	227.04	117.23	6.06	8.29	2.07	17.95	2.54
6100	4/18	5/6	8.30	14.69	74.75	223.53	110.95	6.52	6.30	2.10	1.80	2.75
1056	1/10	11/15	8.30	15.16	75.85	228.29	120.16	4.73	6.62	2.03	15.12	2.64
1481	1/14	4/17	8.30	14.08	75.07	230.15	114.56	4.03	10.43	2.10	5.81	3.03
1427	1/13	12/15	8.30	15.98	74.66	221.06	112.43	4.10	6.49	2.07	3.41	2.44
4388	3/11	6/13	8.30	14.11	75.54	219.54	115.06	7.37	5.12	2.14	2.19	2.74
3740	3/4	6/13	8.30	14.21	75.61	223.79	112.87	15.10	9.10	2.15	2.48	2.93
167	1/3	6/11	8.30	14.52	77.01	226.17	117.14	11.45	6.98	2.15	8.97	2.88
5919	4/15	10/14	8.29	15.23	75.14	220.52	111.14	6.18	8.22	2.11	4.39	2.87
5338	4/8	6/14	8.29	14.86	75.07	226.32	113.02	4.87	5.92	2.22	2.26	2.77
98	1/2	11/17	8.29	14.19	76.04	229.37	119.89	4.90	8.26	2.14	14.78	2.75
3123	2/13	5/11	8.29	14.00	75.54	220.85	111.64	4.50	8.67	2.19	18.65	2.61
1783	1/16	11/15	8.29	14.82	76.30	229.09	120.06	12.48	8.64	2.10	7.86	2.56
3737	3/4	6/10	8.29	14.24	75.30	222.16	113.78	13.44	7.04	2.27	4.55	3.19
9013	11/14	16/17	8.29	14.38	74.77	234.64	121.05	4.69	7.80	1.99	5.70	2.86
8496	8/17	11/14	8.29	14.62	75.25	230.90	115.34	2.46	5.96	2.02	3.32	2.64
1479	1/14	4/15	8.29	14.99	76.00	221.43	112.95	6.63	8.91	2.13	6.43	2.86
6831	5/15	13/18	8.29	15.76	75.09	223.68	111.53	3.25	8.98	2.05	0.99	2.42
1198	1/11	16/17	8.28	14.39	75.23	232.32	121.17	5.43	9.88	2.07	10.51	2.73
1382	1/13	6/15	8.28	15.25	76.08	222.40	112.63	5.27	8.67	2.16	9.19	2.52
166	1/3	6/10	8.28	14.31	75.31	222.49	111.93	8.80	8.77	2.22	20.07	3.09
8008	7/14	16/17	8.28	14.50	74.01	236.85	116.58	2.66	5.42	2.20	4.43	3.03
1476	1/14	4/11	8.28	14.80	75.80	231.61	119.86	6.61	7.13	2.10	5.69	2.77
99	1/2	11/18	8.28	14.21	75.63	227.86	118.01	9.00	6.14	2.10	24.03	2.55
718	1/7	16/17	8.28	14.50	74.47	234.53	116.69	3.39	7.50	2.28	9.24	2.90
5097	4/5	6/18	8.27	14.85	75.10	226.60	117.36	7.14	7.27	2.09	10.70	2.74
96	1/2	11/15	8.27	14.46	76.59	228.26	120.27	6.88	7.85	2.14	11.01	2.55
459	1/5	11/18	8.27	14.62	75.36	223.51	119.82	9.05	7.90	2.07	8.85	2.70
8988	11/13	12/16	8.27	15.52	74.66	225.17	117.39	6.51	7.02	2.01	3.32	2.51
1302	1/12	11/15	8.27	14.99	75.79	232.14	119.27	6.62	6.53	2.17	7.37	2.65
4648	3/14	5/10	8.27	14.63	74.74	227.85	112.75	4.73	8.96	2.21	3.40	2.99
4371	3/11	5/6	8.27	14.29	75.96	226.17	121.39	9.97	6.77	2.27	3.58	2.97
2059	2/3	5/10	8.27	14.41	74.70	229.72	117.07	12.38	10.42	2.12	27.94	2.92
1904	1/17	11/16	8.27	15.07	75.85	233.48	123.34	7.00	7.29	2.03	8.40	2.71
2168	2/4	5/14	8.27	14.36	74.63	222.45	109.05	5.82	8.60	2.11	17.31	2.88
1556	1/14	15/17	8.27	14.15	75.95	225.25	113.45	3.45	10.26	2.09	7.19	2.89
1784	1/16	11/17	8.26	14.60	75.53	234.44	123.91	5.92	9.66	2.01	6.82	2.59
85	1/2	10/11	8.26	14.57	75.75	230.39	118.78	8.83	7.53	2.11	33.39	2.67
5149	4/5	13/14	8.26	14.93	75.57	227.27	110.66	6.66	12.69	2.21	3.80	2.78
4568	3/13	6/10	8.26	14.15	75.39	224.05	111.93	8.14	6.74	2.24	5.00	2.82
3729	3/4	5/14	8.26	14.29	74.86	222.08	111.71	5.17	7.62	2.14	4.27	3.01
1544	1/14	11/17	8.26	13.96	75.75	235.43	120.36	3.43	8.48	2.06	6.44	2.80
5934	4/15	13/14	8.26	15.47	75.38	224.01	113.34	7.36	11.57	2.12	1.68	2.67
6017	4/16	14/17	8.26	15.15	74.45	228.48	118.35	3.46	7.89	2.09	3.27	2.99
6316	5/8	6/14	8.26	15.12	75.72	224.99	110.10	4.41	6.74	2.22	6.61	2.57
6778	5/15	6/13	8.26	15.85	75.17	226.61	114.32	5.21	10.47	2.20	5.33	2.46
168	1/3	6/12	8.25	14.86	75.54	219.97	113.40	10.55	5.62	2.21	5.64	2.95
3092	2/13	3/5	8.25	14.33	75.27	220.66	109.99	7.03	10.24	2.15	16.19	2.67
6951	5/17	11/14	8.25	14.65	76.06	228.90	116.26	2.92	9.07	2.10	5.19	2.97
5564	4/11	5/17	8.25	14.85	75.32	225.53	117.41	4.52	7.89	2.14	4.96	2.98
5544	4/10	14/15	8.25	15.29	74.83	227.10	113.69	3.69	8.03	2.04	3.28	2.95
4570	3/13	6/12	8.25	14.92	75.31	215.70	109.33	8.98	4.43	2.16	1.16	2.72
4116	3/8	6/14	8.25	14.41	75.43	217.56	109.41	7.12	4.29	2.20	5.00	2.88
4878	3/16	10/13	8.25	14.88	74.69	224.01	116.93	3.63	8.14	2.12	2.08	2.70
6828	5/15	13/14	8.25	15.60	75.98	222.30	108.48	3.19	8.88	2.16	2.02	2.58
1542	1/14	11/15	8.25	14.87	76.68	226.71	118.75	6.03	6.96	2.09	7.07	2.63
1749	1/16	7/11	8.25	14.77	75.06	236.40	121.08	7.96	5.38	2.13	20.12	2.57
1781	1/16	11/13	8.24	14.65	75.66	226.64	115.99	6.71	6.50	1.97	6.01	2.43
576	1/6	11/15	8.24	15.33	75.91	229.18	122.02	7.28	7.84	2.16	7.00	2.59
Entry	Parent 1	Parent 2	GY	MOI	AD	PH	EH	SL	ER	TURC	HC	TEX
2387	2/6	5/11	8.24	14.53	75.80	228.38	120.45	6.51	8.64	2.24	21.91	2.68
1480	1/14	4/16	8.24	14.66	75.00	228.37	116.85	7.39	7.72	2.13	9.02	2.94

4021	3/7	6/10	8.24	13.73	73.81	222.94	110.62	6.47	6.48	2.29	6.74	3.03
2362	2/6	3/11	8.24	14.23	76.34	221.87	117.36	7.58	6.74	2.30	7.89	2.85
4377	3/11	5/13	8.24	14.12	75.38	219.84	115.95	5.54	7.58	2.10	3.37	2.68
4387	3/11	6/12	8.24	14.81	75.98	226.30	119.84	10.21	5.61	2.29	1.97	2.96
3234	2/14	5/18	8.24	14.74	75.19	228.24	109.48	7.00	7.90	2.10	26.94	2.66
93	1/2	11/12	8.24	14.66	75.51	225.95	118.81	6.92	4.03	2.17	7.84	2.50
173	1/3	6/17	8.24	13.99	75.41	221.31	111.35	8.19	8.95	2.12	9.82	3.07
1902	1/17	11/14	8.23	14.42	75.90	232.53	115.81	6.42	6.21	2.07	8.51	2.76
3892	3/5	13/18	8.23	15.00	74.35	222.95	113.67	5.11	8.23	2.03	2.77	2.56
1300	1/12	11/13	8.23	15.19	75.37	224.81	113.27	6.29	6.06	2.02	4.86	2.50
169	1/3	6/13	8.23	14.22	75.70	219.87	108.30	9.06	7.23	2.08	7.42	2.80
3825	3/5	6/7	8.22	14.81	75.39	226.76	113.84	11.90	7.19	2.14	16.83	2.82
8460	8/16	11/14	8.22	14.74	74.85	230.08	118.20	4.74	5.62	2.03	4.95	2.44
4007	3/7	5/6	8.22	13.95	74.09	226.61	108.55	11.39	5.73	2.20	10.99	2.92
5843	4/14	10/17	8.22	14.51	73.93	226.67	112.45	5.57	6.72	2.18	4.39	3.19
3233	2/14	5/17	8.22	14.32	75.45	227.26	108.71	6.24	8.49	2.09	19.20	3.02
2171	2/4	5/17	8.22	14.51	74.71	223.88	109.86	7.83	7.30	2.13	18.96	3.03
2327	2/5	10/18	8.22	14.97	74.58	231.07	115.54	8.41	9.67	1.94	27.64	2.62
1558	1/14	16/17	8.22	13.82	74.95	232.19	117.34	4.22	9.07	2.09	9.78	2.97
395	1/5	4/11	8.22	14.58	76.17	227.54	118.65	8.95	7.49	2.12	7.02	2.79
353	1/4	14/17	8.21	14.50	74.96	225.20	110.94	3.61	8.90	2.21	8.20	2.91
2067	2/3	5/18	8.21	14.32	74.68	226.91	113.28	10.90	7.43	2.03	26.92	2.71
293	1/4	6/17	8.21	14.51	75.33	225.43	114.83	6.30	9.22	2.18	9.41	3.08
2172	2/4	5/18	8.21	14.16	74.86	228.93	112.17	8.09	7.19	2.03	31.64	2.67
3804	3/4	14/17	8.21	14.79	74.20	216.29	110.44	1.76	6.63	2.10	6.10	3.16
6012	4/16	13/14	8.21	14.75	75.05	226.87	116.38	8.58	10.86	2.05	4.01	2.81
3075	2/12	11/18	8.21	14.67	74.64	228.55	117.21	5.56	6.37	2.11	18.93	2.53
4654	3/14	5/17	8.21	14.26	74.89	226.32	108.54	4.67	7.31	2.07	3.09	3.00
3227	2/14	5/10	8.21	14.75	75.10	228.63	111.22	9.63	9.59	2.09	27.87	2.91
3098	2/13	3/11	8.21	14.06	75.76	215.55	111.92	3.16	7.55	2.14	7.69	2.56
3732	3/4	5/17	8.21	14.46	74.15	222.94	109.69	6.26	6.13	2.12	2.85	3.01
6884	5/16	11/13	8.21	14.86	75.62	226.50	120.17	4.82	9.40	2.13	5.53	2.58
2243	2/4	14/17	8.21	14.99	74.52	221.33	111.98	2.80	6.66	2.15	10.68	3.05
5997	4/16	10/14	8.21	14.72	74.49	226.41	116.81	6.24	7.54	2.19	4.22	2.95
6782	5/15	6/18	8.21	15.79	75.12	221.89	113.15	6.49	9.72	2.02	4.73	2.50
1555	1/14	15/16	8.21	14.73	75.87	223.47	115.73	6.82	7.55	2.12	10.40	2.81
4428	3/11	12/13	8.21	14.64	75.40	219.98	114.40	5.79	6.42	2.13	1.77	2.67
1903	1/17	11/15	8.21	14.73	76.33	229.10	120.95	7.61	7.89	2.12	10.94	2.83
5885	4/15	6/14	8.20	15.37	75.37	221.84	113.02	6.90	8.81	2.14	1.42	2.85
5391	4/8	14/18	8.20	14.68	74.48	229.96	117.65	4.63	7.10	2.08	7.11	2.55
7988	7/14	10/17	8.20	14.08	73.50	232.95	113.43	0.63	6.83	2.22	7.75	3.08
6624	5/12	11/18	8.20	15.08	74.37	224.19	119.03	5.61	8.14	2.08	3.75	2.68
5620	4/11	13/17	8.20	14.63	75.20	222.22	113.86	7.33	9.57	2.07	4.23	2.83
4392	3/11	6/17	8.20	14.51	75.48	225.25	117.25	7.52	5.78	2.11	3.89	3.00
6644	5/13	6/11	8.20	14.37	76.38	217.24	115.04	4.16	7.91	2.16	7.76	2.52
6854	5/16	7/13	8.20	15.17	74.81	232.96	114.00	4.86	7.36	2.18	11.80	2.63
3597	2/17	11/14	8.20	14.31	75.36	227.79	116.00	1.65	7.35	2.09	10.39	2.86
1062	1/10	12/15	8.20	15.51	75.05	222.49	111.27	3.70	7.87	2.10	7.07	2.70
6894	5/16	13/14	8.20	14.88	75.65	225.16	111.52	4.41	8.18	2.10	4.35	2.72
3483	2/16	10/11	8.20	14.82	75.20	232.44	122.74	7.10	8.29	2.16	19.73	2.59
7505	6/15	10/13	8.20	15.40	74.83	224.80	110.62	3.93	7.47	2.06	5.04	2.38
6563	5/11	13/18	8.20	14.70	75.17	223.30	114.31	2.70	7.60	2.04	2.78	2.42
1543	1/14	11/16	8.20	14.54	75.68	233.65	122.64	6.79	5.77	2.09	9.65	2.71
6834	5/15	14/18	8.20	15.54	75.94	217.58	107.31	4.47	8.14	1.98	1.42	2.62
2244	2/4	14/18	8.20	14.64	74.66	226.37	114.29	3.06	6.54	2.05	23.36	2.69
2439	2/6	11/18	8.20	14.64	75.47	229.22	119.29	3.13	5.62	2.18	19.06	2.50
7987	7/14	10/16	8.20	14.46	73.80	233.91	117.12	2.28	5.83	2.22	7.22	2.96
6812	5/15	10/13	8.20	15.59	75.51	228.90	112.61	1.61	10.45	2.16	2.69	2.58
3829	3/5	6/11	8.20	14.49	77.20	223.92	118.38	9.48	8.75	2.23	7.66	2.90
1293	1/12	10/11	8.20	15.01	75.29	227.58	114.89	6.67	7.66	2.15	18.14	2.80
356	1/4	15/17	8.19	14.73	75.63	223.96	114.78	5.87	9.17	2.10	7.82	2.98
9136	13/14	15/16	8.19	15.42	75.46	221.90	114.19	5.11	7.05	2.01	2.23	2.61
5546	4/10	14/17	8.19	14.69	73.99	225.06	114.10	1.93	8.01	2.17	2.74	3.20
6619	5/12	11/13	8.19	15.40	75.33	224.68	117.45	4.40	8.96	2.18	4.38	2.65
6852	5/16	7/11	8.19	15.05	74.82	235.88	121.61	5.66	7.91	2.19	14.27	2.68
8881	10/14	15/16	8.19	15.16	75.30	224.35	114.56	3.39	7.09	2.07	3.39	2.76
6921	5/17	7/14	8.19	14.70	74.54	233.58	109.27	3.60	7.69	2.17	13.63	2.94
6222	5/6	11/18	8.19	15.05	75.20	224.87	121.10	3.18	7.38	2.15	3.88	2.65
6885	5/16	11/14	8.19	14.77	75.66	228.08	119.13	5.21	8.73	2.11	6.83	2.76
5252	4/7	5/17	8.19	14.89	73.80	230.21	110.42	5.20	6.50	2.21	13.40	2.95
4573	3/13	6/16	8.19	14.13	76.20	216.04	110.75	12.11	5.50	2.16	4.42	2.72
6119	4/18	6/14	8.19	14.96	75.32	226.91	115.28	4.28	6.51	2.26	2.04	2.84
6350	5/8	11/14	8.19	15.00	76.14	224.34	113.41	2.97	6.89	2.14	4.45	2.55
999	1/10	4/15	8.19	14.97	75.69	223.65	111.74	9.74	8.36	2.12	9.12	2.85
3919	3/6	5/10	8.19	14.54	74.47	228.79	117.58	7.78	9.50	2.18	9.39	2.77
1473	1/14	4/8	8.18	14.90	75.71	227.49	111.87	5.29	7.67	2.13	8.93	2.65
1428	1/13	12/16	8.18	15.53	74.48	220.33	113.15	5.70	5.13	2.03	5.14	2.54
6855	5/16	7/14	8.18	15.08	74.85	234.54	112.95	5.25	6.69	2.16	13.09	2.82
2257	2/5	3/11	8.18	14.25	76.18	222.17	118.25	5.76	9.20	2.26	9.08	2.79
4376	3/11	5/12	8.18	14.83	75.82	226.61	120.73	8.38	8.06	2.25	3.16	2.90
5575	4/11	6/17	8.18	15.03	75.41	229.37	120.73	5.63	6.05	2.17	3.48	3.01
1869	1/17	7/11	8.18	14.67	75.20	233.33	118.34	6.93	6.08	2.10	21.47	2.77
3651	2/18	5/14	8.18	14.81	74.22	222.77	111.03	5.77	7.94	2.06	16.97	2.70
3617	2/18	3/5	8.18	14.67	74.79	218.26	111.06	8.56	9.16	2.04	16.06	2.74
3228	2/14	5/11	8.18	14.44	76.08	227.85	113.17	4.86	8.57	2.17	18.46	2.73
690	1/7	10/16	8.18	14.41	74.32	231.24	113.61	3.56	6.08	2.28	21.96	2.87
4854	3/16	7/13	8.18	15.19	74.83	227.30	115.71	5.74	5.60	2.04	2.57	2.62
35	1/2	5/11	8.18	13.99	75.54	218.62	114.53	7.70	8.46	2.20	31.18	2.62
5290	4/7	10/17	8.18	14.60	73.49	225.08	112.22	5.54	5.93	2.30	9.50	3.09
1475	1/14	4/10	8.18	14.61	74.63	226.89	111.17	4.66	8.58	2.14	15.87	3.00
414	1/5	6/18	8.18	14.78	75.09	222.33	114.54	9.28	9.53	2.09	13.77	2.74
3797	3/4	13/14	8.18	14.58	74.96	221.05	113.34	6.96	11.03	2.07	5.25	2.87
3728	3/4	5/13	8.17	14.24	74.91	227.71	112.59	11.46	10.53	2.09	2.00	2.72
4437	3/11	13/17	8.17	14.34	74.89	218.92	111.81	3.10	6.59	1.94	3.69	2.70
1304	1/12	11/17	8.17	14.27	75.46	228.33	118.57	6.38	8.45	2.18	6.25	2.87
3384	2/15	10/18	8.17	15.38	75.63	229.07	113.34	8.11	8.07	1.91	28.37	2.52
1383	1/13	6/16	8.17	14.80	75.90	221.66	113.35	6.88	7.30	2.11	10.92	2.62
1782	1/16	11/14	8.17	14.54	75.51	231.71	118.67	8.71	5.87	2.08	10.15	2.55
1022	1/10	6/15	8.17	15.04	75.28	226.13	113.37	5.93	9.36	2.08	13.74	2.71
6779	5/15	6/14	8.17	15.64	76.02	220.51	110.10	6.43	9.63	2.13	5.76	2.66
1979	1/18	6/11	8.17	15.03	76.32	229.12	120.73	6.25	6.18	2.12	9.40	2.54
815	1/8	11/14	8.17	14.78	75.99	227.97	112.96	6.47	4.03	2.11	7.77	2.33
1356	1/13	4/11	8.17	14.36	76.04	224.23	115.10	11.75	9.17	2.05	6.29	2.64
5016	3/18	5/14	8.17	14.75	74.44	222.40	113.70	5.12	6.96	2.09	3.92	2.83
4569	3/13	6/11	8.17	13.96	76.96	216.46	109.23	7.78	5.87	2.14	2.27	2.67

Entry	Parent 1	Parent 2	GY	MOI	AD	PH	EH	SL	ER	TURC	HC	TEX
3779	3/4	10/14	8.17	14.61	74.65	219.42	114.25	5.30	8.97	2.19	7.32	3.13
4010	3/7	5/10	8.17	14.32	73.94	231.73	115.65	5.98	8.93	2.22	16.48	2.88

4572	3/13	6/15	8.17	14.83	75.71	219.26	110.32	9.84	5.42	2.14	3.06	2.74
6966	5/17	14/18	8.17	14.30	74.53	220.67	106.76	2.97	7.98	2.05	1.81	2.73
6111	4/18	5/17	8.16	14.50	73.79	217.30	107.91	4.56	6.80	2.09	1.58	2.74
454	1/5	11/13	8.16	14.53	76.33	226.14	116.05	4.61	8.44	2.14	7.06	2.57
3725	3/4	5/10	8.16	14.28	74.60	226.07	113.50	9.81	8.47	2.21	4.07	2.97
3888	3/5	13/14	8.16	14.71	75.56	219.34	108.49	2.79	8.35	2.12	5.59	2.78
1523	1/14	8/17	8.16	14.06	75.66	231.31	112.36	2.12	9.02	2.09	9.68	2.68
5494	4/10	6/14	8.16	14.61	74.21	229.03	114.66	5.50	7.85	2.15	4.97	2.96
4754	3/15	6/14	8.16	14.92	75.73	213.08	109.41	9.15	7.18	2.12	4.16	2.97
5710	4/13	5/6	8.16	14.36	75.87	224.72	109.75	6.37	7.36	2.20	2.38	2.67
4803	3/15	13/14	8.16	15.25	75.37	216.08	111.16	3.49	7.22	2.03	3.47	2.67
2918	2/11	5/17	8.16	14.58	75.88	226.49	118.31	7.27	9.41	2.08	21.18	2.95
5918	4/15	10/13	8.16	15.45	75.07	226.24	112.13	10.46	11.01	2.11	4.37	2.66
172	1/3	6/16	8.16	14.17	75.99	221.45	114.37	13.65	6.91	2.25	13.39	2.99
4297	3/10	6/13	8.16	14.14	74.50	226.50	111.82	9.83	6.12	2.12	6.53	2.75
4028	3/7	6/17	8.16	13.97	73.66	221.44	106.11	6.87	4.40	2.20	3.77	3.06
6629	5/12	13/18	8.16	15.40	73.22	220.98	111.00	3.38	7.00	1.99	1.93	2.48
338	1/4	11/17	8.15	14.50	75.94	225.65	117.22	5.10	7.76	2.17	6.43	2.87
1538	1/14	10/17	8.15	13.77	74.58	230.71	111.67	1.48	9.93	2.10	16.63	3.04
5483	4/10	5/14	8.15	14.62	74.83	229.35	113.00	2.37	9.76	2.18	1.99	2.98
1900	1/17	11/12	8.15	14.85	75.10	225.94	118.04	6.05	5.29	2.09	3.98	2.78
6977	5/18	6/14	8.15	15.22	75.97	225.57	112.35	3.82	7.33	2.26	6.39	2.65
2919	2/11	5/18	8.15	14.52	75.72	229.53	119.10	7.48	8.52	2.05	28.64	2.57
2250	2/4	17/18	8.15	14.79	74.74	227.81	115.11	5.07	5.25	2.06	25.01	2.84
6320	5/8	6/18	8.15	15.02	74.45	226.00	114.73	7.58	7.43	2.11	5.27	2.40
8852	10/13	12/15	8.15	16.29	74.19	222.07	109.27	1.97	7.57	2.02	3.38	2.56
1521	1/14	8/15	8.15	14.97	76.58	222.59	110.75	4.72	7.50	2.12	10.31	2.51
2023	1/18	11/15	8.15	15.18	77.13	228.25	120.11	6.43	6.90	2.06	6.86	2.46
1359	1/13	4/15	8.15	15.21	75.93	227.14	113.94	10.91	11.70	2.13	6.41	2.65
6518	5/11	6/18	8.15	15.22	75.43	230.82	123.12	4.71	7.57	2.09	6.04	2.49
2993	2/12	3/11	8.15	14.77	76.20	222.31	116.70	6.00	8.03	2.29	7.47	2.78
4788	3/15	10/14	8.15	15.05	75.46	217.35	112.00	2.46	8.53	2.07	6.49	2.93
6816	5/15	10/18	8.15	15.53	75.47	224.17	111.44	2.89	9.70	1.98	2.10	2.63
2060	2/3	5/11	8.15	14.13	76.21	227.90	115.53	8.31	9.06	2.18	17.62	2.77
5153	4/5	13/18	8.15	14.81	74.82	228.28	115.35	7.70	11.33	2.09	8.15	2.61
4699	3/14	10/17	8.15	14.26	73.95	228.14	113.44	1.49	8.38	2.10	4.16	3.11
5027	3/18	6/14	8.14	14.51	75.68	218.15	111.67	6.53	4.88	2.24	4.78	2.96
1413	1/13	10/11	8.14	14.07	75.43	225.40	112.10	5.00	5.66	2.09	18.20	2.61
6188	5/6	7/18	8.14	14.72	73.33	225.31	108.26	4.60	6.35	2.09	11.30	2.60
1057	1/10	11/16	8.14	14.92	75.35	230.59	123.50	5.16	5.28	2.13	14.35	2.68
5365	4/8	10/14	8.14	14.82	74.37	216.05	109.98	6.80	7.61	2.10	3.82	2.76
4381	3/11	5/17	8.14	14.52	75.31	225.55	118.14	5.70	8.23	2.07	5.08	2.93
515	1/6	4/11	8.14	14.76	76.25	231.38	121.97	10.06	5.65	2.15	5.54	2.82
5014	3/18	5/12	8.14	14.83	73.71	222.91	114.28	7.36	6.11	2.07	0.71	2.72
4557	3/13	5/10	8.14	14.37	74.75	231.75	115.30	5.31	9.24	2.25	5.17	2.79
8032	7/15	10/16	8.14	14.98	75.02	230.78	113.35	6.84	7.50	2.20	6.01	2.77
1518	1/14	8/11	8.14	14.78	76.39	232.77	117.66	4.69	5.72	2.09	9.56	2.42
715	1/7	15/16	8.14	14.71	74.96	232.20	115.94	6.42	6.28	2.32	11.74	2.72
1536	1/14	10/15	8.14	14.68	75.51	221.99	110.06	4.09	8.42	2.13	17.25	2.87
3126	2/13	5/15	8.14	14.89	75.42	227.49	112.52	6.91	10.33	2.12	13.61	2.53
2664	2/8	14/18	8.14	14.51	74.20	227.26	112.24	5.92	6.11	1.97	18.06	2.37
6513	5/11	6/13	8.14	14.58	75.91	224.63	117.53	3.15	7.95	2.21	6.74	2.56
5092	4/5	6/13	8.14	14.68	75.98	228.88	115.34	10.88	11.93	2.23	7.03	2.75
7536	6/16	7/13	8.14	14.58	74.53	224.54	109.51	3.84	4.46	2.16	1.12	2.57
4280	3/10	5/6	8.14	14.16	75.09	226.81	113.28	10.87	8.13	2.18	4.42	2.94
818	1/8	11/17	8.14	14.53	76.28	227.79	118.11	4.85	9.24	2.03	5.94	2.59
3492	2/16	11/14	8.14	14.43	74.96	226.97	118.87	3.93	7.01	2.10	12.02	2.65
5561	4/11	5/14	8.14	14.58	75.71	229.12	118.66	2.86	8.87	2.17	3.68	2.84
2645	2/8	11/14	8.14	14.67	75.44	223.23	113.15	1.70	5.17	2.13	9.65	2.44
3018	2/12	5/11	8.14	14.37	74.99	224.04	114.03	6.89	8.67	2.23	17.83	2.81
5170	4/6	5/13	8.14	14.49	75.92	225.10	111.69	10.07	10.86	2.15	6.38	2.56
1424	1/13	11/17	8.13	14.02	75.25	223.33	114.05	4.29	8.01	2.03	5.68	2.71
6081	4/17	11/14	8.13	14.54	75.75	229.28	116.30	2.43	8.41	2.11	2.77	3.00
171	1/3	6/15	8.13	14.48	76.16	220.59	113.08	11.84	7.31	2.16	11.77	3.08
1076	1/10	15/17	8.13	14.30	75.71	225.86	113.90	2.92	11.00	2.08	8.23	2.90
455	1/5	11/14	8.13	14.81	76.80	225.96	113.88	6.94	7.14	2.19	9.64	2.66
1533	1/14	10/11	8.13	14.49	75.31	232.17	116.97	4.06	6.63	2.10	16.51	2.77
5263	4/7	6/17	8.13	14.49	73.59	225.56	109.59	4.97	4.67	2.27	3.36	3.07
8806	10/11	12/16	8.13	15.26	74.74	229.63	118.86	4.94	8.42	2.19	4.48	2.71
5836	4/14	9/17	8.13	14.84	74.87	225.55	111.11	3.40	5.82	2.16	2.56	2.96
5156	4/5	14/17	8.13	14.71	75.05	222.03	108.16	3.33	7.77	2.24	2.42	3.14
1071	1/10	14/15	8.13	14.88	75.59	226.57	109.33	4.42	7.73	2.16	9.77	2.72
4559	3/13	5/12	8.13	15.14	74.67	223.40	112.70	6.15	6.93	2.17	1.33	2.70
368	1/5	2/11	8.13	14.39	77.69	223.24	118.03	8.59	10.72	2.12	19.02	2.77
3927	3/6	5/18	8.13	14.80	75.46	224.24	116.16	7.71	6.86	2.19	6.37	2.69
7566	6/16	11/13	8.13	14.86	75.65	226.56	119.83	5.13	6.50	2.08	3.40	2.42
5861	4/14	15/17	8.13	15.00	75.32	222.69	112.35	5.51	6.43	2.04	2.41	3.06
1380	1/13	6/12	8.13	15.45	74.91	218.40	110.67	5.05	6.07	2.05	5.92	2.48
7960	7/13	15/16	8.13	15.40	74.55	230.63	114.40	4.71	5.78	2.21	3.57	2.52
4851	3/16	7/10	8.13	15.20	74.60	231.61	119.18	3.54	6.92	2.23	3.10	2.82
5383	4/8	13/14	8.13	14.48	75.16	226.62	110.36	6.42	10.60	2.10	2.99	2.61
5175	4/6	5/18	8.13	14.65	75.64	226.26	115.05	4.91	6.62	2.19	11.09	2.65
1416	1/13	10/15	8.13	14.92	75.33	228.31	110.94	4.15	8.19	2.16	18.32	2.62
4027	3/7	6/16	8.13	13.95	74.62	224.33	110.53	10.61	4.07	2.30	3.59	2.94
5131	4/5	10/14	8.13	14.94	75.56	224.86	110.64	5.68	10.05	2.21	3.96	2.98
3800	3/4	13/17	8.13	14.75	74.25	221.91	111.32	8.05	9.54	2.06	3.83	2.87
1653	1/15	10/11	8.13	14.99	75.48	231.31	116.17	3.91	7.73	2.13	18.29	2.58
331	1/4	10/17	8.13	14.28	74.57	222.85	110.46	6.39	9.03	2.18	18.37	3.05
6448	5/10	6/14	8.13	14.88	74.86	227.70	111.74	5.03	8.67	2.14	9.32	2.76
8418	8/15	10/14	8.13	15.25	75.18	213.99	107.73	3.96	7.17	1.98	2.99	2.56
2386	2/6	5/10	8.13	14.65	74.82	229.57	116.06	12.68	10.13	2.06	33.86	2.69
7524	6/15	13/18	8.12	15.53	76.19	219.78	110.05	3.13	6.45	2.12	0.91	2.33
3025	2/12	6/7	6.45	13.75	75.41	226.67	109.68	6.54	7.00	2.13	19.29	2.64
3667	2/18	7/9	6.43	13.62	75.53	220.86	103.57	7.05	7.06	2.11	10.36	2.31
2616	2/8	7/9	6.42	13.33	75.75	219.68	101.43	8.32	7.81	2.41	10.88	2.43
3033	2/12	6/16	6.42	14.82	76.67	221.61	113.20	4.85	5.80	2.18	14.26	2.76
3037	2/12	7/9	6.37	13.58	74.49	220.14	104.34	5.86	5.92	2.17	13.14	2.40
2932	2/11	7/9	6.36	13.27	76.23	224.12	107.80	6.72	5.92	2.15	10.82	2.37
3060	2/12	9/16	6.34	14.65	75.75	215.07	107.85	4.16	4.72	2.22	8.11	2.52
2478	2/7	4/9	6.30	14.18	75.78	222.70	105.84	7.66	6.64	2.15	4.98	2.60
3552	2/17	6/9	6.30	13.65	75.65	222.76	110.44	2.21	6.51	2.11	13.06	2.60
3027	2/12	6/9	6.28	13.91	76.17	222.09	109.53	1.92	5.17	2.22	9.48	2.43

Appendix 4.3 Grain yield and agronomic trait predictions for exotic x exotic EEDiallel thee-way crosses

Entry	Parent 1	Parent 2	GY	AD	ASI	PH	EH	SL	ER	GLS	TURC	HC	SEN	TEX
239	7/9	1	9.17	72.0	1.4	260.5	131.3	1.9	1.6	1.1	1.4	3.6	2.7	2.9
21	1/4	9	8.85	72.2	1.4	258.5	134.1	4.6	1.5	1.4	1.3	3.7	2.7	3.0
7	1/2	9	8.89	72.9	1.4	257.8	139.1	4.4	1.3	1.3	1.4	3.0	2.7	2.9
28	1/5	9	8.87	73.8	1.4	246.1	136.3	10.9	1.4	1.4	1.3	3.0	2.8	2.9
42	1/7	9	8.96	71.9	1.6	265.0	140.3	12.2	1.9	1.4	1.4	3.0	2.7	3.0
204	5/9	1	8.69	73.2	1.2	248.9	131.2	2.0	1.7	1.9	1.3	2.6	2.9	2.9
99	2/9	1	8.63	72.2	1.7	261.0	136.9	1.7	1.5	1.6	1.3	2.7	3.1	2.8
55	1/9	7	8.88	71.1	1.1	271.5	139.7	12.9	1.9	1.2	1.5	4.0	2.8	3.1
246	8/9	1	8.61	72.2	2.0	257.8	134.2	4.2	1.6	1.2	1.2	4.3	3.0	2.9
176	4/9	1	8.59	71.9	1.8	261.1	132.0	1.6	1.6	1.6	1.3	3.8	2.8	3.0
12	1/3	7	8.65	71.5	0.8	265.4	135.7	2.5	1.4	1.0	1.4	3.3	2.8	2.9
5	1/2	7	8.62	71.9	1.0	266.1	135.4	3.1	1.4	1.1	1.5	3.9	3.0	3.0
190	5/7	1	8.62	72.4	0.7	255.4	130.7	2.7	1.7	1.7	1.4	3.5	3.0	2.9
49	1/8	9	8.58	72.0	1.5	260.9	139.9	11.9	1.5	1.4	1.5	7.9	3.0	2.9
85	2/7	1	8.56	71.5	1.3	267.5	136.3	2.3	1.5	1.4	1.5	3.6	3.2	2.9
205	5/9	2	8.60	73.7	1.2	267.3	149.9	4.8	1.1	1.3	1.6	4.8	3.0	2.9
232	7/8	1	8.54	71.5	1.6	264.2	133.7	4.8	1.6	1.0	1.3	5.2	3.0	3.0
102	2/9	5	8.57	74.5	1.1	255.6	147.1	11.3	1.1	1.5	1.5	4.8	3.1	2.9
70	2/4	9	8.49	72.3	1.0	262.2	141.4	7.7	1.2	1.4	1.5	4.0	2.7	3.1
162	4/7	1	8.52	71.2	1.3	267.5	131.4	2.2	1.6	1.4	1.5	4.7	2.8	3.0
225	6/9	1	8.42	71.7	2.6	253.8	131.4	3.8	1.6	1.3	1.1	2.7	3.1	2.8
154	4/5	9	8.47	73.2	0.9	250.6	138.5	14.3	1.3	1.5	1.5	4.1	2.7	3.1
168	4/7	9	8.56	71.3	1.1	269.5	142.5	15.6	1.8	1.4	1.5	4.1	2.7	3.2
191	5/7	2	8.39	73.5	1.2	269.1	146.7	2.8	1.1	1.3	1.5	4.7	3.2	3.0
77	2/5	9	8.51	73.9	1.0	249.9	143.5	14.1	1.1	1.4	1.5	3.3	2.8	3.0
14	1/3	9	8.44	72.2	1.8	248.0	130.5	2.0	1.7	1.3	1.2	3.7	2.6	2.9
3	1/2	5	8.39	74.0	0.9	258.4	142.0	2.4	1.4	1.9	1.5	4.4	3.2	2.9
91	2/7	9	8.60	72.0	1.2	268.8	147.5	15.4	1.6	1.3	1.5	3.4	2.8	3.1
22	1/5	2	8.33	73.0	1.4	270.5	147.7	2.0	1.3	1.6	1.5	4.5	3.4	2.8
196	5/7	9	8.57	72.9	1.1	257.2	144.7	21.9	1.6	1.5	1.5	3.4	2.8	3.1
149	4/5	2	8.43	73.9	1.3	268.8	149.5	2.2	1.3	1.9	1.6	4.8	3.3	2.9
211	6/7	1	8.34	70.9	2.2	260.3	130.9	4.4	1.6	1.1	1.2	3.7	3.1	2.9
26	1/5	7	8.30	73.2	0.9	260.4	134.5	2.9	1.4	1.2	1.4	5.1	2.9	2.9
240	7/9	2	8.34	72.8	1.0	263.4	143.2	5.6	1.1	1.3	1.5	3.3	3.0	3.0
160	4/6	8	8.37	72.0	4.0	269.2	146.7	5.5	1.2	1.3	1.3	2.8	3.6	2.8
34	1/6	8	8.31	71.6	3.0	263.8	143.1	6.7	1.4	1.2	1.3	4.4	3.5	3.0
35	1/6	9	8.31	71.9	2.1	254.8	138.8	13.3	1.4	1.2	1.4	2.8	2.8	2.9
101	2/9	4	8.33	72.5	1.1	263.8	141.0	5.1	1.4	1.9	1.5	4.0	3.0	3.0
50	1/9	2	8.28	72.3	1.3	264.8	144.1	4.9	1.2	1.6	1.5	3.1	3.1	2.9
249	8/9	4	8.27	72.0	2.6	267.7	140.1	6.4	1.2	1.4	1.3	3.7	3.1	2.9
53	1/9	5	8.31	74.2	0.7	241.1	135.7	11.7	1.4	2.0	1.4	3.0	3.0	2.9
146	3/9	7	8.43	71.4	1.0	270.0	144.7	12.9	1.7	1.3	1.4	2.8	2.8	3.0
104	2/9	7	8.40	71.8	1.2	270.7	144.4	13.4	1.6	1.3	1.5	3.3	3.0	3.1
177	4/9	2	8.38	73.2	1.2	263.2	146.0	5.0	1.2	1.8	1.6	3.3	3.0	3.0
52	1/9	4	8.19	71.3	1.3	265.5	134.2	4.9	1.5	1.7	1.5	4.8	2.8	3.1
141	3/9	1	8.27	71.9	1.3	250.0	129.4	2.4	1.7	1.5	1.2	2.6	2.7	3.0
231	6/9	8	8.28	71.4	2.6	266.9	148.7	14.4	1.4	1.4	1.5	8.0	3.4	3.0
175	4/8	9	8.18	71.4	1.1	265.4	142.1	15.2	1.4	1.4	1.6	8.9	2.9	3.1
61	2/3	7	8.16	72.2	0.9	264.6	140.4	3.1	1.2	1.2	1.3	2.7	3.0	2.9
138	3/8	6	8.15	71.1	4.0	261.1	140.8	4.4	1.4	1.4	1.4	2.8	3.4	3.1
184	5/6	2	8.11	73.4	1.7	269.2	147.3	2.4	1.1	1.2	1.5	4.7	3.4	3.0
19	1/4	7	8.32	71.4	1.2	267.6	134.2	2.4	1.6	1.3	1.4	3.4	3.0	3.1
98	2/8	9	8.23	72.1	1.1	264.7	147.1	15.1	1.2	1.3	1.6	8.2	3.0	3.0
96	2/8	6	8.11	72.1	3.0	265.7	145.4	4.5	1.2	1.2	1.4	2.9	3.6	3.1
36	1/7	2	8.08	72.1	1.3	266.6	141.0	2.8	1.3	1.6	1.4	3.0	3.3	2.9
198	5/8	2	8.11	73.6	1.7	270.7	153.5	2.3	1.1	1.5	1.6	4.7	3.4	2.8
47	1/8	6	8.12	71.1	3.7	259.8	140.3	6.3	1.5	1.3	1.2	2.8	3.5	2.9
71	2/5	1	8.07	72.7	1.0	256.0	136.3	2.4	1.6	2.2	1.4	2.7	3.4	2.8
88	2/7	5	8.08	74.7	1.1	263.4	145.8	2.6	1.2	1.4	1.5	6.0	3.1	2.9
95	2/8	5	8.25	74.8	2.0	274.8	153.7	4.5	1.2	1.3	1.4	4.8	3.3	2.8
83	2/6	8	8.11	72.2	3.0	267.3	151.7	4.5	1.3	1.5	1.5	3.0	3.6	2.9
127	3/7	1	8.19	71.1	0.8	256.5	128.8	3.0	1.7	1.3	1.4	3.5	2.8	3.0
188	5/6	8	8.25	73.4	3.3	271.3	151.8	6.7	1.3	1.2	1.3	3.1	3.5	2.9
203	5/8	9	8.20	72.9	1.1	253.0	144.3	21.6	1.3	1.5	1.6	8.3	3.0	3.0
163	4/7	2	8.18	73.0	1.2	265.0	142.8	3.0	1.3	1.8	1.5	3.3	3.2	3.0
238	7/8	9	8.29	71.1	1.3	271.9	148.3	22.9	1.8	1.4	1.6	8.3	3.0	3.1
197	5/8	1	8.05	72.6	1.3	252.7	133.6	5.0	1.6	1.8	1.3	4.3	3.2	2.9
173	4/8	6	8.06	71.5	3.8	266.1	145.5	4.2	1.5	1.3	1.5	2.8	3.6	3.2
15	1/4	2	8.11	72.5	1.4	266.4	143.7	2.2	1.4	2.1	1.5	3.1	3.4	2.9
226	6/9	2	8.06	72.7	1.6	263.5	143.8	5.2	1.0	1.2	1.5	3.2	3.1	3.1
148	4/5	1	8.03	72.3	1.1	256.0	131.4	2.4	1.7	2.2	1.4	3.8	3.0	3.0
92	2/8	1	7.99	71.7	1.9	264.8	139.3	4.6	1.4	1.5	1.3	4.4	3.4	2.9
247	8/9	2	8.05	72.9	1.6	265.0	150.0	5.2	1.1	1.5	1.6	3.2	3.1	2.9
228	6/9	4	7.96	71.5	2.3	264.6	138.9	5.0	1.5	1.4	1.5	3.8	3.1	3.2
112	3/4	9	8.04	71.7	1.4	252.5	132.8	5.3	1.6	1.3	1.3	4.7	2.6	3.1
94	2/8	4	8.15	72.8	2.8	268.6	144.7	3.6	1.2	1.8	1.4	3.0	3.4	2.7
64	2/4	1	7.97	71.4	1.6	268.1	137.0	2.0	1.5	1.9	1.4	3.9	3.2	3.0
125	3/6	8	8.05	71.3	3.0	264.1	147.5	3.0	1.3	1.4	1.4	3.7	3.5	2.9
20	1/4	8	8.03	72.0	3.2	267.0	140.3	6.0	1.3	1.2	1.2	4.4	3.4	2.8
2	1/2	4	8.07	72.2	1.5	266.4	138.8	2.2	1.5	2.1	1.5	4.1	3.1	3.0
243	7/9	5	7.99	74.9	0.9	246.1	139.5	11.9	1.2	1.5	1.4	4.5	2.9	2.9
63	2/3	9	8.08	72.3	1.4	251.8	137.8	5.2	1.4	1.2	1.3	4.0	2.6	3.0
250	8/9	5	8.17	75.0	1.8	257.4	147.3	13.9	1.2	1.3	1.4	3.4	3.1	2.9
45	1/8	4	8.01	71.7	2.9	270.3	138.0	3.4	1.3	1.6	1.3	3.9	3.2	2.8
169	4/8	1	7.95	71.3	1.9	264.8	134.4	4.5	1.6	1.5	1.3	5.5	3.1	3.1
251	8/9	6	8.01	71.3	3.1	260.8	147.7	15.8	1.3	1.2	1.5	2.8	3.3	3.0
209	5/9	7	8.08	73.1	1.1	265.0	143.5	13.2	1.7	1.5	1.4	4.6	2.9	3.0
213	6/7	3	7.92	71.2	2.4	260.1	136.3	2.6	1.3	1.3	1.3	2.5	3.0	3.0
119	3/5	9	8.06	73.2	1.3	240.2	135.0	11.7	1.4	1.4	1.3	4.0	2.7	3.0
81	2/6	5	7.77	73.8	1.8	271.1	151.3	1.3	1.6	1.2	1.4	5.3	3.2	3.0
161	4/6	9	7.91	71.4	1.6	259.3	141.1	16.6	1.3	1.3	1.5	3.8	2.8	3.1
212	6/7	2	7.86	72.6	1.6	265.3	140.6	3.2	1.1	1.2	1.4	3.2	3.3	3.1
182	4/9	8	8.00	71.7	2.7	270.1	145.9	13.7	1.2	1.3	1.5	7.9	3.4	2.8
56	1/9	8	7.95	71.4	1.7	264.7	142.2	14.8	1.4	1.2	1.4	9.5	3.3	3.0
33	1/6	7	8.02	71.3	1.8	266.1	134.6	7.1	1.6	1.0	1.5	3.6	3.1	3.1
133	3/7	9	8.15	71.3	1.5	259.1	139.0	13.0	1.9	1.3	1.3	4.1	2.6	3.1
201	5/8	6	7.77	72.5	3.1	267.6	149.4	3.5	1.8	1.2	1.3	3.6	3.4	3.0
242	7/9	4	8.00	71.6	1.2	265.6	137.0	5.1	1.4	1.6	1.4	3.5	2.9	3.2
48	1/8	7	7.84	72.6	1.5	265.9	143.5	37.4	1.6	1.2	1.5	4.2	3.1	3.1

Entry	Parent 1	Parent 2	GY	AD	ASI	PH	EH	SL	ER	GLS	TURC	HC	SEN	TEX
183	5/6	1	7.86	72.1	2.0	248.7	130.8	4.6	1.7	1.8	1.2	2.7	3.3	2.8
233	7/8	2	7.85	72.7	1.6	266.9	146.9	3.2	1.1	1.4	1.5	3.2	3.3	2.9
117	3/5	7	7.85	73.5	0.8	258.9	139.5	2.9	1.3	1.3	1.3	3.9	2.9	2.9
84	2/6	9	7.96	72.0	1.7	258.6	146.1	16.4	1.1	1.2	1.5	3.1	2.8	3.0
75	2/5	7	7.82	73.9	1.0	259.6	139.2	3.4	1.2	1.4	1.4	4.4	3.1	3.0
29	1/6	2	7.80	72.1	1.9	266.7	141.5	2.4	1.2	1.5	1.4	3.0	3.5	3.0
39	1/7	5	7.82	74.4	0.7	248.9	134.4	3.0	1.5	2.0	1.4	4.1	3.1	2.9
46	1/8	5	7.99	74.4	1.6	260.2	142.3	4.9	1.5	1.8	1.3	3.0	3.2	2.8
78	2/6	1	7.80	71.1	2.5	260.8	136.4	4.2	1.5	1.6	1.2	2.8	3.5	2.8
156	4/6	2	7.90	72.9	1.7	265.1	143.4	2.6	1.2	1.7	1.5	3.2	3.4	3.0
43	1/8	2	7.79	72.3	1.9	268.3	147.8	2.4	1.3	1.8	1.5	3.0	3.5	2.8
241	7/9	3	7.91	71.7	1.2	253.0	135.0	2.6	1.5	1.2	1.2	3.4	2.7	2.9
189	5/6	9	7.93	72.9	1.6	247.0	143.3	23.0	1.1	1.3	1.5	3.1	2.9	3.0
170	4/8	2	7.89	73.1	1.7	266.6	149.6	2.6	1.3	2.0	1.6	3.2	3.4	2.8
217	6/7	9	8.02	71.0	1.8	265.9	147.3	24.3	1.6	1.3	1.5	3.2	2.8	3.1
218	6/8	1	7.78	71.1	2.8	257.5	133.8	6.7	1.6	1.2	1.1	4.4	3.3	2.9
69	2/4	8	7.83	72.6	3.2	270.5	148.8	3.8	1.1	1.4	1.4	3.0	3.5	2.7
6	1/2	8	7.77	72.2	2.2	265.0	145.2	4.9	1.3	1.4	1.4	4.6	3.4	2.9
181	4/9	7	8.11	71.2	1.4	272.2	143.2	12.8	1.8	1.6	1.4	2.8	3.0	3.2
153	4/5	8	7.97	73.7	3.4	274.5	148.9	6.0	1.1	1.2	1.2	3.1	3.4	2.6
114	3/5	2	7.79	72.5	1.3	262.6	148.6	1.4	1.1	1.7	1.5	4.7	3.2	2.9
27	1/5	8	7.92	73.4	2.4	269.0	145.3	7.1	1.4	1.1	1.2	4.7	3.3	2.9
234	7/8	3	7.82	71.4	1.4	263.0	143.0	1.2	1.2	1.3	1.3	3.4	3.1	2.8
155	4/6	1	7.76	70.8	2.6	260.9	131.5	4.1	1.6	1.6	1.2	3.9	3.1	3.0
229	6/9	5	7.69	74.0	1.6	253.8	144.9	10.7	1.6	1.3	1.4	3.9	3.0	3.0
80	2/6	4	7.85	72.4	2.5	265.5	143.5	2.3	1.5	1.9	1.6	3.1	3.4	3.1
221	6/8	4	7.78	71.8	3.9	269.4	142.7	3.5	1.3	1.3	1.4	2.8	3.5	2.9
31	1/6	4	7.70	71.2	2.7	267.2	136.8	2.0	1.6	1.6	1.5	3.9	3.2	3.2
105	2/9	8	7.74	72.0	1.7	268.2	150.8	12.6	1.3	1.5	1.7	8.2	3.3	2.9
210	5/9	8	7.89	73.2	1.9	272.2	150.9	14.8	1.3	1.3	1.5	8.2	3.3	2.8
110	3/4	7	7.87	71.6	1.0	266.1	139.1	2.5	1.4	1.4	1.2	2.2	3.0	3.1
68	2/4	7	7.84	72.0	1.2	266.8	138.8	3.0	1.3	1.5	1.3	2.7	3.2	3.1
237	7/8	6	7.80	71.5	3.3	265.7	144.0	9.0	1.4	1.2	1.5	2.8	3.6	3.1
111	3/4	8	7.77	71.6	3.2	267.3	144.6	2.4	1.1	1.4	1.3	3.7	3.4	2.7
13	1/3	8	7.71	71.3	2.1	261.8	141.0	3.5	1.3	1.3	1.3	5.3	3.3	2.9
142	3/9	2	7.74	71.9	1.2	256.9	145.1	4.3	1.0	1.6	1.5	3.3	2.9	3.0
216	6/7	8	7.62	72.8	3.0	265.4	152.9	39.2	1.4	1.4	1.4	3.3	3.5	3.1
60	2/3	6	7.62	71.6	3.1	260.8	136.6	2.7	1.2	1.2	1.4	2.9	3.3	3.2
32	1/6	5	7.51	73.4	1.4	256.6	139.9	1.7	1.9	1.7	1.3	3.5	3.2	3.0
37	1/7	3	7.74	71.4	0.7	255.0	133.8	3.1	1.5	1.4	1.2	2.4	2.8	3.0
140	3/8	9	7.77	71.4	1.5	254.9	138.6	12.6	1.6	1.3	1.4	8.9	2.9	3.0
11	1/3	6	7.62	70.6	3.7	254.9	131.5	4.4	1.5	1.3	1.2	2.8	3.2	3.0
113	3/5	1	7.71	72.3	0.6	245.0	128.7	3.2	1.8	2.1	1.3	2.6	3.0	3.0
4	1/2	6	7.58	71.5	2.8	259.5	136.1	4.6	1.3	1.2	1.2	3.0	3.4	2.9
87	2/7	4	7.88	72.4	1.4	266.5	141.6	2.4	1.4	2.1	1.4	2.8	3.2	3.1
219	6/8	2	7.57	72.7	2.2	267.0	147.4	2.8	1.1	1.4	1.5	3.1	3.5	2.9
143	3/9	4	7.61	72.3	1.6	250.9	130.2	5.3	1.6	1.7	1.7	4.0	3.0	3.1
57	2/3	1	7.65	71.3	1.1	257.1	134.4	2.8	1.6	1.8	1.3	2.7	3.1	3.0
235	7/8	4	7.82	71.9	2.8	270.4	140.7	3.6	1.3	1.5	1.2	2.5	3.3	2.9
147	3/9	8	7.69	71.0	1.7	265.0	146.6	11.2	1.3	1.5	1.5	8.8	3.3	2.9
109	3/4	6	7.57	71.0	3.9	261.3	136.7	2.3	1.5	1.4	1.5	2.8	3.3	3.3
227	6/9	3	7.64	71.1	2.9	249.2	130.6	2.6	1.6	1.3	1.3	3.7	2.8	3.1
76	2/5	8	7.71	74.0	2.4	272.5	153.8	4.9	1.2	1.4	1.4	3.3	3.4	2.7
38	1/7	4	7.74	71.2	1.6	268.2	134.8	2.1	1.6	1.8	1.3	3.6	3.0	3.2
67	2/4	6	7.53	72.0	2.9	265.8	141.3	2.5	1.3	1.2	1.5	3.0	3.5	3.2
236	7/8	5	7.68	75.2	1.8	265.2	146.1	5.1	1.3	1.3	1.3	4.5	3.1	2.8
134	3/8	1	7.63	71.3	1.4	253.8	131.8	5.3	1.6	1.4	1.2	4.2	3.0	3.1
18	1/4	6	7.53	71.0	3.5	259.9	136.2	4.2	1.6	1.3	1.3	2.8	3.4	3.1
224	6/8	9	7.65	71.1	1.8	261.7	146.8	23.9	1.3	1.3	1.6	8.0	3.1	3.0
230	6/9	7	7.81	71.1	2.0	270.7	143.6	17.5	1.8	1.3	1.5	3.1	3.1	3.2
106	3/4	1	7.61	71.0	1.2	257.1	129.5	2.7	1.7	1.8	1.4	3.7	2.8	3.1
220	6/8	3	7.56	70.8	3.1	259.2	138.7	1.2	1.3	1.5	1.4	3.6	3.2	3.0
86	2/7	3	7.56	71.3	1.0	258.1	142.2	1.8	1.1	1.6	1.4	2.7	2.9	2.9
128	3/7	2	7.53	71.7	1.2	258.8	141.9	2.3	1.1	1.6	1.5	3.2	3.1	3.0
252	8/9	7	7.63	72.4	1.7	270.4	152.4	47.7	1.8	1.4	1.5	3.7	3.1	3.2
8	1/3	2	7.47	71.2	1.5	260.2	142.9	1.5	1.2	1.9	1.5	3.0	3.3	2.9
145	3/9	6	7.52	70.8	3.2	255.9	138.9	13.9	1.3	1.3	1.5	2.8	3.0	3.1
62	2/3	8	7.51	71.9	2.1	265.3	149.5	1.3	1.1	1.6	1.5	3.9	3.4	2.8
118	3/5	8	7.66	73.1	2.4	269.4	149.7	3.5	1.2	1.3	1.3	3.9	3.3	2.8
103	2/9	6	7.48	71.8	2.2	260.5	143.5	14.0	1.1	1.1	1.5	3.0	3.2	3.0
124	3/6	7	7.57	71.6	1.7	264.6	139.6	7.1	1.4	1.1	1.4	2.5	3.1	3.0
107	3/4	2	7.57	72.1	1.3	258.5	144.7	1.7	1.2	2.2	1.5	3.3	3.2	2.9
82	2/6	7	7.54	72.0	1.9	265.3	139.3	7.7	1.3	1.2	1.5	3.0	3.3	3.1
54	1/9	6	7.48	70.8	2.9	254.6	138.4	15.8	1.4	1.2	1.3	2.9	3.2	2.9
139	3/8	7	7.39	72.8	1.4	264.3	148.4	37.4	1.4	1.3	1.3	3.0	3.1	3.0
97	2/8	7	7.36	73.2	1.6	265.0	148.1	37.9	1.3	1.3	1.4	3.6	3.3	3.1
164	4/7	3	7.48	72.4	1.5	251.3	132.3	2.7	1.5	1.5	1.6	2.7	3.1	3.0
116	3/5	6	7.28	71.9	3.2	262.7	140.6	1.6	1.8	1.2	1.4	3.6	3.1	3.1
248	8/9	3	7.54	71.3	1.9	252.1	137.3	1.3	1.4	1.4	1.3	4.6	2.9	2.9
30	1/6	3	7.47	70.8	2.4	251.2	129.4	3.1	1.6	1.5	1.4	2.6	2.9	3.2
74	2/5	6	7.23	72.9	2.3	267.3	145.2	1.7	1.6	1.1	1.3	3.7	3.3	3.1
152	4/5	7	7.52	73.3	1.2	261.1	137.9	2.8	1.4	1.6	1.3	3.9	3.1	3.1
25	1/5	6	7.24	71.9	2.9	261.4	140.1	3.5	1.9	1.1	1.1	3.6	3.3	2.9
180	4/9	6	7.43	71.2	3.0	260.9	143.6	13.7	1.4	1.2	1.6	2.8	3.2	3.2
126	3/6	9	7.50	71.4	2.0	248.9	137.5	14.0	1.4	1.2	1.4	3.8	2.7	3.0
120	3/6	1	7.43	70.8	2.1	249.8	128.9	4.9	1.7	1.5	1.1	2.7	3.1	3.0
215	6/7	5	7.20	74.2	1.6	261.6	143.7	1.9	1.7	1.3	1.3	5.0	3.1	3.0
222	6/8	5	7.38	74.2	2.5	272.9	151.6	3.9	1.7	1.1	1.2	3.9	3.2	2.9
214	6/7	4	7.51	71.4	2.5	267.3	139.5	2.2	1.6	1.6	1.4	2.5	3.3	3.3
58	2/3	4	7.50	73.2	1.8	251.8	134.8	2.6	1.6	2.2	1.7	3.3	3.3	3.0
167	4/7	8	7.34	73.1	3.1	268.6	150.0	38.5	1.3	1.4	1.3	3.3	3.5	2.9
41	1/7	8	7.28	72.7	2.1	263.1	146.4	39.6	1.5	1.3	1.3	4.9	3.3	3.1
136	3/8	4	7.43	72.6	3.3	255.6	133.9	3.8	1.4	1.6	1.6	3.0	3.4	2.8
59	2/3	5	7.23	74.7	1.6	262.2	144.6	2.9	1.2	1.3	1.6	5.0	3.1	2.8
151	4/5	6	7.18	72.3	3.0	267.7	145.3	1.4	1.9	1.2	1.4	3.6	3.3	3.2
51	1/9	3	7.46	71.3	1.2	244.1	128.1	3.1	1.8	1.5	1.2	3.6	2.6	3.0
9	1/3	4	7.36	72.0	2.0	253.5	128.1	2.3	1.7	1.9	1.7	4.1	3.1	3.1
79	2/6	3	7.29	70.7	2.7	254.3	137.9	1.8	1.2	1.7	1.5	3.0	3.1	3.1
121	3/6	2	7.25	71.6	1.8	258.9	142.5	1.9	1.0	1.6	1.4	3.2	3.2	3.0
245	7/9	8	7.25	72.5	1.7	266.3	152.0	47.3	1.4	1.4	1.6	8.5	3.3	3.1
44	1/8	3	7.37	71.0	1.4	254.1	136.1	1.7	1.4	1.6	1.3	3.5	3.1	3.0
135	3/8	2	7.25	71.8	1.8	260.4	148.8	1.9	1.1	1.8	1.6	3.2	3.2	2.8
208	5/9	6	7.14	72.2	2.4	262.4	147.5	13.0	1.6	1.1	1.4	3.6	3.0	3.0
131	3/7	6	7.30	71.0	3.4	260.8	135.3	7.1	1.4	1.3	1.5	2.7	3.3	3.2
89	2/7	6	7.26	71.9	2.4	265.3	139.8	7.3	1.3	1.1	1.5	2.9	3.5	3.2
144	3/9	5	7.15	74.9	1.4	244.9	138.3	12.2	1.2	1.4	1.5	3.6	2.9	2.9
157	4/6	3	7.22	71.8	3.2	247.5	128.0	2.7	1.6	1.7	1.7	3.0	3.2	3.1

Entry	Parent 1	Parent 2	GY	AD	ASI	PH	EH	SL	ER	GLS	TURC	HC	SEN	TEX
100	2/9	3	7.28	71.2	1.6	247.2	136.5	1.9	1.4	1.6	1.3	4.0	2.8	2.9
40	1/7	6	7.27	70.9	3.1	259.4	134.7	9.0	1.6	1.2	1.3	2.8	3.4	3.0
187	5/6	7	7.22	73.2	1.8	259.6	138.4	7.5	1.4	1.3	1.5	4.2	3.2	3.1
90	2/7	8	7.08	73.4	2.1	266.6	154.9	37.5	1.3	1.5	1.6	3.5	3.4	3.0
202	5/8	7	7.04	74.5	1.5	259.3	147.2	37.7	1.4	1.5	1.4	4.8	3.2	3.0
195	5/7	8	7.22	74.5	2.3	270.7	155.1	39.6	1.4	1.3	1.3	3.6	3.4	3.0
93	2/8	3	7.19	70.8	1.8	257.2	144.6	0.4	1.1	1.8	1.4	3.9	3.2	2.9
166	4/7	6	7.21	71.4	3.2	265.8	140.0	6.9	1.6	1.2	1.6	2.8	3.5	3.3
192	5/7	3	7.00	73.4	1.3	257.7	138.3	3.2	1.3	1.2	1.4	3.0	2.9	2.8
122	3/6	4	7.13	72.2	3.0	252.5	132.7	2.4	1.7	1.7	1.7	3.0	3.4	3.2
178	4/9	3	7.20	72.3	2.0	240.4	126.6	2.7	1.8	1.6	1.5	4.0	2.9	3.0
10	1/3	5	6.97	74.3	1.2	247.7	133.3	3.3	1.5	1.9	1.5	3.2	3.1	2.8
132	3/7	8	7.02	72.4	2.1	263.5	150.8	36.0	1.3	1.5	1.4	4.2	3.4	3.0
171	4/8	3	7.12	72.0	2.2	250.5	134.7	1.3	1.4	1.7	1.6	3.9	3.4	3.0
1	1/2	3	7.11	70.9	1.1	249.2	135.3	2.3	1.4	1.9	1.4	2.9	2.9	3.0
244	7/9	6	7.16	71.2	2.5	260.5	142.2	18.5	1.3	1.1	1.6	2.8	3.2	3.1
66	2/4	5	6.44	75.5	1.3	256.7	134.8	3.0	1.4	1.6	1.7	4.7	3.2	2.8
159	4/6	7	7.25	71.4	2.1	266.8	138.0	7.0	1.5	1.4	1.4	2.5	3.3	3.3
174	4/8	7	7.07	72.7	1.7	266.5	146.9	37.3	1.5	1.6	1.4	3.1	3.3	3.2
194	5/7	6	6.92	72.3	2.5	267.3	143.8	6.2	1.8	1.1	1.4	3.6	3.3	3.2
129	3/7	4	7.16	72.2	1.9	253.5	130.8	2.6	1.6	1.9	1.6	2.7	3.3	3.2
207	5/9	4	6.34	74.2	1.1	251.7	126.3	6.0	1.5	1.7	1.6	4.0	2.9	3.0
16	1/4	3	7.03	72.0	1.5	242.4	125.4	3.2	1.8	1.8	1.6	2.9	3.1	3.1
185	5/6	3	6.74	72.8	3.0	253.9	134.0	3.2	1.3	1.3	1.5	3.3	3.0	3.0
179	4/9	5	6.36	75.7	1.1	239.3	128.5	12.4	1.4	1.7	1.6	3.3	3.0	2.9
130	3/7	5	6.66	75.1	1.4	252.7	137.1	3.5	1.3	1.4	1.5	4.7	3.0	2.8
137	3/8	5	6.84	75.1	2.3	264.0	144.9	5.5	1.3	1.2	1.4	3.6	3.1	2.7
65	2/4	3	6.85	71.9	1.9	245.5	133.9	1.9	1.4	2.0	1.7	3.2	3.2	3.0
206	5/9	3	6.72	73.4	1.8	246.8	132.6	3.3	1.5	1.2	1.4	4.2	2.7	2.8
17	1/4	5	6.18	75.1	0.9	242.1	123.4	3.5	1.7	2.2	1.6	2.9	3.2	2.8
223	6/8	7	6.77	72.6	2.4	265.0	147.3	41.9	1.5	1.3	1.5	3.3	3.4	3.2
199	5/8	3	6.63	73.0	2.0	256.8	140.6	1.8	1.2	1.4	1.5	4.2	3.1	2.8
73	2/5	4	6.22	75.0	1.3	252.6	130.9	3.3	1.5	2.1	1.7	3.2	3.2	2.8
200	5/8	4	6.16	74.5	2.7	256.4	130.0	4.5	1.3	1.6	1.5	3.0	3.3	2.7
24	1/5	4	6.08	73.8	1.5	254.3	124.2	3.0	1.6	1.9	1.6	4.1	3.0	2.9
123	3/6	5	6.35	74.2	2.1	260.4	142.5	2.3	1.7	1.1	1.4	4.1	3.0	2.9
23	1/5	3	6.55	73.0	1.3	248.8	131.4	3.7	1.5	1.5	1.4	3.1	2.9	2.9
72	2/5	3	6.37	72.9	1.6	251.9	139.8	2.4	1.1	1.6	1.5	3.5	3.0	2.8
165	4/7	5	5.87	75.9	1.1	247.2	127.3	3.7	1.4	1.7	1.6	4.4	3.1	2.8
172	4/8	5	6.04	75.9	1.9	258.5	135.1	5.6	1.4	1.5	1.5	3.3	3.2	2.7
186	5/6	4	5.85	74.0	2.4	253.3	128.9	3.1	1.6	1.6	1.7	3.0	3.3	3.0
150	4/5	3	6.30	74.0	2.1	245.2	129.9	3.3	1.5	1.6	1.7	3.5	3.2	2.9
193	5/7	4	5.89	74.0	1.3	254.3	126.9	3.3	1.6	1.8	1.5	2.7	3.2	3.0
158	4/6	5	5.56	75.0	1.8	254.8	132.7	2.4	1.9	1.4	1.5	3.8	3.1	2.9

GY- grain yield, AD-anthesis date, ASI- anthesis silking interval, PH-plant height, EH-ear height, , SL-stem lodging, ER-ear rots, GLS- grey leaf spot, TURC- turcicum, HC-husk cover, TEX-texture.

Appendix 4.4 Grain yield and agronomic trait predictions the highest yielding top 260 of 378 of the EEDiallel double-crosses

Entry	Parent 1	Parent 2	GY	AD	ASI	PH	EH	SL	ER	GLS	TURC	SEN	TEX
20	1/2	7/9	8.76	72.4	1.2	261.9	137.3	3.8	7.4	1.3	1.4	2.9	3.0
15	1/2	5/9	8.64	73.4	1.2	258.1	140.6	3.4	9.3	1.4	1.4	3.0	2.9
69	1/5	2/9	8.60	73.4	1.4	258.3	142.0	6.5	7.9	1.3	1.4	3.1	2.9
164	1/9	5/7	8.59	72.6	0.9	256.3	137.7	12.3	8.2	1.7	1.5	2.9	3.0
62	1/4	7/9	8.59	71.8	1.3	263.0	134.1	3.5	8.4	1.5	1.4	2.8	3.1
83	1/5	7/9	8.58	73.5	1.1	253.3	135.4	6.9	7.4	1.4	1.4	2.8	2.9
152	1/9	2/7	8.58	71.7	1.2	268.2	141.9	8.9	7.4	1.5	1.5	3.0	3.0
41	1/3	7/9	8.54	71.9	1.3	256.7	133.1	2.3	7.9	1.6	1.3	2.7	2.9
161	1/9	4/7	8.54	71.2	1.2	268.5	137.0	8.9	7.6	1.7	1.5	2.8	3.1
111	1/7	2/9	8.52	72.0	1.4	265.8	140.6	7.5	6.7	1.6	1.4	3.0	3.0
13	1/2	5/7	8.50	73.0	0.9	262.3	138.7	2.7	9.4	1.4	1.5	3.1	2.9
269	2/9	5/7	8.48	73.2	1.1	263.1	145.7	12.4	5.8	1.4	1.5	3.0	3.0
11	1/2	4/9	8.48	72.5	1.5	262.1	139.0	3.3	7.9	1.4	1.4	2.9	3.0
48	1/4	2/9	8.48	72.4	1.4	262.4	138.9	3.4	8.0	1.4	1.4	3.0	2.9
264	2/9	4/5	8.45	73.5	1.1	259.7	144.0	8.2	7.0	1.3	1.5	3.0	3.0
63	1/4	8/9	8.44	72.1	2.3	262.7	137.2	5.3	7.9	1.4	1.3	3.0	2.9
168	1/9	7/8	8.41	71.3	1.4	268.1	141.0	13.8	8.9	1.7	1.5	3.0	3.0
84	1/5	8/9	8.39	73.6	1.9	257.6	140.8	9.0	7.5	1.4	1.3	3.0	2.9
123	1/7	5/9	8.39	73.1	1.1	257.0	137.4	7.6	8.2	1.7	1.4	2.9	3.0
266	2/9	4/7	8.37	72.1	1.2	267.3	142.7	9.3	5.8	1.5	1.5	3.0	3.1
146	1/8	6/9	8.35	71.5	2.6	260.3	140.1	9.1	8.8	1.5	1.3	3.3	2.9
120	1/7	4/9	8.35	71.6	1.6	266.6	137.6	7.2	7.6	1.7	1.4	2.9	3.1
9	1/2	4/7	8.35	72.1	1.2	266.3	137.1	2.6	7.9	1.4	1.5	3.0	3.0
116	1/7	3/9	8.35	71.6	1.1	260.0	137.0	7.7	7.6	1.7	1.3	2.8	3.0
240	2/7	5/9	8.34	73.4	1.1	266.1	146.7	9.0	6.4	1.4	1.5	3.0	3.0
21	1/2	8/9	8.33	72.6	1.8	261.4	142.1	4.7	8.5	1.3	1.4	3.0	2.9
67	1/5	2/7	8.32	73.1	1.2	265.5	141.1	2.4	8.6	1.3	1.5	3.2	2.9
105	1/6	8/9	8.31	71.8	2.5	259.3	141.0	10.0	8.0	1.4	1.3	3.2	3.0
141	1/8	4/9	8.30	71.8	2.2	265.6	138.9	7.6	8.6	1.4	1.4	3.1	2.9
150	1/9	2/5	8.29	73.3	1.0	252.9	139.9	8.3	8.0	1.3	1.4	3.1	2.9
144	1/8	5/9	8.29	73.2	1.6	260.6	141.1	8.4	9.8	1.5	1.4	3.1	2.9
159	1/9	4/5	8.25	72.8	1.0	253.3	135.0	8.3	8.2	1.5	1.4	2.9	3.0
237	2/7	4/9	8.24	72.2	1.3	267.7	144.6	8.9	6.5	1.5	1.5	3.0	3.1
255	2/8	5/9	8.24	73.4	1.5	269.7	150.4	9.8	8.0	1.2	1.5	3.1	2.9
18	1/2	6/9	8.24	72.2	2.1	258.6	137.6	4.5	8.1	1.3	1.3	3.1	2.9
149	1/9	2/4	8.23	71.8	1.3	265.2	139.2	4.9	7.4	1.3	1.5	3.0	3.0
7	1/2	4/5	8.23	73.1	1.2	262.4	140.4	2.3	9.9	1.5	1.5	3.2	2.9
46	1/4	2/7	8.22	72.0	1.3	267.0	139.0	2.3	8.7	1.5	1.4	3.2	3.0
339	4/5	8/9	8.22	73.5	2.2	262.6	143.7	10.1	5.9	1.2	1.3	3.1	2.9
147	1/8	7/9	8.21	72.3	1.5	263.4	141.7	24.6	10.9	1.5	1.5	3.0	3.0
249	2/8	4/5	8.20	73.8	2.4	271.7	149.2	4.1	7.6	1.2	1.4	3.3	2.8
19	1/2	7/8	8.20	72.1	1.6	265.6	140.3	4.0	8.6	1.3	1.4	3.2	2.9
252	2/8	4/9	8.19	72.4	1.9	266.6	145.9	9.3	7.5	1.2	1.5	3.2	2.9
60	1/4	6/9	8.19	71.6	2.5	259.2	135.2	4.4	7.6	1.6	1.3	3.1	3.0
132	1/8	2/9	8.19	72.1	1.7	264.6	143.8	7.1	9.3	1.4	1.5	3.2	2.9
253	2/8	5/6	8.18	73.4	2.5	270.2	149.5	4.5	7.5	1.2	1.4	3.4	2.9
166	1/9	6/7	8.18	71.0	2.0	263.1	139.1	14.3	8.1	1.6	1.4	3.0	3.0
40	1/3	7/8	8.18	71.4	1.5	263.6	138.4	3.0	8.4	1.4	1.3	3.1	2.9
61	1/4	7/8	8.18	71.7	2.2	267.3	137.2	4.2	8.6	1.4	1.3	3.2	3.0
257	2/8	6/9	8.17	72.1	2.1	265.2	146.2	9.8	7.4	1.2	1.5	3.3	3.0
157	1/9	3/7	8.17	71.2	1.2	257.8	133.9	8.0	7.9	1.8	1.4	2.7	3.1
197	2/4	7/9	8.17	72.2	1.1	264.5	140.1	5.4	6.0	1.3	1.4	2.9	3.1
104	1/6	7/9	8.17	71.6	1.9	260.5	136.7	10.2	9.5	1.5	1.5	3.0	3.0
103	1/6	7/8	8.17	71.5	2.4	264.9	138.9	6.9	9.5	1.5	1.4	3.3	3.1
212	2/5	7/9	8.17	73.9	1.0	254.8	141.4	8.8	5.0	1.1	1.5	2.9	3.0
198	2/4	8/9	8.16	72.4	2.1	266.4	145.1	5.8	6.9	1.1	1.5	3.1	2.9
270	2/9	5/8	8.15	73.3	1.4	261.9	148.9	11.9	8.3	1.2	1.6	3.2	2.9
345	4/6	8/9	8.14	71.7	2.8	264.3	143.9	11.1	6.4	1.2	1.4	3.2	2.9
37	1/3	6/7	8.13	71.1	2.3	260.2	133.6	3.5	9.1	1.5	1.3	3.0	3.0
250	2/8	4/6	8.13	72.5	2.9	267.2	145.0	4.1	7.0	1.2	1.4	3.5	2.9
165	1/9	5/8	8.13	72.8	1.2	252.9	139.0	13.3	9.4	1.4	1.4	3.1	3.0
182	2/3	7/9	8.12	72.3	1.1	258.2	139.1	4.1	5.5	1.3	1.3	2.8	3.0
68	1/5	2/8	8.12	73.2	1.9	269.8	146.5	4.5	8.7	1.3	1.3	3.4	2.9
356	4/8	6/9	8.12	71.5	2.4	265.7	143.8	9.7	6.8	1.4	1.5	3.3	3.1
126	1/7	8/9	8.12	72.3	1.8	264.1	143.3	25.9	9.4	1.7	1.3	3.0	3.1
213	2/5	8/9	8.11	73.9	1.7	261.2	148.7	9.5	6.5	1.1	1.5	3.1	2.9
153	1/9	2/8	8.11	71.9	1.5	264.7	143.2	9.8	8.6	1.3	1.5	3.2	3.0
125	1/7	6/9	8.11	71.4	2.3	262.2	137.5	10.6	8.8	1.7	1.3	3.1	3.0
82	1/5	7/8	8.11	73.3	1.7	264.7	139.9	5.0	8.2	1.4	1.3	3.1	2.9
16	1/2	6/7	8.10	71.7	1.9	262.8	135.7	3.8	8.2	1.3	1.3	3.2	3.0
366	5/6	8/9	8.09	73.2	2.4	259.1	147.5	14.8	6.0	1.2	1.4	3.2	2.9
233	2/7	3/9	8.08	71.6	1.1	263.5	144.9	8.6	5.1	1.3	1.4	2.8	3.0
14	1/2	5/8	8.08	73.1	1.5	261.7	143.6	3.6	10.5	1.4	1.4	3.3	2.9
42	1/3	8/9	8.08	71.7	2.0	254.9	135.8	2.7	7.9	1.5	1.2	3.0	2.9
47	1/4	2/8	8.07	72.2	2.3	266.7	142.0	4.1	8.2	1.3	1.3	3.4	2.8
273	2/9	7/8	8.07	71.9	1.5	269.4	147.6	13.0	7.2	1.4	1.6	3.2	3.0
162	1/9	4/8	8.07	71.4	1.5	265.1	138.2	9.8	8.8	1.5	1.4	3.0	3.1
139	1/8	4/6	8.06	71.4	3.3	265.0	139.1	4.8	7.8	1.4	1.2	3.4	2.9
25	1/3	2/7	8.06	71.4	1.1	262.8	139.3	2.0	7.4	1.3	1.4	3.0	2.9
333	3/9	7/8	8.06	71.2	1.3	267.5	145.7	12.0	7.0	1.5	1.4	3.0	3.0
142	1/8	5/6	8.06	72.7	2.6	260.0	141.3	5.6	8.9	1.5	1.2	3.4	2.8
90	1/6	2/9	8.05	72.0	2.0	260.8	140.2	7.9	8.1	1.3	1.4	3.2	2.9
363	4/9	7/8	8.05	71.5	2.1	271.2	144.5	13.2	7.2	1.5	1.4	3.2	3.0
89	1/6	2/8	8.05	71.9	2.4	265.2	142.3	4.6	8.1	1.3	1.3	3.5	3.0
81	1/5	6/9	8.05	72.8	2.1	253.8	138.2	7.2	6.4	1.6	1.2	3.0	2.9
378	6/9	7/8	8.04	71.3	2.3	268.8	146.2	15.9	8.1	1.6	1.5	3.3	3.1
267	2/9	4/8	8.04	72.3	1.4	266.0	145.9	8.9	8.4	1.3	1.6	3.2	2.9
228	2/6	8/9	8.03	72.1	2.4	262.9	148.9	10.5	6.9	1.2	1.5	3.2	2.9
39	1/3	6/9	8.03	71.4	2.8	251.5	131.0	3.2	8.6	1.6	1.2	2.9	3.0
268	2/9	5/6	8.02	73.2	1.7	258.1	145.3	12.7	7.2	1.1	1.5	3.1	3.0
326	3/9	4/7	8.02	71.9	1.3	260.4	137.4	9.1	5.4	1.6	1.5	2.9	3.1
195	2/4	6/9	8.01	72.1	2.0	264.0	141.3	5.1	6.2	1.3	1.5	3.1	3.1
99	1/6	4/9	8.01	71.6	2.4	261.0	137.8	7.6	7.5	1.5	1.4	3.0	3.1
98	1/6	4/8	8.01	71.4	2.8	265.5	140.0	4.3	7.5	1.5	1.4	3.3	3.1
138	1/8	4/5	8.00	73.0	2.3	265.3	140.1	4.2	8.8	1.4	1.3	3.2	2.8
6	1/2	3/9	8.00	71.9	1.2	253.5	137.2	3.3	7.3	1.3	1.4	2.8	3.0
30	1/3	4/7	8.00	71.8	1.4	259.4	131.9	2.4	7.5	1.6	1.5	3.0	3.0
338	4/5	7/9	7.99	73.3	1.0	255.9	138.2	8.5	5.9	1.3	1.4	2.9	3.1
371	5/8	6/9	7.99	72.7	2.1	260.3	146.8	12.5	5.7	1.5	1.5	3.2	3.0

Entry	Parent 1	Parent 2	GY	AD	ASI	PH	EH	SL	ER	GLS	TURC	SEN	TEX
12	1/2	5/6	7.99	72.8	1.8	258.9	139.0	3.5	10.1	1.4	1.3	3.3	2.9
375	5/9	7/8	7.98	73.1	1.5	268.6	147.2	14.0	6.8	1.5	1.5	3.1	2.9
145	1/8	6/7	7.98	71.8	2.6	262.8	141.9	21.8	10.1	1.5	1.3	3.3	3.0
234	2/7	4/5	7.98	73.6	1.2	265.0	143.7	2.5	7.6	1.3	1.4	3.2	3.0
221	2/6	4/8	7.98	72.3	2.8	266.4	147.6	3.4	7.0	1.4	1.5	3.5	3.0
137	1/8	3/9	7.98	71.5	1.5	257.5	138.0	6.8	9.2	1.5	1.4	3.0	3.0
331	3/9	6/7	7.97	71.1	2.1	263.0	141.8	13.4	6.9	1.5	1.4	2.9	3.1
322	3/8	6/9	7.96	71.3	2.7	258.0	139.7	8.5	7.8	1.5	1.4	3.1	3.0
27	1/3	2/9	7.96	71.7	1.6	254.1	136.7	1.8	6.9	1.4	1.3	2.9	2.9
130	1/8	2/6	7.95	71.7	2.8	264.0	144.0	4.3	8.4	1.4	1.3	3.5	2.8
282	3/4	7/9	7.95	71.6	1.2	259.3	136.0	3.9	6.4	1.5	1.3	2.8	3.1
292	3/5	7/9	7.95	73.3	1.0	249.6	137.2	7.3	5.4	1.3	1.3	2.8	2.9
351	4/7	8/9	7.95	72.2	2.1	269.1	146.3	27.0	7.8	1.5	1.4	3.1	3.0
108	1/7	2/5	7.95	73.3	1.0	257.8	137.7	2.9	8.0	1.4	1.4	3.2	2.9
224	2/6	5/8	7.94	73.0	2.4	269.2	151.5	2.9	6.8	1.4	1.5	3.4	2.9
271	2/9	6/7	7.94	71.8	1.7	265.6	143.9	13.7	6.0	1.3	1.5	3.1	3.1
53	1/4	3/9	7.94	72.1	1.5	250.4	129.8	3.9	7.6	1.6	1.5	2.9	3.1
242	2/7	6/9	7.93	71.9	1.8	267.1	143.7	11.4	7.5	1.4	1.5	3.1	3.1
58	1/4	6/7	7.93	71.2	2.4	263.8	135.2	3.3	8.3	1.6	1.3	3.2	3.1
140	1/8	4/7	7.93	72.1	2.2	268.1	140.7	20.4	9.9	1.4	1.4	3.1	3.0
260	2/9	3/5	7.92	72.9	1.3	251.4	141.8	6.6	5.9	1.3	1.4	2.9	2.9
10	1/2	4/8	7.92	72.2	1.8	265.7	142.0	3.5	9.0	1.4	1.5	3.2	2.9
143	1/8	5/7	7.92	73.5	1.5	263.0	142.9	21.2	11.1	1.5	1.4	3.2	2.9
102	1/6	5/9	7.91	72.7	1.8	255.7	139.4	7.5	7.9	1.7	1.3	3.0	2.9
101	1/6	5/8	7.91	72.5	2.2	260.2	141.5	4.2	7.9	1.7	1.3	3.3	3.0
88	1/6	2/7	7.91	71.7	1.8	266.4	138.1	4.8	9.7	1.4	1.5	3.3	3.0
107	1/7	2/4	7.91	71.7	1.4	267.4	137.9	2.5	7.4	1.4	1.4	3.2	3.1
106	1/7	2/3	7.91	71.8	1.0	260.8	137.4	3.0	7.5	1.4	1.3	3.1	3.0
265	2/9	4/6	7.90	72.1	1.7	262.2	142.2	9.6	7.2	1.2	1.5	3.1	3.0
283	3/4	8/9	7.90	71.6	2.3	259.9	138.7	3.8	6.3	1.3	1.3	3.0	2.9
222	2/6	4/9	7.90	72.2	2.1	262.0	144.8	9.4	6.4	1.3	1.6	3.1	3.1
128	1/8	2/4	7.90	72.0	2.4	269.3	142.9	2.9	8.3	1.3	1.4	3.3	2.8
369	5/7	8/9	7.90	73.7	1.7	263.9	149.9	30.8	7.4	1.5	1.4	3.1	3.0
32	1/3	4/9	7.90	72.1	1.9	250.7	129.3	2.2	7.0	1.7	1.4	2.9	3.0
163	1/9	5/6	7.89	72.5	1.8	247.8	137.0	13.8	8.6	1.4	1.3	3.1	2.9
129	1/8	2/5	7.89	73.3	1.7	264.3	145.0	3.7	9.4	1.4	1.4	3.4	2.8
95	1/6	3/9	7.89	71.4	2.2	253.0	134.1	8.2	9.0	1.5	1.4	2.9	3.1
178	2/3	6/7	7.89	71.9	2.0	262.7	138.5	2.9	7.0	1.2	1.4	3.1	3.0
94	1/6	3/8	7.89	71.2	2.7	257.5	136.3	4.9	9.0	1.5	1.3	3.2	3.1
350	4/7	6/9	7.88	71.3	2.2	267.6	141.3	11.2	6.9	1.7	1.5	3.1	3.2
155	1/9	3/5	7.88	72.8	1.0	242.6	131.9	7.4	8.4	1.6	1.3	2.8	3.0
151	1/9	2/6	7.88	71.6	2.1	259.7	141.3	10.3	7.8	1.3	1.4	3.1	2.9
210	2/5	6/9	7.87	73.4	1.6	258.6	144.3	7.9	5.1	1.3	1.4	3.0	3.0
148	1/9	2/3	7.87	71.8	1.3	254.4	136.1	4.0	7.7	1.5	1.3	2.9	3.0
225	2/6	5/9	7.87	72.9	1.8	264.8	148.7	8.9	6.1	1.3	1.5	3.0	3.0
97	1/6	4/7	7.86	71.3	2.2	266.7	135.7	4.6	9.0	1.6	1.5	3.1	3.2
4	1/2	3/7	7.86	71.4	1.0	257.6	135.4	2.7	7.4	1.4	1.4	2.9	3.0
293	3/5	8/9	7.86	73.1	1.9	254.8	142.3	7.6	5.9	1.3	1.3	3.0	2.9
180	2/3	6/9	7.85	71.9	2.3	256.3	137.2	3.9	7.2	1.3	1.4	2.9	3.1
262	2/9	3/7	7.84	71.5	1.4	258.9	140.5	7.6	4.7	1.5	1.4	2.9	3.0
243	2/7	8/9	7.84	72.7	1.6	267.7	151.2	26.4	8.4	1.4	1.5	3.1	3.0
181	2/3	7/8	7.84	72.0	1.5	265.0	145.0	2.2	6.7	1.2	1.4	3.2	2.9
160	1/9	4/6	7.84	71.1	2.1	260.1	136.3	10.3	8.0	1.4	1.4	3.0	3.0
196	2/4	7/8	7.84	72.3	2.2	268.6	143.8	3.4	6.9	1.2	1.4	3.3	2.9
171	2/3	4/7	7.83	72.7	1.3	258.2	137.6	2.8	5.7	1.4	1.5	3.2	3.0
8	1/2	4/6	7.83	71.9	2.1	263.0	137.4	3.4	8.6	1.4	1.3	3.3	3.0
226	2/6	7/8	7.83	72.1	2.5	266.3	145.5	6.1	7.8	1.3	1.5	3.4	3.0
336	4/5	6/9	7.82	72.8	2.0	259.2	141.9	7.8	4.5	1.6	1.5	3.0	3.1
45	1/4	2/6	7.82	71.7	2.5	263.1	140.0	3.2	7.9	1.5	1.4	3.4	3.0
154	1/9	3/4	7.82	71.3	1.3	254.8	131.2	4.0	7.9	1.6	1.3	2.7	3.1
376	6/7	8/9	7.82	71.9	2.4	265.6	150.1	31.7	7.9	1.5	1.5	3.2	3.1
281	3/4	7/8	7.82	71.6	2.1	266.7	141.9	2.4	6.8	1.2	1.3	3.2	2.9
230	2/7	3/5	7.82	73.0	1.1	260.8	144.0	2.2	6.3	1.2	1.4	3.0	2.9
131	1/8	2/7	7.82	72.4	1.7	267.1	145.6	19.9	10.6	1.4	1.5	3.3	2.9
301	3/6	7/8	7.81	71.4	2.3	264.3	143.5	5.1	7.6	1.3	1.4	3.3	3.0
34	1/3	5/7	7.81	72.9	1.0	256.6	134.5	2.9	10.2	1.5	1.4	2.9	2.8
219	2/6	4/5	7.81	73.1	2.2	268.3	147.4	1.8	6.2	1.6	1.5	3.3	3.0
254	2/8	5/7	7.81	74.0	1.8	269.9	150.9	21.2	8.6	1.3	1.4	3.3	3.0
343	4/6	7/8	7.81	71.7	3.0	268.0	142.4	6.3	7.8	1.3	1.3	3.5	3.0
259	2/9	3/4	7.81	71.9	1.4	255.5	138.7	3.5	6.0	1.4	1.4	2.9	3.0
280	3/4	6/9	7.80	71.3	2.6	256.9	134.8	3.8	6.6	1.5	1.4	2.9	3.2
183	2/3	8/9	7.80	72.1	1.8	258.6	143.7	3.2	6.9	1.3	1.4	3.0	2.9
258	2/8	7/9	7.80	72.6	1.3	264.8	147.6	26.5	8.5	1.3	1.5	3.1	3.1
315	3/8	4/6	7.79	71.9	3.6	258.4	137.4	4.1	6.6	1.4	1.5	3.4	3.0
173	2/3	4/9	7.79	72.8	1.6	251.8	136.3	3.9	5.9	1.5	1.5	3.0	3.0
329	3/9	5/7	7.79	73.1	1.2	257.5	141.5	12.6	6.6	1.4	1.4	2.8	2.9
66	1/5	2/6	7.79	72.5	2.2	265.9	143.9	2.7	7.7	1.6	1.3	3.3	2.9
59	1/4	6/8	7.78	71.5	3.4	263.4	138.2	5.1	7.8	1.4	1.2	3.4	2.9
117	1/7	4/5	7.78	72.8	1.1	258.6	134.6	2.6	8.8	1.5	1.4	3.1	3.0
303	3/6	8/9	7.78	71.3	2.5	256.5	142.5	8.5	6.4	1.3	1.4	3.1	3.0
113	1/7	3/5	7.78	72.9	0.7	251.9	134.1	3.0	8.9	1.5	1.3	2.9	2.9
321	3/8	6/7	7.77	72.0	2.7	262.7	144.6	20.9	8.8	1.4	1.4	3.2	3.1
79	1/5	6/7	7.77	72.6	1.9	260.9	137.3	3.2	7.2	1.7	1.3	3.1	2.9
100	1/6	5/7	7.77	72.4	1.6	261.3	137.3	4.4	9.4	1.8	1.4	3.1	3.0
211	2/5	7/8	7.77	74.0	1.7	266.1	146.5	4.2	6.5	1.2	1.4	3.2	2.8
361	4/9	6/7	7.77	71.2	2.2	266.6	143.4	13.2	6.1	1.6	1.5	3.1	3.2
251	2/8	4/7	7.76	73.0	2.2	266.8	146.4	20.8	8.1	1.3	1.4	3.3	2.9
227	2/6	7/9	7.75	72.0	1.8	261.9	142.7	12.1	7.1	1.2	1.5	3.1	3.1
291	3/5	7/8	7.75	73.3	1.6	264.1	144.6	3.2	6.4	1.2	1.3	3.1	2.8
86	1/6	2/4	7.75	71.7	2.3	267.0	139.2	2.2	7.6	1.4	1.5	3.3	3.1
2	1/2	3/5	7.75	72.4	1.0	253.8	138.7	2.3	9.3	1.4	1.4	3.1	2.9
337	4/5	7/8	7.75	73.5	2.3	267.8	143.4	4.4	6.6	1.3	1.3	3.2	2.9
368	5/7	6/9	7.75	72.6	1.8	262.2	144.3	14.1	5.8	1.7	1.5	3.0	3.1
93	1/6	3/7	7.75	71.0	2.1	258.6	132.0	5.1	10.6	1.6	1.5	3.0	3.1
135	1/8	3/6	7.74	71.0	2.5	257.0	138.2	4.0	8.4	1.5	1.2	3.3	2.9
364	5/6	7/8	7.74	73.3	2.5	265.5	145.1	7.1	7.4	1.3	1.4	3.4	3.0
256	2/8	6/7	7.74	72.7	2.3	265.4	146.7	21.2	8.0	1.3	1.4	3.4	3.1
112	1/7	3/4	7.74	71.3	1.1	261.6	134.3	2.6	8.3	1.5	1.3	2.9	3.1
312	3/7	6/9	7.72	71.1	2.5	259.9	137.1	10.1	7.9	1.7	1.4	2.9	3.2
245	2/8	3/5	7.72	72.8	1.9	266.0	149.1	2.5	6.8	1.1	1.4	3.2	2.8
229	2/7	3/4	7.72	71.8	1.2	262.3	141.9	2.1	6.4	1.3	1.4	3.1	3.0
278	3/4	6/7	7.72	71.3	2.4	263.7	137.9	2.4	7.1	1.4	1.4	3.1	3.2
362	4/9	6/8	7.71	71.5	2.9	265.5	144.8	13.7	7.1	1.3	1.5	3.3	3.0
167	1/9	6/8	7.71	71.1	2.3	259.6	140.3	15.3	9.3	1.4	1.4	3.2	2.9
248	2/8	3/9	7.71	71.4	1.4	261.0	145.8	7.7	6.7	1.1	1.5	3.1	2.9
74	1/5	3/9	7.71	73.4	1.3	247.5	133.8	7.3	8.7	1.4	1.4	2.8	2.9
36	1/3	5/9	7.71	73.3	1.5	247.9	131.9	2.7	9.7	1.6	1.3	2.8	2.9

Entry	Parent 1	Parent 2	GY	AD	ASI	PH	EH	SL	ER	GLS	TURC	SEN	TEX
217	2/6	3/8	7.70	71.5	2.9	260.8	144.8	3.1	7.2	1.2	1.5	3.3	3.0
158	1/9	3/8	7.70	71.4	1.5	254.4	135.2	9.0	9.1	1.6	1.3	2.9	3.0
175	2/3	5/7	7.70	73.4	1.2	263.4	142.5	3.0	7.8	1.2	1.4	3.1	2.9
220	2/6	4/7	7.69	72.2	2.2	265.4	141.4	5.0	7.2	1.4	1.5	3.3	3.1
133	1/8	3/4	7.69	71.3	2.2	262.2	137.1	2.5	8.2	1.4	1.3	3.1	2.9
193	2/4	6/7	7.68	72.0	2.1	266.3	140.1	2.7	6.2	1.3	1.4	3.3	3.2
134	1/8	3/5	7.68	72.7	1.5	257.2	139.2	3.3	9.4	1.5	1.3	3.2	2.9
110	1/7	2/8	7.68	72.4	1.7	264.9	143.7	21.2	9.3	1.4	1.4	3.3	3.0
51	1/4	3/7	7.68	71.7	1.4	255.0	129.8	2.8	8.3	1.7	1.5	3.0	3.1
194	2/4	6/8	7.68	72.3	3.1	268.2	145.1	3.1	7.1	1.2	1.5	3.5	2.9
17	1/2	6/8	7.68	71.9	2.5	262.3	140.6	4.7	9.3	1.3	1.3	3.4	2.9
188	2/4	3/9	7.67	72.1	1.4	253.9	137.6	4.8	5.1	1.3	1.6	2.9	3.0
244	2/8	3/4	7.67	71.8	2.3	262.9	144.7	2.0	6.3	1.1	1.4	3.3	2.8
109	1/7	2/6	7.67	71.5	2.2	263.0	137.9	5.9	8.7	1.4	1.3	3.4	3.0
279	3/4	6/8	7.67	71.3	3.5	264.3	140.7	2.3	7.0	1.3	1.4	3.3	3.0
238	2/7	5/6	7.67	73.3	1.8	264.4	142.8	4.9	8.6	1.2	1.5	3.3	3.0
38	1/3	6/8	7.67	70.9	2.9	258.4	136.2	4.0	9.1	1.4	1.2	3.3	3.0
290	3/5	6/9	7.67	72.6	2.3	251.5	137.8	6.6	5.5	1.6	1.3	2.9	3.1
177	2/3	5/9	7.66	73.5	1.5	257.0	141.2	4.0	8.0	1.3	1.5	2.9	2.9
223	2/6	5/7	7.66	72.9	1.9	268.2	145.3	4.5	7.0	1.5	1.5	3.3	3.1
307	3/7	4/9	7.65	71.8	1.7	256.3	134.9	7.8	5.6	1.8	1.5	2.9	3.1
87	1/6	2/5	7.65	72.8	1.7	261.6	140.7	2.1	8.0	1.6	1.4	3.3	3.0
246	2/8	3/6	7.65	71.5	2.4	261.5	145.0	2.5	6.2	1.1	1.4	3.4	3.0
327	3/9	4/8	7.65	71.7	1.7	257.9	138.4	8.2	7.0	1.4	1.6	3.2	3.0
85	1/6	2/3	7.63	71.5	2.1	258.9	135.5	2.8	9.2	1.4	1.4	3.2	3.1
218	2/6	3/9	7.63	71.3	2.2	256.4	142.0	9.1	6.5	1.1	1.5	2.9	3.0
357	4/8	7/9	7.62	72.0	1.4	265.9	144.5	26.2	9.5	1.4	1.5	3.1	3.1
372	5/8	7/9	7.62	73.7	1.3	256.2	145.8	29.6	8.5	1.3	1.5	3.1	3.0
272	2/9	6/8	7.61	71.9	2.0	264.3	147.1	13.3	8.5	1.2	1.6	3.3	3.0
373	5/9	6/7	7.61	72.6	1.7	263.7	145.5	13.1	5.0	1.7	1.4	3.0	3.0
96	1/6	4/5	7.61	72.3	2.1	261.9	138.3	1.9	7.4	1.8	1.4	3.2	3.1
136	1/8	3/7	7.61	71.8	1.5	260.0	139.8	19.5	10.5	1.5	1.4	3.1	3.0
317	3/8	4/9	7.60	72.0	2.4	255.3	136.2	8.2	6.7	1.5	1.5	3.1	2.9
332	3/9	6/8	7.60	70.9	2.4	260.5	142.8	12.5	8.4	1.3	1.5	3.1	3.0
26	1/3	2/8	7.59	71.2	1.8	261.0	141.9	2.5	7.4	1.3	1.4	3.3	2.9
1	1/2	3/4	7.59	71.5	1.3	257.8	137.1	2.2	7.8	1.4	1.5	3.0	3.0
296	3/6	4/8	7.59	71.7	3.0	258.3	140.1	2.7	5.6	1.5	1.5	3.5	3.1
91	1/6	3/4	7.59	71.0	2.5	259.2	133.1	2.5	8.5	1.6	1.4	3.0	3.2
313	3/7	8/9	7.58	71.9	1.8	261.3	144.9	24.5	7.8	1.6	1.4	3.0	3.1
323	3/8	7/9	7.58	72.1	1.4	259.6	143.5	25.0	9.0	1.5	1.4	3.0	3.0
344	4/6	7/9	7.58	71.4	1.8	263.0	139.6	11.8	8.1	1.4	1.5	3.1	3.2
127	1/8	2/3	7.58	71.6	1.6	261.2	142.0	2.1	8.9	1.3	1.4	3.3	2.9
335	4/5	6/8	7.58	73.0	3.2	271.1	147.1	3.7	5.1	1.5	1.3	3.4	2.9
80	1/5	6/8	7.58	72.7	2.7	265.2	142.7	5.3	7.3	1.6	1.2	3.3	2.9
353	4/8	5/7	6.56	74.3	1.8	262.5	141.0	21.4	10.0	1.5	1.4	3.3	3.0
346	4/7	5/6	6.54	73.6	2.1	256.5	133.6	5.3	8.5	1.5	1.6	3.3	3.1
277	3/4	5/9	6.53	73.8	1.5	249.2	129.4	4.7	8.7	1.5	1.5	2.8	2.9
275	3/4	5/7	6.45	73.7	1.3	256.0	132.6	3.2	9.1	1.4	1.5	3.0	2.9
340	4/6	5/7	6.40	73.2	1.9	260.8	135.4	4.7	8.4	1.7	1.5	3.2	3.1
276	3/4	5/8	6.40	73.7	2.4	256.6	135.3	3.2	9.1	1.3	1.5	3.2	2.7
284	3/5	4/6	6.39	73.4	2.5	251.2	130.3	2.5	7.1	1.7	1.6	3.2	3.0
70	1/5	3/4	6.31	73.4	1.4	251.5	127.8	3.4	10.6	1.6	1.5	2.9	2.9
199	2/5	3/4	6.30	74.0	1.5	252.2	135.4	2.8	8.7	1.3	1.6	3.1	2.8
274	3/4	5/6	6.29	73.4	2.7	253.6	131.4	3.2	9.4	1.5	1.6	3.1	3.0

GY- grain yield, AD-anthesis date, ASI- anthesis silking interval, PH-plant height, EH-ear height, , SL-stem lodging, ER-ear rots, GLS- grey leaf spot, TURC- turcicum, SEN-senescence, TEX-texture.

Appendix 5.1 Grain yield and agronomic traits of 245 exotic x local three-way hybrids in set 1 in descending order of grain yield

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	HC	EA	TEX
242	SC727	9.98	15.42	62.68	223.69	126.93	9.95	3.83	8.48	1.37	15.08	2.16	3.40
178	DJH161178	8.75	15.57	58.52	223.63	126.48	3.26	4.01	5.30	1.12	8.09	2.63	2.88
244	PAN7M-81	8.49	14.35	59.72	211.23	125.04	-0.84	4.43	4.16	1.37	15.15	2.77	3.16
126	DJH152381	8.27	13.31	55.73	202.65	111.92	4.74	4.78	4.43	2.50	2.91	2.72	3.37
53	DJH152266	8.13	14.65	55.72	207.49	107.34	-0.82	4.14	2.75	2.38	7.95	2.38	1.87
241	SC643	8.09	14.90	56.72	216.69	116.56	1.74	4.69	3.17	1.51	5.02	2.89	3.05
159	DJH152418	7.97	13.94	59.75	208.94	124.62	10.93	3.51	2.99	1.88	3.84	2.84	2.73
37	DJH152099	7.96	14.16	55.92	203.45	105.58	2.94	4.49	4.36	1.62	9.75	2.75	2.60
243	PAN53	7.89	14.68	58.85	201.50	109.96	3.18	4.60	3.08	1.75	4.20	2.66	2.99
236	10C3271	7.80	13.99	55.56	205.71	107.84	6.62	3.98	7.30	3.00	13.21	2.89	3.36
79	DJH16179	7.72	14.64	60.32	216.88	140.94	1.42	5.55	9.67	1.87	2.32	3.20	3.15
83	DJH16183	7.63	14.72	55.93	200.62	110.95	1.31	3.77	6.51	1.63	11.31	3.07	2.68
116	DJH152301	7.63	15.41	58.36	203.86	104.20	7.71	3.61	4.45	1.43	11.15	2.67	2.65
164	DJH161164	7.62	14.92	57.96	212.26	117.09	5.13	4.25	5.47	1.63	12.45	3.03	3.23
158	DJH152416	7.61	15.22	56.62	199.51	114.67	0.50	3.81	2.37	1.63	3.16	2.23	2.68
231	CZH131001	7.58	14.56	56.27	202.43	95.48	6.42	4.76	4.13	1.75	11.66	3.04	2.74
95	DJH152280	7.54	14.80	55.48	210.06	106.89	0.45	3.91	4.23	1.26	12.08	2.39	3.04
147	DJH152404	7.51	14.23	59.79	194.14	116.23	2.45	3.93	3.33	1.75	1.82	2.89	2.80
235	CZH131007	7.50	15.24	59.12	212.35	110.35	1.95	3.66	8.51	1.75	22.79	2.92	3.40
160	DJH152419	7.48	13.97	57.77	206.27	117.47	0.37	4.23	5.85	1.63	1.11	3.08	3.24
232	CZH131013	7.45	15.04	56.79	209.36	104.86	1.47	3.99	10.06	1.37	0.86	2.96	`
233	CZH141028	7.44	14.77	59.90	213.81	125.05	3.35	4.33	4.61	1.50	0.52	3.26	2.85
168	DJH161168	7.42	14.42	57.27	211.89	118.13	0.45	3.36	7.02	1.25	5.48	2.72	2.41
208	DJH152438	7.39	14.94	54.65	212.28	98.49	0.10	4.05	3.21	1.88	2.16	2.91	2.86
46	DJH152259	7.33	15.20	55.83	203.62	111.27	1.43	5.44	2.66	2.13	2.41	2.89	3.04
227	DJH152461	7.31	15.32	58.35	215.99	122.80	10.71	4.02	3.82	2.06	5.60	2.94	2.92
186	DJH161186	7.30	12.85	58.97	206.05	107.39	15.02	4.51	5.47	1.25	2.49	3.06	2.99
97	DJH152282	7.28	14.14	54.60	207.50	110.56	2.69	5.41	4.10	1.88	2.62	3.28	3.10
85	DJH16185	7.21	13.76	55.39	209.19	106.37	5.29	4.72	3.64	1.38	5.92	2.70	3.15
114	DJH152297	7.20	14.94	59.73	213.52	123.05	8.23	4.60	3.29	2.13	6.87	2.86	2.54
87	DJH16187	7.20	13.87	58.09	202.90	111.70	-0.31	4.25	1.75	1.62	4.00	2.75	2.84
239	SC419	7.20	13.22	54.56	214.61	109.84	0.31	5.33	5.83	2.75	2.74	3.09	3.56
234	CZH131006	7.16	15.07	58.56	213.66	108.31	1.94	4.02	3.41	2.13	1.62	2.61	3.06
212	DJH152447	7.15	14.95	54.05	210.32	109.34	2.62	4.82	5.00	1.99	1.85	2.93	3.00
155	DJH152413	7.14	13.88	58.45	194.42	107.89	1.35	4.06	2.41	2.87	-0.63	2.91	3.10
146	DJH152403	7.14	14.91	60.17	202.57	120.70	0.25	2.88	3.77	1.11	3.44	2.68	2.64
84	DJH16184	7.13	14.93	58.23	211.58	115.23	1.50	4.42	2.25	1.56	0.40	2.73	2.76
78	DJH16178	7.10	14.05	58.82	206.73	113.38	4.39	5.13	5.45	1.50	1.43	3.26	3.35
119	DJH152304	7.10	14.17	55.07	215.34	110.84	0.65	3.51	3.23	1.50	1.43	2.84	3.08
64	DJH16164	7.09	14.89	55.03	224.09	124.45	1.38	4.22	5.05	1.25	16.38	2.67	3.00
94	DJH152279	7.02	14.87	57.19	209.19	95.15	5.82	4.11	2.75	2.00	-0.08	2.97	2.72
128	DJH152383	7.01	15.20	57.78	217.34	122.03	0.59	4.17	6.00	1.50	4.72	2.60	2.76
39	VH053121	6.99	12.97	54.39	208.95	109.60	3.41	3.66	3.88	1.75	4.07	2.75	3.55
80	DJH16180	6.97	15.69	56.71	207.62	117.60	2.62	3.93	7.49	1.50	4.31	2.77	3.01
177	DJH161177	6.93	14.13	57.20	201.42	106.66	4.57	4.19	4.44	2.12	5.06	2.84	2.89
90	DJH152274	6.93	12.80	55.77	202.64	104.17	3.26	5.39	3.78	2.00	5.97	3.08	3.26
21	DJH152083	6.93	14.37	56.56	193.28	100.09	3.26	5.01	3.30	2.12	6.70	2.72	2.85
224	DJH152458	6.91	15.31	58.57	204.39	116.38	0.01	3.31	3.82	1.50	1.36	2.82	3.02
193	DJH152421	6.90	14.00	56.87	200.43	107.42	0.75	4.12	2.99	1.87	4.83	2.77	3.04
198	DJH152425	6.88	14.19	57.87	209.95	114.30	2.61	5.05	4.68	2.62	10.19	3.06	2.70
82	DJH16182	6.88	14.95	56.99	201.54	105.55	0.32	3.43	3.28	1.50	15.00	2.34	2.48
51	DJH152264	6.88	14.57	60.55	209.98	121.20	0.02	4.58	4.31	1.82	1.68	2.83	2.87
105	DJH152288	6.84	13.69	56.11	209.07	107.05	-0.52	4.22	2.50	1.62	7.84	2.78	2.78
209	DJH152439	6.84	14.75	57.03	195.20	98.79	3.73	3.36	5.75	2.13	0.13	3.27	2.90
151	DJH152408	6.82	15.18	57.77	208.84	121.49	8.15	3.38	4.42	1.64	-0.15	2.82	3.24
98	DJH152283	6.82	14.32	55.00	203.61	107.83	11.45	4.91	4.03	2.01	7.75	3.08	3.21
33	DJH152094	6.80	13.52	57.00	200.99	109.45	0.06	4.20	5.74	2.12	14.06	2.81	2.75
103	DJH152288	6.79	13.70	55.12	204.64	99.82	3.08	5.04	3.93	2.12	6.42	2.88	2.83
162	DJH161162	6.79	14.36	55.98	218.41	113.55	9.31	4.56	6.77	1.25	3.64	3.06	2.81
171	DJH161171	6.79	14.97	57.61	211.17	112.94	5.31	3.97	6.06	1.88	3.34	2.79	2.94
216	DJH152446	6.78	14.37	55.02	197.22	95.97	7.49	3.70	1.48	2.62	0.23	2.85	3.05
81	DJH16181	6.76	14.64	56.80	210.04	114.41	0.18	4.10	10.19	1.12	11.52	2.83	2.64
199	DJH152427	6.76	13.17	55.66	206.14	106.54	0.57	5.53	6.42	2.75	-0.04	2.85	2.38
100	DJH152285	6.74	14.45	58.90	207.74	110.68	0.16	4.72	4.77	2.50	19.61	3.11	3.24
52	DJH152265	6.73	14.33	56.82	194.13	100.62	17.73	5.50	3.04	2.13	5.10	3.13	2.71
192	DJH161192	6.72	13.88	56.02	211.51	105.63	0.00	5.65	3.85	1.25	9.31	2.86	2.99
31	DJH152093	6.72	14.10	57.01	198.16	108.13	5.76	3.46	5.98	1.75	7.19	2.93	3.26
176	DJH161176	6.71	14.16	56.26	205.10	108.06	3.65	4.25	7.36	1.26	1.93	2.98	2.89
89	DJH16189	6.70	14.37	55.48	208.82	111.40	3.36	4.75	7.48	1.62	10.73	2.99	2.86
135	DJH152392	6.69	14.97	59.89	199.97	115.39	-0.21	5.34	4.86	2.62	1.32	3.06	3.10
196	DJH152424	6.68	13.71	56.78	197.46	94.95	0.03	3.81	7.41	1.25	11.77	3.25	2.75
72	DJH16172	6.67	14.54	58.39	212.08	116.01	-0.18	4.55	3.67	1.75	5.24	2.72	3.02
157	DJH152415	6.66	14.49	60.10	201.31	124.16	0.24	3.38	2.91	2.01	3.08	2.62	2.51
124	DJH152309	6.65	13.93	56.56	192.83	95.19	-1.20	3.86	4.32	1.38	0.04	2.94	3.16
24	DJH152087	6.64	12.92	55.07	206.30	101.96	-0.02	5.64	3.14	1.37	2.30	3.43	3.33
13	CH124004	6.64	13.29	56.45	189.98	103.75	2.64	4.96	8.06	2.38	5.24	3.25	3.14
66	DJH16166	6.64	15.03	54.87	210.09	112.28	5.21	5.97	3.35	1.63	0.87	3.25	3.28
111	DJH152294	6.63	14.16	57.83	201.48	106.97	19.60	3.93	2.72	1.87	4.33	3.00	2.95
214	DJH152449	6.63	14.03	55.04	198.16	107.73	6.62	4.30	4.89	1.37	9.88	2.73	2.62
211	DJH152446	6.63	14.84	54.90	208.24	107.54	21.24	4.90	3.12	2.12	1.06	3.07	2.96
156	DJH152414	6.62	13.60	56.90	199.33	114.61	0.03	3.25	6.57	1.63	2.94	2.85	2.87
117	DJH152302	6.60	14.84	56.18	193.61	100.39	7.74	4.22	6.55	2.13	14.08	2.94	2.59
123	DJH152308	6.60	14.25	57.47	202.26	104.83	5.11	3.62	3.05	1.99	5.77	2.69	2.65
42	DJH152104	6.59	15.10	56.39	198.06	102.00	-1.00	4.14	5.58	1.75	2.80	2.82	2.49
165	DJH161165	6.58	15.65	55.30	209.70	106.49	9.90	4.24	4.68	1.38	-0.07	2.94	2.97
43	DJH152256	6.58	14.26	56.83	203.69	106.22	1.54	4.65	2.88	2.13	2.96	3.03	2.82
107	DJH152290	6.57	14.44	56.83	201.32	101.11	0.09	4.08	4.72	2.50	7.83	2.75	3.08
65	DJH16165	6.57	14.21	55.52	175.94	93.73	4.10	3.18	10.27	1.75	5.89	3.03	3.16
115	DJH152298	6.56	14.32	61.28	204.74	118.06	0.09	5.59	5.60	2.25	0.18	2.88	2.75
88	DJH16188	6.56	13.52	54.37	201.38	103.52	2.10	4.54	5.35	1.50	9.51	2.78	2.58
14	DJH152075	6.54	13.15	55.54	206.88	113.21	-0.16	5.72	3.99	2.13	0.32	2.84	2.95
138	DJH152395	6.54	15.14	59.74	202.40	111.86	0.62	4.10	3.61	2.37	4.22	2.92	3.22
215	DJH152450	6.53	13.54	56.59	195.68	107.14	0.28	3.99	6.86	2.12	1.68	2.89	2.60
122	DJH152307	6.51	13.82	55.80	196.01	96.95	-0.11	3.88	5.22	1.63	0.99	3.00	2.71
137	DJH152394	6.51	14.46	61.14	205.60	121.55	3.65	4.40	6.49	2.12	0.06	3.07	3.00
109	DJH152292	6.51	14.52	55.89	201.44	101.66	-0.41	4.91	7.63	2.63	-0.11	2.90	2.43
30	DJH152092	6.50	14.08	57.14	192.54	88.03	0.62	4.08	6.67	2.24	4.41	2.73	2.84
54	DJH152268	6.49	14.15	56.73	194.98	104.87	0.31	4.40	4.68	1.75	4.98	2.33	2.34
2	DJH152069	6.48	12.79	53.63	195.95	91.98	0.02	4.62	4.21	1.75	1.68	3.10	3.66
Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	HC	EA	TEX

12	CH124163	6.48	13.93	53.68	201.92	98.32	4.76	5.43	5.18	2.00	2.23	3.09	3.30
189	DJH161189	6.47	12.41	54.32	203.94	95.47	0.88	5.68	6.47	1.63	1.70	2.94	2.96
222	DJH152456	6.46	14.76	59.77	219.83	123.46	12.58	4.66	2.28	2.75	0.06	2.78	3.08
204	DJH152434	6.46	13.27	57.11	189.03	100.19	8.57	5.31	2.81	2.25	3.41	3.03	3.12
56	DJH152270	6.44	13.10	54.63	207.33	106.45	7.33	4.93	7.57	2.38	4.46	2.80	2.45
77	DJH16177	6.44	14.63	56.93	184.08	114.90	6.38	4.68	5.39	2.12	1.51	2.80	2.96
148	DJH152405	6.44	14.46	59.77	196.35	115.30	5.57	4.79	4.54	1.50	4.17	3.13	3.06
125	DJH152310	6.43	14.25	57.40	214.21	112.79	10.94	4.82	3.46	2.38	4.24	2.62	2.57
26	DJH152089	6.43	13.32	54.11	192.09	96.09	0.72	3.80	7.41	2.12	10.04	2.98	2.93
173	DJH161173	6.43	14.45	55.22	197.69	108.55	0.20	3.76	3.22	1.37	4.46	2.53	2.06
18	DJH152079	6.41	13.15	56.64	200.53	98.88	4.85	5.50	2.37	2.37	3.90	3.18	3.38
113	DJH152296	6.39	13.92	56.63	203.73	104.94	0.42	3.96	1.90	2.00	0.12	2.76	3.00
142	DJH152399	6.38	15.33	59.78	206.61	121.67	2.78	4.51	2.25	1.87	5.62	2.45	2.90
127	DJH152382	6.37	14.44	57.34	207.86	111.91	7.06	4.50	5.85	1.37	0.94	3.01	3.01
57	DJH152271	6.37	14.30	56.33	205.55	104.08	5.68	4.33	2.97	2.37	-0.01	2.92	2.52
161	DJH152420	6.35	13.42	59.36	211.98	126.01	2.38	3.45	8.64	2.12	2.38	2.99	2.77
102	DJH152287	6.34	14.06	56.41	205.19	108.52	-0.05	4.37	4.96	1.62	18.70	3.11	3.03
16	DJH152077	6.34	13.89	56.26	194.56	108.92	-0.15	4.29	8.31	2.88	2.47	3.01	2.97
163	DJH161163	6.33	14.29	57.24	195.09	108.67	5.74	4.73	8.12	1.88	1.55	2.92	2.88
41	DJH152103	6.33	14.66	58.21	203.71	109.97	1.22	4.05	4.61	1.75	2.76	2.94	3.07
238	SC403	6.32	13.03	49.85	207.79	106.48	3.85	4.47	10.76	2.37	4.09	3.43	3.41
121	DJH152306	6.31	14.16	56.02	201.29	100.22	0.66	4.02	5.06	1.99	5.34	2.77	2.85
59	DJH16159	6.30	12.77	53.98	196.37	105.47	3.73	4.85	3.66	1.89	0.49	3.24	3.36
180	DJH161180	6.28	15.51	55.43	198.78	107.73	-1.18	3.16	4.48	1.25	7.62	2.15	2.28
63	DJH16163	6.28	15.88	57.99	213.15	115.58	0.84	4.63	4.55	1.25	6.10	2.66	3.12
175	DJH161175	6.27	14.80	54.74	195.17	97.99	0.63	3.62	8.80	1.49	6.34	2.84	2.76
229	DJH152464	6.27	14.33	56.64	203.07	105.15	22.64	4.79	3.61	2.12	1.79	2.96	2.76
91	DJH152276	6.26	14.48	57.75	200.99	109.45	-0.20	3.97	6.17	1.37	5.61	3.06	2.94
1	DJH161001	6.26	13.85	60.38	201.16	108.44	0.10	5.00	5.00	2.88	2.02	2.74	2.37
86	DJH16186	6.24	15.08	55.48	194.03	98.85	4.96	4.11	3.65	1.38	2.04	2.50	2.63
132	DJH152389	6.24	13.84	61.89	193.50	113.49	5.44	5.42	9.38	1.74	0.08	3.25	2.76
120	DJH152305	6.23	14.52	55.94	208.92	107.61	3.06	4.73	2.74	1.38	2.32	2.76	2.23
15	DJH152076	6.20	14.19	59.12	201.37	107.15	0.12	3.76	6.20	2.12	2.89	3.13	2.97
202	DJH152432	6.18	14.44	57.31	205.56	103.07	4.61	4.39	6.74	1.50	9.19	2.79	2.78
49	DJH152262	6.18	14.69	56.65	206.80	106.71	-1.59	5.32	7.98	2.75	2.47	2.67	2.44
4	CH131279	6.16	14.74	55.68	196.79	111.95	0.40	5.01	1.57	2.00	0.17	2.71	2.59
92	DJH152277	6.16	15.02	57.38	211.44	112.88	2.06	5.28	4.16	1.51	3.56	2.68	2.20
17	DJH152078	6.15	13.76	58.09	186.08	94.86	-0.51	4.20	5.31	2.12	1.49	3.00	3.25
205	DJH152435	6.15	15.14	59.80	191.95	105.09	6.82	4.99	3.01	1.38	3.57	2.67	2.58
230	DJH152465	6.14	14.11	57.62	199.59	108.22	8.69	4.42	4.04	2.38	9.62	2.87	2.74
5	CH131280	6.13	14.77	59.29	202.87	102.93	-0.18	3.92	5.57	2.12	16.48	3.14	3.22
183	DJH161183	6.10	13.63	54.49	218.90	103.91	-0.93	3.78	6.55	1.13	6.65	2.60	2.59
45	DJH152258	6.09	14.46	56.27	214.28	107.69	0.44	4.31	4.01	1.37	7.52	2.64	2.97
190	DJH161190	6.09	14.90	55.74	194.05	102.98	0.60	4.64	3.21	1.43	4.14	2.87	2.76
35	DJH152096	6.09	13.77	49.73	183.40	105.52	3.09	5.39	5.94	2.75	5.58	3.02	2.76
74	DJH16174	6.07	14.05	56.19	206.80	99.32	9.24	4.81	8.16	1.75	3.66	3.03	2.62
139	DJH152396	6.07	14.64	60.62	203.37	110.66	3.75	5.43	3.16	2.12	-0.19	3.03	2.99
11	CH124004	6.05	13.60	55.57	206.07	116.90	4.40	4.01	5.27	1.57	0.10	3.07	3.11
19	DJH152080	6.03	13.74	60.02	202.62	105.70	2.57	5.23	6.08	1.88	3.17	3.29	3.34
187	DJH161187	6.03	15.17	58.21	206.01	105.27	0.63	4.26	5.67	1.25	2.88	2.77	2.83
20	DJH152081	6.02	13.76	57.61	200.79	116.73	1.96	4.54	4.33	2.63	0.89	3.04	3.36
174	DJH161174	6.01	13.99	56.65	199.73	95.32	6.26	3.89	5.62	2.13	6.36	2.62	1.94
237	SC301	5.99	12.93	48.62	194.64	83.32	-0.29	5.60	3.08	2.62	2.55	3.29	3.07
6	DJH152070	5.99	13.85	55.19	209.11	110.37	0.70	5.06	4.67	1.51	-0.23	2.77	3.16
29	CH131042	5.99	13.34	56.90	210.88	104.80	1.80	3.50	6.66	2.38	6.22	5.26	3.18
217	DJH152450	5.98	13.36	57.93	195.48	101.02	2.84	3.43	3.75	2.88	8.89	2.80	2.75
58	DJH152272	5.98	13.32	58.33	198.78	94.67	1.86	4.48	2.32	10.01	2.08	2.91	2.61
71	DJH16171	5.96	13.81	57.83	204.26	108.47	-0.10	4.49	6.20	1.62	4.10	3.11	2.67
34	DJH152095	5.92	13.17	56.64	207.35	102.32	7.30	5.48	2.92	2.25	4.95	2.92	3.11
10	DJH152073	5.90	14.61	56.69	197.85	91.07	0.31	4.30	4.03	1.38	8.49	2.92	3.31
203	DJH152433	5.90	15.00	58.39	187.65	104.93	-1.35	4.42	6.60	1.99	3.84	2.70	2.02
185	DJH161185	5.85	14.21	59.29	209.45	115.52	1.88	3.57	6.82	1.38	0.93	2.51	2.98
69	DJH16169	5.83	15.37	55.21	189.42	93.42	2.63	4.27	5.26	1.25	1.35	2.83	2.70
99	DJH152284	5.80	14.53	58.66	203.58	104.17	0.24	3.72	3.54	1.50	3.01	2.79	2.51
44	DJH152257	5.80	14.69	55.64	198.11	99.17	2.75	5.55	6.26	2.12	13.01	2.62	2.09
27	DJH152090	5.80	14.01	56.76	197.88	108.41	2.49	4.17	4.83	1.99	3.58	3.13	2.84
38	DJH152100	5.79	13.76	54.65	196.80	94.96	0.65	3.89	4.90	1.50	15.87	2.83	2.89
40	DJH152102	5.76	13.51	55.23	202.43	84.48	0.47	4.42	5.42	1.62	0.09	2.72	3.41
75	DJH16175	5.74	13.97	57.17	200.90	99.87	-0.12	4.53	4.02	2.25	0.24	2.96	3.01
154	PAN413	5.73	13.32	55.35	185.15	99.33	4.24	3.58	9.40	1.74	0.13	3.34	3.72
200	DJH152428	5.73	14.29	56.28	202.22	101.64	0.73	4.49	4.54	2.50	2.34	2.77	2.68
179	DJH161179	5.73	15.19	58.19	194.01	105.58	-0.36	3.28	3.82	1.25	0.03	2.91	2.67
67	DJH16167	5.72	13.69	53.66	195.03	99.32	-0.06	3.05	5.82	1.38	4.81	2.93	3.12
62	DJH16162	5.70	14.19	54.00	207.01	109.13	-0.34	4.33	9.07	1.37	7.20	3.21	2.53
152	DJH152410	5.69	13.69	60.31	198.51	109.43	2.05	3.83	6.67	2.00	4.72	3.00	3.30
191	DJH161191	5.68	14.10	56.60	203.03	105.33	2.66	4.67	5.72	1.88	-0.06	3.12	3.05
149	DJH152406	5.68	14.55	58.94	202.40	106.57	0.33	2.77	18.79	1.75	6.77	2.61	2.64
167	DJH161167	5.67	14.37	57.01	202.24	106.75	0.57	4.39	7.15	1.39	9.08	2.69	2.59
240	SC513	5.65	12.46	56.11	198.72	110.35	4.60	5.18	7.30	1.25	4.52	3.55	3.45
166	DJH161166	5.63	14.18	55.10	195.47	101.46	0.10	3.52	5.25	1.25	-0.17	2.99	2.37
60	DJH16160	5.61	13.86	53.86	207.40	108.07	1.02	5.17	11.78	1.25	4.91	3.10	2.95
9	CH124163	5.59	13.44	53.15	211.45	102.91	0.15	4.59	5.41	2.12	2.19	2.87	3.19
8	DJH152072	5.58	13.86	55.25	184.33	92.80	1.33	4.07	7.80	1.75	8.69	3.10	3.29
136	DJH152393	5.54	14.51	61.43	201.30	117.75	0.51	3.83	4.56	2.25	0.03	3.08	2.73
140	DJH152397	5.53	14.17	57.08	187.05	102.28	3.04	3.94	5.16	2.13	1.04	2.69	3.01
22	DJH152084	5.53	13.71	56.62	196.99	97.85	2.15	4.60	5.57	1.88	7.65	2.81	2.73
130	DJH152387	5.52	14.36	57.89	194.41	108.84	1.70	3.99	5.05	1.25	0.78	2.80	2.86
245	PHB30G19	5.51	14.97	57.78	202.14	112.06	1.40	4.63	4.52	1.88	1.85	3.08	2.78
210	DJH152440	5.50	14.38	57.87	191.21	103.63	7.56	4.69	4.47	2.13	6.12	2.63	2.29
48	DJH152259	5.50	14.81	55.15	212.30	102.20	6.30	5.18	1.79	2.50	-0.09	3.07	3.08
7	DJH152071	5.47	13.50	55.60	190.94	110.59	2.25	3.98	4.89	2.37	2.33	2.82	3.32
76	DJH16176	5.47	13.54	56.30	211.31	109.86	2.07	5.88	3.69	2.24	11.61	3.18	2.99
73	DJH16173	5.46	14.57	56.41	207.03	108.88	0.72	4.84	7.65	2.24	2.96	3.05	3.36
110	DJH152293	5.46	13.69	56.16	189.69	98.83	4.72	3.65	3.10	1.87	3.96	2.56	3.02
108	DJH152291	5.44	14.47	56.42	202.10	106.71	1.49	3.90	5.92	2.25	8.51	2.75	2.78
153	DJH152411	5.43	13.70	56.72	202.99	114.22	0.01	4.20	3.01	1.74	-0.07	2.75	2.80
96	DJH152281	5.40	13.98	57.02	200.96	99.14	8.56	4.06	4.74	1.74	7.55	2.72	2.86
25	DJH152088	5.37	13.75	55.63	202.26	98.21	0.15	4.34	2.39	1.73	3.92	2.83	2.97
104	DJH152282	5.37	14.68	54.61	214.01	103.82	1.84	4.58	4.68	1.88	1.94	2.62	3.09
141	DJH152398	5.36	14.29	61.45	195.82	114.78	1.16	3.77	6.20	2.12	2.46	2.59	2.80
150	DJH152407	5.35	14.40	57.23	207.91	119.81	2.95	3.02	5.10	2.24	6.00	2.61	2.62
220	DJH152453	5.34	13.93	57.10	208.15	100.10	6.84	5.71	2.65	3.00	2.05	3.09	2.72
112	DJH152295	5.34	14.52	56.84	207.36	100.25	4.94	3.95	2.73	1.75	8.05	2.58	2.95
143	DJH152400	5.33	13.17	59.17	201.37	116.02	0.00	3.43	6.79	2.75	0.02	2.64	2.97
197	DJH152422	5.32	14.34	54.26	202.37	100.68	4.85	5.60	2.94	2.50	1.80	3.05	3.10
195	DJH152423	5.32	13.88	55.62	184.47	89.91	8.22	3.79	5.10	1.25	0.43	3.01	2.47
181	SC635	5.29	13.81	57.67	212.60	98.83	8.19	3.96	4.18	1.33	5.20	3.19	3.14
Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	HC	EA	TEX

144	DJH152401	5.29	13.66	62.48	213.09	118.46	0.85	4.81	3.65	2.74	0.33	2.86	3.00
50	DJH152263	5.25	14.78	54.71	186.53	83.07	-0.05	3.97	5.43	2.50	0.11	2.80	2.66
213	DJH152448	5.23	15.05	55.42	198.84	97.88	15.65	4.43	1.40	1.24	-0.45	2.50	2.70
206	DJH152436	5.22	13.51	60.50	201.93	103.77	2.79	5.14	5.81	2.00	1.76	3.24	2.68
55	DJH152269	5.21	13.29	56.47	191.01	87.14	0.91	3.78	3.19	2.37	0.95	2.82	2.73
221	DJH152455	5.17	13.83	56.88	193.85	114.66	0.71	4.84	3.93	2.37	4.40	2.74	2.90
133	DJH152390	5.16	14.03	60.27	193.82	111.08	11.89	3.83	8.03	2.13	8.10	3.20	3.10
131	DJH152388	5.10	13.24	58.67	192.40	98.28	8.40	4.00	4.97	2.12	2.78	2.98	2.49
207	DJH152437	5.09	12.88	54.07	209.47	104.72	6.84	4.55	1.48	2.38	1.89	2.51	2.99
201	DJH152431	5.08	14.24	57.96	200.19	102.63	7.51	5.01	7.83	2.25	4.87	3.12	2.60
28	CH131155	5.05	12.58	55.97	184.30	98.03	-0.15	4.95	5.21	2.12	0.05	2.82	2.87
223	DJH152457	5.04	14.49	58.07	200.19	103.58	3.41	3.33	3.46	2.87	-0.38	2.64	3.18
182	DJH161182	5.00	14.45	58.42	195.72	110.94	0.94	3.95	6.65	1.25	2.36	3.01	2.54
36	DJH152097	4.98	13.62	56.94	206.29	107.75	0.75	4.50	3.78	2.38	2.04	3.17	3.00
3	CH131277	4.95	13.07	53.32	190.26	90.27	2.62	4.31	5.65	1.75	5.53	2.92	3.05
101	DJH152286	4.93	15.19	56.13	194.66	99.66	0.05	3.63	1.65	1.24	4.22	2.81	2.84
32	CH124165	4.92	14.52	54.67	208.74	100.42	3.33	4.52	3.79	2.12	9.06	2.84	3.06
172	DJH161172	4.85	14.98	59.46	199.52	112.08	10.85	3.69	11.93	1.12	1.15	2.79	2.79
218	DJH152451	4.80	14.81	60.91	196.09	108.44	-0.14	3.86	3.09	2.50	2.17	2.67	2.60
194	DJH152422	4.80	14.48	56.68	192.22	91.22	7.84	4.73	2.37	1.87	4.23	3.03	2.99
23	DJH152085	4.80	14.47	55.87	196.90	107.57	0.30	3.82	5.70	1.37	1.66	2.79	2.81
169	DJH161169	4.77	14.14	59.63	198.73	109.84	5.68	3.60	8.10	1.25	12.71	2.91	2.75
61	DJH16161	4.75	14.56	57.35	202.37	108.54	-0.03	4.36	6.59	1.38	8.29	2.80	2.77
68	DJH16168	4.71	13.31	59.73	180.90	105.03	7.84	4.33	9.61	1.99	6.52	3.16	3.53
145	DJH152402	4.68	13.73	61.53	214.60	126.84	0.06	3.96	8.30	2.13	5.99	2.75	2.84
47	DJH152260	4.63	13.98	55.61	184.02	93.10	3.63	3.96	3.54	1.37	0.21	3.03	2.69
184	DJH161184	4.60	14.57	56.56	206.24	109.78	2.50	3.17	7.28	1.12	4.45	2.26	2.13
118	DJH152303	4.58	23.08	56.22	211.77	106.88	10.02	4.01	3.79	1.88	4.67	2.75	2.70
226	DJH152460	4.54	14.00	55.99	206.62	102.94	3.79	3.66	2.28	2.38	1.49	2.49	2.26
70	DJH16170	4.49	14.29	53.71	188.94	98.95	0.17	5.36	7.92	1.75	3.74	3.42	3.31
219	DJH152452	4.44	14.39	57.26	207.71	101.88	10.34	3.46	2.90	1.99	2.42	2.43	2.44
170	DJH161170	4.10	13.83	58.55	209.67	114.81	0.48	3.37	3.32	1.38	0.21	2.43	2.48
228	DJH152462	4.08	13.76	54.98	213.58	104.97	3.54	5.00	0.65	1.75	0.76	2.67	2.42
225	DJH152459	3.92	14.76	56.71	203.63	106.82	0.21	3.41	6.95	1.95	3.26	2.61	2.37
188	DJH161188	3.89	14.54	57.37	199.84	104.64	0.13	3.18	3.13	1.25	-0.09	2.22	1.96
106	DJH152289	3.76	13.55	56.86	216.79	112.51	-0.45	4.29	7.54	1.37	12.63	2.99	2.75
129	DJH152384	3.71	12.38	60.98	193.91	108.59	7.95	4.38	8.38	2.26	1.43	3.31	3.16
93	DJH152278	3.49	14.04	57.42	207.79	114.98	8.57	3.63	4.05	1.50	3.01	2.52	2.77
134	DJH152391	2.69	12.10	59.80	205.33	112.85	-0.10	4.02	9.18	1.74	0.02	2.95	3.01
Mean		6.19	14.23	56.97	202.57	107.13	3.20	4.33	5.09	1.90	4.44	2.87	2.88
LSD		1.41	2.08	2.55	16.73	15.16	9.89	1.37	5.99	1.50	9.72	0.43	0.65
CV		11.64	7.43	2.28	4.21	7.21	0.00	15.95	59.90	40.09	111.56	7.67	11.41
Heritability		0.75	0.30	0.82	0.50	0.62	0.26	0.58	0.09	0.39	0.32	0.77	0.35

GY- grain yield, MOI- moisture AD-anthesis date, , PH-plant height, EH-ear height, SL-stem lodging SEN-senescence, ER-ear rots, GLS- grey leaf spot, HC-husk cover, EA- ear aspect, TEX-texture.

Appendix 5.2 Grain yield and agronomic traits of 200 exotic x local three-way hybrids in set 2 in descending order of grain yield

Entry	Hybrid	GY	AD	MOI	PH	EH	SL	SEN	ER	GLS	TURC	EA	TEX
207	SC727	9.67	70.89	16.71	234.30	130.00	6.60	4.70	10.59	1.97	1.74	2.66	3.53
199	CZH141028	8.68	65.71	16.05	237.70	141.60	5.48	4.91	3.09	1.53	1.75	2.88	2.65
202	10C3271	8.47	63.05	16.36	233.30	120.00	3.95	5.37	3.52	3.03	1.91	2.44	2.97
209	PAN7M-81	8.40	67.28	15.55	240.00	134.60	1.93	4.24	4.37	1.62	1.82	2.50	2.88
91	CH124294	8.39	63.82	15.99	224.40	110.40	-0.17	4.18	2.54	1.85	1.66	2.38	2.77
147	DJH152994	8.23	65.96	15.85	212.90	113.50	5.08	4.50	2.41	1.30	1.60	2.88	2.69
152	DJH153000	8.18	65.65	16.40	219.20	106.70	6.53	4.41	2.30	1.85	1.74	2.60	2.49
201	CZH131007	8.18	67.55	16.90	214.50	109.30	5.49	5.15	16.57	2.26	1.86	3.06	5.70
87	DJH162087	8.13	66.44	16.64	209.30	122.20	1.30	5.42	5.08	2.46	1.81	2.74	2.21
153	DJH153001	8.13	65.22	16.42	215.10	108.80	10.79	5.60	5.68	2.03	1.78	2.89	2.84
158	DJH153006	8.07	63.80	15.66	210.30	109.30	0.83	4.53	6.11	1.68	1.59	2.74	2.89
67	DJH152759	8.06	64.80	16.37	206.20	102.60	4.08	4.85	1.84	1.88	1.66	2.15	2.43
132	DJH152825	8.02	67.02	16.77	218.90	118.90	2.51	5.06	2.57	1.78	1.70	2.60	2.68
206	SC643	7.96	65.55	16.58	224.50	119.10	8.58	4.50	4.98	2.13	1.80	2.44	2.46
144	DJH152991	7.94	65.05	16.42	207.70	102.70	1.63	4.75	2.92	1.58	1.69	2.70	2.28
198	CZH131013	7.94	65.55	17.14	219.30	102.20	3.35	4.94	5.04	1.60	1.64	2.76	2.81
135	DJH152981	7.92	65.22	15.91	221.60	109.40	-0.44	5.28	3.41	2.13	1.70	2.49	2.64
93	CH133348	7.89	67.55	16.32	226.40	119.20	5.42	4.65	2.58	1.78	1.76	2.88	2.48
92	DJH152782	7.87	65.47	15.76	207.10	113.20	0.36	5.58	2.64	1.78	1.56	2.57	2.34
72	DJH152763	7.86	62.64	16.41	223.90	118.80	3.68	5.68	4.53	2.00	1.72	2.94	3.32
89	DJH152780	7.86	66.89	16.44	207.70	117.50	4.46	4.79	4.29	2.03	1.82	3.00	3.07
99	DJH152785	7.86	66.39	16.70	230.40	123.20	3.81	4.20	5.18	1.71	1.66	2.83	2.93
184	DJH153031	7.86	64.47	17.05	223.10	116.90	3.67	4.55	2.62	1.83	1.98	2.58	2.14
97	CH133697	7.81	66.97	16.29	217.80	113.70	0.06	5.53	5.37	1.90	1.72	2.95	2.94
109	DJH152796	7.80	64.30	16.60	206.40	103.80	3.50	4.87	4.49	2.29	1.60	2.15	2.26
128	DJH152820	7.80	65.72	17.60	211.10	110.40	4.69	4.83	1.71	2.03	1.59	2.69	2.22
208	PAN53	7.75	65.89	17.19	209.90	107.80	1.25	5.57	4.34	2.34	1.75	2.55	2.71
88	DJH152779	7.74	66.64	16.86	213.30	116.00	0.90	4.67	3.85	1.60	1.63	2.49	2.76
102	DJH152789	7.74	65.56	16.79	222.30	113.30	6.24	4.88	3.74	2.31	1.48	2.63	2.51
107	DJH152794	7.73	68.05	15.79	207.10	105.50	1.42	5.50	4.24	2.03	1.79	2.69	2.98
116	DJH152803	7.73	63.30	16.04	211.60	110.00	6.05	5.44	3.67	2.13	1.67	2.74	2.13
204	SC419	7.72	62.39	15.87	229.00	120.00	1.06	5.64	5.77	1.96	1.95	2.87	3.18
40	DJH152614	7.70	62.22	17.22	205.20	88.70	8.26	4.93	3.12	1.87	1.57	2.38	3.84
84	DJH152775	7.67	66.14	16.10	221.70	113.10	3.91	6.10	6.13	2.31	1.89	2.82	3.02
56	DJH152631	7.62	64.22	16.91	196.20	98.27	0.25	4.63	5.66	1.88	1.66	2.82	2.51
142	DJH152989	7.61	65.47	16.85	219.20	106.30	3.57	5.53	8.19	2.03	1.69	2.83	3.06
100	DJH152786	7.60	65.89	16.94	201.00	103.30	2.03	4.75	2.65	1.55	1.77	2.97	3.19
36	DJH152610	7.59	66.89	16.73	219.90	115.50	0.23	5.12	6.48	1.63	1.77	2.72	2.72
134	DJH152828	7.57	65.11	16.61	214.40	115.40	5.83	5.52	3.28	2.28	1.64	2.74	2.11
3	DJH152498	7.56	62.55	16.39	207.70	99.02	2.62	5.53	6.17	1.30	1.52	2.67	2.49
127	DJH152819	7.56	64.14	16.22	209.50	102.50	11.99	4.28	2.06	2.26	1.66	2.67	2.23
35	DJH152609	7.53	63.05	16.55	202.10	103.00	7.65	5.56	3.86	1.40	1.60	2.68	2.49
165	DJH153012	7.52	68.22	15.30	223.90	121.60	1.62	5.26	5.50	1.90	1.59	2.74	2.60
5	DJH152500	7.46	63.72	16.82	235.90	113.30	3.46	6.22	9.11	1.58	1.73	2.82	2.90
140	DJH152987	7.46	67.05	15.62	210.30	94.35	4.59	4.95	6.57	2.16	1.58	2.77	3.02
173	DJH153020	7.45	65.00	16.83	227.20	116.80	1.05	4.41	9.07	1.69	2.07	2.75	3.03
83	DJH152774	7.43	64.80	16.23	517.40	116.10	4.87	5.28	4.17	2.28	1.69	2.80	2.92
10	DJH152504	7.42	62.30	16.97	221.40	109.30	2.56	5.82	7.32	1.83	1.72	2.57	2.93
117	DJH152803	7.38	66.33	16.17	214.10	111.40	2.27	6.31	5.05	2.28	1.87	3.04	2.50
154	DJH153002	7.37	64.22	15.98	216.10	104.90	5.17	5.61	6.75	2.21	1.82	2.78	2.95
197	CZH131001	7.36	64.22	16.60	215.10	100.60	1.08	6.09	4.65	1.99	1.60	2.88	1.95
160	DJH153008	7.34	62.05	15.45	213.50	109.80	3.44	5.20	6.44	1.69	1.68	2.75	2.49
12	DJH152503	7.32	64.55	16.13	229.20	115.80	4.46	5.54	4.36	1.93	1.77	2.77	3.32
32	DJH152605	7.30	61.97	15.69	213.30	98.15	2.63	5.88	2.72	1.80	1.49	2.92	2.99
155	DJH153003	7.30	63.80	15.50	197.50	91.39	1.64	5.42	3.28	1.60	1.69	2.84	3.08
133	DJH152826	7.27	65.05	16.98	221.30	118.00	5.65	5.21	3.81	1.65	1.91	2.66	2.36
104	DJH152791	7.26	63.64	16.12	237.10	114.50	3.32	5.44	5.07	2.25	1.59	2.66	2.90
17	DJH152509	7.25	63.39	15.48	214.40	109.80	1.28	4.80	4.11	1.68	1.58	2.61	2.43
143	DJH152990	7.24	68.47	15.91	212.70	117.90	7.97	4.56	5.28	1.40	1.54	3.00	3.06
37	DJH152611	7.19	64.72	16.79	219.10	100.20	1.72	5.70	3.68	1.65	1.71	2.69	2.61
187	DJH153029	7.18	64.39	17.05	218.90	111.80	0.42	5.87	4.23	1.52	1.72	2.77	3.03
29	DJH152524	7.17	62.97	16.34	193.80	100.30	8.25	6.14	2.55	1.80	1.74	5.34	2.94
62	DJH152640	7.17	65.72	17.49	232.20	114.70	8.91	5.17	5.44	1.58	1.81	2.78	2.60
16	DJH152504	7.15	62.30	16.86	209.60	98.68	1.57	4.99	3.96	1.93	1.64	2.75	3.13
177	DJH153025	7.14	64.14	16.37	249.00	115.60	2.44	6.20	4.13	2.10	1.93	2.83	2.48
136	DJH152982	7.13	65.55	15.62	217.10	106.40	0.89	5.69	5.62	2.21	1.85	2.91	3.74
63	CH142227	7.11	62.80	15.92	222.10	115.80	3.98	5.65	3.80	1.94	1.58	2.58	3.15
137	DJH152984	7.11	64.55	16.16	211.60	102.20	0.96	5.55	3.45	2.33	1.60	2.84	2.66
168	DJH153015	7.10	66.80	15.50	217.60	111.70	1.11	5.91	6.98	2.35	1.66	2.94	2.77
200	CZH131006	7.08	66.39	16.31	224.70	108.10	4.54	5.31	4.33	1.91	1.81	2.38	2.91
171	DJH153018	7.07	64.72	16.74	213.50	108.10	0.46	5.63	5.36	1.83	1.97	2.65	2.96
77	DJH152766	7.06	66.05	16.52	208.60	109.80	6.57	4.59	3.76	1.85	1.73	2.68	3.10
55	DJH152630	7.05	66.30	16.43	212.20	110.50	1.11	4.69	6.02	1.47	1.75	2.94	2.89
166	DJH153013	7.05	66.14	14.98	213.60	112.20	2.45	5.72	3.95	2.05	1.57	2.97	3.15
188	DJH153035	7.05	62.05	16.19	210.80	94.52	0.04	4.80	5.11	1.88	1.87	2.73	3.12
103	DJH152790	7.02	65.05	15.88	214.30	111.00	1.17	5.50	2.90	1.55	1.68	2.60	1.98
139	DJH152986	7.02	65.05	15.99	211.60	103.10	1.64	5.47	6.06	1.65	1.71	2.53	2.94
9	DJH152503	7.00	64.55	16.47	205.40	104.20	2.13	5.43	3.58	2.06	1.67	2.75	2.85
151	DJH152998	7.00	67.14	16.68	195.20	110.60	12.83	5.44	6.19	2.26	1.67	2.57	2.61
156	DJH153004	7.00	67.09	15.64	217.20	120.50	0.09	5.29	7.71	1.90	1.67	3.01	2.84
71	DJH152762	6.98	65.97	16.20	220.90	129.00	8.91	5.43	3.57	2.26	1.61	2.66	2.77
145	DJH152992	6.98	64.89	16.51	211.40	108.20	1.27	5.11	9.36	2.47	1.63	2.81	2.99
185	DJH153032	6.98	64.97	16.89	210.00	109.50	-0.07	5.27	14.07	1.47	1.78	2.98	2.57
54	DJH152629	6.97	62.89	16.77	216.10	102.20	0.92	6.00	4.17	1.72	1.76	2.72	2.24
57	DJH152632	6.96	64.30	16.67	210.60	105.20	2.82	5.94	3.56	1.44	1.45	2.64	2.02
112	DJH152799	6.96	65.64	16.64	220.90	117.20	2.43	4.96	5.93	2.28	1.89	2.88	2.53
121	DJH152809	6.94	66.05	16.68	238.60	121.70	1.78	6.47	9.25	2.51	1.93	2.56	2.81
46	DJH152620	6.93	64.80	16.52	198.80	95.20	2.63	5.12	6.79	1.54	1.76	2.72	2.74
138	DJH152985	6.90	64.55	15.92	207.90	102.10	9.06	5.20	4.35	1.60	1.63	2.97	2.81
159	DJH153007	6.90	66.14	16.44	212.00	108.90	0.20	5.43	4.97	1.83	1.63	2.86	2.86
186	DJH153033	6.90	63.17	16.54	210.20	101.20	2.77	5.27	8.64	1.96	1.91	2.67	2.88
180	DJH153028	6.89	64.30	16.72	226.70	116.30	0.85	6.12	5.05	1.62	1.61	2.93	2.52
175	DJH153022	6.87	64.89	16.85	210.70	102.50	0.16	5.07	3.12	2.10	1.77	2.81	2.95
76	DJH153053	6.86	65.00	16.32	217.50	117.60	1.99	4.57	7.30	1.93	1.76	2.85	2.83
131	DJH152824	6.85	63.86	17.26	199.80	96.22	1.75	5.69	2.43	2.10	1.56	2.90	2.16
146	DJH152993	6.85	65.30	16.26	214.90	108.40	0.33	5.23	2.87	1.42	1.72	3.08	3.06
196	DJH153052	6.85	65.14	16.99	208.30	109.90	1.09	4.85	5.34	1.90	1.73	3.07	3.04
111	DJH152798	6.84	64.72	15.91	218.70	113.20	5.18	5.74	7.39	2.02	1.67	2.96	2.65
195	DJH153049	6.84	67.39	17.29	222.40	125.50	0.15	5.14	3.83	1.93	1.87	3.15	2.73
Entry	Hybrid	GY	AD	MOI	PH	EH	SL	SEN	ER	GLS	TURC	EA	TEX

38	DJH152612	6.83	62.47	17.02	212.20	95.36	0.91	5.46	5.32	1.55	1.63	2.93	2.68
150	DJH152996	6.82	64.72	15.77	203.80	104.40	1.19	4.82	3.83	1.81	1.73	2.94	3.30
23	DJH152515	6.78	62.22	15.74	202.30	91.03	0.12	5.62	3.28	1.97	1.68	2.66	2.34
120	DJH152807	6.77	68.22	16.14	220.30	123.20	6.09	4.47	4.32	1.93	1.65	2.99	2.51
79	DJH152768	6.76	65.97	17.24	225.60	129.30	1.58	5.43	3.13	1.97	1.77	2.63	2.93
181	DJH153029	6.75	65.02	16.18	217.80	108.70	3.78	5.33	6.03	1.47	1.75	2.61	2.77
114	DJH152801	6.74	63.55	17.42	220.00	112.50	9.55	6.40	3.63	2.13	1.77	3.18	2.93
41	DJH152615	6.72	62.14	17.58	214.50	102.60	6.65	6.35	4.80	1.50	1.81	2.64	2.80
118	DJH152804	6.72	65.55	16.38	213.00	113.80	5.98	4.86	4.18	1.62	1.72	2.85	2.48
157	DJH153005	6.72	68.72	15.71	218.20	109.50	0.04	4.43	2.28	1.65	1.79	2.72	2.24
164	DJH153011	6.72	67.72	15.88	204.70	118.50	1.95	5.81	4.67	1.75	1.50	2.90	2.86
113	DJH152800	6.71	65.47	16.91	198.40	98.25	7.14	5.15	5.05	1.77	1.62	2.77	2.40
163	DJH153010	6.71	66.05	15.10	211.70	117.30	2.55	6.30	4.39	1.52	1.77	3.00	2.98
30	DJH152525	6.68	66.72	16.20	209.40	107.40	3.35	5.54	5.57	2.09	1.55	2.81	2.31
51	DJH152625	6.66	62.55	16.79	202.40	103.70	-0.35	4.64	5.59	1.62	1.54	2.69	2.89
73	CH124280	6.66	63.55	16.62	212.00	113.90	1.38	4.97	2.78	1.85	1.72	2.87	3.02
167	DJH153014	6.66	65.30	15.60	208.70	106.60	0.05	5.66	6.32	2.28	1.64	2.97	2.60
59	DJH152634	6.65	62.22	16.27	211.30	98.59	2.33	6.01	2.90	1.75	1.63	2.54	2.54
108	DJH152795	6.65	64.64	17.25	203.90	101.10	0.34	5.25	7.70	1.40	1.75	2.73	2.75
148	DJH152995	6.65	65.39	15.90	219.10	107.30	3.73	4.49	4.43	1.58	1.61	2.78	2.66
52	DJH152626	6.64	64.22	16.43	213.60	105.20	2.65	6.16	5.17	1.90	1.63	2.45	4.63
90	DJH152781	6.64	65.30	15.91	210.40	102.90	3.91	4.99	5.30	2.12	1.65	2.32	2.64
123	DJH152812	6.64	62.74	16.27	208.40	104.90	0.19	4.84	2.80	2.18	1.51	2.59	2.58
39	DJH152613	6.63	63.90	16.50	219.50	114.40	8.47	5.22	3.67	1.35	1.64	2.82	2.62
170	DJH153017	6.62	67.05	16.14	209.40	110.90	1.09	4.64	1.79	1.47	1.62	2.61	3.25
174	DJH153021	6.62	63.55	16.53	215.70	107.60	0.06	6.20	7.98	1.47	1.81	2.91	2.93
192	DJH153044	6.61	64.80	17.09	518.60	103.80	-0.09	5.03	3.85	1.55	1.69	2.67	2.90
61	DJH152639	6.60	65.47	16.13	212.40	105.70	4.02	5.98	5.37	1.90	1.66	2.92	2.35
110	DJH152797	6.59	66.22	16.61	229.80	121.40	0.07	6.15	9.32	2.08	1.70	3.06	2.78
149	DJH152997	6.59	63.72	15.88	206.60	104.60	1.07	4.90	4.09	1.52	1.61	3.07	2.69
161	DJH153009	6.57	60.64	15.16	203.00	95.01	0.29	6.14	5.91	2.00	1.82	3.03	2.86
21	DJH152513	6.56	63.05	15.19	206.30	101.60	3.27	6.26	4.75	1.83	1.79	3.04	2.12
24	DJH152516	6.56	63.89	15.84	216.90	104.80	5.76	6.60	3.92	1.83	1.73	2.77	2.65
101	DJH152787	6.56	64.97	16.56	196.90	103.20	6.45	5.97	5.89	1.93	1.74	2.89	3.15
141	DJH152988	6.56	67.64	16.27	212.70	107.50	-0.02	4.59	5.32	2.21	1.78	2.65	3.10
22	DJH152514	6.55	63.39	15.85	184.90	83.12	2.73	5.27	3.58	1.62	1.58	3.03	2.70
86	DJH152777	6.53	67.20	16.71	214.20	108.10	16.49	4.86	5.67	1.96	1.64	2.96	3.11
105	DJH152792	6.53	63.05	16.09	226.10	113.70	1.30	5.82	9.44	1.83	1.86	3.04	2.91
176	DJH153023	6.52	65.89	16.64	206.90	101.30	0.87	5.67	8.27	1.69	1.72	2.82	2.77
66	DJH152758	6.50	64.47	16.44	198.60	108.50	0.36	5.52	3.60	1.37	1.53	2.69	2.62
162	CH14404	6.50	67.72	15.95	209.10	129.30	0.66	5.03	7.18	2.51	1.86	2.73	2.22
6	DJH152501	6.47	66.14	15.52	222.20	113.90	1.41	5.16	1.39	2.08	1.75	2.56	2.65
65	DJH152756	6.47	66.55	16.21	219.90	118.50	4.37	4.64	4.79	2.35	1.81	2.57	2.55
26	DJH152521	6.46	65.89	15.73	177.70	91.93	11.26	5.15	5.89	2.18	1.74	2.93	2.34
48	DJH152622	6.46	65.28	16.70	215.90	105.60	0.97	5.62	6.76	2.19	1.72	2.87	2.79
172	DJH153019	6.46	64.74	16.33	207.80	110.40	0.86	4.05	2.89	1.65	1.87	2.90	3.23
183	DJH153029	6.46	64.30	16.57	215.50	105.80	1.82	5.70	6.14	1.77	1.67	2.64	3.13
18	DJH152510	6.45	65.72	15.84	219.20	109.40	-1.08	5.59	5.92	1.55	1.74	2.88	2.85
42	DJH152616	6.45	63.55	17.09	216.10	103.60	6.66	5.33	3.38	1.88	1.62	2.58	2.89
75	DJH152765	6.45	65.64	16.00	199.40	106.60	-0.88	5.14	6.09	1.97	1.59	2.97	2.60
27	DJH152522	6.44	63.22	15.63	213.70	108.60	3.68	5.54	6.91	1.93	1.62	2.86	2.28
70	DJH152761	6.44	65.72	16.20	207.50	116.70	7.10	5.39	5.09	2.34	1.71	2.81	3.09
31	DJH152604	6.41	65.80	15.99	206.30	108.40	9.40	6.06	3.98	1.47	1.62	2.98	2.21
28	DJH152523	6.40	62.64	16.37	217.80	103.60	8.24	6.32	2.90	1.72	1.65	2.64	2.31
125	DJH152816	6.38	67.97	16.53	222.40	122.50	1.16	5.69	4.45	2.00	1.64	2.92	2.52
43	DJH152617	6.37	62.64	16.65	204.00	95.64	7.28	5.48	0.83	1.44	1.57	2.86	2.72
74	DJH152764	6.37	64.91	16.34	195.70	99.64	6.38	5.17	6.42	1.50	1.71	3.02	2.86
20	DJH152512	6.32	65.89	16.29	220.00	107.40	3.34	6.22	3.12	2.38	1.64	2.81	2.23
78	DJH152767	6.31	67.97	15.99	222.40	115.90	0.25	5.09	6.54	1.75	1.62	2.99	2.85
7	DJH152502	6.30	64.72	16.94	216.80	101.40	0.02	6.45	6.91	1.47	1.70	2.75	2.77
124	DJH152815	6.30	65.22	16.36	211.70	110.90	3.29	5.37	3.74	2.19	1.85	2.70	2.77
50	DJH152624	6.29	62.93	16.26	208.20	102.30	3.85	6.00	5.63	2.21	1.84	2.67	2.21
85	DJH152776	6.27	65.01	16.20	204.70	104.20	0.69	5.81	2.95	2.01	2.02	2.88	2.72
1	DJH152496	6.26	62.39	15.35	216.70	99.80	4.36	5.66	4.01	1.62	1.55	2.90	3.04
106	DJH152793	6.26	67.74	16.20	216.10	118.70	3.96	4.80	4.94	1.87	1.95	3.45	2.74
169	DJH153016	6.26	65.89	15.66	215.50	116.40	7.00	5.26	4.18	2.47	1.90	3.13	2.68
82	DJH152771	6.25	66.74	17.01	227.80	110.50	-0.23	5.48	4.75	2.59	1.96	2.97	2.82
68	CH142238	6.24	65.28	15.46	214.80	108.00	3.87	4.83	9.47	2.18	1.76	2.77	2.78
13	DJH152506	6.18	62.97	16.83	212.90	101.10	8.66	5.20	3.13	1.52	1.68	2.71	2.20
44	DJH152618	6.16	62.80	15.84	198.70	99.70	-0.04	5.10	5.47	1.59	1.54	2.89	2.32
49	DJH152623	6.16	64.47	16.27	217.90	105.60	6.25	5.88	1.84	1.97	1.68	2.73	2.63
178	DJH153026	6.14	65.55	16.09	220.00	104.60	5.73	5.64	6.41	2.00	1.80	2.43	2.36
4	DJH152499	6.13	65.80	16.71	204.60	92.96	8.85	6.28	6.68	1.78	1.57	2.70	2.45
8	DJH162008	6.13	63.55	16.81	207.50	99.20	6.74	5.47	4.05	1.68	1.67	2.66	2.25
47	DJH152621	6.12	62.97	16.83	212.90	109.30	5.47	4.83	1.55	1.37	1.68	2.80	2.10
115	DJH152802	6.12	64.05	17.41	206.40	95.75	3.20	4.49	1.65	1.44	1.68	2.85	2.39
95	DJH152784	6.09	62.90	15.43	220.20	115.60	1.76	5.83	2.29	1.75	1.64	2.70	3.03
179	DJH153027	6.09	63.22	15.97	198.60	94.84	5.72	5.67	4.17	1.69	1.79	2.75	2.54
34	DJH152608	6.06	63.39	16.61	213.80	108.30	7.47	5.86	2.46	1.62	1.72	2.63	1.91
193	DJH153045	6.06	68.72	15.70	220.70	119.80	6.80	5.78	4.94	2.28	1.73	2.97	2.46
122	DJH152811	6.04	65.47	15.89	216.00	108.10	4.45	6.14	5.99	2.51	1.73	2.75	2.60
80	DJH152769	5.99	69.72	16.48	211.70	114.90	1.53	4.75	6.28	1.75	1.78	2.76	2.74
64	DJH152755	5.97	63.55	16.26	214.50	103.10	1.69	5.19	5.89	1.84	1.89	3.02	2.98
205	SC513	5.96	63.72	15.00	218.30	108.50	8.54	5.45	5.92	1.52	1.92	3.30	2.98
129	DJH152821	5.95	61.72	15.54	220.00	107.60	5.02	6.61	1.19	1.87	1.68	2.72	2.14
190	DJH153038	5.95	60.80	15.86	213.70	110.60	3.02	5.72	4.36	1.69	1.81	2.94	2.72
69	DJH152760	5.93	64.55	15.92	227.60	117.90	4.26	6.02	8.77	1.83	1.75	2.48	2.93
203	SC301	5.91	58.30	14.99	203.80	91.15	2.55	6.46	5.32	2.96	1.89	3.11	2.90
189	DJH153037	5.90	64.74	16.18	205.90	107.30	0.15	5.38	4.47	1.60	1.89	2.72	2.93
81	DJH152770	5.88	67.55	16.38	217.10	102.20	3.32	5.52	8.01	2.53	2.05	2.96	3.19
126	DJH152817	5.86	66.39	17.25	202.80	108.60	4.68	5.53	6.47	2.09	1.71	2.75	2.55
33	DJH152606	5.84	62.46	15.95	217.80	106.50	6.20	6.21	3.65	1.80	1.75	2.83	2.60
60	DJH152638	5.79	66.89	17.09	213.60	117.60	3.74	5.02	4.00	1.47	1.77	2.44	2.52
119	DJH152805	5.71	65.14	16.36	228.30	117.90	8.77	4.75	4.06	1.87	1.65	2.87	2.08
25	DJH152517	5.58	63.30	16.25	220.30	102.40	-0.52	5.79	5.46	1.93	1.94	2.78	2.40
45	DJH152619	5.58	63.55	16.41	203.90	111.90	1.52	5.79	5.17	1.55	1.56	2.82	2.28
19	DJH152511	5.55	63.89	15.99	221.30	113.80	1.41	5.93	5.36	1.47	1.83	2.65	2.34
15	DJH152508	5.44	65.30	16.79	210.90	91.73	1.00	5.42	3.27	1.40	1.73	2.66	2.65
58	DJH152633	5.40	67.22	17.77	215.60	110.50	0.45	4.90	5.47	1.78	1.75	2.75	2.85
98	CH124275	5.37	68.55	16.03	194.30	104.10	0.43	4.36	4.81	2.16	1.63	3.06	2.77
191	DJH153042	5.37	63.05	16.45	214.70	102.80	0.25	6.00	1.32	1.97	1.74	2.78	2.82
Mean		6.80	64.98	1.45	216.60	110.20	5.36	3.35	4.94	1.88	1.72	2.82	2.73
LSD		1.38	3.52	1.38	83.78	59.64	9.20	1.14	6.27	0.82	0.27	0.86	0.81
CV		10.36	2.76	4.31	19.70	27.57	39.60	10.70	64.55	22.21	7.89	15.46	15.12
Heritability		0.51	0.44	0.48	0.06	0.05	0.56	0.00	0.01	0.24	0.33	0.08	0.41

Appendix 5.3 Grain yield and agronomic traits of 195 exotic x local three-way hybrids in set 3 in descending order of grain yield

Entry	Hybrid	GY	AD	ASI	MOI	PH	EH	SL	SEN	ER	GLS	TURC	EA	TEX
192	SC727	8.47	64.05	3.01	14.07	212.14	125.17	0.40	4.75	11.33	1.46	1.81	2.28	3.12
114	DJH153523	7.96	61.91	2.37	13.94	199.99	97.57	2.52	4.98	6.29	1.38	1.48	2.34	2.94
162	DJH153564	7.87	60.23	2.16	12.28	196.73	108.59	0.12	5.03	8.03	1.21	1.64	1.92	2.56
194	PAN7M-81	7.58	61.98	0.45	25.86	212.07	119.37	1.69	4.33	4.87	1.46	1.81	2.15	2.95
183	CZH141028	7.56	61.00	0.35	13.61	211.26	107.99	0.95	5.48	1.54	1.21	1.56	2.05	2.75
39	DJH153122	7.39	57.39	1.66	14.67	188.25	97.27	4.21	4.51	4.04	1.21	1.56	2.35	2.44
71	DJH153275	7.36	59.36	2.08	14.09	200.73	102.37	5.40	4.93	4.51	1.38	1.64	2.05	2.48
133	DJH153541	7.34	60.32	1.31	13.90	197.84	101.82	3.75	4.16	1.64	1.13	1.64	2.46	2.54
139	DJH153547	7.04	60.37	2.90	13.49	197.71	103.33	2.05	4.76	4.11	1.29	1.56	2.53	2.85
182	CZH131013	7.03	60.42	2.13	13.45	200.46	91.76	0.78	5.45	2.26	1.29	1.56	2.29	2.73
122	DJH153531	6.97	59.24	0.87	13.71	200.08	106.47	1.43	4.97	7.91	1.54	1.73	2.17	2.96
1	DJH153084	6.93	60.72	1.88	14.43	195.10	96.17	6.68	5.67	2.25	1.29	1.64	2.34	2.70
191	SC643	6.92	59.79	1.90	12.50	206.32	104.21	2.13	5.70	2.76	1.29	1.73	2.09	2.28
150	DJH153557	6.91	62.28	2.17	13.78	207.51	108.65	1.76	4.68	5.70	1.71	1.73	2.21	2.67
113	DJH153522	6.91	62.20	2.06	14.46	195.68	111.14	0.79	4.96	4.90	1.63	1.56	2.10	2.27
143	DJH153550	6.86	61.14	3.03	13.94	186.65	105.84	12.73	4.66	4.07	1.13	1.48	2.46	3.13
34	DJH153117	6.86	59.35	1.41	13.97	184.89	105.03	1.43	5.15	2.72	1.46	1.48	2.18	2.71
61	DJH153142	6.85	61.36	2.79	13.55	190.51	110.47	0.63	5.05	8.81	1.13	1.73	2.54	2.80
24	DJH153107	6.79	58.54	0.64	13.54	182.88	96.27	1.88	6.03	5.42	1.21	1.64	2.35	2.89
193	PAN53	6.79	61.09	3.33	13.58	198.59	108.07	2.29	5.58	2.47	1.79	1.64	2.15	2.89
99	DJH153431	6.78	61.60	0.94	12.85	199.09	101.69	3.88	4.97	3.37	1.21	1.73	1.91	2.45
181	CZH131001	6.77	60.76	1.16	13.06	195.26	88.37	0.36	5.30	6.76	1.38	1.81	2.50	2.69
40	DJH153123	6.77	61.27	1.15	13.56	192.03	102.72	2.66	5.49	6.91	1.54	1.64	1.98	2.83
131	DJH153539	6.77	59.74	0.83	13.55	198.56	102.85	0.72	5.11	7.11	1.21	1.48	2.66	2.99
186	10C3271	6.74	58.98	2.40	14.03	211.67	106.81	16.85	4.96	5.19	1.63	1.39	2.45	2.78
136	DJH153544	6.73	61.69	1.20	13.64	198.82	101.73	1.40	4.93	5.13	1.63	1.64	2.35	2.89
73	DJH153281	6.70	58.98	0.90	13.59	199.77	99.86	0.67	5.28	5.98	1.21	1.64	2.43	2.66
152	DJH153559	6.67	60.95	1.45	13.53	201.46	100.97	2.80	5.13	5.39	1.29	1.64	2.22	2.89
154	DJH151859	6.64	60.47	1.89	13.96	210.43	102.76	6.16	5.06	3.55	1.29	1.56	2.09	2.56
13	DJH153097	6.64	59.62	1.16	13.97	193.20	96.04	1.27	5.72	3.50	1.04	1.39	2.59	3.02
9	DJH153093	6.62	59.72	1.09	13.69	192.64	100.32	15.02	5.42	4.34	1.21	1.56	2.33	2.62
128	DJH153537	6.59	59.73	0.78	12.74	193.25	101.89	3.69	5.76	11.54	1.78	1.56	2.49	2.80
189	SC419	6.55	58.13	0.88	12.93	204.54	102.11	3.91	5.76	3.20	1.38	1.73	2.39	3.14
120	DJH153529	6.53	59.79	1.67	12.61	183.62	100.86	10.55	5.49	8.75	1.21	1.56	2.77	3.06
167	DJH153565	6.52	60.31	2.69	13.67	199.05	97.65	2.91	4.90	2.56	1.46	1.56	2.20	2.67
161	DJH153563	6.51	61.86	1.72	13.73	204.03	99.26	2.94	4.67	2.75	1.38	1.48	2.26	2.17
125	DJH152759	6.47	60.34	0.08	13.34	199.35	99.63	5.25	4.84	0.70	1.46	1.64	1.92	2.67
78	DJH153286	6.40	60.02	2.67	13.30	196.67	89.98	0.74	4.77	3.19	1.54	1.48	2.42	2.37
153	DJH153560	6.37	60.90	2.44	12.29	199.16	105.46	2.22	5.47	13.63	1.63	1.81	2.12	2.51
75	DJH153283	6.37	61.79	1.59	13.65	195.94	102.06	21.24	4.96	2.58	1.21	1.64	2.04	1.92
42	DJH153125	6.35	58.61	1.49	13.73	188.43	91.76	0.14	5.67	3.80	1.21	1.48	2.80	2.80
104	DJH153436	6.34	58.40	0.40	12.66	191.33	93.56	4.34	5.07	2.44	1.13	1.64	2.49	2.62
53	DJH153134	6.32	60.14	1.72	13.22	203.69	100.85	0.54	5.18	5.53	1.21	1.64	2.26	2.80
54	DJH153135	6.30	59.05	1.12	13.84	198.33	105.03	-0.07	5.39	2.57	1.29	1.64	2.48	3.06
91	DJH153422	6.29	58.86	0.36	13.53	190.71	93.91	8.87	5.24	6.18	1.29	1.64	2.47	2.52
21	DJH153104	6.29	60.57	2.88	13.19	196.10	95.29	13.78	4.50	3.27	1.13	1.56	2.13	2.89
10	DJH153094	6.25	60.36	1.50	13.89	190.90	98.84	0.72	5.29	8.92	1.29	1.56	2.35	2.76
180	DJH153575	6.22	59.90	3.36	12.71	196.41	105.36	4.83	4.84	10.51	1.54	1.64	2.37	2.96
127	DJH153536	6.21	60.04	0.51	13.45	190.96	94.47	5.13	5.24	2.99	1.38	1.64	2.23	2.85
7	DJH153091	6.19	58.92	0.72	14.02	198.14	93.15	6.51	6.11	8.87	1.21	1.81	5.12	2.96
184	CZH131006	6.19	61.48	0.81	14.35	199.03	103.39	1.43	5.06	3.76	1.38	1.66	2.36	2.67
86	DJH153295	6.16	62.98	1.03	13.58	199.90	107.44	2.38	5.27	4.73	1.54	1.64	2.20	2.82
135	DJH153543	6.16	57.44	1.42	13.03	191.32	87.33	-0.56	4.78	2.98	1.63	1.81	2.46	2.50
98	DJH153429	6.13	57.99	1.12	13.56	198.36	95.28	2.91	5.87	6.64	1.04	1.56	2.38	2.90
47	DJH153129	6.10	59.42	2.15	14.40	195.52	102.80	5.34	4.44	7.12	1.13	1.56	2.28	2.30
79	DJH153287	6.10	57.36	2.30	13.64	191.65	84.08	-0.40	4.56	4.27	1.54	1.48	2.16	2.32
170	DJH152804	6.10	60.19	2.40	12.94	193.59	100.89	11.76	5.44	5.99	1.38	1.56	2.45	2.76
12	DJH153096	6.09	57.38	0.55	13.34	195.84	98.43	4.38	5.83	5.25	1.13	1.56	2.10	2.66
118	DJH153528	6.07	60.26	1.62	13.57	206.10	104.29	2.63	5.02	10.86	1.38	1.56	2.56	2.90
2	DJH153086	6.06	61.39	0.64	13.73	188.99	98.06	3.07	4.72	1.85	1.04	1.56	2.27	2.47
8	DJH153092	6.06	60.68	3.10	13.19	196.06	96.41	10.54	5.02	4.91	1.21	1.56	2.14	3.15
5	DJH153089	6.06	59.63	0.57	13.27	201.22	111.08	9.59	5.84	4.12	1.04	1.73	1.86	2.95
15	DJH153097	6.05	58.19	1.79	13.73	190.04	92.61	3.20	5.85	3.06	1.12	1.29	2.09	3.13
29	DJH153112	6.04	58.17	1.93	12.88	197.38	98.06	2.08	5.57	4.29	1.46	1.56	2.11	2.26
92	DJH153423	6.03	59.80	0.61	14.40	199.53	100.18	1.00	5.57	6.77	1.29	1.64	2.28	2.67
30	DJH153113	6.02	61.79	1.93	13.34	188.81	98.96	3.99	5.71	2.92	1.33	1.38	2.37	2.96
49	DJH153127	6.00	59.41	1.96	13.90	188.71	101.18	0.27	5.35	5.00	1.21	1.73	2.02	3.14
174	CH14362	5.99	62.18	2.16	13.57	191.02	107.93	11.90	4.92	4.83	1.54	1.39	2.28	2.66
185	CZH131007	5.98	63.06	1.21	13.88	200.98	103.42	5.52	5.27	7.82	1.38	1.64	2.34	3.08
16	DJH153099	5.98	60.93	2.98	14.50	180.96	93.70	5.58	4.89	8.66	1.13	1.48	2.36	2.35
6	DJH153090	5.92	58.87	1.08	14.43	201.09	103.80	4.85	5.58	7.32	1.38	1.64	2.53	3.15
172	DJH153569	5.91	61.25	1.60	12.74	204.75	106.74	0.95	5.60	3.11	1.46	1.56	2.02	3.04
32	DJH153115	5.87	60.79	1.30	14.04	195.56	107.10	2.07	5.16	8.79	1.13	1.56	2.32	2.76
59	DJH153140	5.87	61.49	2.56	13.64	184.27	99.58	4.28	4.69	4.18	1.38	1.39	2.32	3.14
46	DJH153127	5.86	58.89	1.67	13.44	195.48	92.83	0.19	5.26	3.40	1.18	1.76	2.59	3.06
18	DJH153097	5.86	58.72	1.71	13.46	205.45	100.31	-0.02	5.03	1.70	1.13	1.39	2.11	3.19
176	DJH152814	5.83	60.11	1.42	13.70	210.87	108.32	0.53	6.39	5.00	1.88	1.39	2.31	2.51
148	DJH153555	5.80	58.94	0.73	13.80	197.50	100.04	3.90	5.10	3.38	1.38	1.73	2.13	2.77
164	CH123787	5.76	61.46	1.48	13.67	219.03	113.95	0.71	5.37	5.60	1.13	1.58	1.79	2.20
142	DJH153549	5.75	60.29	1.67	13.43	192.86	101.53	0.70	4.62	3.33	1.46	1.64	2.53	2.76
123	DJH153532	5.75	61.10	1.00	13.18	187.99	91.35	0.67	5.22	8.16	1.88	1.48	2.43	3.03
95	DJH153427	5.73	57.72	1.41	26.33	197.13	100.71	3.03	5.52	4.87	1.13	1.56	2.55	2.58
4	DJH153088	5.72	60.36	1.32	13.82	192.32	94.09	3.50	5.40	3.84	1.13	1.64	2.20	2.93
171	2.00E+05	5.72	62.62	1.44	13.84	183.48	91.39	3.77	4.48	1.28	1.54	1.56	2.23	2.74
82	DJH153290	5.70	63.77	0.80	14.05	194.22	88.93	0.19	5.06	11.04	1.71	1.39	2.31	2.56
159	CH123788	5.67	59.17	1.22	12.85	191.02	95.34	0.82	5.10	4.82	1.29	1.64	2.47	2.79
188	SC403	5.67	55.66	2.59	12.41	194.89	95.88	0.48	5.92	6.02	1.54	1.48	2.46	2.90
38	DJH153121	5.65	58.65	1.17	12.63	179.05	87.16	8.40	5.48	5.25	1.29	1.39	2.28	2.75
112	DJH153521	5.63	58.70	2.91	13.27	190.30	97.98	2.56	4.72	4.54	1.54	1.56	2.72	2.99
145	DJH152773	5.62	59.06	1.03	13.25	194.06	103.50	-0.10	4.69	2.07	1.38	1.64	2.25	3.00
17	DJH153100	5.61	58.79	1.00	13.77	192.80	96.81	5.75	5.05	5.75	1.13	1.48	2.32	3.17
23	DJH153106	5.61	57.01	1.55	13.94	196.48	85.48	2.09	6.18	5.52	1.21	1.56	1.93	2.37
109	DJH153443	5.60	58.76	1.57	13.07	181.71	95.52	1.04	6.23	5.40	1.46	1.56	2.54	2.61
126	DJH153534	5.58	59.39	0.36	13.49	201.66	99.57	-0.10	5.95	8.66	1.13	1.64	2.35	3.05
66	DJH153148	5.57	60.39	1.63	14.62	185.54	101.44	9.16	5.11	2.49	1.38	1.56	2.67	2.80
76	DJH153281	5.56	60.85	0.99	13.61	198.02	95.22	2.81	5.37	2.78	1.38	1.64	2.24	2.76
56	DJH153137	5.55	59.50	1.17	13.58	179.12	92.24	-0.65	5.34	3.67	1.13	1.48	2.52	2.70
51	DJH153132	5.54	60.23	1.33	13.39	177.70	79.99	2.69	5.12	2.10	1.21	1.56	2.36	2.76
27	DJH153110	5.53	59.38	2.24	13.42	205.77	98.58	4.67	5.53	11.18	1.21	1.64	1.86	2.66
108	SC635	5.45	59.44	3.89	11.93	195.57	96.64	4.88	5.83	6.88	1.29	1.73	2.60	3.16

Entry	Hybrid	GY	AD	ASI	MOI	PH	EH	SL	SEN	ER	GLS	TURC	EA	TEX
158	CH123932	5.44	58.99	1.21	13.64	203.16	107.89	-0.43	5.40	9.36	1.13	1.28	2.34	3.17
124	DJH153533	5.40	60.67	1.37	13.14	206.57	103.07	2.73	5.26	7.04	1.38	1.56	2.60	2.77
168	DJH153566	5.40	60.65	2.61	13.71	199.24	92.41	0.12	5.31	6.82	1.29	1.56	2.30	2.48
58	DJH153139	5.39	59.84	2.48	13.16	189.44	99.66	5.30	5.53	3.34	1.04	1.48	2.34	2.77
11	DJH153095	5.38	60.26	1.50	13.62	200.78	96.94	11.44	5.62	5.21	1.38	1.39	2.35	2.32
62	DJH153143	5.37	59.36	2.96	13.39	214.86	117.27	0.14	5.91	4.05	1.29	1.48	2.56	3.14
45	DJH153128	5.34	59.32	1.60	13.75	187.44	98.21	3.67	4.97	1.21	1.13	1.48	2.74	2.85
177	DJH152817	5.31	61.50	1.34	13.80	196.95	106.60	10.21	5.34	5.30	1.46	1.56	2.23	2.66
111	DJH153520	5.30	59.77	1.13	13.55	205.64	107.07	-0.35	5.71	3.89	1.79	1.64	2.18	2.81
57	DJH153138	5.30	60.26	0.81	13.95	185.46	96.59	8.80	5.23	5.07	1.04	1.39	2.96	2.80
155	DJH153561	5.27	60.51	2.12	13.56	194.02	90.56	0.79	5.72	8.67	1.71	1.73	2.41	2.56
94	DJH153426	5.26	57.75	1.09	14.54	195.26	83.61	1.29	6.09	2.99	1.13	1.56	2.21	2.92
81	DJH153289	5.25	59.94	1.52	13.32	200.96	96.78	5.88	5.65	3.43	1.62	1.29	1.92	2.31
129	CH124278	5.25	59.88	1.39	13.94	194.13	97.47	1.01	5.31	8.11	1.13	1.64	2.60	3.06
175	DJH153572	5.24	60.82	1.54	13.00	209.97	118.37	5.81	6.43	3.95	1.46	1.81	2.54	2.72
50	DJH153131	5.22	58.50	1.16	14.08	178.48	90.97	4.23	4.92	2.43	1.21	1.48	2.32	2.65
105	DJH153437	5.17	59.19	1.35	12.87	197.10	90.81	5.19	6.00	6.23	1.38	1.56	2.58	2.95
144	DJH153551	5.16	61.22	1.00	13.33	208.01	108.92	-0.03	5.68	4.40	1.46	1.56	2.47	2.76
26	DJH153109	5.15	58.73	1.89	13.45	203.77	108.48	4.03	5.93	-0.17	1.13	1.58	2.11	2.42
55	DJH153136	5.13	58.83	0.50	13.46	206.84	103.84	2.99	5.16	4.56	1.21	1.64	2.58	2.89
80	DJH153288	5.12	59.45	0.89	14.24	197.86	98.71	4.79	5.45	5.73	1.46	1.56	2.30	2.75
140	DJH153548	5.11	60.17	1.43	13.21	206.16	113.44	1.62	5.67	11.31	1.88	1.89	2.09	2.61
141	CH14537	5.10	61.22	2.71	13.47	200.26	106.95	4.86	5.03	7.00	1.54	1.56	2.40	3.11
160	CH123937	5.08	61.42	2.12	13.64	192.51	94.25	3.94	5.54	3.95	1.71	1.64	2.35	2.61
96	DJH153428	5.08	60.16	1.02	13.48	194.06	90.59	14.07	5.51	3.06	1.29	1.48	2.69	2.62
190	SC513	5.06	57.88	1.42	11.98	196.88	98.66	10.76	5.32	7.95	1.29	1.56	2.58	2.91
44	DJH153127	5.06	59.99	0.85	13.95	193.04	97.77	2.24	4.62	2.80	1.21	1.48	2.31	2.94
103	DJH153435	5.04	59.49	1.99	12.71	195.37	94.35	7.71	5.50	4.12	1.29	1.48	2.24	2.47
130	DJH153538	5.00	57.87	1.10	12.85	194.50	99.61	0.37	4.89	7.34	1.13	1.56	2.34	2.90
37	DJH153120	4.99	60.34	2.36	13.60	192.71	92.02	1.78	4.97	2.41	1.46	1.39	2.66	2.53
195	PHB30G19	4.99	60.26	4.08	13.15	196.00	107.47	14.28	5.64	19.55	1.29	1.56	2.48	2.77
67	DJH153149	4.99	61.86	2.46	14.36	193.50	103.75	2.79	5.32	7.50	1.21	1.56	2.37	2.61
151	DJH153558	4.98	60.97	0.90	13.53	199.70	101.88	6.59	5.34	10.95	1.46	1.89	2.23	2.52
48	DJH153130	4.98	60.06	1.58	12.82	182.33	94.29	10.61	5.04	4.11	1.38	1.39	2.72	2.99
33	DJH153116	4.96	61.02	2.74	13.26	181.72	97.67	10.01	4.74	10.67	1.29	1.48	2.29	3.17
163	CH123936	4.95	62.34	3.58	13.64	193.49	97.60	2.32	5.17	19.46	1.46	1.56	2.85	3.11
43	DJH153126	4.94	58.19	0.72	13.57	204.50	100.01	4.70	5.91	1.25	1.04	1.48	2.14	2.74
107	DJH152625	4.94	58.33	1.74	13.35	185.22	91.45	0.22	5.54	2.38	1.29	1.39	2.35	2.59
20	DJH153103	4.91	57.72	1.75	13.10	182.49	89.71	0.23	5.54	3.75	1.13	1.48	2.44	2.75
87	DJH153296	4.88	58.69	1.55	12.96	190.75	87.36	0.51	5.25	7.29	1.13	1.64	2.37	2.87
63	DJH153144	4.87	59.81	1.53	12.82	196.66	102.18	5.66	6.14	7.21	1.28	1.56	2.51	2.80
134	DJH153542	4.87	60.16	0.55	13.24	186.30	94.83	1.57	5.53	2.21	1.63	1.64	2.61	2.97
166	CH123932	4.86	59.58	2.26	14.12	203.06	94.46	2.70	5.60	6.19	1.13	1.56	2.19	2.73
173	DJH152809	4.85	60.49	5.42	13.15	207.88	119.49	-0.39	6.42	11.87	1.63	1.64	2.30	3.03
83	DJH153291	4.83	58.52	0.91	13.86	196.21	99.08	1.52	6.03	3.49	1.88	1.64	2.28	2.22
178	DJH153573	4.82	60.51	1.93	13.05	203.71	108.03	3.13	6.20	3.95	1.38	1.73	2.25	3.06
137	DJH153545	4.82	57.61	1.52	13.61	192.00	96.72	-0.42	5.84	6.53	1.29	1.56	2.34	2.86
60	DJH153141	4.75	59.15	1.96	13.47	183.82	102.39	5.47	5.77	4.84	1.38	1.48	2.23	2.47
19	DJH153102	4.74	60.47	0.81	13.20	187.10	92.73	8.84	5.55	11.00	1.21	1.39	1.95	5.67
138	DJH153546	4.68	60.94	1.82	13.33	200.00	117.01	1.92	5.73	4.80	2.04	1.64	2.47	2.84
41	DJH153124	4.68	60.42	1.93	13.74	191.39	94.69	4.99	5.62	1.50	1.79	1.56	2.35	2.38
52	DJH153133	4.67	60.31	0.50	13.73	201.20	99.77	10.36	5.43	8.84	1.13	1.39	2.43	3.01
31	PAN413	4.67	60.59	2.65	12.48	188.20	94.31	5.41	4.55	7.39	1.29	1.48	2.72	3.32
90	DJH153418	4.65	60.03	2.31	13.07	199.21	89.46	1.29	5.94	7.09	1.63	1.56	2.29	2.69
77	DJH153285	4.61	59.25	1.89	13.58	174.79	87.82	7.51	5.44	1.92	1.63	1.39	2.54	2.91
156	DJH153562	4.60	59.60	0.97	14.53	212.54	97.43	11.24	6.03	5.80	1.63	1.56	2.00	2.77
157	CH123939	4.57	60.59	2.70	13.76	194.35	100.31	8.63	5.35	4.99	1.38	1.66	2.37	2.64
36	DJH153119	4.56	60.50	0.41	13.40	188.08	97.34	1.55	4.28	4.26	1.21	1.48	2.41	2.65
121	DJH153530	4.51	59.90	1.49	12.94	189.68	95.79	4.78	4.74	4.66	1.29	1.64	2.15	2.66
70	DJH153274	4.47	60.03	1.01	13.55	205.45	87.90	0.41	5.22	4.71	1.38	1.56	2.42	2.66
115	DJH153525	4.44	60.96	1.39	13.18	200.05	101.79	0.17	4.63	2.14	1.38	1.64	2.53	2.81
110	DJH153444	4.42	60.13	0.85	13.93	194.14	100.84	3.33	5.60	3.16	1.13	1.56	2.46	2.61
85	DJH153294	4.41	60.37	0.53	13.10	177.96	95.59	2.79	4.79	8.28	1.63	1.48	2.68	2.96
74	DJH153282	4.39	59.84	1.76	13.22	184.31	88.69	4.12	5.94	2.32	1.88	1.48	2.38	2.53
28	DJH153111	4.39	59.09	3.87	13.10	186.39	92.01	0.90	5.88	4.73	1.29	1.48	2.36	2.72
97	DJH153430	4.37	56.83	1.77	13.54	189.14	100.65	3.10	5.67	7.37	1.21	1.48	2.29	2.56
169	DJH153567	4.33	58.46	1.82	12.66	220.21	112.26	0.75	6.36	11.61	1.13	1.64	1.83	2.74
117	DJH153527	4.27	60.27	1.20	13.23	196.12	103.22	4.87	4.17	1.19	1.63	1.81	2.17	3.01
35	DJH153118	4.25	60.04	1.21	12.74	187.63	94.05	1.39	4.61	6.70	1.29	1.48	2.19	2.93
88	DJH153297	4.23	60.41	2.04	13.88	193.89	97.92	6.23	5.24	5.55	1.71	1.64	2.17	2.66
3	DJH153087	4.22	60.40	2.09	14.14	190.70	93.08	2.48	6.12	4.95	1.63	1.48	2.28	2.46
165	CH123938	4.16	58.75	0.92	13.27	192.28	96.56	5.85	6.64	16.64	1.48	1.96	2.40	3.31
65	DJH153147	4.14	59.58	1.74	13.49	198.27	99.84	-0.61	5.82	2.01	1.46	1.48	2.58	2.95
93	DJH153425	4.12	59.21	1.61	13.51	192.82	98.72	6.51	6.29	6.13	0.94	1.47	2.51	2.87
22	DJH153105	4.11	59.81	0.91	12.68	191.78	95.78	6.98	5.31	4.35	1.04	1.39	2.12	2.86
119	CH133139	4.11	61.52	1.83	13.53	193.11	105.56	9.07	4.68	5.29	1.46	1.39	2.31	3.10
187	SC301	4.09	56.04	2.39	12.48	186.60	89.82	0.17	6.35	5.06	1.71	1.64	2.67	2.51
101	DJH153433	4.07	59.89	2.08	12.29	191.84	96.45	23.07	6.01	5.16	1.46	1.64	2.73	3.11
89	DJH153416	4.05	59.48	0.70	12.11	200.94	96.42	-0.15	5.44	3.25	1.29	1.64	2.60	3.05
68	DJH153150	4.03	61.22	2.04	13.31	182.64	100.00	6.13	4.78	4.46	1.63	1.64	2.42	3.07
14	DJH153098	3.98	58.52	1.15	12.81	191.63	101.08	-1.06	5.44	3.64	1.13	1.48	2.35	2.95
147	DJH153553	3.94	61.85	1.30	13.20	207.79	104.91	9.65	6.35	8.74	1.54	1.73	2.50	2.77
146	DJH153552	3.80	58.93	1.30	12.97	195.58	101.04	0.84	5.34	5.80	1.88	1.64	2.18	2.43
106	DJH153439	3.77	59.68	1.24	13.23	195.88	95.78	0.66	5.67	6.29	1.13	1.64	2.63	2.65
179	DJH153574	3.62	61.07	2.69	13.62	192.44	102.29	1.79	4.91	7.02	1.38	1.64	2.27	2.62
69	DJH153273	3.59	59.89	1.91	13.80	192.18	93.00	1.33	4.80	3.82	1.46	1.64	2.55	2.67
64	DJH153146	3.46	59.08	3.68	13.17	174.41	88.14	3.97	5.09	5.18	1.21	1.48	2.46	2.99
102	DJH153429	3.43	59.16	1.54	13.48	193.81	82.84	6.56	5.59	5.36	1.03	1.58	2.83	3.06
149	DJH153556	3.12	59.97	1.62	13.39	194.71	102.32	3.50	5.91	6.89	1.63	1.73	2.42	2.47
25	DJH153108	3.06	60.95	2.22	13.44	192.11	99.55	3.22	5.27	3.91	1.79	1.48	2.13	2.92
132	DJH153540	3.01	61.26	1.92	13.48	186.19	97.88	4.30	4.53	0.94	1.96	1.56	2.37	2.76
100	DJH153432	2.76	61.06	0.65	13.28	183.32	95.20	5.73	5.71	5.83	1.21	1.48	2.48	5.13
84	DJH153292	2.66	61.13	9.24	13.23	202.66	95.03	8.01	5.76	6.73	1.88	1.64	2.49	2.78
72	DJH153280	2.52	60.77	1.97	14.08	187.32	92.11	2.26	4.30	3.12	1.54	1.56	2.32	2.51
116	DJH153526	2.24	61.71	2.38	13.36	186.73	93.91	7.26	6.07	6.69	1.83	1.28	2.45	2.75
Mean		5.46	59.97	1.69		195.28	99.18	3.96	5.34	5.42	1.37	1.57	2.36	2.80
LSD		2.34	2.83	2.38	4.12	23.07	15.58	12.01	0.87	8.91	0.62	0.61	0.74	0.97
CV		21.74	2.40	71.60	15.41	6.01	7.99	154.22	8.21	83.63	23.01	19.63	16.02	17.60
Heritability		0.28	0.31	0.18		0.00	0.29	0.00	0.70	0.00	20.00	0.00	0.12	0.08

GY- grain yield, AD-anthesis date, MOI- moisture, PH-plant height, EH-ear height, SL-stem lodging, SEN-senescence ER-ear rots, GLS- grey leaf spot, TURC- turcicum, HC-husk cover, EA- ear aspect, TEX-texture.

Appendix 5.4 Grain yield and agronomic traits of 220 exotic x local three-way hybrids in set 4 in descending order of grain yield

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	HC	EA	TEX
178	DJH152318	8.00	15.72	65.88	185.38	108.91	5.84	5.58	6.22	1.25	11.03	2.63	2.45
218	PAN7M-81	7.48	18.15	65.88	214.95	125.66	2.75	5.27	5.11	1.26	8.25	2.25	2.79
80	DJH152183	7.01	18.05	67.00	206.01	115.79	10.68	6.35	6.94	1.27	11.52	2.63	2.27
112	DJH152221	6.69	18.21	67.50	207.42	119.95	3.12	5.34	5.01	1.26	2.56	2.19	1.73
78	DJH152181	6.54	17.46	65.75	201.05	116.24	19.98	5.77	7.91	1.51	9.73	2.76	2.23
213	SC419	6.34	16.77	62.75	202.98	104.55	6.45	5.51	8.41	2.00	7.59	2.68	2.58
172	DJH152313	6.26	16.76	65.25	206.94	111.94	3.09	5.01	3.79	1.02	3.17	2.63	2.63
136	DJH152241	6.11	17.65	67.63	206.65	117.67	-0.15	6.40	5.13	1.49	10.74	2.68	2.46
188	DJH152329	6.02	17.47	68.13	201.18	115.99	5.69	6.21	3.80	1.50	4.32	2.39	2.63
44	SC608	5.94	16.48	64.65	196.68	115.71	1.20	5.93	14.18	1.25	4.14	2.95	3.11
35	CH14668	5.91	17.98	66.25	178.33	111.54	0.00	4.96	6.44	1.28	11.34	2.52	2.39
121	DJH152231	5.86	15.86	64.00	207.96	110.43	16.79	5.81	7.51	1.73	3.63	2.25	2.42
100	DJH152206	5.84	17.12	66.75	206.42	120.58	0.07	5.09	8.50	1.51	10.15	2.73	2.62
18	DJH152124	5.83	16.52	65.36	204.50	100.55	3.62	6.47	4.90	1.49	3.81	2.75	2.09
176	DJH152318	5.80	16.31	65.13	185.23	104.10	0.10	6.10	10.52	1.03	6.59	2.63	2.36
216	SC727	5.79	17.96	68.88	213.49	123.40	1.59	5.24	10.80	1.51	10.93	2.50	2.66
134	DJH152239	5.76	16.82	66.38	195.77	92.16	16.98	6.33	5.18	1.51	6.25	2.56	1.68
4	DJH152108	5.75	17.05	66.00	209.11	117.70	1.55	5.21	6.84	2.23	6.77	2.25	2.98
153	DJH152836	5.68	16.94	65.63	211.76	113.27	1.07	5.93	8.19	1.25	7.74	2.62	2.07
114	DJH152223	5.64	18.52	66.88	203.01	122.53	2.80	6.06	6.05	1.51	5.20	2.44	2.38
139	DJH152244	5.58	16.65	66.00	202.26	109.81	3.81	5.55	7.31	1.24	5.95	2.37	2.07
75	DJH152178	5.55	17.65	66.50	195.14	103.20	1.12	5.72	5.64	1.52	14.63	2.44	2.03
195	DJH152336	5.49	16.71	65.50	188.04	102.55	9.60	5.65	7.69	1.52	4.17	2.75	2.51
111	DJH152220	5.47	16.25	67.92	202.15	115.81	0.07	5.75	6.90	2.76	9.91	2.69	2.09
24	DJH152130	5.45	16.09	65.63	197.47	107.48	8.88	6.42	4.02	1.48	7.38	2.38	2.53
189	DJH152330	5.44	17.19	68.13	206.36	122.01	9.08	5.96	4.76	1.26	3.41	2.57	2.47
150	DJH152254	5.41	18.12	67.13	193.25	111.61	4.85	6.04	4.35	1.51	10.00	2.63	2.09
57	DJH152162	5.38	18.31	66.49	201.40	120.59	5.33	5.47	8.33	1.25	5.79	2.93	2.11
81	DJH152184	5.30	18.10	69.13	203.55	117.63	7.65	6.74	5.34	1.48	10.19	2.57	2.56
2	DJH152106	5.30	18.45	66.25	179.78	89.06	25.40	5.32	11.16	1.75	13.85	2.44	2.13
26	DJH152132	5.29	18.96	67.25	195.07	114.40	0.20	5.66	6.96	1.26	3.81	2.75	2.22
162	DJH152847	5.28	16.20	65.50	196.35	106.36	5.38	6.80	8.37	1.25	4.80	2.50	2.41
41	DJH152145	5.25	17.16	69.38	198.40	111.16	9.68	4.52	6.20	1.00	17.09	2.81	1.79
209	CZH131007	5.24	18.29	68.21	198.39	110.60	2.48	4.92	10.20	1.50	11.79	2.82	2.52
39	DJH152143	5.21	17.84	68.13	208.47	128.24	13.50	5.90	8.58	1.49	22.28	2.69	2.21
164	DJH152851	5.21	16.62	65.88	191.44	99.48	8.50	5.47	6.08	1.26	8.16	2.43	2.03
69	DJH152172	5.17	19.44	67.13	200.64	125.72	1.53	5.76	9.65	1.01	4.13	2.56	2.28
110	DJH152219	5.16	17.54	69.25	207.66	124.79	1.10	6.21	3.64	1.51	1.00	2.43	2.15
174	DJH152316	5.15	17.51	65.00	196.90	98.29	-0.11	5.92	8.82	1.02	0.96	2.81	2.81
217	PAN53	5.13	17.37	65.88	195.45	95.15	0.01	6.28	6.09	1.49	3.97	3.12	2.51
140	DJH152245	5.08	17.65	65.38	201.01	106.51	14.25	5.29	5.36	1.49	2.94	2.45	1.96
56	DJH152160	5.07	18.55	65.13	188.37	108.28	7.83	5.96	7.43	1.52	0.74	2.51	2.01
220	PAN413	5.06	17.02	66.88	179.14	92.43	5.79	4.75	7.61	1.76	3.89	2.63	2.76
180	DJH152320	5.06	17.26	68.13	200.44	119.68	7.74	5.55	6.57	0.99	7.49	3.06	2.39
60	CH124029	5.04	17.77	64.63	188.23	105.30	9.30	6.23	5.28	1.23	2.68	2.88	2.74
206	CZH131013	5.02	17.00	64.78	203.37	99.13	4.80	6.39	7.17	1.49	9.74	2.93	2.26
36	DJH152140	5.02	15.72	66.50	195.63	110.68	8.04	5.57	4.34	1.47	12.15	2.95	2.10
177	DJH152315	5.01	17.84	64.88	180.29	95.69	4.64	5.64	5.65	1.48	6.42	2.62	2.73
77	DJH152180	5.01	18.09	68.38	198.81	113.21	5.00	5.19	10.38	1.53	11.88	2.44	2.14
14	DJH152119	5.00	16.05	66.50	197.74	108.37	0.03	5.29	7.04	1.00	8.10	2.69	2.18
185	DJH152326	5.00	16.34	66.00	204.84	113.43	2.58	6.18	7.55	1.26	6.36	2.81	2.33
142	DJH152247	4.99	18.57	66.64	204.29	107.18	1.79	5.80	2.71	1.51	2.50	2.42	2.47
59	DJH152164	4.99	18.21	64.63	199.12	105.12	4.45	6.70	6.28	1.48	8.04	2.67	2.57
207	CZH141028	4.97	16.41	66.88	203.76	112.72	-0.05	4.67	8.39	1.25	7.85	2.68	2.14
122	DJH152232	4.95	18.36	66.00	192.41	104.70	7.23	6.03	8.64	1.27	3.51	2.50	2.50
83	DJH152186	4.94	17.19	64.22	199.50	117.05	9.45	5.09	10.57	1.25	14.75	2.83	2.15
89	DJH152192	4.91	17.75	64.99	205.87	116.88	3.47	6.00	5.32	1.00	5.68	2.59	1.97
193	DJH152334	4.90	16.16	65.75	189.88	106.35	9.71	5.65	5.21	1.27	3.67	2.62	2.74
187	DJH152328	4.90	17.44	68.63	206.47	114.00	7.80	6.28	8.42	1.26	10.29	2.55	2.72
15	DJH152120	4.89	16.84	65.49	194.55	104.80	3.79	5.17	8.46	1.52	0.83	2.82	2.41
107	DJH152216	4.88	16.62	68.50	200.09	119.70	9.77	5.85	6.95	1.50	5.56	2.93	2.18
141	DJH152246	4.88	16.30	65.92	203.19	114.62	8.37	5.83	8.43	0.99	2.83	2.56	2.21
7	DJH152110	4.87	15.16	64.88	193.09	104.96	18.61	6.38	7.65	1.47	7.29	2.57	2.09
28	DJH152134	4.86	16.87	67.21	193.92	104.12	8.08	5.42	13.39	1.25	16.09	2.38	2.14
125	DJH152234	4.86	17.24	66.92	201.52	119.12	0.14	5.48	7.23	1.49	4.25	2.23	2.28
71	DJH152174	4.84	17.77	70.88	186.74	105.51	5.99	5.65	9.85	1.49	0.00	2.32	2.10
210	10C3271	4.83	16.05	63.88	209.13	114.80	8.74	6.11	8.56	3.25	4.53	2.51	2.44
3	DJH163004	4.82	15.41	68.07	199.07	107.62	6.99	6.68	9.26	2.00	9.17	3.00	1.78
149	DJH152253	4.72	16.36	67.00	189.50	102.51	6.52	6.11	7.36	1.76	0.00	2.62	2.43
12	DJH152116	4.71	15.52	66.38	193.92	102.91	1.50	5.86	4.18	1.49	11.98	2.69	2.75
82	DJH152185	4.70	16.90	68.75	202.77	118.42	3.11	5.36	7.16	1.49	6.54	2.88	1.72
101	DJH152208	4.68	15.84	67.35	210.08	122.83	13.16	4.98	2.56	1.77	0.00	2.50	2.43
74	DJH152177	4.68	17.57	67.63	208.90	120.57	8.06	5.58	5.80	1.51	8.37	2.69	2.31
208	CZH131006	4.67	15.88	66.50	202.91	107.01	0.19	6.10	6.67	1.25	6.02	2.93	2.64
29	SC637	4.66	15.41	66.49	185.38	95.35	8.19	6.26	5.10	1.48	9.53	2.31	2.20
55	DJH152159	4.66	16.91	64.75	210.25	117.67	4.19	5.33	6.48	1.52	7.24	2.51	2.05
19	DJH152125	4.65	16.29	66.25	201.56	102.24	1.61	5.83	5.87	1.73	6.72	2.81	2.50
47	DJH152151	4.65	16.22	67.36	195.40	112.38	8.51	4.75	7.87	1.77	9.29	2.48	2.22
30	CH124234	4.64	18.05	61.25	191.66	110.15	5.31	4.79	12.45	1.73	1.79	2.60	2.04
11	DJH152115	4.62	15.74	65.38	174.51	104.42	1.16	5.34	5.49	1.26	0.00	2.94	2.68
108	DJH152217	4.62	17.19	79.00	199.03	109.12	2.19	5.40	6.36	1.52	2.50	2.60	2.38
85	DJH152188	4.61	18.23	65.50	208.74	120.35	1.12	5.88	0.48	1.26	0.23	2.12	2.18
92	DJH152194	4.61	17.54	66.38	207.09	123.60	-0.13	6.02	5.90	1.49	5.00	2.44	1.88
34	CH14670	4.60	17.04	66.50	197.61	114.54	9.30	5.08	3.29	1.49	5.24	2.45	1.82
25	DJH152131	4.60	18.02	64.88	190.08	106.27	7.82	5.64	7.05	1.23	1.14	2.38	2.24
109	DJH152218	4.55	17.51	68.75	208.49	122.97	4.12	6.07	4.58	1.51	7.08	2.57	1.98
192	DJH152333	4.55	14.93	67.22	186.04	92.05	15.63	5.29	8.14	1.28	1.06	2.95	2.65
42	DJH152146	4.54	16.22	65.63	191.95	102.93	0.00	5.71	5.40	1.74	2.18	2.62	2.00
196	DJH152337	4.54	16.27	68.88	196.54	108.17	4.00	4.85	7.64	1.25	7.02	2.88	2.98
91	DJH152193	4.53	16.02	64.38	186.96	101.83	1.23	5.68	3.81	1.52	4.13	2.77	2.30
102	DJH152209	4.52	16.17	65.25	193.41	111.80	1.56	5.58	5.24	1.53	6.61	2.37	1.97
145	DJH152250	4.47	16.82	66.13	198.41	103.86	9.85	6.04	5.94	1.02	11.77	2.80	2.21
58	DJH152163	4.46	16.70	65.00	196.26	104.05	8.40	5.52	12.08	1.23	9.09	2.32	2.19
168	DJH152855	4.46	16.40	66.50	196.71	111.37	5.98	5.38	7.96	0.99	2.74	2.63	1.84
182	DJH152322	4.46	16.45	66.50	198.01	115.97	9.17	5.30	6.53	1.25	2.43	2.82	2.37
179	DJH152319	4.45	17.09	66.38	201.15	113.75	2.22	5.56	12.01	1.51	8.21	2.56	2.38
126	DJH151817	4.45	16.57	67.00	179.63	96.12	-0.04	5.22	8.60	1.49	2.82	2.73	2.27
17	DJH152122	4.45	16.24	65.00	194.94	108.93	18.51	5.85	7.21	1.23	0.00	2.31	2.31
143	DJH152248	4.45	15.50	64.38	208.72	118.52	0.15	6.29	2.15	1.49	0.74	2.57	2.20
154	DJH152838	4.45	16.25	64.92	184.60	93.21	14.99	4.86	8.23	1.00	1.32	2.81	2.29

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	HC	EA	TEX
66	DJH152169	4.42	16.61	66.38	191.58	116.22	1.46	5.63	7.86	1.27	17.63	3.00	2.48
169	DJH152856	4.38	16.95	66.13	187.72	102.66	0.16	6.14	4.79	1.24	3.40	2.81	2.10
113	DJH152222	4.36	16.41	64.38	199.25	113.12	1.36	5.34	6.34	1.50	4.02	4.19	2.04
197	DJH152338	4.36	15.75	66.07	189.22	96.76	-0.26	5.98	6.05	1.47	1.14	2.75	2.47
167	DJH152854	4.36	16.01	64.13	199.13	105.73	5.51	6.37	6.95	0.99	0.83	2.60	2.08
159	SC633	4.34	14.80	65.75	203.64	117.33	4.22	6.14	9.33	1.01	14.17	3.12	2.91
46	DJH152150	4.33	16.35	65.50	190.16	109.58	21.55	6.43	9.30	1.50	9.74	2.56	1.90
23	DJH152129	4.32	15.56	67.00	192.91	101.52	3.37	5.44	7.18	1.23	8.24	3.00	2.42
202	DJH152343	4.31	16.31	65.38	180.31	98.76	-0.09	6.33	4.97	1.24	0.00	2.57	1.82
203	DJH152344	4.30	16.51	66.50	190.98	104.77	0.01	5.78	3.33	1.24	1.88	2.75	2.39
138	DJH152243	4.30	16.77	68.07	190.96	101.91	0.06	5.63	10.44	1.24	0.66	2.75	2.29
50	DJH152154	4.27	16.45	68.21	203.82	123.18	-0.03	5.09	6.71	1.49	4.26	2.44	2.21
163	DJH152849	4.27	15.92	66.25	204.59	100.45	8.54	6.26	6.78	1.47	12.98	2.31	1.58
51	DJH152155	4.26	17.66	66.35	190.13	111.59	7.57	5.38	5.73	1.50	0.83	2.69	2.05
106	DJH152214	4.26	17.05	67.50	201.07	97.08	8.32	5.51	5.39	1.77	3.57	2.44	1.81
181	DJH152321	4.25	16.15	65.64	179.25	97.42	3.22	5.49	10.41	1.25	9.38	2.81	2.72
68	DJH152171	4.24	17.29	68.63	210.42	127.16	2.70	5.80	3.49	1.50	5.00	2.69	2.02
204	DJH152345	4.23	15.94	67.00	195.79	104.47	13.82	5.50	6.92	1.50	2.82	2.77	2.27
170	DJH152311	4.23	14.87	64.50	196.80	104.81	6.70	5.44	7.82	1.53	2.94	2.81	2.65
95	DJH152198	4.22	17.04	66.63	200.51	121.73	0.10	5.58	9.29	0.98	3.84	2.94	2.00
146	CH142176	4.19	15.50	60.00	196.96	105.81	0.02	5.61	8.55	1.52	3.13	2.68	2.02
127	DJH152235	4.17	17.81	65.78	198.61	107.15	0.02	6.53	7.97	1.25	4.58	2.75	2.58
93	DJH152195	4.17	17.69	64.88	193.72	111.06	-0.04	5.72	6.51	1.25	3.39	6.57	2.07
104	CH14685	4.15	17.09	66.63	202.45	112.91	9.01	5.13	2.95	1.49	4.82	2.69	1.71
137	DJH152242	4.15	16.16	65.75	212.17	107.47	3.50	6.52	4.59	1.50	7.66	2.44	1.99
117	DJH152227	4.14	16.31	68.13	198.11	110.67	-0.02	5.97	4.07	1.52	1.79	2.87	2.08
157	DJH152843	4.14	16.85	66.00	190.21	99.19	5.38	5.80	6.35	1.28	1.39	2.63	2.49
94	DJH152197	4.13	15.71	64.92	189.29	106.85	33.42	5.51	11.96	1.49	9.74	3.06	2.37
219	PHB30G19	4.13	17.14	65.38	196.83	108.93	5.27	5.36	7.70	1.02	4.29	2.94	2.55
63	DJH152166	4.12	17.94	66.38	189.47	112.03	9.31	5.43	9.92	1.01	19.53	2.82	2.27
215	SC643	4.10	16.29	66.00	212.37	117.99	-0.23	5.93	4.85	1.29	9.75	2.56	2.14
67	DJH152170	4.09	17.36	65.50	197.93	113.45	8.50	6.63	7.45	1.52	1.47	2.94	2.36
200	DJH152341	4.09	15.61	66.88	181.64	96.86	-0.15	5.24	3.49	1.27	2.50	2.80	2.05
76	DJH152179	4.08	16.49	63.64	199.94	112.31	9.87	5.99	6.97	1.74	5.48	2.81	1.97
45	DJH152149	4.06	15.82	64.75	194.95	107.18	4.14	5.65	8.35	1.50	7.23	2.38	2.18
65	DJH152168	4.06	17.05	66.75	204.35	115.74	4.45	6.01	12.99	1.24	4.16	2.50	2.11
198	DJH152339	4.06	16.05	68.25	189.80	102.61	5.12	5.82	3.94	1.50	0.00	2.62	2.29
6	CH123975	4.06	16.84	67.13	202.82	102.05	3.05	4.93	7.63	1.02	4.26	2.60	2.51
98	CH132200	4.06	17.11	67.13	192.42	102.06	6.97	5.54	4.52	1.50	12.12	2.37	2.21
124	CH142244	4.03	16.36	67.07	208.15	109.89	6.98	5.47	8.93	1.28	4.29	2.87	2.64
132	DJH152237	4.03	16.29	67.25	201.23	104.54	9.09	5.82	10.02	1.53	13.57	2.57	2.09
133	DJH152238	4.02	16.81	68.88	204.97	109.18	4.50	5.19	7.03	1.76	1.79	2.66	2.14
73	DJH152176	4.00	16.82	68.38	192.84	116.28	2.22	5.46	5.06	1.23	4.80	2.82	2.16
183	DJH152323	3.99	17.44	67.63	195.72	103.39	-0.02	6.22	12.39	1.00	0.96	2.87	2.94
199	DJH152340	3.98	15.97	65.88	189.44	98.71	1.05	5.48	9.53	1.26	4.51	2.81	2.10
118	DJH152228	3.96	15.74	67.38	189.70	107.31	1.81	5.25	8.14	1.48	7.36	2.94	1.90
130	CH12760	3.96	16.09	65.88	188.15	98.32	1.58	5.40	4.56	1.01	1.67	2.75	2.37
61	CH124172	3.95	16.61	67.63	190.86	108.22	14.97	4.99	10.69	1.25	9.91	3.00	2.15
191	DJH152332	3.95	16.26	67.13	196.33	106.26	-0.02	5.87	7.00	1.50	4.67	2.63	2.34
49	DJH152153	3.93	16.68	66.38	191.02	98.29	0.01	5.82	3.56	1.23	0.00	2.19	1.92
214	SC513	3.92	14.71	64.35	188.45	113.02	3.95	6.45	7.38	1.49	0.96	3.12	2.67
144	DJH152249	3.92	16.29	66.00	182.97	98.09	3.74	6.44	2.79	1.48	1.25	2.63	1.95
128	DJH152236	3.91	16.48	63.93	200.78	105.82	5.21	6.29	7.73	1.04	3.66	2.90	2.56
171	DJH152312	3.90	17.69	63.35	184.78	102.57	-0.15	6.01	37.88	0.99	8.60	2.74	2.46
1	DJH152105	3.90	16.69	67.88	198.03	111.39	4.90	5.30	3.02	1.49	8.93	2.67	2.37
27	CH132165	3.89	16.81	66.38	199.64	119.08	0.08	5.97	9.61	1.23	13.39	2.87	2.11
205	CZH131001	3.88	15.79	62.07	186.10	99.29	5.28	6.14	10.36	1.27	0.89	6.34	2.50
160	DJH152845	3.88	14.47	64.78	194.82	109.06	10.19	6.41	6.81	1.26	1.67	2.75	2.34
5	DJH152109	3.85	16.98	67.38	186.72	100.81	1.96	5.29	10.69	1.26	7.29	2.75	2.17
72	DJH152175	3.85	17.00	66.00	197.70	113.12	1.55	4.73	8.70	1.27	2.61	2.62	2.08
131	DJH152235	3.85	16.91	64.50	199.57	108.14	7.73	6.08	6.06	0.98	6.08	2.65	2.60
123	DJH152233	3.85	17.99	66.78	196.48	112.26	10.20	5.85	6.35	1.51	0.00	2.38	2.23
87	DJH152190	3.83	16.70	66.00	211.40	119.78	3.03	5.98	7.04	1.52	0.74	2.66	2.32
37	DJH152141	3.82	16.27	65.64	192.52	102.34	5.93	6.40	3.31	1.49	6.19	2.76	2.08
13	DJH152117	3.81	16.97	65.13	207.32	105.35	3.26	6.24	3.61	1.49	3.19	2.82	2.54
79	DJH152182	3.81	15.31	64.78	195.44	110.07	22.96	5.88	4.47	1.48	5.00	2.74	2.08
62	DJH152165	3.81	16.69	66.75	213.83	123.68	4.11	5.00	7.80	1.50	9.20	2.44	2.60
148	DJH152252	3.78	16.56	67.00	186.59	101.58	-0.07	6.06	4.88	0.98	1.04	2.31	1.96
99	DJH152205	3.77	15.54	68.78	185.19	116.54	5.52	4.85	5.12	1.23	12.34	2.56	1.95
211	SC301	3.77	13.41	61.13	199.10	89.24	17.43	6.32	10.11	2.24	4.01	3.13	2.24
38	SC719	3.76	17.21	69.78	219.54	130.28	1.42	5.01	9.40	1.22	0.69	2.12	2.43
48	DJH152152	3.75	14.90	66.38	200.37	107.04	5.44	6.14	5.23	1.26	3.54	2.63	2.02
212	SC403	3.71	13.87	62.38	199.84	102.97	0.07	6.43	8.29	1.48	4.45	3.00	2.35
97	DJH152201	3.67	17.40	69.00	198.40	113.96	10.99	5.55	6.65	1.49	0.00	2.63	1.85
90	CH142171	3.66	15.58	65.50	203.06	119.13	3.29	5.76	6.91	1.74	2.10	3.00	2.11
165	DJH152852	3.66	16.47	65.75	190.81	97.14	9.70	5.44	17.10	1.24	3.56	2.53	2.34
166	DJH152853	3.66	15.95	65.13	192.07	110.24	4.67	5.85	6.53	1.51	6.08	2.62	2.04
156	DJH152842	3.63	14.31	66.07	191.52	105.70	8.97	5.56	13.61	0.98	13.23	2.95	2.48
52	DJH152156	3.57	15.11	66.65	179.81	104.60	1.89	5.19	6.19	1.74	5.32	2.37	2.20
32	DJH152138	3.57	15.71	66.35	195.45	105.03	4.59	5.33	8.05	1.49	2.88	2.75	2.27
84	DJH152187	3.54	16.21	65.13	197.82	113.14	4.97	5.03	5.88	1.04	11.31	2.74	3.53
173	DJH152315	3.54	16.21	65.25	196.89	93.75	4.96	5.61	8.39	1.25	6.11	2.62	2.67
201	DJH152342	3.54	16.91	66.13	186.21	101.71	1.07	5.63	7.86	1.23	1.70	2.44	1.89
103	DJH152212	3.52	17.04	67.13	197.15	116.60	11.43	6.15	8.76	1.48	4.40	2.53	2.07
10	DJH152113	3.49	15.27	65.92	204.40	112.48	1.80	5.39	3.42	1.51	4.64	2.63	2.14
86	CH124647	3.47	16.50	65.88	210.61	120.94	-0.09	5.46	3.13	1.23	3.85	2.31	2.06
88	DJH152191	3.44	16.79	66.13	189.51	111.96	8.18	5.35	6.71	1.24	13.78	2.51	2.12
20	DJH152126	3.41	14.45	65.63	205.95	110.53	3.12	5.41	10.28	1.24	12.50	2.80	2.07
161	DJH152846	3.31	16.21	64.88	205.80	110.04	17.20	4.92	3.87	1.00	2.34	2.70	2.03
116	DJH152226	3.27	15.95	66.75	213.05	121.39	4.34	5.85	5.83	1.24	9.73	2.63	2.04
186	DJH152327	3.23	15.27	66.25	186.52	100.18	1.55	6.05	12.42	1.77	2.63	2.94	2.87
31	DJH152137	3.22	15.49	65.35	183.54	97.71	23.31	5.23	22.40	1.01	4.44	2.82	2.06
105	DJH152213	3.18	13.72	68.88	192.74	104.98	12.57	5.23	4.11	1.24	3.82	3.01	2.38
155	DJH152841	3.18	16.28	67.21	199.38	105.83	10.03	5.40	10.08	1.25	0.00	2.65	2.54
8	DJH152111	3.17	15.81	65.25	196.06	102.99	2.01	6.51	6.65	1.52	3.16	2.75	2.49
70	SC303	3.17	14.49	66.00	198.17	121.92	5.27	5.45	5.86	1.23	12.08	2.81	2.26
190	DJH152331	3.17	16.87	67.63	183.60	101.96	1.26	5.46	20.49	1.26	1.47	2.94	2.63
9	DJH152112	3.14	15.30	67.63	207.04	119.95	8.19	6.13	6.68	1.23	2.21	2.94	2.57
64	DJH152167	3.13	16.77	63.49	199.13	110.81	2.67	6.23	3.57	1.49	0.69	2.88	2.23
158	DJH152844	3.10	15.31	65.38	181.97	99.83	0.17	6.25	6.23	1.00	13.08	2.63	2.21
120	DJH152230	3.05	14.79	66.32	194.08	117.95	1.14	5.58	16.04	1.25	4.37	2.60	2.19
16	DJH152121	3.01	15.74	66.07	191.80	103.08	-0.02	5.39	12.32	1.51	5.68	3.00	2.55
40	DJH152144	2.97	15.42	66.64	202.72	121.30	2.14	6.40	7.61	2.01	0.00	2.75	2.13
184	DJH152324	2.96	14.81	67.21	196.76	107.24	-0.06	6.19	6.10	1.49	3.57	2.88	2.27
129	CH12756	2.93	14.99	65.21	181.56	99.53	7.39	5.30	4.67	1.22	0.00	2.79	2.30
53	DJH152157	2.91	15.44	64.88	214.80	118.13	1.35	6.14	6.64	1.49	5.63	2.68	2.61
115	DJH152225	2.90	15.79	68.49	192.01	109.84	4.33	4.81	6.20	1.50	11.24	4.82	1.88

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	HC	EA	TEX
151	DJH152255	2.88	14.81	67.00	196.34	108.87	-0.06	5.53	5.00	1.52	5.10	2.63	2.08
135	DJH152240	2.87	14.74	65.25	206.45	109.77	8.23	6.63	11.88	1.50	2.86	7.46	2.38
96	DJH152199	2.86	14.61	66.35	207.46	117.00	0.00	5.64	6.19	1.46	3.17	2.88	2.62
152	DJH152833	2.73	14.89	68.07	192.66	99.17	2.08	4.70	11.90	1.24	9.08	3.17	2.56
33	DJH152139	2.73	14.40	65.75	191.96	115.15	9.09	5.41	11.52	1.25	12.60	2.94	2.05
119	DJH152229	2.69	14.70	65.49	191.52	110.51	-0.20	6.26	3.58	1.26	1.35	2.81	1.79
194	DJH152335	2.64	15.31	65.75	174.43	88.38	17.28	5.67	8.97	1.23	2.68	2.72	2.35
21	SC635	2.56	13.95	65.49	183.42	103.30	17.52	6.07	5.75	1.23	1.14	3.41	2.51
43	DJH152147	2.47	15.55	66.31	199.30	107.17	-0.12	4.96	12.32	1.26	0.00	3.18	2.11
22	DJH152128	2.29	15.27	64.63	195.62	111.67	2.72	5.52	7.12	0.99	5.47	2.50	2.47
175	DJH152317	2.28	15.94	66.25	179.76	95.78	-0.15	5.16	3.94	1.24	1.14	2.94	2.57
147	DJH152251	2.12	14.49	69.00	199.61	105.88	2.09	6.41	13.27	1.49	1.14	3.19	2.28
54	GV665A	1.52	13.18	64.25	208.08	116.55	1.62	5.71	5.70	1.26	1.04	2.46	2.27
Mean		4.35	16.47	66.28	196.91	109.10	5.41	5.70	7.43	1.39	5.61	2.75	2.28
LSD		2.22	2.90	7.44	18.62	15.68	15.49	0.84	10.78	0.46	10.64	1.48	0.55
CV		25.91	8.95	5.71	4.82	7.32	0.00	7.39	73.92	16.80	96.52	27.46	12.28
Heritability		0.34	0.06	0.07	0.37	0.50	0.02	0.64	0.00	0.66	0.21	0.33	0.49

GY- grain yield, MOI- moisture, AD-anthesis date, PH-plant height, EH-ear height, SL-stem lodging, SEN-senescence ER-ear rots, GLS- grey leaf spot, HC-husk cover, EA- ear aspect, TEX-texture.

Appendix 5.5 Grain yield and agronomic traits of 230 exotic x local three-way hybrids in set 5 in descending order of grain yield

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	TURC	HC	TEX
229	PAN7M-81	8.23	15.86	67.31	209.20	125.43	4.09	3.93	3.60	1.00	2.00	4.44	2.69
226	SC643	8.19	15.50	65.83	209.82	112.32	2.67	5.13	5.24	1.00	1.75	3.85	2.87
144	DJH152585	8.17	15.67	69.06	219.84	132.58	5.82	4.88	2.20	1.50	1.75	1.28	3.12
227	SC727	7.99	14.77	73.56	224.78	136.50	1.51	4.39	2.26	1.25	1.50	4.55	3.05
172	DJH152653	7.96	15.35	70.80	212.09	136.21	1.05	4.07	4.96	1.25	1.75	0.00	2.35
173	DJH152654	7.89	12.29	69.78	218.42	135.03	-2.21	5.02	3.51	1.25	2.00	0.00	2.81
95	DJH152536	7.81	15.69	67.42	215.32	124.66	19.63	4.31	2.39	1.50	2.00	1.39	3.13
178	DJH152659	7.73	15.97	70.38	200.06	130.16	-0.15	4.21	5.21	1.00	1.75	7.69	2.93
187	DJH152670	7.67	14.25	69.80	217.44	132.02	1.94	3.82	8.12	1.50	1.50	2.38	2.80
228	PAN53	7.64	14.59	67.23	207.31	107.34	12.08	4.48	6.16	1.75	1.50	6.49	2.75
110	DJH152551	7.52	15.26	68.37	197.87	110.98	-0.03	4.29	4.26	1.25	1.50	8.89	2.75
1	DJH165001	7.51	13.85	62.54	213.56	103.98	14.45	4.57	5.39	1.25	1.50	4.23	3.11
58	DJH152378	7.50	16.28	64.78	201.46	109.65	0.22	4.41	1.69	1.00	1.50	6.25	2.18
9	DJH165009	7.49	16.57	62.23	201.81	105.36	4.09	4.66	2.29	1.00	1.75	2.56	2.75
68	DJH165068	7.48	15.46	66.78	202.76	121.11	5.31	4.16	7.14	1.00	1.50	13.35	2.95
217	CZH131001	7.48	15.17	68.32	217.49	115.96	2.92	4.91	3.15	1.00	1.75	2.47	3.07
73	DJH165073	7.47	15.19	66.41	209.59	103.86	0.08	5.33	4.72	1.50	1.75	3.03	2.82
21	DJH165021	7.45	15.89	68.43	199.57	120.73	0.67	4.27	4.79	1.00	1.75	7.95	2.51
48	DJH152368	7.41	16.37	68.43	197.34	115.53	4.47	3.83	6.48	1.50	1.75	8.33	2.44
84	DJH165084	7.39	14.63	66.86	201.66	112.67	6.88	5.07	5.54	2.00	1.75	8.66	2.69
219	CZH141028	7.39	15.14	67.22	220.00	129.63	-0.96	3.34	3.30	1.00	1.75	0.00	2.70
201	DJH152685	7.36	15.14	70.63	219.07	126.99	-0.45	4.28	4.11	1.25	1.50	11.70	2.82
189	DJH152672	7.31	15.60	70.32	208.06	130.44	0.27	4.56	2.68	2.00	1.75	7.39	2.31
167	CH14649	7.27	15.26	70.88	215.32	123.96	1.37	4.68	4.89	1.25	2.00	11.48	3.18
224	SC419	7.23	13.77	65.38	208.29	116.05	1.18	5.18	8.01	2.25	1.50	0.00	3.19
221	CZH131007	7.18	15.18	68.73	204.39	110.06	-0.54	3.79	5.89	1.00	1.50	14.36	3.13
14	DJH165014	7.14	15.80	70.83	204.58	110.53	1.53	4.29	3.74	1.00	1.50	6.85	2.56
19	DJH165019	7.14	14.24	68.54	207.45	128.23	0.57	5.19	9.79	1.00	1.50	2.22	3.00
20	DJH165020	7.14	13.08	70.37	205.35	117.04	28.99	5.16	7.32	1.25	1.75	0.00	2.94
175	DJH152656	7.14	14.56	72.02	215.40	127.41	0.35	4.67	2.36	1.25	1.75	0.00	2.32
209	DJH152693	7.14	15.05	67.16	204.10	121.16	1.02	4.15	8.92	1.00	1.50	12.26	2.25
170	CH14651	7.13	14.50	70.81	219.32	127.97	1.50	4.34	3.49	1.25	1.50	0.98	2.94
207	DJH152691	7.07	15.34	69.48	178.06	117.12	2.81	4.26	1.99	1.25	1.75	4.72	2.57
45	DJH152365	7.06	15.70	68.74	216.25	120.11	4.81	5.16	11.27	1.00	1.75	6.04	2.75
198	DJH152682	7.02	14.68	72.65	212.56	123.02	-0.70	4.04	4.77	1.00	1.75	0.00	2.62
36	DJH152356	6.98	14.90	66.84	194.21	108.27	12.40	4.59	7.14	1.25	1.75	16.64	2.74
174	DJH152655	6.98	14.85	67.13	208.03	111.72	15.01	5.24	3.74	1.00	1.75	0.00	2.83
103	DJH152544	6.97	15.60	67.54	205.60	110.15	28.08	5.56	3.48	1.25	1.75	2.78	5.69
190	DJH152673	6.97	14.97	66.18	219.20	138.12	-0.23	4.30	5.03	1.75	1.75	8.33	2.94
59	DJH152379	6.96	15.01	64.94	207.68	116.57	5.37	4.60	9.18	1.00	1.50	1.28	2.56
130	DJH152571	6.96	15.36	66.43	209.40	114.25	11.62	4.56	2.31	1.25	1.50	1.28	2.56
200	DJH152684	6.96	15.33	70.46	197.02	128.09	9.91	4.52	2.82	1.25	1.75	1.11	2.54
203	DJH152687	6.96	15.90	70.99	223.77	137.48	1.01	5.13	3.12	1.75	1.75	1.67	2.69
216	DJH152700	6.96	14.14	69.66	203.42	115.59	8.08	4.30	3.28	1.75	1.50	6.21	2.63
42	DJH152362	6.95	14.97	66.00	198.02	96.79	2.26	5.64	4.88	1.75	1.75	0.00	2.50
161	DJH152602	6.95	14.05	65.16	197.74	112.90	3.11	4.61	3.20	1.75	1.75	12.96	2.20
206	DJH152690	6.95	15.40	69.63	217.04	124.14	4.46	4.40	4.86	1.00	1.50	3.13	2.35
85	DJH152526	6.94	14.64	63.02	218.97	114.90	19.91	4.78	2.07	1.25	1.50	0.00	2.57
208	DJH152692	6.92	15.77	71.71	207.33	138.33	-1.92	3.76	7.18	1.00	1.75	0.00	3.18
152	DJH152593	6.91	14.82	65.08	196.38	108.64	0.33	5.09	6.22	1.50	1.75	4.96	2.69
179	CH124326	6.90	14.43	67.32	204.12	117.98	-0.88	4.05	8.75	1.00	1.75	0.00	3.00
79	DJH165079	6.89	16.40	65.77	196.40	117.14	8.26	4.81	0.95	1.25	1.50	0.00	2.45
67	DJH165067	6.86	15.35	64.98	184.63	98.49	1.15	3.83	4.54	1.25	1.50	9.55	2.56
72	DJH165072	6.86	14.18	64.35	206.45	114.42	16.35	5.02	2.18	1.00	1.50	4.76	3.00
140	DJH152581	6.86	14.19	65.58	214.98	118.84	-0.01	5.32	5.65	1.00	1.50	11.11	2.69
46	DJH152366	6.85	15.67	68.57	204.71	122.33	15.94	6.27	5.75	1.75	1.75	4.62	2.82
168	CH14383	6.84	13.77	69.92	208.34	129.58	9.02	3.89	6.20	1.75	1.50	2.08	2.81
222	10C3271	6.84	14.59	62.60	205.88	111.70	13.16	4.59	3.07	3.25	2.25	5.56	2.88
63	DJH165063	6.82	14.13	68.49	199.65	108.03	2.15	5.46	3.86	2.00	1.50	4.72	2.32
77	DJH165077	6.82	14.88	69.18	205.91	117.49	3.43	5.52	12.74	1.00	1.50	8.89	2.67
176	DJH152657	6.82	14.94	70.65	224.75	120.43	5.08	4.41	2.39	1.25	1.50	3.33	4.07
116	DJH152557	6.81	16.28	67.42	197.46	115.06	29.45	5.19	6.77	1.00	1.50	5.79	2.50
194	CH132222	6.81	16.41	70.64	208.12	120.91	0.22	4.08	6.56	1.25	1.75	8.53	2.32
108	DJH152549	6.78	15.15	65.12	196.76	102.94	-0.83	4.92	4.70	1.00	1.75	0.00	2.38
81	DJH165081	6.77	13.26	66.46	196.37	114.78	2.40	4.30	11.93	1.00	1.50	16.62	2.56
10	DJH165010	6.76	15.02	66.34	199.31	112.20	2.21	4.48	4.40	1.00	1.50	4.08	2.81
133	DJH152574	6.75	16.01	69.98	197.56	116.00	1.15	4.26	2.85	1.00	1.50	4.29	2.75
154	DJH152595	6.75	15.55	67.41	198.80	114.01	1.10	5.03	3.85	1.25	1.75	4.85	2.87
87	DJH152528	6.70	15.27	63.38	200.21	111.02	20.17	4.69	6.15	1.00	1.75	2.38	2.49
16	DJH165016	6.69	15.57	68.83	199.66	114.84	0.61	4.52	6.52	1.00	1.50	3.33	2.32
218	CZH131013	6.68	15.72	64.66	213.25	100.38	0.15	5.20	6.97	1.00	1.50	8.24	2.70
162	DJH152603	6.67	14.63	71.43	204.51	118.95	9.35	4.02	4.97	1.50	1.75	1.11	2.81
98	DJH152539	6.66	15.35	68.30	200.04	105.45	2.32	4.41	4.47	2.00	2.00	8.89	2.68
104	DJH152545	6.65	15.10	64.71	199.95	111.79	-0.11	4.02	6.39	1.75	1.50	0.00	2.82
78	DJH165078	6.61	14.67	65.71	201.86	111.68	7.80	4.63	4.55	1.00	1.75	0.00	2.50
76	DJH165076	6.60	13.86	64.23	214.60	109.01	4.10	4.96	2.57	1.50	1.50	3.57	2.56
160	DJH152601	6.56	15.98	67.98	193.01	108.30	27.55	5.11	6.38	1.00	1.50	2.38	2.93
204	DJH152688	6.55	15.83	70.38	220.99	130.07	1.14	5.80	4.22	1.75	2.00	1.28	2.50
132	DJH152573	6.54	14.66	67.81	200.80	112.69	0.85	4.42	3.53	1.25	1.50	6.73	2.32
23	DJH165023	6.51	13.70	63.07	210.42	120.27	4.32	4.69	7.42	1.25	1.50	0.00	2.62
138	DJH152579	6.51	15.56	64.12	187.93	100.19	16.70	4.78	4.60	1.00	1.50	0.00	2.95
22	DJH165022	6.50	14.89	66.94	202.29	114.04	0.14	4.83	2.55	0.99	1.75	0.00	2.47
93	DJH152534	6.50	14.45	65.26	203.52	117.18	20.94	4.18	7.61	1.01	1.50	1.19	2.93
148	DJH152589	6.49	14.55	65.07	208.93	116.81	25.36	5.25	3.46	1.00	1.75	3.33	2.25
69	DJH165069	6.46	14.81	67.86	205.44	113.44	1.05	4.60	4.45	1.25	1.50	6.39	2.63
13	DJH165013	6.45	14.83	67.77	195.99	108.72	15.64	4.08	2.71	1.00	1.50	1.28	2.31
89	DJH152530	6.45	15.71	65.56	204.34	113.91	1.71	4.82	5.38	1.00	1.75	0.00	2.77
83	DJH165083	6.43	14.24	63.10	201.72	118.69	0.56	4.56	4.61	1.00	1.50	4.62	2.62
56	DJH152376	6.41	13.31	62.59	197.05	116.58	7.31	5.01	4.73	1.50	1.50	8.79	2.94
196	DJH152680	6.40	14.16	70.22	200.46	121.72	1.08	4.81	4.47	1.00	2.00	13.77	2.32
34	DJH152354	6.37	14.59	67.74	196.66	103.33	19.59	5.37	4.50	1.50	1.50	9.08	2.63
64	DJH165064	6.34	14.06	65.58	193.26	116.18	11.39	4.84	9.04	1.00	1.75	7.78	3.18
90	DJH152531	6.34	15.75	68.06	198.15	107.13	12.22	4.35	1.94	1.25	1.50	2.94	2.75
205	DJH152689	6.34	14.19	69.46	204.35	118.95	-0.41	4.09	3.99	1.50	1.75	1.39	2.32
32	DJH152352	6.33	14.18	65.99	183.45	96.32	4.46	4.38	9.17	1.00	1.50	4.90	3.00
131	DJH152572	6.33	14.43	63.61	198.14	102.94	7.45	6.09	3.65	1.00	1.75	0.00	2.56
180	CH124327	6.32	14.25	71.47	208.93	122.45	-2.01	4.19	6.60	1.00	1.75	1.85	2.69
44	DJH152364	6.30	14.74	66.62	206.73	111.60	9.70	4.79	8.05	1.75	1.50	8.58	2.87
177	DJH152658	6.30	14.46	69.09	208.97	118.82	-0.91	4.69	1.85	1.00	1.50	0.00	2.56
128	DJH152569	6.29	14.31	66.14	193.36	107.76	6.58	4.34	6.28	1.50	1.75	7.41	2.83

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	TURC	HC	TEX
139	DJH152580	6.29	15.65	64.92	218.13	119.68	-0.66	4.67	5.13	1.75	1.50	6.18	2.88
141	DJH152582	6.29	12.85	66.72	190.60	115.88	12.23	4.36	2.08	1.00	1.75	4.90	2.54
121	DJH152562	6.28	15.11	68.51	204.19	109.61	1.61	5.32	5.38	1.00	1.50	0.00	2.69
171	DJH152652	6.27	15.36	72.45	214.21	120.97	0.51	4.45	5.43	1.00	1.50	1.52	2.82
220	CZH131006	6.27	14.31	65.41	205.06	101.85	0.82	4.75	2.66	1.00	1.50	4.17	2.93
6	DJH165006	6.26	15.23	65.20	207.19	110.34	7.65	4.84	4.01	1.00	1.75	0.00	2.68
91	DJH152532	6.24	14.84	65.85	205.51	105.17	3.06	4.96	6.82	1.25	1.50	12.08	2.68
41	DJH152361	6.23	14.95	68.56	199.31	112.63	12.13	5.16	7.52	1.24	1.50	3.03	2.43
135	DJH152576	6.23	14.40	68.89	204.30	111.65	11.06	5.39	9.02	2.26	1.75	6.55	2.73
127	DJH152568	6.22	15.03	64.57	202.18	102.77	58.22	4.71	1.24	1.00	1.50	0.00	2.82
57	DJH152377	6.21	15.36	64.50	189.56	100.62	0.33	4.59	3.60	1.00	1.50	6.84	2.59
66	DJH165066	6.21	14.08	62.87	180.43	101.39	23.67	3.79	4.08	1.25	1.50	9.96	2.41
15	DJH165015	6.19	15.57	69.46	198.41	112.91	5.73	4.86	3.68	1.25	1.75	1.28	2.69
215	DJH152699	6.18	15.60	66.41	202.57	116.17	0.47	2.84	5.11	1.25	1.50	10.23	3.88
18	DJH165018	6.16	14.16	65.55	207.65	108.73	5.92	4.93	8.37	1.00	1.50	0.00	2.75
61	DJH152381	6.16	13.39	67.38	203.80	114.97	11.40	4.92	4.96	1.25	1.75	5.90	2.56
124	DJH152565	6.15	15.51	65.62	190.49	103.75	-1.22	4.69	5.13	1.00	1.50	0.00	2.68
156	DJH152597	6.15	15.07	63.45	193.54	106.26	7.68	4.83	4.00	1.50	1.50	17.95	2.69
214	DJH152698	6.15	14.71	67.73	204.82	122.46	0.57	4.08	6.75	1.25	1.50	6.79	2.31
33	DJH152353	6.12	13.58	65.94	184.42	106.20	10.26	4.31	8.63	1.25	1.50	4.74	2.56
38	DJH152358	6.09	15.00	65.86	212.86	115.71	4.44	5.92	11.01	1.75	1.50	8.97	2.63
111	DJH152552	6.09	14.87	64.62	200.22	116.57	44.05	4.74	3.42	0.99	2.00	3.33	2.75
149	DJH152590	6.09	13.59	68.81	190.45	108.76	19.89	5.76	2.96	1.50	1.50	6.25	2.99
29	DJH152349	6.08	15.34	64.56	197.36	112.08	3.61	5.41	5.80	1.50	1.50	11.09	2.38
119	DJH152560	6.08	15.34	65.47	189.18	106.85	37.24	4.63	8.01	1.00	1.50	0.00	2.81
74	DJH165074	6.07	12.63	64.11	188.07	107.85	0.73	3.88	0.98	1.00	1.50	0.00	3.00
164	DJH152605	6.07	14.57	68.40	224.15	123.53	0.44	4.53	5.82	1.00	1.50	7.41	2.75
185	SC635	6.06	13.95	70.96	217.45	134.70	19.87	4.23	1.36	1.50	1.50	0.00	2.57
197	DJH152681	6.06	14.75	69.98	193.17	123.50	13.01	4.34	6.39	1.25	1.50	0.00	2.69
7	DJH165007	6.04	15.00	64.94	199.77	105.50	5.58	4.35	3.16	1.25	1.50	15.66	2.50
17	DJH165017	6.04	14.62	67.53	205.32	111.79	1.08	5.74	5.27	1.75	1.75	1.39	2.56
25	DJH165025	6.03	15.68	63.69	205.79	112.85	7.81	5.24	1.22	1.00	1.50	0.00	2.20
8	DJH165008	6.02	14.59	63.18	199.04	113.97	12.23	4.40	5.61	1.00	1.50	0.00	2.75
165	DJH152606	6.02	14.76	68.89	202.02	111.44	5.97	4.20	3.35	1.25	1.50	2.78	2.69
26	DJH165026	6.00	13.60	66.12	212.27	116.30	0.01	4.69	3.89	1.50	1.50	2.08	2.56
106	DJH152547	6.00	15.27	64.40	182.19	87.26	5.86	4.35	3.83	1.75	1.50	5.56	2.19
117	DJH152558	6.00	14.21	65.48	198.93	108.83	44.71	4.65	2.07	1.25	1.50	2.95	2.51
183	DJH152664	5.99	13.80	71.56	207.08	124.11	0.60	4.12	1.31	1.25	1.75	6.67	2.81
4	DJH165004	5.98	15.29	65.91	194.28	108.49	14.22	4.27	5.84	1.00	1.50	1.39	2.64
71	DJH165071	5.97	14.12	66.05	198.76	106.29	2.79	5.46	4.21	1.25	1.50	5.36	2.74
118	DJH152559	5.97	14.60	63.55	211.84	117.36	30.11	5.52	7.28	1.00	1.50	0.00	2.87
136	DJH152577	5.97	12.68	64.99	207.63	106.35	8.85	5.38	4.40	1.25	1.50	2.38	2.80
35	DJH152355	5.96	13.97	64.95	199.65	110.17	9.11	5.16	7.07	1.25	1.75	10.21	2.75
184	DJH152665	5.96	13.38	74.25	211.42	124.28	1.35	4.32	7.83	1.50	1.75	2.94	2.76
75	DJH165075	5.95	15.50	64.62	199.67	109.59	0.74	4.54	3.27	1.50	1.50	1.28	2.18
47	DJH152367	5.94	15.73	69.03	208.07	125.78	19.09	5.38	5.44	1.75	1.75	6.36	2.88
5	DJH165005	5.93	13.94	65.39	187.12	101.19	7.99	4.82	10.83	1.00	1.75	15.37	2.63
101	DJH152542	5.93	14.28	65.73	204.87	113.70	18.34	5.34	6.55	1.75	1.50	22.90	2.56
115	DJH152556	5.93	15.43	64.49	191.86	106.41	7.49	4.41	4.78	1.24	1.75	13.87	6.85
54	DJH152374	5.92	14.72	65.88	196.46	104.02	48.98	4.85	6.78	1.25	1.75	0.00	2.81
157	DJH152598	5.90	14.88	65.14	194.37	103.46	6.63	5.59	5.03	1.25	1.50	2.50	2.45
151	DJH152592	5.87	14.33	63.74	196.14	107.73	-0.52	4.77	4.15	1.75	1.75	1.39	2.58
107	DJH152548	5.85	14.50	65.73	199.90	112.92	8.71	5.16	4.68	1.25	1.50	0.00	2.64
191	DJH152674	5.84	16.45	67.63	200.68	119.63	5.62	4.61	4.00	1.00	1.50	0.00	2.38
55	DJH152375	5.83	13.05	65.92	214.82	113.92	29.56	5.33	4.59	1.50	1.75	7.42	2.81
60	DJH152380	5.83	14.39	64.14	209.92	121.34	8.73	5.09	6.93	1.25	1.50	14.67	2.63
153	DJH152594	5.83	15.23	62.76	201.22	100.74	11.44	6.52	3.68	1.50	2.00	5.56	2.44
143	DJH152584	5.79	14.75	63.95	209.31	115.32	-0.55	4.60	3.22	1.50	1.50	4.23	2.76
24	DJH165024	5.78	14.67	65.87	204.98	112.08	3.47	4.08	2.83	1.24	1.50	5.56	2.25
195	CH123968	5.78	13.74	74.04	202.60	124.98	1.04	4.78	5.02	1.00	1.50	0.00	3.13
147	DJH152588	5.77	13.67	66.06	198.96	116.13	0.62	4.80	5.94	1.25	1.50	12.08	2.88
129	DJH152570	5.76	14.96	65.92	204.81	106.51	5.09	4.62	7.31	1.50	1.50	0.00	2.50
120	DJH152561	5.74	13.77	66.68	198.55	113.95	21.81	5.14	4.36	1.25	1.50	11.67	2.81
28	DJH152348	5.73	13.98	64.94	205.22	102.48	22.74	5.17	7.68	1.25	1.50	4.52	2.81
50	DJH152370	5.70	13.83	65.28	203.59	108.36	18.67	4.53	6.72	1.50	1.50	3.33	2.31
80	DJH165080	5.69	14.72	66.47	206.55	117.62	-1.69	3.67	4.51	1.00	1.50	6.55	5.57
112	DJH152553	5.69	14.48	66.60	185.32	101.46	4.90	4.31	6.30	1.25	1.50	2.38	2.20
155	DJH152596	5.69	14.66	65.60	187.39	109.06	0.29	4.02	3.99	1.25	1.50	2.78	2.56
181	SC403	5.69	12.61	58.52	197.14	103.73	2.88	5.24	8.20	1.75	1.50	4.08	2.69
39	DJH152359	5.68	13.52	68.61	196.88	111.91	2.97	3.95	13.18	1.00	1.75	3.33	2.99
169	CH14386	5.67	14.19	71.54	203.97	111.48	-0.74	4.66	2.40	1.25	1.50	0.00	2.75
150	DJH152591	5.66	14.78	66.59	207.30	111.66	29.27	5.43	6.97	1.50	1.75	5.16	2.96
40	DJH152360	5.64	14.53	66.24	196.02	114.34	27.20	4.88	7.26	0.99	1.50	11.67	2.94
3	DJH165003	5.63	12.24	67.76	202.46	108.52	7.72	4.81	5.58	1.00	1.50	0.00	2.88
37	DJH152357	5.63	14.56	63.86	202.61	109.73	12.40	5.05	2.40	1.00	1.50	2.08	2.32
97	DJH152538	5.63	15.12	66.14	193.93	109.64	1.08	4.20	2.38	1.00	1.50	12.73	2.25
123	DJH152564	5.63	14.03	63.89	201.22	104.14	41.70	4.65	3.07	2.00	1.75	0.00	3.00
11	DJH165011	5.62	14.24	65.41	197.23	113.24	6.51	5.21	9.10	1.00	1.75	3.33	2.92
105	DJH152546	5.62	13.62	65.06	189.18	110.57	9.18	4.36	1.15	1.25	1.50	4.51	6.88
223	SC301	5.62	12.77	60.49	197.28	93.75	9.56	5.93	2.27	1.50	1.50	4.96	2.63
186	DJH152669	5.61	13.87	71.68	205.58	125.62	5.59	4.36	4.90	1.00	1.50	4.76	2.57
199	DJH152683	5.61	14.27	67.63	218.86	126.38	0.51	3.52	0.97	1.25	1.50	0.00	2.12
43	DJH152363	5.57	13.33	63.49	204.90	113.04	8.01	5.13	3.34	1.50	1.50	3.85	2.74
113	DJH152554	5.57	15.32	65.46	200.47	106.19	1.12	5.10	2.80	1.00	1.50	2.08	2.20
145	DJH152586	5.56	14.73	64.76	205.24	103.68	32.57	5.24	8.81	1.00	1.50	14.77	3.01
70	DJH165070	5.55	15.13	63.42	193.41	107.11	5.05	4.83	7.29	1.25	1.75	12.18	3.01
65	DJH165065	5.53	13.93	68.60	205.70	126.79	1.67	3.88	4.13	1.50	1.50	0.00	3.32
30	DJH152350	5.50	14.07	63.75	199.66	98.97	29.68	5.62	3.84	1.25	1.50	0.00	3.12
51	DJH152371	5.47	14.17	63.10	188.97	105.61	2.24	4.52	2.97	1.25	1.50	1.28	2.62
137	DJH152578	5.46	14.12	63.19	206.46	110.24	2.85	4.62	0.91	1.25	1.50	1.52	2.67
86	DJH152527	5.43	13.79	65.74	197.88	114.58	4.85	4.92	6.19	1.00	1.75	0.00	2.25
159	DJH152600	5.40	14.50	66.14	186.62	98.79	9.35	3.94	2.13	1.25	1.50	4.72	2.45
109	DJH152550	5.39	14.41	67.71	202.91	110.98	29.76	4.21	6.67	1.50	1.50	16.67	2.25
27	DJH152347	5.38	13.81	63.37	210.99	111.19	10.19	5.52	4.03	2.26	1.75	8.89	3.00
134	DJH152575	5.38	14.25	65.50	192.30	109.32	1.92	4.16	2.31	1.50	1.50	0.00	2.56
202	DJH152686	5.31	13.52	68.60	205.96	118.55	1.54	4.54	3.58	1.75	1.75	5.37	2.76
210	DJH152694	5.31	13.01	71.19	195.96	105.25	4.23	4.18	1.94	1.49	2.00	1.67	2.82
212	DJH152696	5.31	14.34	73.04	203.80	119.01	0.18	3.59	6.29	1.00	1.50	2.78	2.75
96	DJH152537	5.30	15.11	64.88	188.13	106.97	6.42	4.90	6.95	1.01	1.50	8.01	2.75
146	DJH152587	5.30	14.86	63.99	206.18	115.33	-0.62	4.49	7.47	1.25	1.50	13.03	2.63
125	DJH152566	5.28	13.14	65.53	190.53	101.75	30.50	4.63	5.08	1.00	1.50	4.08	2.45
230	PHB30G19	5.27	14.73	66.78	198.35	99.35	1.80	5.20	7.63	1.25	1.50	2.78	2.76
49	DJH152369	5.26	14.51	66.58	198.15	105.94	6.27	4.74	4.97	1.75	1.75	10.47	2.94
31	DJH152351	5.21	14.32	65.79	189.15	102.00	35.72	4.93	5.09	1.00	1.75	0.00	2.63
52	DJH152372	5.19	14.49	67.22	197.65	117.54	6.80	4.74	4.98	1.25	1.50	22.56	2.42
53	DJH152373	5.19	13.66	67.50	191.77	104.20	-1.80	5.19	5.30	1.26	1.50	2.08	2.57
102	DJH152543	5.19	14.21	65.26	202.82	100.23	15.25	4.89	4.51	1.00	1.75	4.22	2.19

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	TURC	HC	TEX
193	DJH151820	5.16	13.48	69.52	207.78	119.37	0.35	4.44	1.96	1.25	1.50	8.10	2.75
114	DJH152555	5.06	13.92	63.73	208.49	109.76	5.05	4.10	3.21	1.00	2.00	0.00	2.20
99	DJH152540	5.05	15.06	68.02	192.76	100.67	6.95	4.34	1.97	1.00	1.75	1.28	2.76
82	DJH165082	5.03	14.32	65.44	205.16	107.73	9.99	4.12	8.97	1.25	1.50	12.14	2.67
211	DJH152695	5.03	12.97	75.69	184.88	114.10	1.88	5.36	6.04	1.00	1.75	0.00	3.00
166	DJH152607	5.01	13.57	69.08	193.80	112.13	3.06	3.81	4.52	1.00	1.50	0.00	2.94
158	DJH152599	4.97	14.16	64.30	212.04	112.21	-0.63	4.95	3.06	1.25	1.50	5.00	2.62
188	DJH152671	4.94	12.80	75.17	194.97	120.37	0.05	4.14	3.64	1.00	1.75	0.00	2.37
126	DJH152567	4.83	13.38	68.42	201.22	116.59	1.07	3.91	5.17	1.25	1.75	7.41	2.56
12	DJH165012	4.81	13.75	67.13	193.99	96.44	11.74	3.17	9.12	1.25	1.75	18.95	2.88
192	CH132212	4.74	12.82	74.18	185.45	125.89	1.09	4.67	11.15	1.25	1.75	4.55	3.19
225	SC513	4.73	12.80	64.57	193.51	106.89	3.42	4.98	10.61	1.00	1.50	4.76	3.26
182	DJH152663	4.60	13.55	73.71	203.43	123.60	0.54	4.63	4.63	1.25	1.50	7.41	2.88
213	DJH152697	4.60	13.14	72.51	207.25	138.36	2.40	4.20	3.17	1.25	1.50	5.42	2.94
88	DJH152529	4.52	12.49	69.50	176.50	86.58	0.42	4.20	5.60	1.25	1.75	3.06	2.69
122	DJH152563	4.31	13.69	67.92	183.72	97.45	3.51	4.56	5.66	1.99	1.75	8.70	2.95
142	DJH152583	4.16	13.32	69.13	186.98	98.59	13.84	5.41	6.22	1.00	1.75	2.38	2.40
2	DJH165002	4.14	13.23	64.87	190.44	105.25	0.44	4.18	7.23	1.00	1.75	2.56	2.24
92	DJH152533	3.98	13.38	67.17	187.92	101.27	40.39	3.72	5.90	1.50	1.75	3.03	2.57
163	DJH152604	3.84	13.22	67.61	191.75	106.29	7.46	4.79	5.46	1.00	1.50	0.00	2.91
100	DJH152541	3.79	13.77	65.81	193.83	100.57	40.48	4.89	9.90	1.00	1.75	8.33	2.60
94	DJH152535	3.77	13.63	64.03	195.18	98.44	54.26	4.79	3.15	1.25	1.75	0.00	2.68
62	DJH152382	3.35	12.81	68.70	178.47	95.53	5.69	4.67	21.05	1.00	1.50	8.93	3.32
Mean		6.18	14.54	67.01	201.91	113.13	8.18	4.67	5.14	1.27	1.62	4.83	2.76
LSD		1.64	2.23	3.10	17.52	16.32	21.11	1.05	6.97	0.66	0.39	11.99	1.49
CV		13.50	7.81	2.35	4.42	7.35	130.01	11.29	69.07	26.37	12.25	126.35	27.58
Heritability		0.58	0.20	0.86	0.59	0.65	0.59	0.39	0.06	0.46	0.16	0.16	0.45

GY- grain yield, MOI- moisture, AD-anthesis date, PH-plant height, EH-ear height, SL-stem lodging, SEN-senescence ER-ear rots, GLS- grey leaf spot, TURC-turcicum, HC-husk cover, TEX-texture.

Appendix 5.6 Grain yield and agronomic traits of 250 exotic x local three-way hybrids in set 6 in descending order of grain yield

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	ER	TURC	HC	EA	TEX
248	PAN7M-81	9.66	13.93	67.25	232.15	149.69	4.25	3.14	1.75	8.31	2.27	2.82
246	SC727	9.66	13.60	70.00	225.35	129.99	11.07	1.49	1.75	14.42	2.19	3.00
30	DJH166030	9.02	13.22	67.50	196.09	106.89	2.21	2.43	1.51	-0.17	2.43	2.63
25	DJH166025	8.80	14.43	68.25	217.30	132.03	2.55	2.26	1.50	0.82	2.50	2.39
43	DJH166043	8.68	14.17	69.50	212.18	118.92	1.74	2.37	1.49	5.76	2.38	2.57
41	DJH166041	8.66	14.05	65.00	213.72	126.90	3.67	5.09	1.50	1.40	2.50	2.70
238	DJH166238	8.61	14.32	66.25	215.00	113.80	-0.73	3.68	1.50	4.17	2.00	2.64
209	DJH166209	8.50	14.36	67.00	213.12	116.96	2.92	4.98	1.75	11.70	2.39	2.50
52	DJH166052	8.49	13.87	69.25	212.32	122.92	1.51	1.46	1.50	2.31	2.18	2.36
214	DJH166214	8.48	14.12	69.25	216.76	118.28	-0.23	3.30	1.76	8.87	2.32	2.07
216	DJH166216	8.40	14.34	67.75	210.75	114.53	4.12	7.79	1.75	5.84	2.56	2.57
55	SC608	8.30	13.88	66.50	202.47	119.15	3.16	2.82	1.50	7.46	2.30	3.01
202	DJH166202	8.21	13.89	68.50	209.49	124.06	4.37	2.33	2.00	5.65	2.25	2.57
146	DJH166146	8.20	14.06	66.25	209.27	125.17	3.80	1.96	1.50	4.47	2.06	2.68
200	DJH166200	8.19	14.81	65.25	211.25	115.58	3.42	3.58	1.75	5.19	5.21	2.63
80	DJH166080	8.19	14.26	66.50	191.16	106.28	6.12	5.42	1.75	0.06	2.48	3.06
15	DJH166015	8.18	13.86	68.75	226.75	145.28	1.98	6.03	1.51	0.12	2.57	2.75
164	DJH166164	8.15	13.92	69.25	217.20	131.41	0.97	2.15	1.49	1.89	2.21	2.00
240	10C3271	8.13	14.23	67.00	204.73	113.24	10.99	10.52	2.00	7.27	2.38	2.88
184	DJH166184	8.07	14.59	70.25	198.50	111.92	3.68	9.63	1.51	16.50	2.25	2.89
153	DJH166153	8.03	15.00	66.75	203.71	109.41	-0.06	2.77	1.50	7.86	2.61	2.61
24	DJH166024	8.03	14.13	65.00	217.69	126.03	0.70	0.95	1.50	2.53	2.06	2.25
150	DJH166150	7.99	14.01	70.50	208.06	124.81	6.71	1.84	1.51	2.89	2.37	2.44
165	DJH166165	7.96	13.43	65.75	195.21	100.80	4.08	9.00	1.75	10.45	2.24	2.62
92	DJH166092	7.96	14.02	67.75	207.31	111.97	4.05	3.83	1.50	3.42	2.37	3.06
18	DJH166018	7.95	14.06	67.50	208.40	121.92	0.06	3.40	1.50	3.07	2.39	2.63
245	SC643	7.95	14.03	65.50	216.03	119.55	7.97	2.68	2.00	10.67	2.26	2.63
118	DJH166118	7.94	12.77	67.25	199.14	101.66	1.55	3.89	1.51	3.87	2.63	3.05
189	DJH166189	7.92	14.51	66.75	213.54	119.75	-0.72	2.72	1.74	4.52	2.13	2.19
76	DJH166076	7.90	14.52	68.50	209.97	118.95	2.08	4.13	1.50	12.63	2.62	2.89
128	DJH166128	7.89	13.71	69.00	213.03	121.01	3.28	3.97	1.49	9.47	2.38	2.76
102	DJH166102	7.89	13.67	64.50	218.67	123.47	2.66	5.35	1.50	0.96	2.51	2.81
132	DJH166132	7.89	14.05	66.75	213.91	118.41	4.01	2.63	1.50	5.13	2.63	3.05
98	DJH166098	7.84	13.01	67.25	205.23	112.64	6.17	3.83	1.51	10.73	2.42	3.04
133	DJH166133	7.82	13.84	69.50	210.37	120.09	9.17	5.25	1.50	4.81	2.64	2.88
183	DJH166183	7.81	14.42	66.50	199.06	115.63	1.42	5.09	1.50	10.21	2.44	2.68
237	DJH166237	7.81	13.76	69.00	219.38	128.26	7.10	2.64	1.50	1.66	2.49	2.63
117	DJH166117	7.80	13.80	66.25	208.76	130.28	1.57	3.29	1.74	7.99	2.74	3.24
227	DJH166227	7.77	13.64	69.75	209.03	131.21	0.44	5.83	1.50	1.74	2.44	2.75
201	DJH166201	7.76	13.30	65.75	211.65	106.82	4.30	2.58	1.75	4.56	2.07	3.26
90	DJH166090	7.75	12.62	66.00	215.76	125.49	1.36	5.92	1.50	4.99	2.58	3.66
160	DJH166160	7.71	14.39	67.75	208.25	114.52	0.84	5.40	1.50	9.67	2.72	2.70
134	DJH166134	7.70	13.39	66.25	206.34	114.16	5.71	4.10	2.00	4.10	2.55	3.17
77	DJH166077	7.69	13.25	69.00	204.22	108.38	9.75	3.36	1.75	0.01	2.31	2.51
48	DJH166048	7.64	13.91	65.75	198.76	114.55	2.62	5.63	1.50	3.97	2.50	2.86
179	DJH166179	7.61	13.32	67.00	194.21	114.00	2.75	7.01	1.51	-0.16	2.50	3.00
78	DJH166078	7.61	13.77	66.75	221.85	125.85	4.92	2.31	1.74	0.00	2.19	2.50
211	DJH166211	7.60	14.32	68.00	200.75	112.16	1.11	8.40	1.49	2.07	2.54	3.11
213	DJH166213	7.60	14.41	71.00	210.00	119.98	3.55	2.96	1.49	4.67	2.39	2.31
17	DJH166017	7.60	13.35	69.75	209.45	99.93	2.92	0.76	1.50	0.19	2.38	2.61
187	DJH166187	7.57	13.83	66.50	205.76	119.14	1.84	6.74	1.50	2.27	2.49	2.81
231	DJH166231	7.56	14.05	68.75	190.24	114.82	3.84	2.90	1.49	-0.20	2.12	2.75
192	DJH166192	7.55	13.84	65.75	200.06	104.01	0.99	5.26	1.51	4.80	2.57	2.50
120	DJH166120	7.54	13.69	67.25	201.21	104.32	-0.43	4.55	1.50	8.93	2.27	2.75
127	DJH166127	7.54	13.85	66.75	213.10	117.97	3.47	4.17	1.75	-0.11	2.39	3.07
236	DJH166236	7.54	13.67	63.25	216.45	107.17	1.24	2.88	1.50	2.40	2.62	2.80
230	DJH166230	7.54	13.60	66.25	195.58	114.91	3.08	2.87	1.75	2.32	2.65	2.95
95	DJH166095	7.53	14.20	65.75	204.44	117.87	5.60	2.32	1.75	3.23	2.55	2.47
50	DJH166050	7.51	14.07	70.75	196.91	113.25	2.79	7.02	1.75	2.29	2.43	2.49
247	PAN53	7.51	14.11	68.25	214.24	117.19	0.87	2.81	1.50	-0.13	2.26	2.70
239	DJH166239	7.49	14.27	68.75	210.16	108.14	2.42	4.26	1.50	12.15	2.62	3.18
42	SC719	7.48	13.89	65.75	208.51	108.69	1.11	7.13	1.50	16.23	2.62	2.93
195	DJH166195	7.46	13.61	69.50	204.59	117.28	1.96	1.44	1.50	8.78	2.45	2.50
224	DJH166224	7.46	13.95	68.75	216.49	127.38	2.85	2.16	2.00	6.04	2.24	2.10
31	DJH166031	7.46	13.82	68.25	202.68	119.54	3.24	2.71	1.49	1.66	2.63	3.25
11	DJH166011	7.46	14.22	67.75	197.01	111.85	0.31	2.38	1.50	1.32	2.53	2.89
13	DJH166013	7.45	14.35	70.50	219.22	129.18	3.86	4.67	2.01	1.63	2.56	2.68
44	DJH166044	7.44	13.66	67.50	200.79	119.93	1.14	4.42	1.49	2.19	2.45	2.62
33	SC637	7.43	13.67	67.75	216.80	119.62	-0.26	2.00	1.75	0.05	2.58	2.99
182	DJH166182	7.42	13.61	68.00	196.14	117.96	0.04	6.53	1.74	2.69	2.68	3.05
10	DJH166010	7.41	13.17	69.00	196.16	104.41	2.04	4.24	1.75	1.83	2.29	2.51
197	DJH166197	7.41	14.23	68.50	202.40	114.66	-0.08	5.11	1.75	3.12	2.33	2.38
94	DJH166094	7.40	13.27	67.00	227.14	135.84	2.77	8.05	1.49	2.63	2.75	2.81
35	DJH166035	7.38	13.18	68.75	207.62	112.81	2.99	2.88	1.75	2.38	2.68	2.82
6	DJH166006	7.37	13.52	64.75	205.07	106.16	2.06	4.87	1.50	0.09	2.45	2.94
129	DJH166129	7.37	13.62	67.00	205.96	111.94	7.43	6.62	1.48	-0.09	2.50	2.76
16	DJH166016	7.35	13.67	66.50	209.10	109.85	1.71	1.90	1.75	13.64	2.45	2.31
208	DJH166208	7.32	13.46	64.25	202.96	102.79	0.17	3.76	1.74	7.28	2.33	2.75
46	DJH166046	7.31	13.22	65.75	200.98	113.16	2.58	3.76	1.49	3.01	2.26	3.03
144	DJH166144	7.30	13.22	69.50	217.45	115.72	3.38	2.41	1.75	1.49	2.40	2.81
103	DJH166103	7.30	14.55	69.75	219.02	137.97	5.77	6.15	1.75	10.76	2.32	2.75
130	DJH166130	7.28	13.34	68.75	209.40	119.86	5.86	3.92	1.75	1.44	2.36	2.50
131	DJH166131	7.27	13.66	68.75	223.51	133.90	1.10	2.06	1.50	4.94	2.44	2.82
12	DJH166012	7.26	14.03	67.00	218.02	120.17	4.70	1.73	1.75	9.59	2.44	2.61
101	DJH166101	7.25	13.56	68.00	206.34	116.98	7.10	2.06	1.51	9.79	2.30	2.94
162	DJH166162	7.25	13.45	65.75	198.61	105.95	3.56	3.50	1.50	6.19	2.33	2.44
97	DJH166097	7.22	13.58	69.25	221.71	112.14	4.84	4.10	1.49	6.55	2.37	2.87
37	DJH166037	7.22	13.49	69.50	223.99	135.56	4.51	4.47	1.50	1.73	2.46	2.97
107	DJH166107	7.22	12.74	67.50	205.45	108.16	3.05	10.38	1.50	6.15	2.36	2.94
79	DJH166079	7.22	13.55	67.25	223.78	124.54	3.31	4.72	1.50	6.01	2.67	2.86
173	DJH166173	7.22	13.69	67.00	203.03	116.44	3.95	1.96	1.51	1.06	2.38	2.39
106	DJH166106	7.19	13.71	66.75	209.29	113.11	3.12	4.50	1.75	4.27	2.39	2.63
166	DJH166166	7.18	14.84	69.50	201.28	119.41	2.13	3.45	1.50	5.12	2.31	2.68
123	DJH166123	7.16	13.98	66.75	203.22	112.13	5.68	7.28	1.50	0.47	2.45	2.87
108	DJH166108	7.15	13.33	63.75	201.02	108.51	1.99	3.31	1.50	0.26	2.62	3.18
3	DJH166003	7.15	13.79	67.75	198.88	106.72	5.20	3.33	1.74	0.06	2.55	2.87
53	DJH166053	7.14	14.21	66.50	215.42	116.88	3.74	2.97	1.50	4.95	2.44	3.07
115	DJH166115	7.10	12.99	69.75	199.50	120.67	5.07	4.79	1.49	1.53	2.54	2.74
140	DJH166140	7.10	13.52	71.50	203.56	120.33	3.32	9.49	1.50	4.37	2.77	2.61
Entry	Hybrid	GY	MOI	AD	PH	EH	SL	ER	TURC	HC	EA	TEX

215	DJH166215	7.09	13.64	65.00	207.90	102.09	4.63	3.64	1.50	4.01	2.62	2.49
190	DJH166190	7.08	13.25	65.00	200.01	100.82	0.20	4.15	1.51	0.06	2.18	2.50
70	DJH166070	7.07	14.03	70.50	204.04	123.96	2.70	4.41	1.75	1.10	2.43	2.57
125	DJH166125	7.06	13.81	68.25	221.33	125.51	2.39	2.88	1.50	2.49	2.39	3.14
2	DJH166002	7.05	13.99	64.75	197.30	114.94	4.66	4.08	1.50	0.14	2.75	3.19
219	DJH166219	7.02	13.68	64.75	211.69	106.16	2.53	1.88	1.49	13.65	2.56	2.55
45	DJH166045	7.01	13.49	65.75	209.35	112.00	4.50	2.52	1.49	5.63	2.31	2.75
21	DJH166021	7.01	13.38	65.75	200.03	115.68	4.90	2.63	1.51	2.21	2.47	2.30
207	DJH166207	7.01	13.67	66.00	202.96	124.80	6.07	3.32	1.75	6.04	2.25	2.43
93	DJH166093	6.99	13.80	67.75	208.53	118.50	3.09	2.26	1.50	0.12	2.49	2.58
36	DJH166036	6.96	13.39	66.00	209.83	99.43	1.94	6.40	1.50	3.10	2.32	2.75
158	DJH166158	6.96	13.73	68.25	200.46	97.95	0.96	3.32	1.50	9.03	2.55	2.81
226	DJH166226	6.95	13.40	68.25	211.50	119.42	8.44	4.40	1.50	8.36	2.56	2.80
111	DJH166111	6.93	13.55	67.00	215.18	126.07	12.07	1.33	1.50	1.79	2.49	2.94
86	DJH166086	6.93	13.70	71.50	199.98	121.81	3.79	6.03	2.01	-0.10	2.13	2.49
38	DJH166038	6.93	13.75	68.75	208.24	121.62	2.01	4.85	1.50	4.27	2.65	3.15
69	DJH166069	6.92	13.65	65.25	207.69	110.33	1.65	2.39	1.51	0.32	2.23	2.56
191	DJH166191	6.90	14.26	66.25	206.14	117.46	1.30	4.20	1.76	9.55	2.44	2.82
49	DJH166049	6.90	13.98	65.50	212.51	122.34	4.39	4.47	1.50	1.84	2.24	2.80
56	DJH166056	6.88	13.19	69.50	238.02	130.72	3.60	8.07	1.75	3.49	2.75	2.99
243	SC419	6.87	13.29	64.00	213.99	104.60	6.22	3.86	1.75	0.13	2.51	3.36
137	DJH166137	6.87	13.11	65.25	209.19	110.45	5.33	1.87	1.49	5.19	2.24	2.94
141	DJH166141	6.86	13.46	70.00	206.28	121.94	2.19	5.65	1.76	7.33	2.38	2.48
54	DJH166054	6.85	12.89	65.25	214.85	123.27	4.38	3.90	2.01	3.21	2.55	3.19
175	DJH166175	6.85	13.60	67.75	203.22	116.29	3.05	3.92	1.51	3.96	2.27	2.37
82	DJH166082	6.82	12.94	68.50	213.98	128.25	6.90	3.05	1.50	11.27	2.39	2.70
180	DJH166180	6.82	13.91	66.75	202.56	125.09	1.31	3.16	1.75	2.37	2.49	2.70
72	DJH166072	6.81	13.09	67.50	188.73	112.43	1.09	4.27	1.50	2.60	2.43	2.94
204	DJH166204	6.80	13.49	68.00	195.12	103.97	1.11	4.65	1.50	1.41	2.34	2.68
143	DJH166143	6.80	13.12	69.25	212.02	110.48	1.83	2.96	1.49	5.64	2.50	2.51
176	DJH166176	6.80	13.85	68.50	197.63	123.80	2.21	2.65	1.49	4.17	2.33	2.06
233	DJH166233	6.78	13.73	68.50	192.49	117.81	1.63	6.25	1.50	9.84	2.19	2.26
119	DJH166119	6.78	13.09	.	204.91	103.87	2.74	6.84	1.75	1.39	2.79	2.79
74	DJH166074	6.78	14.69	69.25	206.63	113.93	-0.03	5.18	1.50	2.02	2.38	2.37
188	DJH166188	6.78	13.94	68.00	198.27	113.15	6.20	1.64	1.50	0.87	2.68	2.82
218	DJH166218	6.77	13.95	66.75	214.97	117.93	2.04	5.62	2.00	5.47	2.57	2.63
163	DJH166163	6.75	13.13	67.50	200.52	114.42	3.53	3.62	1.49	-0.04	2.38	2.70
223	DJH166223	6.73	13.31	68.00	207.83	120.13	2.21	3.37	1.51	1.33	2.46	2.45
147	DJH166147	6.71	13.32	69.75	198.01	110.38	5.17	2.76	2.00	5.58	2.42	2.87
135	DJH166135	6.71	12.98	68.75	210.54	108.12	1.24	3.07	1.50	10.94	2.54	2.81
145	DJH166145	6.71	13.87	68.75	203.97	115.94	5.11	3.34	1.75	1.45	2.38	2.69
27	DJH166027	6.69	12.64	65.25	217.35	121.13	3.84	3.08	1.50	4.73	2.51	2.75
8	DJH166008	6.69	13.39	67.75	223.52	135.26	4.62	3.12	1.49	2.83	2.32	2.69
89	SC633	6.67	11.98	65.48	204.68	116.36	0.48	6.07	1.75	7.02	2.82	3.49
203	DJH166203	6.66	13.35	68.00	195.56	107.06	3.44	4.16	1.50	8.33	2.57	2.95
172	DJH166172	6.65	13.30	67.50	207.05	116.71	5.81	2.67	1.50	2.40	2.50	2.61
174	DJH166174	6.64	13.12	68.50	199.83	129.20	3.70	4.06	1.50	1.81	2.67	2.88
51	DJH166051	6.64	13.63	68.00	207.18	121.44	2.18	5.02	1.51	2.74	2.61	2.79
138	DJH166138	6.64	13.11	67.75	191.21	106.01	8.14	6.50	1.49	3.29	2.65	3.20
59	DJH166059	6.62	12.91	65.00	207.46	131.71	1.72	5.25	1.50	3.05	2.61	7.00
234	DJH166234	6.61	13.51	68.75	192.17	115.85	1.38	3.38	1.75	7.41	2.18	2.57
159	DJH166159	6.61	13.01	64.00	202.76	111.87	3.95	5.50	1.50	1.28	2.68	3.00
235	DJH166235	6.60	13.13	64.00	200.49	95.41	6.60	2.31	1.75	7.36	2.13	2.45
124	DJH166124	6.58	13.59	67.50	200.27	103.70	1.52	2.67	1.50	8.84	2.50	3.19
217	DJH166217	6.58	12.31	65.75	199.97	111.09	2.01	6.16	1.51	0.16	2.65	2.80
75	DJH166075	6.56	13.55	67.50	201.10	113.02	-0.41	4.62	1.50	1.76	2.38	2.81
154	DJH166154	6.56	13.94	70.50	208.34	117.76	4.91	5.43	1.50	2.51	2.43	2.82
116	DJH166116	6.54	12.68	69.00	207.95	113.77	1.64	4.22	1.75	2.19	2.51	2.37
61	DJH166061	6.54	13.26	67.25	196.30	108.34	1.76	1.86	1.49	3.20	2.14	2.37
151	DJH166151	6.53	13.25	70.00	209.42	126.10	3.14	5.88	1.50	5.17	2.30	2.43
157	DJH166157	6.50	13.86	68.00	198.31	103.97	1.71	5.93	1.76	4.68	2.57	3.00
148	DJH166148	6.49	13.86	69.50	186.09	117.91	4.31	6.98	1.50	4.74	2.51	2.63
220	DJH166220	6.49	12.64	66.50	193.90	112.87	9.49	8.13	1.50	24.51	2.92	3.26
71	DJH166071	6.48	13.30	68.25	215.12	120.87	4.93	6.56	1.52	1.07	2.48	2.74
83	DJH166083	6.48	13.31	67.50	211.14	131.29	6.13	1.46	1.50	3.94	2.55	3.00
222	DJH166222	6.48	13.32	65.00	199.15	120.21	3.46	2.36	2.00	2.42	2.44	3.06
170	DJH166170	6.47	12.75	67.75	203.27	122.66	3.21	4.33	1.49	5.59	2.58	2.89
210	DJH166210	6.46	13.96	69.00	192.32	104.17	4.65	1.55	1.50	4.78	2.52	2.70
249	PHB30G19	6.43	13.57	68.00	206.77	110.28	10.84	2.86	1.50	5.38	2.77	2.83
87	DJH166087	6.42	13.19	67.25	204.88	119.14	7.64	3.59	1.51	1.53	2.49	2.75
178	DJH166178	6.42	13.26	64.50	197.51	118.19	1.04	4.20	1.50	3.50	2.30	3.01
136	DJH166136	6.42	12.91	67.25	203.19	110.54	13.03	4.98	1.76	7.95	2.73	3.10
122	DJH166122	6.41	13.24	68.75	220.35	117.81	3.31	3.29	1.75	5.16	2.43	2.68
112	DJH166112	6.35	12.64	69.00	215.33	115.94	0.36	2.00	1.50	-0.05	2.68	3.15
64	DJH166064	6.34	13.49	68.50	212.31	125.79	5.57	8.57	1.51	0.02	2.81	3.31
161	DJH166161	6.33	13.36	68.00	206.74	105.96	4.23	4.02	1.50	5.14	2.39	2.37
181	DJH166181	6.32	12.64	67.25	202.89	117.69	2.35	4.05	2.00	3.41	2.62	2.94
14	DJH166014	6.31	14.37	70.50	200.87	125.56	8.53	2.25	1.50	3.52	2.25	2.20
57	DJH166057	6.31	13.04	65.25	216.83	114.25	4.59	6.37	1.75	8.93	2.49	2.85
68	DJH166068	6.31	13.03	71.00	208.88	131.52	4.33	6.23	1.99	1.90	2.57	2.86
96	DJH166096	6.27	13.55	66.25	217.11	122.72	3.25	6.62	1.50	6.93	2.37	3.14
28	DJH166028	6.27	13.50	72.25	188.64	120.60	2.10	2.88	1.51	1.82	2.94	2.81
177	DJH166177	6.22	13.75	67.50	200.06	108.15	3.95	4.50	1.49	-0.07	2.49	2.51
29	DJH166029	6.22	14.14	72.50	207.67	122.75	5.38	5.19	1.74	6.53	2.76	3.44
84	GV665A	6.19	11.85	65.50	218.42	112.02	7.08	4.24	1.51	11.35	2.26	2.37
73	DJH166073	6.17	13.90	67.75	210.95	114.65	0.63	3.36	1.74	-0.01	2.45	2.82
156	DJH166156	6.16	13.33	69.00	203.10	108.19	15.42	4.51	1.50	1.13	2.36	2.37
228	DJH166228	6.15	13.84	64.75	217.27	126.62	6.13	3.96	1.49	2.67	2.56	3.05
206	DJH166206	6.15	12.72	67.75	197.36	114.15	-0.79	5.52	1.50	4.56	2.55	2.73
63	DJH166063	6.10	12.96	69.00	220.81	130.06	7.15	15.47	2.00	27.04	2.25	2.49
142	DJH166142	6.09	13.19	69.75	203.80	114.88	1.73	3.86	1.50	3.54	2.55	2.88
19	DJH166019	6.06	13.22	67.25	201.56	121.28	0.54	4.69	1.73	3.61	2.25	2.49
5	DJH166005	6.05	13.19	64.75	212.37	109.67	6.43	1.30	1.50	12.45	2.76	2.50
26	DJH166026	6.04	12.82	68.25	205.43	115.44	1.39	5.52	1.50	2.82	2.94	3.24
171	DJH166171	6.04	13.20	68.50	203.63	111.74	2.21	3.76	1.75	-0.02	2.32	1.95
155	DJH166155	6.03	13.41	68.25	197.91	93.78	3.64	5.26	1.51	4.85	2.68	2.61
40	DJH166040	5.99	13.29	69.75	207.40	117.04	15.98	1.47	1.76	7.45	2.11	2.63
205	DJH166205	5.98	14.69	68.00	191.86	100.10	1.24	5.56	1.75	-0.13	2.45	2.45
62	DJH166062	5.96	12.36	65.00	209.06	141.78	4.05	5.43	1.75	8.08	2.52	3.02
22	DJH166022	5.96	13.57	67.25	217.72	116.59	5.15	1.33	1.50	0.06	2.34	2.77
109	DJH166109	5.92	13.59	64.75	209.57	113.30	2.17	5.11	1.50	7.60	2.32	2.82
225	DJH166225	5.88	12.97	68.75	192.99	113.04	5.64	7.19	1.50	3.66	2.68	3.43
100	DJH166100	5.88	13.08	66.75	215.41	129.80	2.45	4.64	1.74	0.06	2.27	2.63
212	DJH166212	5.86	13.19	66.50	192.08	106.53	0.63	4.34	1.51	7.97	2.62	2.82
81	DJH166081	5.80	13.45	71.25	206.69	119.03	9.78	4.74	1.49	1.86	2.56	2.88
167	DJH166167	5.77	13.44	63.25	198.38	97.09	1.00	2.15	1.50	2.18	2.62	2.81
104	DJH166104	5.77	13.60	71.75	220.05	122.99	4.19	4.03	1.75	7.02	2.30	2.56
Entry	Hybrid	GY	MOI	AD	PH	EH	SL	ER	TURC	HC	EA	TEX

194	DJH166194	5.76	12.57	68.75	200.97	123.20	1.94	3.74	1.75	2.23	2.69	2.88
126	DJH166126	5.74	13.27	69.00	185.44	98.21	7.74	6.10	1.50	0.14	2.81	2.88
39	DJH166039	5.74	13.50	67.00	206.44	124.41	2.39	6.57	1.75	19.21	2.70	2.99
242	SC403	5.68	12.64	65.75	210.94	111.42	1.64	3.74	2.00	2.27	2.55	2.67
149	DJH166149	5.67	13.31	66.75	202.62	114.70	8.74	7.19	1.50	1.31	2.35	2.96
34	DJH166034	5.61	13.00	68.50	205.69	107.62	2.36	6.45	1.49	1.24	2.75	3.07
7	DJH166007	5.61	12.52	68.25	222.81	130.83	1.55	4.21	1.50	1.19	2.52	3.09
114	DJH166114	5.55	12.51	65.75	203.42	107.94	1.26	3.77	1.75	2.70	2.52	3.15
4	DJH166004	5.55	13.82	70.00	198.52	108.75	-0.57	2.47	1.50	1.33	2.51	2.87
110	DJH166110	5.52	12.89	69.75	216.62	118.12	5.20	6.15	1.50	1.40	2.83	3.00
198	DJH166198	5.49	12.63	67.75	203.22	116.41	1.06	10.03	1.50	5.86	2.74	2.75
121	DJH166121	5.49	13.36	70.50	204.97	113.68	9.79	16.52	1.50	21.07	2.69	3.00
1	DJH166001	5.49	13.02	66.00	214.15	117.70	12.73	1.81	1.50	0.04	2.26	2.57
67	DJH166067	5.47	13.43	65.50	212.80	129.68	10.72	7.95	2.00	6.76	2.40	2.69
241	SC301	5.46	12.86	59.50	195.11	81.23	-0.16	2.79	1.75	5.09	2.87	2.87
185	DJH166185	5.46	12.40	69.50	194.05	104.62	2.69	7.04	1.75	3.86	2.80	2.87
221	DJH166221	5.43	13.17	67.00	212.08	111.48	0.34	5.82	1.50	1.51	2.26	2.81
250	PAN413	5.40	12.69	65.50	184.87	104.38	3.86	12.98	1.76	7.58	2.99	3.24
244	SC513	5.31	12.47	63.50	206.83	112.72	5.24	9.64	1.50	5.03	2.73	3.25
88	SC303	5.31	12.71	58.25	186.27	81.13	4.07	2.90	1.50	1.27	2.57	2.81
113	DJH166113	5.27	13.61	69.25	206.00	127.84	6.12	4.98	1.51	7.66	2.44	2.26
152	DJH166152	5.25	13.12	70.25	183.34	118.01	11.18	10.18	1.50	-0.11	2.74	3.13
47	DJH166047	5.16	13.27	65.25	206.34	119.67	8.37	5.88	1.51	13.00	2.50	2.80
229	DJH166229	5.14	13.40	68.25	207.87	113.41	3.18	2.57	1.75	1.30	2.57	2.50
232	DJH166232	5.13	13.56	68.50	200.91	122.37	3.13	3.24	1.49	0.83	2.76	2.94
23	SC635	5.13	12.44	69.25	211.65	118.24	8.73	6.43	1.49	5.98	2.94	3.51
20	DJH166020	5.13	11.85	70.75	209.81	130.62	4.30	8.35	1.50	1.44	2.46	2.93
186	DJH166186	5.06	13.68	64.75	197.64	110.77	0.48	7.93	1.74	4.08	2.62	2.92
169	DJH166169	5.01	12.99	70.00	206.01	120.99	3.45	9.01	1.50	3.06	3.00	3.27
139	DJH166139	4.99	13.25	69.00	202.51	116.91	2.14	5.86	1.75	2.49	2.57	3.01
99	DJH166099	4.98	12.98	67.25	207.13	114.33	5.51	3.26	1.49	15.91	2.70	3.14
65	DJH166065	4.94	13.22	67.25	199.91	114.05	4.79	3.36	1.50	-0.02	2.44	2.82
58	DJH166058	4.92	12.35	66.00	211.90	109.96	3.72	1.46	1.50	4.63	2.30	2.93
32	DJH166032	4.90	13.50	68.00	199.43	112.87	1.37	7.06	1.50	-0.02	2.54	2.55
66	DJH166066	4.88	13.14	64.00	198.80	114.11	5.13	1.41	1.75	0.04	2.38	2.82
168	DJH166168	4.87	12.93	68.50	192.62	120.97	5.22	7.90	1.50	-0.06	2.70	2.82
193	DJH166193	4.84	12.50	67.00	198.12	115.18	0.60	3.86	1.50	6.19	2.44	2.43
91	DJH166091	4.80	12.34	67.75	206.90	112.00	9.18	2.35	1.75	6.27	2.39	2.64
85	DJH166085	4.80	22.58	67.75	203.59	117.32	9.93	2.07	1.75	4.94	2.56	2.62
9	DJH166009	4.54	12.93	66.00	219.49	127.40	3.93	5.24	1.49	0.02	2.30	2.81
199	DJH166199	4.36	12.91	68.50	188.57	113.07	7.21	1.48	1.75	1.82	2.55	2.87
105	DJH166105	4.28	13.05	66.75	208.39	108.05	5.11	3.05	1.75	16.20	2.39	3.02
60	DJH166060	4.17	12.43	70.50	169.69	100.55	-0.22	4.62	1.50	0.01	3.01	3.25
196	DJH166196	2.89	33.41	66.50	210.01	123.18	0.54	4.92	1.49	15.67	2.55	3.07
Mean		6.76	13.60	66.43	206.33	116.25	3.74	4.45	1.60	4.54	2.49	2.80
LSD		2.02	4.21	48.53	17.59	16.73	8.64	5.99	0.37	9.95	0.64	0.95
CV		15.19	15.75	7.09	4.34	7.33	117.36	68.47	11.55	111.62	13.15	17.24
Heritability		0.52	0.00	0.37	0.56	0.62	0.00	0.15	0.26	0.35	0.20	0.24

GY- grain yield, MOI- moisture, AD-anthesis date, PH-plant height, EH-ear height, SL-stem lodging, ER-ear rots, TURC-turcicum, HC-husk cover, EA-ear aspect, TEX-texture.

Appendix 5.7 Grain yield and agronomic traits of 275 exotic x local three-way hybrids in set 7 in descending order of grain yield

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	ER	HC	TEX
81	SC635	8.26	11.46	63.91	190.28	101.93	5.06	6.19	10.02	2.76
263	DJH167263	7.62	14.39	65.89	221.11	135.00	0.21	1.07	2.67	2.10
265	DJH167265	7.42	13.67	67.72	200.74	107.62	-0.34	19.88	21.00	3.26
274	PAN7M-81	7.34	13.38	66.07	217.04	130.23	6.01	7.03	3.87	2.79
219	DJH167219	7.20	13.81	71.30	213.71	130.84	3.46	8.24	3.38	2.14
229	DJH167229	7.03	13.85	70.44	202.04	124.90	1.90	2.91	0.32	2.80
170	DJH167170	6.97	13.38	66.01	200.21	101.52	1.30	8.92	10.28	2.31
272	SC727	6.97	12.82	71.26	198.27	116.67	6.00	25.17	31.93	3.52
164	DJH167164	6.96	13.85	65.17	199.03	101.67	0.22	23.71	9.87	2.48
203	DJH167203	6.87	14.64	70.08	200.64	119.46	3.69	26.96	4.18	2.84
212	DJH167212	6.86	14.82	68.80	190.82	108.49	-0.10	20.50	10.76	2.68
125	DJH167125	6.82	13.86	64.04	185.10	92.64	6.49	2.84	0.76	2.36
243	DJH167243	6.75	13.01	66.87	183.73	95.70	1.74	8.57	2.19	2.87
222	DJH167222	6.71	12.51	70.12	213.95	109.77	-0.08	7.62	7.77	1.92
193	DJH167193	6.68	13.43	68.17	202.00	111.65	-1.71	6.28	2.65	2.66
4	DJH167004	6.64	14.19	66.36	195.78	92.26	0.64	3.00	3.81	2.53
97	DJH167097	6.59	14.31	63.58	210.01	99.28	0.27	8.83	-0.17	2.53
207	DJH167207	6.58	13.87	70.81	206.52	135.00	0.15	27.84	0.78	2.68
216	DJH167216	6.54	13.83	67.29	202.46	110.21	0.87	5.76	1.78	3.07
271	SC643	6.54	13.55	64.36	197.57	112.61	5.92	31.44	1.13	2.59
221	DJH167221	6.48	13.69	67.77	201.95	122.39	1.46	3.73	11.55	2.74
209	DJH167209	6.46	13.96	70.69	190.24	103.60	1.39	11.96	4.66	2.67
89	DJH167089	6.44	13.63	64.46	199.13	113.37	1.75	8.04	4.85	2.85
194	DJH167194	6.44	14.06	70.17	204.94	117.22	0.40	10.89	4.86	2.24
53	DJH167053	6.43	13.18	63.09	182.29	97.31	0.33	9.97	-0.84	2.38
53	DJH167053	6.43	13.18	63.09	182.29	97.31	0.33	9.97	-0.84	2.38
226	DJH167226	6.43	13.83	70.55	213.66	126.32	0.79	17.70	20.78	2.86
140	DJH167140	6.42	13.60	62.87	199.88	99.94	0.92	1.82	9.96	2.45
80	DJH167080	6.38	13.45	68.13	206.09	125.94	4.50	29.90	0.31	2.58
5	DJH167005	6.35	13.75	67.13	181.80	97.13	1.44	18.44	0.85	2.61
208	DJH167208	6.35	14.23	68.49	199.81	118.25	1.27	10.86	2.81	2.52
177	DJH167177	6.31	13.50	66.52	196.10	105.72	0.27	10.69	0.13	2.67
70	DJH167070	6.28	13.86	63.90	183.51	97.64	0.71	12.24	2.18	3.16
188	DJH167188	6.28	13.89	67.35	191.55	103.20	0.05	6.17	0.73	2.71
255	DJH167255	6.27	10.71	65.89	194.98	112.88	12.21	3.47	1.24	2.68
261	DJH167261	6.24	13.22	63.89	198.87	96.08	0.30	6.92	5.97	2.66
22	DJH167022	6.23	13.56	67.12	188.83	96.61	2.92	10.43	1.20	2.85
171	DJH167171	6.22	13.11	66.09	193.03	99.36	3.97	6.61	23.52	2.58
245	DJH167245	6.22	13.68	68.43	193.73	105.61	0.07	12.55	1.13	2.18
34	DJH167034	6.21	13.48	67.74	190.65	102.47	-0.01	10.03	4.00	2.75
131	DJH167131	6.21	13.29	64.44	188.84	86.92	1.46	4.24	-0.43	2.96
252	DJH167252	6.21	13.29	68.62	185.31	99.32	0.22	6.77	7.34	2.54
72	DJH167072	6.19	13.48	64.73	170.01	89.65	1.94	8.64	7.89	2.93
218	DJH167218	6.19	14.17	69.19	206.12	121.37	2.35	9.00	5.33	2.96
266	10C3271	6.19	12.19	63.15	200.88	97.03	2.00	8.95	2.83	3.08
124	DJH167124	6.17	12.82	64.19	191.78	100.98	1.07	23.35	3.40	3.09
154	DJH167154	6.17	14.21	62.81	202.89	114.58	2.32	6.49	14.71	2.49
14	DJH167014	6.16	13.94	66.98	199.71	98.67	2.08	10.24	3.71	2.10
223	DJH167223	6.16	14.34	69.81	206.45	122.14	-0.25	12.28	6.23	2.53
273	PAN53	6.15	12.93	66.47	191.68	102.28	4.72	3.82	8.88	3.00
237	DJH167237	6.14	12.88	68.58	206.74	120.86	1.78	13.43	7.51	2.64
233	DJH167233	6.13	14.09	69.27	206.00	125.45	0.10	11.02	0.65	2.08
239	DJH167239	6.13	13.70	63.96	201.29	110.04	4.04	3.62	1.64	2.15
256	DJH167256	6.13	13.46	67.68	199.95	109.31	-0.02	4.94	0.39	2.69
264	DJH167264	6.13	13.45	65.31	215.44	110.98	2.25	0.64	3.99	2.45
78	DJH167078	6.12	13.69	67.24	196.03	92.41	3.07	26.79	1.91	2.87
121	DJH167121	6.12	13.89	64.60	185.06	93.35	18.54	10.42	6.37	2.47
191	DJH167191	6.11	13.85	69.53	202.81	116.17	0.42	4.39	3.22	2.65
206	DJH167206	6.10	13.33	65.83	190.12	104.53	0.96	19.37	2.27	2.30
77	DJH167077	6.09	13.64	65.59	185.00	94.01	-0.27	1.70	2.10	2.64
57	DJH167057	6.07	13.92	65.07	209.20	102.87	1.48	1.57	7.00	2.23
109	DJH167109	6.06	14.16	64.62	200.09	103.81	4.25	7.02	6.66	2.34
169	DJH167169	6.06	12.92	64.32	209.42	104.64	4.50	10.54	13.90	2.90
55	DJH167055	6.05	12.92	66.41	175.43	97.42	3.73	2.27	0.80	2.62
179	DJH167179	6.04	12.65	68.95	200.36	114.82	1.57	14.40	2.85	3.09
141	DJH167141	6.02	11.94	58.91	186.27	81.39	22.86	9.10	2.50	2.64
228	DJH167228	6.02	14.18	70.75	219.60	139.31	3.54	26.52	1.80	2.25
238	DJH167238	6.02	13.12	69.16	212.32	116.67	1.47	3.14	10.24	2.75
86	DJH167086	6.00	11.90	64.65	192.49	105.35	0.14	1.48	9.85	2.67
174	DJH167174	5.96	13.44	64.15	171.39	89.52	0.25	13.78	10.65	2.75
185	DJH167185	5.96	13.77	68.04	194.00	105.28	6.13	3.13	15.01	2.65
105	DJH167105	5.94	13.15	63.60	181.61	84.12	2.23	10.45	4.10	2.84
103	DJH167103	5.92	12.91	62.56	189.53	91.00	1.08	15.17	9.15	3.02
110	DJH167110	5.90	13.91	64.94	192.76	101.46	0.11	53.88	10.19	2.66
68	DJH167068	5.87	12.96	63.68	185.81	99.16	0.23	11.35	11.68	2.73
197	DJH167197	5.86	11.37	68.17	199.16	108.32	0.15	11.58	1.92	3.10
214	DJH167214	5.85	13.64	69.64	211.41	132.65	0.37	2.20	3.71	2.52
93	DJH167093	5.83	13.07	67.29	202.42	95.38	2.91	3.28	0.90	2.51
257	DJH167257	5.83	12.87	72.38	189.45	102.26	1.89	4.76	0.17	2.31
91	DJH167091	5.82	13.81	63.09	173.92	89.04	1.40	38.64	4.71	2.91
115	DJH167115	5.82	13.66	63.99	194.70	98.07	-0.56	13.41	11.02	2.06
40	DJH167040	5.81	13.08	64.27	200.00	100.31	-0.16	3.72	-1.25	2.79
76	DJH167076	5.81	14.31	69.29	184.84	99.06	1.48	15.40	8.39	2.50
175	DJH167175	5.80	13.25	66.60	206.06	107.28	0.58	1.74	7.76	2.40
16	DJH167016	5.79	12.73	64.30	186.29	90.17	1.71	1.01	2.94	2.89
35	DJH167035	5.79	13.43	64.95	185.15	90.25	0.11	7.57	4.04	2.67
153	DJH167153	5.79	12.94	53.09	193.73	80.84	-0.23	9.51	2.58	2.76
187	DJH167187	5.79	13.20	68.54	206.46	114.56	-0.33	17.59	6.71	2.71
236	DJH167236	5.78	12.78	66.72	202.36	120.40	0.39	2.40	0.89	2.51
161	DJH167161	5.77	13.61	63.55	198.83	103.19	0.12	4.23	2.65	2.98
192	DJH167192	5.77	13.82	71.01	211.88	116.32	1.82	12.42	2.87	2.37
112	DJH167112	5.75	13.08	66.58	193.51	99.21	-0.37	15.05	5.13	2.19
127	DJH167127	5.75	13.51	64.19	199.11	90.73	1.87	17.00	5.23	2.85
51	DJH167051	5.73	12.31	64.11	192.17	98.73	1.26	5.81	10.69	2.57
83	DJH167083	5.73	12.90	67.65	199.67	104.56	0.03	6.34	3.26	2.69
198	DJH167198	5.73	13.35	64.30	197.95	107.20	7.13	24.44	3.53	3.01
210	DJH167210	5.73	12.73	69.49	192.84	113.07	1.91	19.90	-0.05	2.76
138	DJH167138	5.72	12.71	68.31	187.88	91.66	1.61	13.09	6.33	2.07
180	DJH167180	5.71	14.04	70.06	208.74	109.74	1.61	3.62	3.65	3.03
Entry	Hybrid	GY	MOI	AD	PH	EH	SL	ER	HC	TEX

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	ER	HC	TEX
217	DJH167217	5.71	13.72	68.52	202.84	119.97	3.58	4.25	8.65	2.17
8	DJH167008	5.70	13.74	64.03	184.01	100.63	-0.06	26.13	1.08	2.56
28	DJH167028	5.70	12.39	65.02	192.63	108.50	1.50	25.92	3.36	2.64
1	DJH167001	5.68	12.67	63.86	188.14	94.39	-0.27	1.40	6.48	2.32
56	DJH167056	5.68	14.14	65.59	187.26	103.10	0.13	13.10	9.58	2.50
120	DJH167120	5.68	14.29	67.32	183.09	94.02	2.40	1.53	-0.83	2.64
135	DJH167135	5.67	13.32	63.58	175.29	88.03	0.72	10.25	2.70	3.30
128	DJH167128	5.66	13.62	64.03	185.85	91.10	1.44	4.74	2.72	3.00
215	DJH167215	5.64	13.12	70.07	201.71	107.13	3.54	16.74	46.42	2.82
269	SC419	5.64	12.38	63.03	202.35	108.64	5.11	4.39	3.35	3.25
45	DJH167045	5.62	13.28	63.22	182.81	90.85	3.51	9.47	7.87	2.81
201	DJH167201	5.62	13.17	70.97	200.16	117.91	1.97	8.41	4.13	3.15
241	DJH167241	5.61	13.63	64.70	186.54	89.42	1.83	11.64	5.52	2.69
9	DJH167009	5.59	13.01	68.02	203.12	112.51	1.26	2.05	0.04	2.18
262	DJH167262	5.59	11.60	64.09	185.79	87.70	0.18	5.84	9.58	2.66
27	DJH167027	5.58	13.33	65.60	201.55	100.53	-0.08	25.28	9.00	2.32
102	DJH167102	5.57	14.38	70.29	207.49	112.66	-0.18	3.84	9.65	2.20
211	DJH167211	5.57	14.43	71.45	209.20	124.63	6.96	3.04	9.13	2.44
59	DJH167059	5.56	13.38	70.71	184.69	99.12	0.30	4.15	-0.08	2.48
61	DJH167061	5.55	12.97	64.72	182.85	95.54	1.51	18.96	12.25	2.66
98	DJH167098	5.55	10.83	63.91	198.04	103.13	0.94	4.94	0.81	3.10
156	DJH167156	5.55	11.84	67.48	189.15	81.53	1.19	9.96	1.91	2.23
247	DJH167247	5.55	12.46	63.26	177.46	89.19	-0.06	10.15	7.21	3.12
195	DJH167195	5.54	12.70	65.36	185.74	98.74	0.07	9.28	8.31	3.03
224	DJH167224	5.54	14.05	71.02	200.14	128.55	1.87	18.28	4.09	2.70
240	DJH167240	5.54	12.97	67.61	187.96	86.26	5.71	11.11	-0.85	2.73
6	DJH167006	5.53	13.16	65.97	187.66	92.87	4.57	1.86	0.51	2.84
150	DJH167150	5.53	12.01	64.16	188.42	93.68	3.39	3.96	2.67	2.93
100	DJH167100	5.52	13.92	66.18	197.26	96.11	3.43	12.20	7.22	2.07
155	DJH167155	5.52	14.28	64.43	189.12	106.62	1.76	17.71	13.24	3.08
60	DJH167060	5.50	13.36	65.27	193.50	103.38	-0.74	14.83	8.07	3.06
108	DJH167108	5.49	12.04	63.60	176.65	74.14	-0.13	4.74	7.45	2.99
234	DJH167234	5.49	11.68	65.92	194.67	102.66	-0.01	11.11	0.22	3.66
253	DJH167253	5.48	13.09	69.81	197.21	95.10	0.59	6.12	5.08	2.89
17	DJH167017	5.47	13.45	65.68	199.42	94.95	2.60	11.20	5.69	2.59
41	DJH167041	5.46	13.22	64.33	198.91	93.07	3.94	10.98	1.06	2.83
107	DJH167107	5.46	12.46	68.24	209.49	107.23	8.33	1.77	-0.84	6.15
246	DJH167246	5.46	13.69	67.40	214.17	121.18	1.14	14.25	10.29	2.24
249	DJH167249	5.45	13.25	68.48	207.94	119.93	0.31	7.04	5.63	3.07
36	DJH167036	5.44	13.54	64.06	194.60	103.74	1.31	15.35	10.24	2.65
250	DJH167250	5.44	14.31	66.57	197.91	110.88	0.06	1.00	0.62	2.21
137	DJH167137	5.43	12.30	64.38	178.82	83.44	4.51	13.28	5.40	2.91
204	DJH167204	5.43	13.16	68.68	204.04	114.09	-0.70	18.44	-0.33	2.17
139	DJH167139	5.41	12.74	63.68	180.25	84.12	4.08	20.86	10.93	3.31
39	DJH167039	5.38	12.06	66.76	179.13	89.38	3.17	28.61	0.18	3.26
200	DJH167200	5.38	13.80	69.73	202.32	114.54	0.35	11.55	4.62	2.74
62	DJH167062	5.37	13.59	65.77	199.73	102.73	1.52	28.03	6.93	2.92
71	DJH167071	5.37	12.99	65.87	185.57	92.91	0.08	6.72	5.90	2.62
162	DJH167162	5.36	13.44	63.83	202.66	92.90	1.55	2.19	2.27	2.77
54	DJH167054	5.34	13.04	65.29	176.54	89.45	0.09	13.59	0.24	2.89
117	DJH167117	5.34	13.44	63.48	187.72	88.98	0.12	0.56	6.21	2.83
165	DJH167165	5.33	13.07	64.94	181.85	94.18	2.95	24.27	-0.19	2.82
23	DJH167023	5.32	12.74	66.09	186.89	108.53	5.34	1.04	0.95	2.32
114	DJH167114	5.31	13.01	64.62	205.47	115.87	8.31	36.70	12.11	3.00
133	DJH167133	5.31	13.40	66.35	195.21	102.34	2.06	10.32	11.28	2.49
19	DJH167019	5.30	12.89	60.46	192.45	87.85	4.83	1.96	3.73	2.19
119	DJH167119	5.30	13.24	67.30	181.73	91.23	8.99	2.75	6.75	2.48
244	DJH167244	5.30	12.89	64.83	184.42	94.15	3.00	19.32	-0.11	2.50
32	DJH167032	5.29	13.33	62.76	191.87	80.87	1.06	4.02	3.54	2.72
172	DJH167172	5.29	13.01	67.33	200.87	102.08	0.27	12.13	0.43	2.52
275	PHB30G19	5.29	13.46	66.85	196.23	102.83	0.17	15.11	4.49	2.58
69	DJH167069	5.27	14.56	65.61	205.74	106.40	5.58	16.28	-0.22	2.60
104	DJH167104	5.27	13.44	63.54	199.19	88.03	-0.08	11.79	0.34	2.83
184	DJH167184	5.27	13.08	67.40	189.20	92.59	3.98	3.18	0.54	2.37
254	DJH167254	5.27	13.44	67.17	203.48	110.29	-0.04	3.57	4.13	2.68
66	DJH167066	5.26	13.39	62.63	187.10	100.27	0.55	9.99	17.50	2.74
85	DJH167085	5.25	13.96	68.72	196.45	104.15	-0.25	9.95	6.24	2.63
90	DJH167090	5.25	13.13	66.36	193.73	90.07	-1.76	11.24	3.80	2.70
118	DJH167118	5.24	12.46	65.37	171.67	86.53	-0.10	5.34	5.28	2.81
7	DJH167007	5.23	12.66	67.15	191.94	97.08	3.09	5.17	6.75	2.92
242	DJH167242	5.23	13.17	67.85	194.54	96.79	0.11	8.56	11.30	2.89
167	DJH167167	5.22	12.88	65.65	189.09	84.52	0.37	14.09	9.19	2.93
159	DJH167159	5.19	12.76	64.57	201.12	99.09	0.04	5.92	17.14	2.43
43	DJH167043	5.18	12.99	66.10	188.83	90.85	0.88	15.25	5.23	2.42
189	DJH167189	5.18	13.22	68.45	198.87	102.03	3.63	1.29	-0.55	2.86
248	DJH167248	5.18	13.29	68.41	197.34	109.63	0.50	3.88	6.25	2.94
3	DJH167003	5.16	13.39	63.64	185.17	88.14	2.16	16.64	4.72	2.55
29	DJH167029	5.16	12.58	64.49	179.80	77.77	4.44	6.43	4.35	2.48
111	DJH167111	5.16	13.10	62.96	190.79	99.30	1.18	15.90	6.35	2.57
122	DJH167122	5.15	14.41	67.98	179.72	91.06	0.01	1.90	2.03	2.09
168	DJH167168	5.15	13.83	61.69	181.75	85.92	1.11	8.30	3.05	2.93
220	DJH167220	5.15	14.06	70.81	206.86	115.44	13.64	17.92	4.43	2.09
99	DJH167099	5.14	13.34	66.27	178.58	90.93	2.38	9.08	6.52	2.83
173	DJH167173	5.13	11.06	61.65	187.33	98.75	0.62	4.60	9.43	2.40
20	DJH167020	5.08	12.59	65.76	179.65	86.75	6.80	6.85	3.10	3.09
146	DJH167146	5.08	13.99	67.16	165.96	98.60	3.01	1.77	-0.62	2.67
15	DJH167015	5.07	12.53	64.05	194.29	104.88	2.29	7.55	1.19	3.08
31	DJH167031	5.07	13.74	67.32	184.85	100.24	3.81	4.96	4.50	2.46
130	DJH167130	5.05	13.74	64.96	198.88	99.79	-0.59	1.98	-0.15	2.28
178	DJH167178	5.05	14.23	64.53	189.08	105.06	2.24	1.01	3.09	2.57
84	DJH167084	5.03	13.08	65.34	188.65	98.64	-1.14	8.45	4.73	2.88
235	DJH167235	5.00	12.71	66.82	202.29	98.19	1.34	46.18	-0.73	2.84
183	DJH167183	4.99	13.95	68.57	210.50	110.19	3.09	28.95	12.56	2.68
48	DJH167048	4.98	10.90	67.08	196.97	98.04	2.42	2.78	0.94	2.90
64	DJH167064	4.98	13.27	64.08	191.72	102.51	3.88	1.85	1.49	2.34
82	DJH167082	4.96	12.68	64.03	204.58	99.82	0.60	1.60	8.58	2.22
74	DJH167074	4.94	13.63	64.05	198.02	92.31	0.20	4.10	5.18	2.42
18	DJH167018	4.92	12.63	61.95	208.97	107.58	-0.17	15.13	14.55	2.40
21	DJH167021	4.92	13.01	67.31	201.00	101.61	1.56	8.65	2.47	2.82
190	DJH167190	4.92	13.61	67.59	211.04	118.29	-0.14	16.66	0.45	2.72
148	DJH167148	4.90	14.11	67.19	165.29	79.37	1.22	1.92	2.77	2.47
176	DJH167176	4.90	13.28	65.44	206.26	103.94	0.30	2.01	4.18	2.64
75	DJH167075	4.88	12.51	65.42	178.48	90.37	0.05	1.16	8.15	3.18
95	DJH167095	4.87	13.26	66.22	176.44	90.37	6.05	8.56	6.60	2.68
25	DJH167025	4.84	14.12	66.11	199.04	101.24	4.34	16.37	0.32	2.68
225	DJH167225	4.84	10.92	70.27	189.38	111.10	2.19	11.14	-0.02	2.99
88	DJH167088	4.83	13.99	64.72	194.59	92.45	1.39	3.85	4.63	2.67

202	DJH167202	4.83	13.51	69.90	220.24	133.46	3.43	36.11	4.53	2.77
123	DJH167123	4.81	12.22	65.33	185.42	92.96	0.70	4.63	-0.19	3.18
136	DJH167136	4.81	13.46	64.67	182.91	80.95	6.18	4.60	4.67	2.95
196	DJH167196	4.81	13.59	70.52	184.94	106.77	-0.10	6.20	0.76	2.01
38	DJH167038	4.80	13.07	66.53	187.35	88.77	3.99	11.89	4.13	2.56
129	DJH167129	4.80	12.96	65.97	174.92	90.69	1.16	8.42	5.05	2.68
160	DJH167160	4.80	13.25	65.58	189.48	100.51	2.95	10.54	18.36	2.86
158	DJH167158	4.79	13.54	64.64	188.20	80.59	8.93	3.02	11.11	2.64
26	DJH167026	4.77	13.19	65.67	198.36	97.53	6.37	3.28	0.22	2.59
132	DJH167132	4.76	13.86	66.68	192.62	97.93	-0.44	9.58	0.12	2.66
134	DJH167134	4.76	13.63	64.63	187.46	106.28	0.05	-0.10	-0.04	2.55
268	SC403	4.75	11.97	61.28	191.15	94.06	1.05	26.21	5.52	2.88
46	DJH167046	4.72	13.39	63.72	198.77	87.88	0.34	16.70	0.01	3.02
52	DJH167052	4.71	12.66	63.62	172.83	80.87	2.55	10.97	0.06	2.63
96	DJH167096	4.70	13.16	65.36	193.44	82.39	2.92	14.58	7.80	2.84
144	DJH167144	4.69	12.90	64.16	186.22	90.32	2.18	2.25	5.37	2.24
231	DJH167231	4.69	13.48	71.74	204.33	112.15	4.79	15.95	7.06	2.78
143	SC637	4.66	13.92	67.60	192.04	107.29	0.17	8.60	0.18	2.65
258	DJH167258	4.65	13.26	70.90	193.61	107.20	2.71	19.82	-0.23	2.90
42	PAN413	4.61	11.95	64.43	180.02	88.55	0.00	40.17	1.02	3.55
50	DJH167050	4.60	12.79	66.61	197.72	97.39	-0.13	2.26	0.34	2.31
113	DJH167113	4.60	14.24	65.80	190.51	99.12	3.15	4.24	-0.06	2.49
152	DJH167152	4.60	12.01	63.33	188.87	96.18	2.32	15.44	10.21	2.83
251	DJH167251	4.60	12.81	66.38	195.76	110.09	1.02	10.57	0.52	2.67
47	DJH167047	4.59	11.92	64.50	184.48	85.60	0.27	14.93	0.82	2.74
186	DJH167186	4.59	13.16	68.23	192.70	99.43	-0.08	16.13	1.17	2.74
30	DJH167030	4.54	14.62	66.19	190.32	102.80	18.24	1.60	-0.35	2.37
2	DJH167002	4.49	13.29	65.86	178.51	90.59	2.42	1.92	6.27	3.16
227	DJH167227	4.47	14.16	69.10	200.46	131.81	4.29	12.82	7.38	2.81
101	DJH167101	4.45	13.77	65.49	202.04	105.91	0.04	17.51	27.95	2.67
126	DJH167126	4.44	13.47	65.74	170.32	82.79	0.11	2.23	3.64	2.52
49	DJH167049	4.43	12.74	65.23	194.33	99.66	0.04	2.33	0.44	2.84
65	DJH167065	4.43	13.53	62.68	193.36	106.52	3.91	18.47	-0.54	2.42
58	DJH167058	4.40	13.06	64.75	195.75	106.39	0.01	4.97	2.34	3.16
33	DJH167033	4.39	12.34	64.30	190.06	98.00	2.49	15.28	1.58	3.00
94	DJH167094	4.37	13.09	63.87	175.65	87.31	5.01	12.87	2.76	2.84
151	DJH167151	4.35	12.76	65.79	178.05	80.82	-0.89	8.01	2.16	2.68
106	DJH167106	4.32	13.04	67.88	181.62	91.73	3.03	5.18	2.70	2.50
87	DJH167087	4.30	12.46	66.04	190.88	96.28	1.23	9.02	2.33	3.51
92	DJH167092	4.29	14.21	67.76	203.03	104.86	5.61	9.77	17.83	2.85
213	DJH167213	4.28	13.61	70.43	198.87	112.05	5.85	31.65	13.08	2.66
145	DJH167145	4.27	11.89	64.80	183.21	94.63	0.58	14.93	2.28	2.55
260	DJH167260	4.27	13.98	68.07	188.12	103.96	3.10	0.37	0.89	2.35
13	DJH167013	4.21	13.46	62.75	197.59	91.00	1.79	0.76	0.51	2.84
157	DJH167157	4.21	14.11	63.96	188.37	94.87	0.13	-0.16	0.16	1.95
79	DJH167079	4.19	12.87	64.66	199.72	105.23	6.43	3.57	6.08	2.41
163	DJH167163	4.18	13.01	66.29	184.69	88.76	0.04	13.43	8.28	2.57
230	DJH167230	4.18	12.88	71.54	202.67	118.99	4.24	1.20	-0.78	2.60
116	DJH167116	4.16	13.41	63.30	178.24	83.48	0.40	1.14	1.92	1.98
10	DJH167010	4.15	12.60	66.60	163.34	79.22	4.34	16.89	2.48	2.65
181	DJH167181	4.09	10.44	67.48	188.35	89.90	-0.06	3.88	2.27	3.00
166	DJH167166	4.07	12.83	63.33	170.45	77.09	1.30	3.39	6.05	2.66
182	DJH167182	3.88	13.98	69.64	191.64	106.94	5.74	12.85	2.94	2.57
73	DJH167073	3.83	14.13	63.95	190.76	97.01	17.88	1.43	8.29	2.58
24	DJH167024	3.82	13.28	65.75	182.18	92.75	3.30	5.62	6.09	2.36
199	DJH167199	3.80	13.68	69.81	197.36	106.28	5.86	10.09	8.38	2.84
259	DJH167259	3.74	13.96	73.40	193.66	101.15	3.02	3.29	1.79	2.50
11	DJH167011	3.72	12.82	64.22	192.81	87.15	-0.46	3.20	11.08	3.15
232	DJH167232	3.54	14.22	69.31	196.78	113.75	4.25	9.06	0.32	2.58
270	SC513	3.52	11.81	64.86	186.69	96.15	8.58	4.24	5.22	3.38
44	DJH167044	3.49	12.32	66.07	182.16	79.45	5.50	9.70	11.02	2.75
142	DJH167142	3.44	13.95	63.45	164.05	84.19	6.27	7.75	8.42	2.76
67	DJH167067	3.42	12.86	64.46	170.66	83.66	-0.23	30.38	33.23	2.67
205	DJH167205	3.41	13.53	71.12	203.19	116.95	0.21	4.15	0.53	2.54
63	DJH167063	3.31	12.51	67.68	186.40	95.30	0.08	1.28	5.69	3.00
147	DJH167147	3.24	14.62	67.81	187.06	100.45	5.62	3.28	24.47	2.22
12	DJH167012	3.20	13.55	64.40	180.39	98.57	4.54	4.40	11.13	2.81
37	DJH167037	2.97	12.74	68.33	176.19	82.48	1.58	9.38	-0.03	2.57
149	DJH167149	2.49	10.13	68.43	179.22	91.78	2.07	4.66	-0.24	2.92
267	SC301	2.49	30.12	57.00	177.67	70.93	0.30	0.46	2.07	2.92
Mean		5.37	13.30	66.20	193.00	100.77	2.27	10.25	5.23	2.69
LSD		2.04	3.61	3.22	22.41	20.55	8.00	22.38	12.92	0.99
CV		19.35	13.80	2.47	5.91	10.38	179.60	111.12	125.81	18.82
Heritability		0.31	0.00	0.83	0.47	0.66	0.11	0.14	0.40	0.07

GY- grain yield, MOI- moisture, AD-anthesis date, PH-plant height, EH-ear height, SL-stem lodging, ER-ear rots, HC-husk cover, TEX-texture.

Appendix 5.8 Grain yield and agronomic traits of 100 exotic x local three-way hybrids in set 8 in descending order of grain yield

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	TURC	EA	TEX
97	SC727	9.48	12.35	73.22	251.44	149.70	13.64	4.53	4.13	2.00	1.75	2.29	3.95
87	DJH168087	8.61	12.45	70.95	236.18	172.02	0.00	4.50	4.02	1.25	1.52	2.86	2.67
58	DJH168058	8.59	12.87	66.20	223.81	124.37	24.68	4.33	6.06	1.25	1.25	2.48	3.08
91	10C3271	8.51	10.90	62.54	234.69	125.47	4.17	4.51	2.13	3.25	1.98	2.49	3.39
99	PAN7M-81	8.49	12.32	68.88	228.62	135.23	11.54	3.61	0.09	1.25	1.24	2.47	3.56
90	DJH168090	8.27	11.26	68.74	228.68	119.60	0.00	4.93	-1.39	1.50	1.24	2.82	2.26
12	DJH168012	7.78	12.95	72.24	236.29	149.38	0.00	4.64	0.01	1.00	1.53	2.66	2.54
22	DJH168022	7.71	12.07	68.99	232.88	132.63	0.00	4.92	13.21	1.50	1.26	2.84	3.54
96	SC643	7.46	10.98	67.71	228.94	133.63	0.00	5.13	10.74	1.50	1.23	3.00	2.83
68	DJH168068	7.41	11.00	66.35	227.35	124.01	3.85	5.57	7.64	1.50	1.27	2.74	2.96
43	DJH168043	7.26	11.85	64.76	229.42	113.93	19.87	4.70	2.07	1.50	1.74	2.50	2.57
63	DJH168063	7.25	11.57	67.47	224.13	112.77	11.11	4.26	3.00	1.25	1.51	2.92	3.06
71	DJH168071	7.19	11.68	67.06	227.00	122.49	7.69	5.17	5.05	1.00	1.73	2.46	2.72
85	DJH168085	7.17	12.02	64.08	217.94	95.50	29.17	5.20	4.39	1.00	1.50	2.74	2.59
66	DJH168066	7.16	10.11	65.56	222.10	91.97	0.00	4.31	6.30	1.25	1.77	2.83	3.37
15	DJH168015	7.14	11.19	68.56	236.17	123.05	0.00	4.40	3.43	1.50	1.26	2.86	3.36
45	DJH168045	7.07	11.03	66.83	230.73	119.94	7.69	5.76	10.03	1.25	1.51	3.21	3.29
86	DJH168086	7.07	11.78	66.13	222.16	106.09	23.08	5.06	6.67	1.25	1.23	3.03	3.17
7	DJH168007	7.01	11.55	69.14	223.14	134.93	8.33	5.88	6.97	1.25	1.24	2.51	3.04
46	DJH168046	6.95	11.92	66.83	227.38	117.49	15.28	4.78	2.62	1.25	1.48	2.93	2.87
72	DJH168072	6.92	12.43	68.19	242.77	130.12	5.00	3.88	4.46	1.25	1.54	2.09	1.87
8	DJH168008	6.87	11.21	62.72	229.13	119.83	4.17	5.16	9.53	1.25	1.25	2.85	3.23
89	DJH168089	6.84	11.65	69.57	225.22	125.95	7.69	4.24	13.88	1.50	1.24	3.22	3.98
100	PHB30G19	6.78	11.37	68.82	227.33	117.27	0.00	4.98	16.47	1.00	1.25	2.74	3.04
57	DJH168057	6.76	11.94	67.15	238.67	123.62	8.33	4.95	4.13	1.50	1.25	2.79	2.47
32	DJH168032	6.63	10.59	65.22	223.07	121.22	18.18	4.94	5.17	1.50	1.25	2.62	2.83
56	DJH168056	6.61	12.40	69.87	251.78	146.64	0.00	5.10	6.03	1.50	1.22	2.60	3.59
14	DJH168014	6.60	11.80	65.58	225.75	123.50	0.00	4.81	4.45	1.25	1.46	3.08	3.05
38	DJH168038	6.56	10.59	61.51	234.60	118.35	4.17	5.36	0.97	1.00	1.47	2.99	2.89
98	PAN53	6.55	11.79	68.37	232.38	117.94	3.85	4.96	16.82	1.50	1.49	2.68	3.09
16	DJH168016	6.45	10.91	67.17	236.35	132.90	0.00	4.97	14.75	1.00	1.24	3.03	3.65
27	DJH168027	6.44	10.72	67.26	230.41	133.57	20.19	5.27	6.11	1.00	1.78	3.11	3.68
49	DJH168049	6.42	11.83	64.71	220.68	114.88	5.00	4.94	-0.04	1.50	1.24	2.37	2.49
88	DJH168088	6.36	12.53	67.54	224.64	114.54	8.39	4.74	4.93	1.25	1.49	2.68	3.09
2	DJH168002	6.35	11.08	65.62	231.73	127.68	11.25	4.59	3.71	1.00	2.00	2.43	3.27
39	DJH168039	6.33	11.40	65.52	213.85	108.19	27.50	5.37	5.38	1.25	1.26	1.95	3.15
62	DJH168062	6.32	11.33	67.57	259.53	148.38	0.00	4.01	2.11	1.25	1.49	2.15	3.15
64	DJH168064	6.32	10.80	66.58	211.86	111.45	0.00	4.50	12.07	1.25	1.26	3.00	3.30
24	DJH168024	6.30	12.13	67.82	222.72	127.17	18.18	3.73	4.04	1.25	1.52	2.65	3.53
35	DJH168035	6.27	11.73	64.33	208.86	113.47	4.55	4.98	7.49	1.25	1.30	3.06	2.75
76	DJH168076	6.26	11.50	68.34	212.07	106.94	14.55	4.66	10.19	2.00	1.52	2.84	2.95
6	DJH168006	6.16	11.17	68.45	224.30	114.78	0.00	5.95	4.35	1.75	1.47	2.56	2.82
17	DJH168017	6.13	11.81	69.08	246.16	132.47	0.00	4.12	10.01	1.00	1.23	2.47	2.51
74	DJH168074	6.09	13.14	70.44	234.78	132.33	5.00	4.95	9.46	1.25	1.01	2.49	3.09
23	DJH168023	6.07	11.60	70.17	233.28	138.08	0.00	5.43	8.97	1.50	1.23	2.97	3.40
84	DJH168084	6.06	10.90	67.73	223.76	108.31	5.56	4.76	1.68	1.00	1.49	2.51	2.78
33	DJH168033	6.04	10.58	68.86	208.92	134.22	4.17	5.13	7.67	1.50	1.75	2.48	3.81
79	DJH168079	6.01	10.53	63.83	213.67	100.72	9.09	5.44	3.65	2.00	1.48	2.88	2.13
44	DJH168044	6.00	10.69	62.91	218.25	105.85	50.00	4.95	2.48	1.25	1.23	2.78	2.98
80	DJH168080	5.97	11.33	67.78	224.21	111.21	3.85	5.09	7.75	1.50	1.74	2.86	3.16
41	DJH168041	5.96	11.88	68.73	233.05	133.90	0.00	5.54	10.36	1.50	2.02	2.30	2.66
70	DJH168070	5.95	10.80	60.52	230.74	103.59	7.14	5.63	0.56	1.00	1.21	2.73	3.18
92	SC301	5.94	9.80	58.67	212.80	111.51	0.00	5.96	3.97	1.75	2.01	2.82	2.83
11	DJH168011	5.92	11.61	69.08	228.81	129.16	11.11	4.36	9.69	1.75	1.77	2.51	2.58
21	DJH168021	5.92	11.31	71.35	229.28	134.79	7.69	5.15	8.65	1.50	1.24	2.93	2.54
60	DJH168060	5.90	11.55	68.36	234.27	131.13	27.69	5.17	6.30	1.25	1.24	3.19	3.30
94	SC419	5.89	11.08	62.92	231.65	119.02	8.01	5.00	5.63	1.75	2.04	2.70	3.15
93	SC403	5.86	10.05	60.44	232.44	112.92	11.54	5.33	5.23	1.50	1.74	2.97	3.10
37	DJH168037	5.78	11.62	68.12	209.41	113.83	21.59	4.30	4.15	1.00	1.46	2.80	3.19
65	DJH168065	5.75	12.08	69.63	216.81	111.17	0.00	3.39	3.01	1.00	1.28	2.29	2.90
42	DJH168042	5.70	10.44	65.84	236.31	119.41	6.25	4.76	5.75	1.50	1.52	2.46	2.76
54	DJH168054	5.65	10.81	67.03	232.03	127.43	18.75	4.55	-0.17	1.50	1.27	2.74	2.82
25	DJH168025	5.56	11.39	67.43	221.98	110.61	3.85	5.10	8.24	1.25	1.24	2.89	3.61
75	DJH168075	5.54	10.93	68.68	222.65	108.60	41.96	4.55	3.31	1.50	1.25	2.81	2.52
4	DJH168004	5.51	12.25	72.11	215.31	122.55	0.00	3.56	9.17	1.75	1.75	3.17	2.99
51	DJH168051	5.49	12.38	65.26	216.48	103.68	6.25	3.90	5.34	1.00	1.49	2.30	2.51
95	SC513	5.48	9.72	64.00	224.73	126.70	19.23	6.04	6.47	1.50	1.51	3.19	3.82
3	DJH168003	5.47	12.16	67.71	209.04	118.03	5.56	4.08	12.38	1.25	0.98	2.87	2.88
34	DJH168034	5.34	10.95	64.45	232.78	127.16	6.25	4.94	4.56	1.50	1.51	2.65	3.09
1	DJH168001	5.30	12.09	66.23	225.13	123.70	10.56	4.09	6.86	1.00	1.49	2.65	3.29
5	DJH168005	5.29	11.26	70.16	219.73	140.73	0.00	5.01	2.07	1.25	1.24	2.62	2.39
13	DJH168013	5.29	11.86	69.98	237.98	123.03	16.67	4.75	1.60	1.50	1.00	2.72	3.20
78	DJH168078	5.22	10.91	65.99	223.71	109.42	30.56	5.28	8.36	1.25	1.23	2.67	3.10
82	DJH168082	5.22	13.35	68.64	257.04	129.46	0.00	4.33	1.60	1.50	1.47	2.08	2.41
31	DJH168031	5.21	10.51	65.69	232.54	113.87	15.00	5.03	8.25	1.50	1.49	2.94	3.50
18	DJH168018	5.18	10.21	64.12	237.63	122.43	0.00	4.88	8.89	1.00	1.27	2.78	3.08
28	DJH168028	5.16	10.91	61.98	244.45	106.41	0.00	4.87	2.72	1.25	1.01	2.61	3.12
36	DJH168036	5.16	12.28	67.31	231.69	133.27	0.00	5.53	18.40	1.50	1.04	3.17	4.11
30	DJH168030	5.10	11.45	64.26	232.41	123.79	0.00	4.89	0.33	1.50	1.51	2.62	3.21
55	DJH168055	5.07	12.48	66.02	221.88	122.79	0.00	4.63	5.73	1.00	1.23	2.42	2.84
69	DJH168069	5.07	11.09	66.44	221.82	107.62	0.00	4.82	0.95	1.25	1.26	2.03	3.29
50	DJH168050	5.02	10.81	66.02	220.01	115.99	0.00	4.43	6.19	1.25	1.74	2.73	2.59
67	DJH168067	5.01	12.84	64.42	227.58	122.43	0.00	4.61	4.87	1.00	1.27	2.46	2.81
48	DJH168048	4.99	13.23	69.01	225.29	128.04	5.00	4.21	8.54	1.00	1.52	2.55	3.13
20	DJH168020	4.95	12.37	70.76	216.66	125.50	18.06	4.12	12.35	1.25	1.29	2.68	2.91
73	DJH168073	4.88	10.54	65.37	209.21	103.83	0.00	4.63	2.28	1.25	1.50	2.99	2.68
26	DJH168026	4.87	10.37	68.85	217.60	117.76	0.00	4.77	4.16	1.50	1.52	2.59	2.97
29	DJH168029	4.87	11.30	65.06	213.59	103.96	0.00	4.69	5.66	1.25	1.26	2.90	2.67
9	DJH168009	4.75	11.39	65.26	232.76	123.12	5.00	4.83	9.81	1.00	1.51	2.64	3.64
53	DJH168053	4.69	11.31	66.29	233.90	116.76	48.75	4.56	11.51	1.25	1.48	8.33	2.54
47	DJH168047	4.68	11.59	67.29	232.35	124.02	78.57	5.25	2.40	1.25	1.22	2.15	2.65
10	DJH168010	4.60	11.49	67.27	227.83	125.28	0.00	4.50	14.22	1.25	1.24	2.85	3.64
81	DJH168081	4.40	8.84	68.13	190.67	97.48	0.00	4.32	2.73	1.25	1.53	2.94	3.15
52	DJH168052	4.32	11.76	65.41	232.99	101.98	42.86	4.45	2.92	1.00	1.25	2.62	2.19
61	DJH168061	4.24	11.60	65.35	213.46	98.60	25.00	4.53	2.41	1.75	1.27	2.59	2.67
59	DJH168059	4.15	12.70	71.38	196.07	116.07	0.00	5.32	6.61	1.50	1.26	3.11	3.68
77	DJH168077	4.14	10.99	65.95	210.36	91.17	0.00	5.26	3.00	1.75	1.50	2.71	2.34
83	DJH168083	3.76	11.25	66.68	219.48	125.66	5.56	5.15	9.52	1.25	1.48	3.15	2.78
19	DJH168019	3.51	11.72	70.97	221.74	113.49	33.33	5.54	12.08	1.00	1.50	3.28	3.08
Entry	Hybrid	GY	MOI	AD	PH	EH	SL	SEN	ER	GLS	TURC	EA	TEX

40	DJH168040	2.43	10.58	72.84	220.56	118.59	12.50	4.57	5.64	1.00	1.73	2.92	2.75
Mean		6.00	11.45	67.01	226.39	120.57	9.69	4.81	6.11	1.35	1.42	2.77	3.01
LSD		2.56	1.68	2.70	25.02	26.47	19.70	0.96	10.76	0.58	0.60	1.77	0.66
CV		21.47	7.41	2.03	5.57	11.07	10.24	10.06	88.78	21.68	21.42	32.07	11.11
Heritability (broad sense)		0.39	0.46	0.89	0.40	0.50	0.72	0.66	0.14	0.57	0.13	0.00	0.72

GY- grain yield, MOI- moisture, AD-anthesis date, PH-plant height, EH-ear height, SL-stem lodging, SEN-senescence ER-ear rots, GLS- grey leaf spot, TURC-turcicum, EA-ear aspect, TEX-texture.

Appendix 5.9 Grain yield and agronomic traits of 135 exotic x local three-way hybrids in set 9 in descending order of grain yield

Entry	Hybrid	GY	MOI	AD	PH	EH	SL	ER	GLS	TURC	TEX
132	SC727	11.39	14.41	78.50	208.52	115.84	0.00	8.46	1.27	1.50	3.78
124	CZH141028	10.73	14.53	73.50	217.76	122.94	0.00	2.88	1.00	1.75	2.83
6	DJH152203	10.34	15.50	75.60	211.58	121.73	0.00	3.17	1.46	1.75	2.97
131	SC643	9.53	14.25	71.59	192.62	105.83	0.00	5.45	1.27	1.50	3.06
119	DJH151818	9.38	13.87	76.94	202.22	108.08	0.00	3.55	1.75	1.50	2.83
121	DJH153479	9.24	12.76	79.86	207.34	111.92	0.00	4.26	1.26	1.50	2.59
134	PAN7M-81	9.10	13.09	73.98	200.17	119.07	0.00	4.03	1.75	1.75	3.35
73	DJH152916	8.90	13.84	71.81	193.18	101.24	0.00	6.98	1.01	1.50	3.41
128	10C3271	8.81	14.07	71.07	182.44	93.58	11.54	9.34	3.01	1.75	3.50
122	CZH131001	8.78	13.19	69.90	185.30	77.72	0.00	1.59	1.24	1.50	2.45
123	CZH131013	8.65	13.34	71.75	194.41	85.41	0.00	5.30	1.00	1.50	2.63
81	DJH152972	8.63	13.83	79.01	200.72	114.71	19.23	6.13	1.74	1.50	3.17
43	CH124152	8.62	13.92	75.05	193.71	104.28	0.00	3.26	1.24	1.50	2.83
33	DJH152347	8.60	11.81	71.14	192.42	96.25	0.00	9.15	2.01	1.50	3.57
106	DJH153398	8.43	13.10	73.69	186.85	84.91	10.10	5.10	1.73	1.75	2.01
5	DJH152202	8.25	13.97	77.65	211.05	113.14	0.00	5.81	1.24	1.50	2.83
87	DJH153166	8.22	12.99	72.30	187.81	100.61	4.55	6.94	1.52	1.75	3.57
133	PAN53	8.21	13.14	73.34	196.14	96.57	3.85	3.74	1.73	1.50	3.11
75	DJH152937	8.11	13.56	72.86	200.41	94.43	3.85	10.88	1.24	1.50	3.46
24	DJH16024	7.99	13.83	72.63	187.88	94.03	0.00	3.42	0.98	1.50	3.03
63	CH13905	7.96	12.92	72.12	184.63	93.73	8.33	9.78	1.50	1.50	3.04
8	DJH152210	7.91	13.94	72.07	197.03	99.37	0.00	6.88	1.99	1.75	2.80
69	CH1126	7.83	13.49	76.93	199.28	121.15	4.17	3.70	1.48	1.75	2.72
107	DJH153402	7.80	12.27	70.97	177.44	84.78	0.00	14.58	1.50	1.75	2.87
85	DJH153154	7.79	13.84	71.10	185.30	108.37	0.00	4.21	1.26	1.75	3.16
56	DJH152701	7.76	13.74	77.97	191.34	112.19	0.00	6.29	1.23	1.50	2.23
27	DJH16027	7.73	13.74	72.41	199.19	102.66	0.00	9.75	1.01	1.50	3.02
45	CH142214	7.72	12.66	77.26	181.19	103.17	29.55	3.25	1.51	1.50	2.91
70	DJH152899	7.72	13.01	70.98	198.53	104.21	0.00	7.42	1.01	1.75	3.10
79	DJH152954	7.62	12.75	72.58	187.40	91.97	4.17	5.91	1.23	1.50	3.34
113	DJH153420	7.53	12.46	71.09	185.64	86.58	5.56	7.01	1.26	2.00	2.90
129	SC403	7.50	11.61	65.90	179.73	86.31	0.00	5.15	2.24	1.50	2.74
126	CZH131007	7.45	13.55	77.61	181.81	95.85	0.00	10.29	1.26	1.50	3.53
127	CH132095	7.40	12.72	74.32	188.98	101.95	0.00	7.09	2.00	1.75	2.27
84	DJH153153	7.36	13.90	73.67	189.72	99.00	0.00	7.81	1.25	1.50	3.10
65	DJH152884	7.30	13.17	72.82	194.48	94.05	5.56	8.49	1.00	1.50	3.16
72	CH14468	7.24	13.44	76.71	172.75	97.90	5.00	9.97	1.77	1.50	3.03
20	DJH16020	7.24	13.78	74.53	183.92	103.55	3.85	10.25	1.50	1.50	3.08
20	DJH16020	7.24	13.78	74.53	183.92	103.55	3.85	10.25	1.50	1.50	3.08
74	DJH152936	7.23	13.97	75.40	199.85	104.84	0.00	7.25	1.53	1.75	3.80
21	DJH16021	7.23	14.26	73.09	192.41	98.10	0.00	3.31	0.97	1.50	2.72
21	DJH16021	7.23	14.26	73.09	192.41	98.10	0.00	3.31	0.97	1.50	2.72
91	DJH153193	7.21	13.75	74.77	191.75	99.00	40.21	3.05	1.76	1.50	2.25
120	DJH153470	7.21	14.62	73.10	194.09	107.91	0.00	4.55	0.99	1.50	2.62
125	CZH131006	7.16	13.49	74.70	192.67	102.80	0.00	2.99	1.76	1.50	2.97
93	DJH153231	7.16	13.36	72.14	168.25	78.84	4.17	5.90	1.23	1.75	2.99
4	DJH152200	7.11	13.67	70.26	195.62	100.03	0.00	4.91	1.23	1.75	2.40
26	DJH16026	7.11	13.22	73.44	194.52	95.72	0.00	4.92	1.00	1.75	2.82
105	DJH153393	7.08	13.00	70.17	192.78	87.21	0.00	4.52	1.01	1.75	3.35
76	DJH152943	7.03	13.29	74.23	193.06	104.57	0.00	11.26	0.99	1.50	2.89
28	DJH152365	7.01	13.30	73.33	193.42	103.32	0.00	2.73	1.27	1.75	3.08
78	DJH152950	6.99	13.23	75.85	185.34	92.65	0.00	7.58	1.02	1.50	2.67
29	DJH152371	6.99	13.60	72.03	182.70	93.97	0.00	1.36	2.50	1.50	3.10
90	DJH153176	6.95	12.02	72.20	192.29	91.95	0.00	6.00	1.01	1.75	3.00
67	DJH152888	6.95	11.98	77.49	192.21	94.63	0.00	10.95	1.00	1.50	3.08
86	DJH153164	6.93	13.72	72.51	167.69	89.16	0.00	12.54	1.27	1.50	2.92
47	DJH152649	6.92	14.03	79.40	214.90	119.16	0.00	2.82	1.49	1.75	3.20
17	DJH152325	6.91	13.23	70.77	171.03	85.69	0.00	7.61	1.53	1.50	3.49
25	DJH16025	6.90	13.83	72.15	190.58	105.29	0.00	1.72	1.02	1.50	1.88
88	DJH153171	6.89	13.37	74.97	187.78	104.77	4.55	2.56	1.49	2.00	3.40
115	DJH153429	6.83	13.68	71.99	196.40	96.80	0.00	12.33	1.27	1.50	3.15
57	DJH152702	6.82	14.08	78.14	196.46	110.95	0.00	2.47	0.99	1.50	2.36
66	DJH152886	6.78	13.62	74.81	190.51	104.95	0.00	9.05	1.23	1.75	3.26
130	SC513	6.77	11.82	70.28	184.05	90.84	7.69	6.38	0.99	1.75	3.63
80	DJH152962	6.77	13.02	77.96	203.50	109.31	0.00	6.48	1.02	1.50	3.08
10	DJH152215	6.71	13.28	73.74	194.42	111.76	0.00	3.38	2.52	1.50	2.54
135	PHB30G19	6.69	13.91	72.88	208.79	106.76	0.00	5.10	1.01	1.75	2.33
11	DJH152835	6.65	12.93	69.09	180.21	82.94	0.00	2.85	0.98	1.50	3.52
117	DJH153441	6.63	13.48	71.80	202.42	102.67	0.00	2.74	1.03	1.75	3.02
89	DJH153174	6.61	12.99	73.19	196.99	111.81	6.25	20.61	1.51	1.75	2.57
112	DJH153419	6.60	13.55	72.36	174.07	86.46	26.92	2.69	1.50	1.50	2.31
103	DJH152541	6.54	13.49	74.96	191.62	101.16	0.00	5.73	1.03	1.50	3.11
2	DJH152136	6.51	13.59	71.45	173.16	86.35	0.00	6.96	1.23	1.50	2.48
111	DJH153417	6.47	13.08	71.54	182.68	86.33	4.17	6.44	1.04	1.75	2.79
31	DJH16031	6.43	13.69	72.87	195.01	101.67	12.50	7.27	0.98	1.75	2.39
58	DJH152710	6.43	13.00	80.64	190.00	105.89	0.00	5.80	1.03	1.75	2.68
51	DJH152671	6.43	14.08	78.33	199.34	111.97	0.00	8.62	0.97	1.50	2.97
3	DJH152196	6.38	13.39	73.11	207.43	116.65	11.11	5.45	1.48	1.50	2.64
68	DJH152892	6.37	13.62	74.68	189.92	96.02	0.00	3.65	1.50	1.75	2.24
39	DJH152575	6.36	12.49	76.81	186.93	90.89	0.00	5.61	2.04	1.50	2.82
83	DJH152976	6.32	13.82	78.36	181.41	100.10	10.56	2.04	1.48	1.50	3.38
48	DJH152651	6.31	13.67	76.22	203.86	112.17	0.00	4.16	1.74	1.50	3.16
109	DJH153414	6.30	14.03	73.32	176.09	90.13	17.50	13.15	1.98	1.50	2.52
98	DJH153311	6.28	12.92	72.23	193.26	92.20	7.14	9.51	1.52	1.50	2.75
42	DJH152641	6.20	14.32	76.10	205.56	121.86	22.22	1.66	1.74	2.00	2.17
92	DJH153208	6.18	13.59	76.94	175.63	105.95	0.00	7.21	2.00	1.50	2.28
100	DJH153333	6.11	12.79	71.58	191.62	83.52	0.00	4.68	2.00	1.75	2.84
64	CH13897	6.03	12.82	73.90	186.20	95.58	3.85	5.76	1.49	1.50	2.80
15	DJH152261	6.03	12.94	72.25	183.96	89.49	0.00	21.21	2.23	1.75	2.60
116	DJH153434	5.97	13.59	70.63	169.78	80.35	5.56	3.61	0.99	1.50	2.98
71	CH14466	5.95	15.17	74.29	182.62	99.60	0.00	7.38	1.24	1.50	3.07
62	DJH152728	5.90	13.34	76.50	197.70	111.27	0.00	7.36	1.99	1.75	2.97
23	DJH16023	5.89	13.05	71.86	176.65	90.90	0.00	3.95	1.50	1.50	3.07
9	DJH152211	5.84	13.24	73.22	197.44	107.56	0.00	9.01	1.51	1.50	2.53
18	DJH16018	5.79	13.25	75.33	189.58	102.77	0.00	4.93	0.98	1.50	2.93
77	DJH152945	5.76	12.75	75.24	186.73	102.05	0.00	9.33	1.00	1.50	3.37
7	DJH152207	5.74	13.83	70.81	197.41	99.18	0.00	2.37	1.24	1.50	2.59
96	DJH153245	5.66	13.91	74.82	179.64	90.09	0.00	3.73	2.50	1.75	2.41
52	DJH152677	5.64	14.36	75.93	197.43	120.09	0.00	0.62	1.51	1.50	2.53
Entry	Hybrid	GY	MOI	AD	PH	EH	SL	ER	GLS	TURC	TEX

118	DJH153462	5.63	13.05	77.34	216.30	106.01	5.56	4.21	1.51	1.75	3.16
94	DJH153235	5.63	13.81	72.45	166.96	80.66	37.50	5.65	1.52	1.75	2.03
36	DJH152563	5.62	13.93	76.75	205.38	110.82	0.00	4.91	1.74	2.00	3.27
110	DJH153415	5.57	13.17	72.28	186.45	96.46	7.69	12.12	1.00	1.50	2.69
108	DJH153413	5.49	13.38	71.74	191.39	88.32	0.00	23.50	1.51	1.50	3.00
104	DJH153368	5.48	13.08	73.54	180.16	87.19	0.00	7.42	1.74	1.75	2.54
14	DJH152850	5.47	12.82	71.06	185.66	89.69	0.00	2.22	1.23	1.50	2.90
16	DJH152267	5.47	12.52	67.93	201.46	80.62	0.00	5.71	1.49	1.75	2.58
30	DJH16030	5.47	13.95	71.89	170.68	83.95	0.00	7.46	0.98	1.50	2.76
19	DJH16019	5.35	14.87	70.77	180.97	76.79	0.00	3.18	0.96	1.50	2.62
50	DJH152667	5.32	13.88	78.92	188.70	108.50	0.00	0.97	1.46	2.00	2.62
1	DJH152133	5.28	12.92	74.09	190.14	100.88	0.00	8.34	1.50	1.50	2.02
114	DJH153424	5.28	12.86	72.47	186.13	82.75	13.64	8.62	1.75	1.75	2.55
60	DJH152712	5.28	15.23	79.25	192.77	114.90	0.00	2.13	1.02	1.50	2.26
55	DJH152691	5.27	13.79	77.87	190.68	116.83	0.00	6.11	2.50	1.50	2.40
44	CH142214	5.17	12.97	73.41	192.14	112.77	0.00	2.99	1.48	1.50	2.88
101	DJH153335	5.13	13.61	71.35	199.40	96.36	0.00	4.68	0.98	1.50	3.02
41	DJH152601	5.06	13.09	74.47	184.83	93.40	4.55	3.60	1.48	1.50	2.33
34	DJH152561	5.01	13.27	72.66	193.77	92.74	0.00	4.44	1.73	1.50	2.95
54	DJH152689	4.99	13.44	80.46	208.12	111.62	5.56	6.49	1.48	2.00	3.02
97	DJH153253	4.98	12.38	71.72	164.69	77.90	0.00	12.40	1.51	1.75	2.66
95	DJH153243	4.93	14.83	75.37	181.87	93.15	0.00	2.61	1.50	1.50	2.80
59	DJH152711	4.77	13.95	82.08	189.23	115.45	0.00	0.92	1.76	1.50	2.82
61	DJH152713	4.74	13.66	76.32	204.01	112.96	0.00	4.33	2.50	1.75	3.08
22	DJH16022	4.72	13.13	70.89	167.19	83.58	0.00	5.61	1.27	1.50	2.43
35	DJH152352	4.72	13.21	71.11	183.34	96.23	33.33	2.99	1.48	1.50	3.10
49	DJH152666	4.69	13.01	76.60	201.27	102.62	0.00	6.10	1.02	1.50	2.53
99	DJH152480	4.59	13.24	73.17	181.60	100.66	0.00	20.99	1.27	1.50	2.61
102	DJH153343	4.49	13.67	73.17	176.27	81.13	0.00	21.41	1.49	1.50	1.89
37	DJH152566	4.47	14.08	73.89	171.54	87.23	0.00	4.60	1.27	1.75	2.64
12	DJH152839	4.46	14.10	74.92	191.47	90.76	0.00	4.68	1.01	1.75	3.14
38	DJH152573	4.43	14.36	72.56	191.83	100.84	0.00	2.68	1.51	1.50	2.16
13	DJH152840	4.42	12.91	75.45	194.10	109.99	7.14	2.78	1.21	2.00	2.85
53	DJH152683	4.41	14.08	77.58	194.07	106.01	0.00	8.94	1.76	1.75	2.58
32	DJH16032	4.38	13.84	71.36	174.23	86.99	0.00	3.42	1.03	1.50	1.94
46	CH14367	4.33	14.03	79.22	206.75	107.98	0.00	2.65	1.53	1.75	3.36
82	DJH152974	4.17	14.21	84.07	181.33	110.51	7.14	9.32	2.28	1.75	2.80
40	DJH152590	3.76	13.18	70.98	188.57	95.15	5.56	2.81	2.25	1.75	2.13
Mean		6.61	74.05	13.47	190.34	99.30	3.19	6.30	1.44	1.61	2.83
LSD		2.45	3.17	1.49	19.32	16.46	18.56	10.03	0.53	0.40	0.61
CV		18.74	2.17	5.60	5.16	8.42	92.81	80.78	18.68	12.59	11.02
Heritability (broad sense)		0.63	0.86	0.39	0.62	0.74	0.18	0.26	0.74	0.04	0.72

GY- grain yield, MOI- moisture, AD-anthesis date, PH-plant height, EH-ear height, SL-stem lodging, ER-ear rots, GLS- grey leaf spot, TURC-turcicum, TEX-texture.