GENOTYPIC AND PHENOTYPIC CHARACTERIZATION OF MAIZE TEST CROSS HYBRIDS UNDER STRESSED AND NON STRESSED CONDITIONS

A Dissertation

by

ROSAN PATERSON GANUNGA

Submitted to the Office of Graduate Studies of Texas A&M University in partial fulfillment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

December 2005

Major Subject: Plant Breeding

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Approved by:

Chair of Committee, Javier Betrán Committee Members, C. Wayne Smith

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ABSTRACT

Genotypic and Phenotypic Characterization of Maize Test Cross Hybrids Under Stressed and Non Stressed Conditions. (December 2005)

Rosan Paterson Ganunga, B.Sc., University of Malawi; M.Sc., University of Zambia Chair of Advisory Committee: Dr. Javier Betrán

Drought and low soil nitrogen are major factors limiting maize production in Sub-Saharan Africa. Genotypic and phenotypic characterization of maize testcross hybrids developed from four biparental populations: CML441 x CML444, CML440 x COMPE, CML444 x K64R and CML312 x NAW was conducted. The objectives were (a) to evaluate the performance of $F_{2:3}$ line testcrosses across stressed and non-stress conditions, (b) to estimate heritabilities for grain yield and secondary traits, (c) to assess the relationship between testing environments, (d) to estimate genetic correlations among relevant traits, (e) to estimate direct and indirect genetic gain from selection, and (e) to have a preliminary assessment of the efficiency of marker-assisted selection. Studies were conducted under no nitrogen fertilization, low nitrogen, drought, wellwatered and high nitrogen in Malawi and Zimbabwe. About 100 entries from each population were tested using an alpha lattice design with two replications at all locations. Traits measured were grain yield, plant height, anthesis date, anthesis-silking interval, ears per plant, grain moisture at harvest and leaf senescence.

Highest grain yield across environments was obtained from population CML444 x K64R $(3.82 \text{ Mg ha}^{-1})$ and the lowest from CML440 x COMPE $(3.64 \text{ Mg ha}^{-1})$. Testcrosses from CML441 x CML444 and CML444 x K64R had higher heritability estimates compared to CML440 x COMPE and CML312 x NAW. Drought and high nitrogen environments had higher heritability estimates than low nitrogen and well-watered conditions. Drought and well-watered environments discriminated testcrosses in a similar manner as well as high and low nitrogen environments. All populations had

negative correlations between grain yield and anthesis silking interval, while positive correlations were observed between grain yield and ears per plant. No consistent differences were observed between overall means of best and worst marker based selected line testcrosses across populations and environments. Highest direct expected genetic gains were observed from high nitrogen environments. Direct selection under specific environments (e.g. drought) was estimated to be more beneficial than indirect selection in other environments.

DEDICATION

To my lovely parents Paterson and Hannah Ganunga

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CHAPTER I INTRODUCTION

Maize (*Zea mays*, L.) is the first world's staple cereal food crop. It is Africa's second most important food crop behind cassava. Per capita consumption of maize in Africa is highest in Eastern and Southern Africa. Maize consumption in Kenya, Tanzania, Malawi, Zambia, Zimbabwe and Swaziland averages over 100 kg per year (CIMMYT, 1990), giving maize a similar position in terms of dietary importance in those countries to rice in Asia. Uses of maize are multiple: animal feeding, sweet corn (syrup), food uses including fresh (green maize boiled), as a thick porridge using maize flour, tortillas, making syrup and soft drinks (Nhlane, 1990; Smale, et al., 1994). Maize is grown almost everywhere in the world because it is adapted to a wide range of environmental conditions.

Maize production is limited by several factors including low soil fertility, little or no use of inorganic fertilizers especially nitrogen, drought, use of unimproved traditional varieties, pests and diseases. Maize production can be variable, for example, in Eastern and Southern Africa, annual maize production averaged 16.2 million tons over the past twenty years, barely resulting in food self-sufficiency. During the same period, production levels fluctuated between 7.3 and 22.4 million tons in the same region indicating how variable and uncertain maize production can be (Banziger et al., 2000). In the Southern Africa Development Community (SADC) region, over one hundred million people live in the rural areas, in large households that farm 0.5 to 3.0 hectares. The average yield for maize grown in this region is 1.1 tons per hectare, but in droughtaffected years or on widespread, infertile areas farmers obtain less.

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This dissertation follows the format and style of Crop Science.

Farmers are trapped in low-input, low risk, but low productivity systems because they are trying to deal with an unstable climate, declining soil fertility, rising population pressure, high input cost and poor credit systems (Banziger et al., 2000).

Drought is one of the key factors that limit the productivity of maize in most parts of the world with Sub-Saharan Africa being the region that suffers from the greatest impact of drought in the world. On average, drought reduces maize yield by 36% in the lowland areas and 21% in subtropical areas, and affects about 23% of the total land area (CIMMYT, 1988). Drought affects maize grain yield to some degree at almost all the stages of crop growth. However, three stages i.e. early growth stage (when plant stand are established), flowering and mid-to late grain filling stage are considered critically sensitive stages for maize plant to drought. Among these stages, flowering is the most susceptible (Claassen and Shaw, 1970). Extreme sensitivity seems to be confined to the period minus two to twenty days after silking with a peak at seven days and almost complete barrenness can occur if the maize is stressed in the interval from just before tassel emergence to the beginning of grain fill (Grant et al., 1989). Maize is more susceptible to drought at flowering than other rain fed crops because its female florets develop virtually at the same time and are usually borne on a single ear on a stem. Unlike other cereals, the male and female flowers in maize are separated by as much as one meter, and pollen and fragile stigmatic tissue are exposed to a dry and hostile atmosphere during pollination which limits pollination under drought. Drought at flowering is known to reduce the capacity of developing kernels to use available assimilates because the functioning of a key enzyme, acid invertase, is impaired (Westgate, 1997). Drought also affects the rate of photosynthesis, resulting in reduced supply of current assimilates. Since the developing silk is a weak sink, growth is delayed leading to an increase in the anthesis-silking interval, and kernel and ear abortion (Bolanos and Edmeades, 1996). However, once the kernels are in the linear phase of biomass accumulation about two to three weeks after pollination, they develop the capacity to access reserve assimilate in different plant parts and they normally grow at

least 30% of the weight of the kernels on unstressed plants, even though drought may become more severe (Bolanos and Edmeades, 1996).

Drought induced yield losses can be substantial, and researchers have been attempting to improve the tolerance of crops to limiting supplies of water for decades. Physiologists, breeders, biochemists, agronomists, and molecular biologists have all used specific tools from their disciplines to unravel the complexities of drought response. Their efforts have resulted in increased knowledge of drought tolerance and genetic improvement for stress tolerance. For the past decade, the International Maize and Wheat Improvement Centre (CIMMYT) has conducted extensive research on screening and developing maize genotypes for drought tolerance using conventional methods. This has been accomplished by improving the locally adapted, elite germplasm for drought and low nitrogen tolerance, improving non-adapted but drought and/or low nitrogen tolerant populations for local adaptation, and formation of new breeding germplasm through introgression (Banziger, et al., 2000). This work has been conducted at CIMMYT-Mexico, CIMMYT-Zimbabwe and CIMMYT-Kenya. Some success has been achieved, for example, CIMMYT-Zimbabwe recently released ZM421, ZM521 and ZM621 open pollinated varieties (OPVs) which are tolerant to drought and are grown in Malawi, South Africa, Tanzania and other countries in the SADC region (Banziger, 2002).

In addition to drought, low soil fertility, especially nitrogen, is another factor limiting maize production in the tropics. Tropical soils themselves vary greatly, giving rise to differences in moisture and nitrogen at a single site within the same year. In contrast to drought, low nitrogen tolerance is a more predictable stress, since often one has prior knowledge of the soil nitrogen status. Nitrogen status levels too can be more easily adjusted through controlled fertilizer applications (Vasal et al., 1997). However, most farmers in the Sub-Saharan Africa region use very little or no fertilizers at all because of high price.

The development of drought and low nitrogen tolerant varieties requires appropriate strategies. These range from the establishment of an appropriate selection environment, like the establishment of off-season nurseries, ability to control water and fertility levels, well trained personnel, and adequate equipment to evaluate parameters related to stress tolerance (Edmeades et al., 1999). Although success has been accomplished using phenotypic breeding for drought and low nitrogen tolerance, the approach is faced with many challenges. Firstly, it is time consuming, laborious and expensive to screen and develop germplasm. Due to the polygenic nature of genes associated with drought tolerance, it is also difficult to introgress favorable genes for drought tolerance into one line or cultivar.

Correlation measures the degree of association among traits and helps to ascertain the degree to which these are associated with economic productivity. This correlation has also implications in the magnitude of direct and indirect response to selection. The causes of correlations can be genetic and/or environmental (Hallauer and Miranda, 1988). If genetic correlation exists, selection for one trait will cause changes in other traits. This is called correlated response. Correlations between characters have three main causes: pleiotrophy, genetic linkage and environment. Pleiotropic effects occur when the same gene or genes condition the expression of correlated traits. The genetic correlations arising from pleiotropy expresses the extent to which two characters are expressed by the same genes. This type of correlation is common in populations which have been randomly mated for a long time (Falconer, 1989). In contrast, linkage causes transient correlations which have can be broken by recombination. Environmental correlations reflect a similarity or dissimilarity in the response of a trait to a common environment (Falconer, 1989). This exists because measurements of several traits are taken from the same individual or from the same family. For example, a positive environmental correlation is expected to occur between plant height and ear height in the same plants because a microenvironment that favors plant height also favors ear height, and vice versa (Hallauer and Miranda, 1988). Genetic correlation is also determined by

genetic linkage. Linkage in coupling causes positive correlation, while repulsion causes negative correlation. The knowledge of the sign and magnitude of the correlation are both important for the understanding of the relationship between a quantitative character and the fitness in natural populations and for prediction of correlated responses to selection in breeding programs (Falconer, 1989). Characters like grain yield have such complex inheritance and are associated with several secondary traits (Stuber and Moll, 1996). For example, selection for grain yield under drought and low nitrogen has been unsuccessful because of low heritability for this trait under these conditions and recommended the use of secondary traits which are correlated with grain yield (Bolaños and Edmeades, 1996). This means that the selection for one trait may cause an indirect response in another trait. Genetic correlations are reported to be more useful if indirect selection gives greater response than direct selection for the same trait (Hallauer and Miranda, 1988). Phenotypic correlations between two traits are due to genetic and environmental effects. If the heritability of the traits are low, the phenotypic correlation is due to environmental effects.

The effectiveness of selection also depends on the relative importance of genetic and non genetic factors in the expression of phenotypic differences in a population which is called heritability (Fehr, 1993). The heritability of a trait affects the method chosen for population improvement. For example, traits with high heritabilities can be easily improved with single plant selection and less evaluation, while those with low heritabilities require family selection and wider testing (Hallauer and Miranda, 1988). This shows that heritability estimates also determine the extent to which replicated testing is required for selection to be effective. However, heritability estimates are not always a constant value. Because they are affected by so many factors, they can be controlled by the breeder in order to maximize genetic improvement with the available resources. So, any precautions a breeder takes to control the experimental error, will improve the heritability of a character (Fehr, 1993). These factors include the environment where the population was tested, reference population used, sample of

genotypes evaluated, use of random samples, method of calculation be it on plot or family basis, and the generation or progenies used because different progenies exploit different proportions of additive and dominance variance components. For example, heritability estimates for the same trait decrease depending on the family used in the following order $S_2 > S_1 >$ half-sib > full-sib (Hallauer and Miranda, 1988).

The development of molecular markers has contributed extensively to the understanding of the genetic diversity of the maize genome, and facilitated the study of past selection history, genetic drift, recombination, heritability, estimation of genetic relationships between inbreds and the extent of haplotype sharing within diverse groups of maize inbreds. The identification of quantitative trait loci (QTLs) uses both phenotypic and genotypic data. Unfortunately, large numbers of genes will fall within the same chromosomal segments where QTLs are located. The identification of key genes responsible for drought tolerance would facilitate the potential of marker assisted selection. Molecular tools can assist in selection in the following ways: (a) allow selection outside the target environment, (b) reduce linkage drag during backcrossing, (c) select transgressive segments, and (d) transfer genomic regions associated with a quantitative trait to elite backgrounds. For the past decade, the International Maize and Wheat Improvement Center (CIMMYT) has conducted mapping of QTLs for drought tolerance in several populations. These mapping studies have allowed the identification of QTLs consistent across mapping populations and environments (Ribaut et al., 2004). Hence, it is possible to select genotypes based on the marker allele composition at these QTLs. This constitutes the foundation of this dissertation.

Rationale and objectives

Drought, low nitrogen, pests and diseases, weeds (*Striga*) and low pH are common problems that limit maize production in Africa. In an effort to solve these problems, scientists in Africa established sites where they are screening and selecting against different stresses (Fig.1). In this scenario, there are several issues that affect maize improvement for stress tolerance:

- \triangleright Genetic gain in plant breeding depends on the heritability of the target trait(s) under the target environment.
- \triangleright Little is known about heritability and correlations between grain yield and other traits under drought and low N stress conditions.
- ¾ Estimating the relationship between optimal and stress environments will facilitate breeding for tolerance and broad adaptation.
- ¾ Marker assisted selection (MAS) can assist breeders in selecting for stress tolerance.

It is therefore important that African farmers should have varieties which are tolerant to drought and low nitrogen because these are the conditions prevailing within their farming environment. An enhanced knowledge about the issues listed above will facilitate the development of these varieties. The objectives of this study were:

- (a) To evaluate the performance of $F_{2:3}$ test crosses across stressed and optimal conditions.
- (b) To estimate heritabilities for grain yield and secondary traits.
- (c) To assess the relationship between testing environments.
- (d) To estimate genetic correlations among relevant traits.
- (e) To estimate direct and indirect response to selection.
- (f) Have a preliminary assessment of the efficiency of MAS.

Source: Vivek, et al., 2004.

Fig. 1. Managed stress testing sites for drought, low N, low pH, stem borers and *Striga* **in Africa.**

CHAPTER II REVIEW OF LITERATURE

Maize in Africa

Maize was introduced in Africa by the Portuguese explorers in the beginning of the $16th$ century (Reader, 1997). It has since become Africa's second largest important crop after cassava. Maize is grown over a wide range of environmental and geographical regions ranging from lowland (Niger's northern Sahel), mid-altitude and Ethiopia's sub-tropical highland environments to converted forest lands of Sierra Leone (Zaidi, 2004). The popularity of maize as a food crop developed because of low labor requirement and ease of processing compared to sorghum and millet which were common crops. In Southern Africa, palatability is considered to be the major factor that contributed to the increase in maize production.

Maize production in Africa is mostly done by poor resource smallholder farmers who are characterized by fragmented small land holdings (3 ha or less) and low input agriculture. In Eastern and Southern Africa alone (South Africa, Lesotho, Botswana, Swaziland, Mauritius, Democratic Republic of Congo, Seycheles, Mocambique, Zambia, Malawi, Tanzania, Angola, Kenya, Ethiopia, Rwanda, Uganda and Burundi) more than 250 million people derive their food and income from maize with an average yield of 1.1 metric tons per hectare (CIMMYT-Zimbabwe, 2000). In this region, rate of growth for maize production has reduced from the 1980s to the 1990s (Table 1). This is probably because Southern Africa is one of the most variable in terms of production as it faces a lot of variability due to environmental conditions and limited resource use. From table 1, the general decline of maize production in Southern Africa from the 1980s to the 1990s is due to increased number of production constraints, including low soil fertility and drought, little or no use of inorganic fertilizers, resurgence of new pests and diseases. As a result, yield stability across seasons has not been achieved despite it being a goal for most governments.
Region	1970-1979	1980-1989	1990-1997	
West Africa	-2.2	15.4		
East Africa	5.9	$0.0\,$	-1.6	
Southern Africa	4.1	7.2	3.9	
Africa	24		0.5	
$-$ _ . _ _ _ .				

Table 1. Rate of growth (%) of maize production in Africa per region.

Source: FAO (1998).

Maize is consumed in multiple forms in different parts of the world. In Africa, maize (mainly white grained) is the staple food crop for most of the countries. This means that stable and sustainable yields must be maintained in order to achieve food self sufficiency. However, this has not been achieved because population growth rate exceeds food production, resulting in net food deficit. In most Southern African countries, maize is mainly consumed as a thick porridge produced from maize flour which is produced by hand pounding (usually preceded by soaking) or grinding in a hammer mill, followed by boiling. It is also eaten fresh as a snack (boiled green maize). This form of consumption fetches more income per unit area of maize compared to dried grain. Despite this attraction, farmers mostly sell green maize grown from off season production after they have harvested the dried grain from the main season. Dried maize grain is either hand pounded or milled and used to prepare a soft porridge eaten for breakfast, or a thick porridge eaten at lunch and diner. In countries like Malawi, Zambia, Mozambique, Kenya, Tanzania, Zimbabwe and South Africa, maize is mostly hand pounded in a mortar, soaked for at least three days, dried and milled to produce fine and white maize flour which is used to prepare a thick porridge called *nsima, mshima, nsima, ugali, ugali, sadza* and *papa,* respectively (same thing with different names). This is eaten with relish (beans, vegetables, meat or fish). In Uganda the thick porridge is wrapped in banana leaves and heated again before it is eaten. Where hand pounding is common, households prefer those harder, flint-type varieties whose endosperm and embryo can be milled together. In contrast, households and commercial grain milling companies that mill their grain generally prefer dent varieties because flour extraction is higher. Dry maize grain is also roasted and eaten as a snack or as pop corn.

In West Africa, dry maize is processed to produce soft flour used to make porridge which is mixed with milk and sugar. The flour is also mixed with water and steamed at least three times to produce *cous-cous* which is eaten with sauce (beef, vegetables or beans). Alternatively, the flour is boiled with water to produce a very thick porridge and eaten with sauce (Karim Triori, personal communication).

In North Africa, e.g., Egypt, a maize flat bread called *aish merahra* is widely consumed. This is made from a soft dough spiced by 5% fenugreek seeds, aimed to increase the protein content and digestibility and increase the shelf life of the bread. Aish merahra can easily keep fresh for seven to ten days. In almost all parts of Africa, maize is also used for production of different types of beer, which are produced by germinating the seed for several days followed by exposing the grain to the sun to stop the germination process, then milling the germinated grain. In Malawi for example, the malt is cooked and the extract is strained off, cooled and allowed to stand for three days for fermentation to take place, after which the product is ready for consumption as beer (FAO, 1989).

Problems with maize production in Africa

Most farmers in Africa produce higher maize yields per unit area than sorghum and millet, possibly because maize is mostly grown in well-watered areas than the other crops. However, Edmeades et al. (1992), reported that maize suffers more yield loss due to moisture and nutrient stress than either sorghum or millet, resulting in maize a loss of approximately 1.8 million tons per year in Eastern and Southern Africa alone. CIMMYT, (1988) produced a list of potential constraints to maize production in Africa that are outlined in Table 2.

Contraint	%Lowland tropical	%Sub-tropical	% Highland	%Area
Drought	36	21	U	23
Striga	30	20		21
E.turcicum	21	35	100	40
H. maydis	56		θ	28
P.sprghi		42	58	28
P.polysora	26			23
Maize streak virus	73	37		60
Buseola fusca		69	76	37
Weevils	20	41	38	20
Termites	12	15		19

Table 2. Principal maize production constraints across agro-ecologies in Africa.

Source: CIMMYT, 1988.

This list shows that maize streak virus is the most widespread maize disease in Africa, affecting 60% of the continent's maize growing areas and some Indian Ocean Islands. This could be because viruses which spread easily cause this disease. Severe epidemics of maize streak virus occur irregularly both in space and time, but it is common to find infection scattered in most parts of the maize fields resulting in significant grain yield losses (CIMMYT-Zimbabwe, 2000). The second problematic disease is the *turcicum* leaf blight (produced by *Helminthosporium turcicum*) a fungal infection that affects 40% of the maize grown in Africa and affects almost all the maize grown in highland areas. Yield losses of 40, 52 and 82% have been reported in Ethiopia, Uganda and Kenya, respectively. Stem borers, especially *Buseola fusca* are more problematic in the sub-tropical and highland areas and affect 37% of all the maize grown (CIMMYT, 1998). Southern Africa has also suffered from another outbreak of grey leaf spot (*Cercospora zea-maydis*) since the mid 1990s. This disease has been reported to cause major crop losses in Zimbabwe, Malawi, South Africa, Zambia, Swaziland and Botswana. It is common in warm and humid regions. In susceptible varieties, severity reaches 60 to 100% of plant to leaf coverage resulting in maize grain yield loss of up to 20 to 100%. Severe blighting also causes weakening of stems leading to lodging (CIMMYT-Zimbabwe, 2000). Downey mildew has been reported to be a major disease of maize in West Africa, Democratic Republic of Congo and Mozambique, while

weevils and large grain borer remain the most devastating post harvest pests affecting maize in storage (CIMMYT, 1990).

Maize breeding research in Sub-Saharan Africa

Most of the research on maize breeding in Sub-Saharan Africa is conducted or coordinated by National Agricultural Research Systems (NARS) of the Ministry of Agriculture. Collaboration by international research organizations like CIMMYT or IITA with the national programs is also common. Research is mostly done on white grained maize, although some small pockets of yellow maize are also grown.

During the early days of maize research, development of improved open pollinated maize varieties was common using recurrent selection methods as described by (Shull,1908; Hallauer and Miranda,1988). Such varieties were preferred because farmers would select seed from their field for the next cropping season. However, the yield potential of these varieties was not high enough to justify the use of inorganic fertilizers and create a profitable agricultural business and sustainable yields. These varieties were also more susceptible to storage pests than the traditional maize varieties. Open pollinated varieties also suffered from low uptake by the private sector for seed production distribution because farmers would not buy the seed every year (Heisey et al., 1998). Due to shortage of seed for these improved open pollinated varieties, most farmers continued to grow their undeveloped local varieties.

Later, maize research focused on production of hybrid maize varieties to exploit heterosis. Two types of hybrids have been developed depending on the processing needs of the consumers. Both farmers who mill their maize and milling companies prefer dent grained varieties, while farmers who use a hammer mill or pound in a mortar prefer harder flint-grained maize varieties, because the extraction rates of the final products are higher for each variety and processing technique. For example, breeders in Zimbabwe

released a single cross hybrid called SR52 which yielded 46% more than local varieties (Weinmann, 1975). This hybrid was widely adopted by most commercial and smallholder farmers. In Malawi, the two flint grained three way hybrids (MH17 and MH18) that were released in 1990 to meet the processing needs of the farmers (hand pounding) received wider adoption than the dent hybrids that were released previously (Zambezi, 1997). Despite that hybrids are high yielding and widely promoted by the private companies, the uptake and land grown to hybrid maize is below 20%, even after sixty years hybrids were first introduced (Morris, 1998). The same author indicated that about 63% of the maize grown in Africa is still unimproved or landrace. The low uptake of hybrids is due to the high cost of hybrid seed and the need to buy the seed every year, which most smallholder farmers cannot afford. In addition, hybrid production requires use of high rates of inorganic fertilizers. However, due to the removal of subsidies on fertilizer prices, most farmers are unable to purchase or use inorganic fertilizers.

Success stories about the wide adoption in Ghana of quality protein maize (QPM), which is high in lysine and triptophan has resulted in work initiated to promote this type of maize. CIMMYT-Zimbabwe through the Southern Africa Drought and Low Soil Fertility Project (SADLF) in collaboration with national agricultural research systems (NARS), non governmental organizations, local farmers, high school agricultural teachers and agricultural extension agents are introducing these high protein maize varieties (mostly OPVs) to the farming community. These high protein maize varieties are aimed at helping to improve the nutritional levels of the local communities, which are characterized by high rates of malnutrition through Mother/Baby Approach. In this approach, experiments are set up within the farming communities, and farmers grow a sub-set of the tested varieties so that they make better and educated choices when deciding which varieties to buy from the market. The strength of this approach is that it also helps breeders to understand the criteria farmers use in selecting varieties. Other common areas of research related to maize in Southern Africa are striga tolerance by IITA, CIMMYT-Kenya and NARS (Malawi); stem borers (CIMMYT-Kenya); diseases

(CIMMYT-Zimbabwe in collaboration with NARS), and drought and low nitrogen tolerance (coordinated by CIMMYT-Zimbabwe through the SADLF Project and collaborated with NARS). National Agricultural Research Systems of each country also have programs that meet specific needs of the people in their respective countries. For example, earliness, flint grain texture, maize streak virus and grey leaf spot tolerance are some specific breeding goals for Malawi's Maize Breeding Research Program.

Abiotic stresses

Drought-- the problem

Most parts of the world are subject to drought, but the duration and intensity vary greatly from one climatic zone to another. Losses incurred from drought include reduction in yield, poor quality product and loss of economic value amounting from few to hundreds of millions of dollars (Quizenberry, 1982). Indirect losses are more difficult to evaluate but include losses from crops not planted, abandonment of land, and land use changes following the drought. The effects of drought can only be alleviated with precipitation or irrigation. If irrigation is not available, then cultural practices that help accelerate the use of the available moisture would help reduce the effects of the drought.

In some parts of the world, especially semi-arid regions, where most poor people live drought is endemic. Even well-watered places experience occasional drought during some periods of the growing season (Bennetzen, 2000). Because irrigation is not always a possibility for most of the poor resource farmers, development of varieties with improved tolerance to drought is a major focus of most plant breeding programs. However, drought tolerance is a complex issue because it is associated with polygenic genes.

CIMMYT, (1988) estimated that about 23% of the total land in Africa suffers from drought effects and that Southern Africa is at the highest risk of drought. In Sub-Saharan Africa, drought is one of the key factors that limit cereal production, and it is the region which receives the greatest drought impact in the world (Ribaut et al., 2002). The FAO estimates that Southern Africa suffers an annual maize grain yield loss of 44% due to drought effects alone. This makes drought the most important abiotic stress constraint to maize production (Heisey and Edmeades, 1999).

Biological immunity against drought is not a possibility to reduce the effects of drought, as a result productivity under drought is normally less than under optimal moisture. However, through plant breeding you can develop some degree of tolerance to reduce the effects of drought, in a manner analogous to disease and pest resistance. Thus, the term "drought tolerance" means the ability of a maize genotype to produce grain with a given amount of soil moisture stress (Quizenberry, 1982). Both conventional and molecular approaches are currently available to improve drought tolerance.

Effects of drought on maize

Maize is one of the crops that is highly susceptible to drought. In general, drought reduces maize production by decreasing plant stand during the seedling stage, by decreasing leaf area development and photosynthetic rate during the pre-flowering period, by decreasing ear and kernel set during the two weeks bracketing flowering, and by inducing early leaf senescence during grain filling. At the cellular level, drought results in the accumulation of abscisic acid (ABA) mainly in the roots where it stimulates growth. When passed to the leaves, it causes leaf rolling, stomatal closure and accelerates leaf senescence. Although ABA helps the plant to survive under drought, it does not contribute to productivity (Zhang et al., 1987). Cell division is inhibited under severe drought stress which results in lack of full cell expansion even if the stress is removed. Conversion of sucrose to starch in the grain decreases under drought because the activity of acid invertase, a key enzyme that converts sucrose to hexose sugars, is

diminished (Westgate, 1997). Drought is also reported to reduce cell expansion and photo-oxidation of chlorophyll and loss of photosynthetic capacity (Banziger et al., 2000).

The low nitrogen problem

Most of the maize in developing countries is produced under low nitrogen conditions because of continuous cropping and monocropping which have resulted in a decline in soil fertility. There is also little or no use of inorganic fertilizer due to increased price following the removal of subsidies on fertilizer and other inputs by most governments. As a result, nitrogen will continue to be a major nutrient limiting maize production in most farmers' fields (CIMMYT, 1992). Population pressure has also exacerbated this problem by reducing fallow periods, leading to reduced soil fertility. Increased production of crops which have a higher monetory value leaves maize to be grown in less fertile areas. These changes imply that more maize will be grown in the marginal areas in the future. Poor weed control and leaching due to heavy rain in some seasons increases the incidence of nitrogen stress in many cases. In addition to reduced yield, N stress has been observed to reduce ear biomass at flowering and under drought conditions (Edmeades, et al., 1992).

One approach to reducing the impact of nitrogen deficiency is to select cultivars that are superior in the utilization of available nitrogen, due either to enhanced uptake capacity or more efficient use of absorbed nitrogen for grain production (Lafitte and Edmeades, 1994). Blum (1988) suggested that selection for grain yield in the target environment (in this case low nitrogen environments) should be more efficient than selection for yield potential alone. However, such environments are not favored by maize breeders because increased environmental variability is exposed as soil fertility declines, resulting in a decline in heritability for grain yield.

Breeding for drought and low nitrogen stress tolerance has been an ongoing program at CIMMYT since 1986. It has been established that successful strategies to develop drought and low nitrogen tolerant maize requires knowledge of the plant, environment and the magnitude of the interaction of the two (Edmeades et al., 1992). One such approach is the development of stress tolerant maize under carefully managed drought and low nitrogen stress sites. The advantage of using managed stress sites is that it displays genetic variation for drought or low nitrogen adaptive traits to best advantage even if the stress is more severe than that encountered in the target environment.

Another approach to increasing the efficiency of selection in low nitrogen environments is the use of correlated secondary traits (Blum, 1988). These are improved N uptake by seedlings, high plant nitrate uptake and increasing nitrate reductase activity . Feil et al. (1993) reported positive correlations between between nitrate reductase activity measured in growing plants in a growth cabinet and total N uptake and grain yield observed in the field. Other traits which are also positively correlated with grain yield under limited nitrogen environments are large leaf area, high specific leaf N, an increased leaf chlorophyll per unit area, total biomass and N at anthesis, plant height at anthesis and length of the duration of grain filling (Lafitte and Edmeades, 1988).

Other options for breeding for low nitrogen tolerance are breeding under high nitrogen environment, hoping that there is a positive correlation between a low nitrogen environment and selection for low nitrogen tolerance using marker assisted selection.

How farmers deal with drought and low nitrogen problems

Farmers' fields are rarely characterized by one abiotic stress alone, because drought also occurs where nitrogen stress is also common. In a season when rainfall is plentiful, maize crops are often sevely nitrogen deficient due to leaching. When drought comes early in the season, farmers have the option to either plant another short season or apply artificial water through irrigation which is not possible with smallholder farmers. Some farmers just abandon their farms and migrate to other areas where the rainfall pattern is better. In areas where the probability of drought stress is high, farmers often respond by reducing the application of nitrogen fertilizer (McCown et al., 1992). Under low nitrogen conditions, farmers can improve such soils by applying organic or inorganic fertilizers. However, most smallholder farmers in Africa apply little or no fertilizer at all because of high price. Where land is not a big problem, farmers can practice fallowing using multipurpose tree species, but some farmers just abandon poor soil.

Breeding for tolerance to drought and low N

There are several options to select for drought and low nitrogen tolerance: Selection approaches for drought tolerance:

- 1. Select best genotypes under well- watered conditions assuming that the selected genotypes will also perform also well under drought (Indirect selection).
- 2. Select under rain fed conditions in target environments (random stress).
- 3. Select under managed drought stress environments.
- 4. Select using molecular markers.

Selection approaches for low nitrogen tolerance:

- 1. Select under optimal fertilization assuming positive correlation between low nitrogen and high nitrogen.
- 2. Select under low nitrogen environments.
- 3. Select using molecular markers.

Conventional breeding for drought tolerance is a great challenge and complex. However, tolerance to drought can be developed through selection for genetic variation for stress tolerance traits that can be identified and exploited through evaluation and selection (Bernardo, 2002). The most common approach that has been used for breeding drought tolerance is to select for drought tolerance components. Bolanos and Edmeades (1996) reported that selection for drought tolerance based on grain yield under drought may result in limited progress due to low genetic variation and low heritability for that trait. Also, heritability of maize grain yield reduces under drought, which reduces the yield potential. As drought intensity increases, genetic variance for grain yield is decreased, which weakens the selection intensity of the tested genotypes. Alternatively, use of secondary traits of adaptive value, and genetic variation increases under drought, can increase the selection efficiency. The most efficient are those whose variance is largest when drought stress is induced during the flowering stage, heritability is high and have a high relationship with grain yield. These are anthesis-silking interval (ASI), ears per plant, leaf senescence, tassel size and grain yield (Fischer et al., 1983). However, other secondary traits like leaf and stem elongation rate, canopy temperature, leaf photooxidation, leaf chlorophyll concentration and seedling survival under drought are not good indicators of drought tolerance (Banziger et al., 2000). Consistent selection for drought tolerance using anthesis silking interval during flowering should be done with great care to avoid increasing the frequency of male-sterile genotypes, because delayed anther extrusion could be easily confused with a short anthesis silking interval.

There are a number of approaches with regards to the best selection environment to use in order to obtain higher yields in drought stressed environments (Quizenberry, 1982). The first is to develop varieties that are highly adapted to a moisture stress environment. It is based on the principle that varieties selected for high yield under optimal moisture conditions will not necessarily have high yield when they are grown under moisture

stress conditions (Hurd, 1976; Falconer, 1989). This approach is mostly effective where the plants must complete their life cycle on soil moisture stored during the previous season. However, the use of this approach suffers from the problem of uneven precipitation from year to year especially in most semiarid regions. In such a case, a variety developed through this approach may not be able to respond in years of above normal precipitation or below normal precipitation. The second approach is to develop varieties that are adapted to a broad range of environmental conditions. This approach would be most effective when plants receive precipitation during the growing season or in a more optimal growing climate where periodic droughts may occur. Deday et al. (1973) suggested that selection for drought tolerance should be done under favorable environments because of greater genetic variance and high heritability. Another approach was suggested by Oppenheimer (1961) and Banziger et al., (2000) called the physiogenetic approach which combines the use of moisture stress environments and optimal moisture conditions. This assumes that yield and drought tolerance are different traits that are controlled by different genes or systems. Thus, screening germplasm should be done under both moisture stresse and under optimal moisture conditions. Only the best germplasm (i.e. genotypes with drought tolerance that have good yields under optimal moisture conditions) should be advanced to the next testing phase. Testing of the selected genotypes should be done under managed drought stress conditions, random drought conditions (representing farmers' growing conditions) and under optimal moisture conditions. This means that there is duplication of work especially during the early years of screening, which makes the approach expensive, time consuming and laborious.

The approach described by Banziger et al. (2000) has been used by CIMMYT scientists for the past three decades in order to develop drought tolerant genotypes with emphasis on the period before and during flowering and selection of genotypes with a short anthesis-silking interval. Selection was done on early generation lines, inbreds, hybrids, testcrosses and OPV's which were later evaluated in replicated trials at one or two

drought stress levels during a rain-free period using irrigation. Drought was applied during flowering and grain filling such that average grain yield in these trials was reduced to 30% (severe stress level, grain-filling stress) or 15-30% (intermediate stress level, combined flowering and grain-filling stress), respectively, of unstressed yields. The same progenies were also grown under well-watered conditions during the main season. Selection was for an index that seeks to maintain time from sowing to anthesis, maintain or increase grain yield under well-watered conditions, increase grain yield under drought, and decrease anthesis-silking interval (ASI), barrenness, the rate of leaf senescence, and leaf rolling under drought (Bolaños and Edmeades 1993; Bolaños et al. 1993; Banziger et al. 1999; Edmeades et al. 1999). Other breeding goals, such as yield potential, disease resistance, and grain quality, were also considered, based on observations made with the same progenies in trials grown during the main cropping season. However, despite some significant progress, the approach is slow, time consuming with uncertain potential for further progress. After so many years of research, CIMMYT researchers recommended that managed stress environments are more effective and cost effective for screening and selecting maize germplasm for drought tolerance. In addition, rapid and short term improvement for yield under non moisture stressed conditions can be made in elite maize germplasm through recurrent selection.

Drought tolerance can also be improved through the identification of genetic regions whose expression controls the plant's tolerance to drought and evaluation for yield potential under field conditions. Ribaut et al., (1997) indicated that a combination of marker assisted selection strategy based on best quantitative trait loci (QTLs) for different traits directly or indirectly related to yield would be the best way to breed for drought tolerance, in contrast to traditional breeding where breeders have relied on secondary traits like anthesis-silking interval.

Heritability of traits under drought and low N

Lafitte and Edmeades (1988) reported that realized heritabilities were generally larger for yield under high nitrogen than under low nitrogen both at C_0 and C_2 cycles. Values of $h²$ for grain yield across nitrogen levels, chlorophyll concentration and senescence rate tended to be smaller than those of grain yield.

Bolaños and Edmeades (1996) reported on the importance of anthesis-silking interval in breeding for drought tolerance in tropical maize. They observed that in all cases and for all the traits, $S_{2:3}$ progenies had larger heritabilities (by around 0.10 to 0.15) than S_1 progenies across all the yield levels. They also observed that heritability estimates tended to decrease with increase in moisture stress from around 0.60 under well watered environments to 0.40 with increasing stress. However, the heritability for days to anthesis remained fairly constant across all moisture regimes. Largest heritability estimates were generally for morphological and phenological traits like days to anthesis (0.80), leaf angle score (0.78), tassel branch number (0.79) and plant height (0.70).

Banziger et al. (2000) evaluated selection for grain yields under drought conditions. They reported that by using grain yield alone limited progress is achieved because of the low genetic variability for this trait under drought and because heritability for grain yield reduces under drought. Lafitte and Edmeades (1994) reported that realized heritabilities for different cycles of half sib recurrent selection under high and low nitrogen were larger for grain yield under low nitrogen than under high nitrogen. They also found that all the traits evaluated had higher heritabilities under cycle 0 compared to recurrent selection.

Correlation among traits, indirect selection and selection indices

A review of many publications on genetic correlation by Finne et al. (2000) showed that although correlation estimates are helpful in determining the components of a complex trait such as yield in white clover, they do not provide an exact picture of the relative importance of the component characters. In maize, correlations between grain yield and secondary traits like ears per plant, anthesis-silking interval and plant height have been reported by several writers (Bolanos and Edmeades, 1996; Banziger et al., 2000; Badu-Apraku et al., 2004) when selection was done for drought tolerance. Banziger and Lafitte (1997) reported that the use of secondary traits for grain yield was 20% more efficient than selection for yield alone. However, Badu-Apraku et al. (2004) indicated that cutting off irrigation two weeks before flowering appears to be too severe to properly elicit true differences among families because it resulted in negative variances which made it impossible to calculate genetic correlations in some instances.

Fisher et al. (1983) reported that genetic correlations between yield in unstressed and stressed environments remain positive but tend to be non significant where stress reduces yield by 50%. Reduced plant height was also reported by the same authors to be associated with reduced anthesis-silking interval and increased tolerance to drought. Banziger and Lafitte (1997) reported that genetic correlations between grain yield and anthesis-silking and ears per plant interval under stress were -0.6 and 0.9, respectively, suggesting that these traits are good surrogates for grain yield under severely stressed environments. Betran et al. (2003) reported that genetic correlations were positive and significant for ears per plant and grain yield in hybrids and inbreds under stressed and non stressed conditions.

Lafitte and Edmeades (1988) reported on the improvement of tolerance to low soil nitrogen in tropical maize. They found significant phenotypic correlations between grain yields and other secondary traits. Ear leaf chlorophyll concentration per unit area, plant height, ear leaf area, kernels per ear, ears per plant, and number of green leaves below the ear under low nitrogen were positively correlated with grain yield, while anthesissilking interval was negatively correlated with grain yield. Weak correlations were observed between grain yield and mass per kernel. Genetic and phenotypic correlations observed also generally agreed in sign and magnitude, but they also observed some differences between the two. While genetic and phenotypic correlations are useful in describing expected changes in secondary traits with selection, may be misleading in cases where field variability for the level of the limiting factor is large.

Bolaños and Edmeades (1996) reported on correlations between traits used in selection and grain yield. They observed that there were no consistent differences between the genetic correlations of most traits and grain yield between S_1 and S_2 :3 progenies. Genetic correlations between grain yield and kernels per plant, ears per plant and were consistently high (0.7 to 0.8). However, these showed no significant trends as water availability changed. Both days to anthesis and anthesis-silking interval correlated more strongly and more negative with grain yield as moisture stress intensified.

Badu-Apraku et. al. (2004) evaluated methodologies for screening for drought tolerance in maize. They reported large and positive genetic correlations between yield and moisture content, plant and ear height. However, in another study, they unexpectedly found positive genetic correlations between grain yield and anthesis-silking interval. But generally, correlation coefficients were higher in the non-stressed than the stressed environments. However, traits which had negative genetic variances could not calculate genetic correlations. Negative variances are attributed to sampling error in the production of progenies for evaluation, field design, data collection and the statistical analysis to estimate the variance components (Hallauer and Miranda, 1988). Negative variance component estimates could also be due to experimental problems or failure of the data to fulfill the assumption of genetic or statistical methods (Gousnard and Gallais, 1992).

The use of direct vs. indirect selection has produced contradictory realized gains from selection. Byrne et al., (1995) working with maize found little or no gain under drought when these crops were selected under irrigated conditions. Contrary to this, Johnson and Geadelmann (1989) measured similar gains for drought-stressed conditions when maize was selected either under irrigated or drought stressed conditions.

Atlin and Frey (1990) compared predicted responses of grain yield to indirect and direct selection to asses the value of high yielding or well-watered selection for improving grain yields in low yielding or drought stresses environments. Although heritabilities for grain yield were low under stress conditions, they concluded that direct selection was often superior to indirect selection in targeting stress environments.

Banziger et al. (1997) indicated that selection under high nitrogen for performance under low nitrogen was significant and more efficient than selecting under low nitrogen when yield was reduced by 40% under nitrogen stress. The same authors also suggested that when negative genetic correlations exist between yield in unstressed and stressed environments, this would mean that the two should be bred for separately. In addition, the same study suggested that the superiority of selection under either stress or non stress conditions may depend on the stress intensity in the target environment. Thus, as genetic correlations between grain yields under low and high N decreased with relative decrease in yield reduction under low N, indirect selection under high N became less efficient. Similar results were observed by Banziger et al., (1999) where they reported that correlated responses from selection under optimal conditions may be expected to decrease as N stress increases.

Marker- assisted selection (MAS)

Marker-assisted selection has been a useful tool in plant breeding through the identification of important agronomic traits such as resistance to nematodes, insects,

pathogens, tolerance to abiotic stresses, quality plant aspects and quantitative traits (Mohan et al., 1997). This type of selection is dependent on the availability of a large number of genetic markers which are known to have a strong genetic linkage with the component that is to be selected. Marker assisted selection has also proved to be most effect in early generation selection of breeding materials.

The international Maize and Wheat Improvement centre (CIMMYT), has developed a program using marker assisted selection for drought tolerance and insect resistance in maize and wheat. The Centre for Tropical Agriculture (CIAT) in Colombia is currently transferring drought tolerance from tepary to *Phaseolus* beans using molecular markers. Additionally, The International Crops Research institute for the Semi-Arid Tropics (ICRISAT) has developed genomic maps for sorghum using maize markers and has also mapped for drought tolerance in sorghum and millet (Visser, 1994).

Achievemnets with marker- assisted selection

There has been a lot of work done using marker assisted selection (MAS) as a plant breeding tool over the past twenty years. A review by Young (1999) indicated that despite the large number of articles (over 400) visited; very few of them led to the release of cultivars or germplasm. Most of them have concentrated on mapping loci which are known to be of agricultural interest.

Ragot et al. (1995) indicated that the efficiency of MAS is highest when the expression of a trait is controlled by a single gene or a gene responsible for a high percentage of the phenotypic variance of a trait. As such when you transfer a single genomic region from the donor parent to the recipient plant, you can achieve a large genetic improvement for that trait. In addition, for line conversion to be successful, the number of target genes and the expected level of conversion must be established long before the MAS is started because they will determine the size of population to be used, the number, position and nature of molecular markers and the number of genotypes to be selected (Ribaut et al., 2002). Ribaut et al. (1999), also indicated that for MAS experiments to be successful, they should not be based only on the QTL involved in the yield components because only a few QTLs are stable across environments but should consider QTLs involved in the expression of secondary traits that are correlated with grain yield under drought. These QTLs should also account for a large percentage of the phenotypic variance and be stable across environments.

Cregan et al. (1999) found that selection for one or two single sequence repeat markers linked to the *rhg*1 locus was highly effective in screening for resistance to cyst nematodes in soybeans. In pearl millet, marker assisted backcrossing has been successfully done in improving drought tolerance for the elite inbred pollinator H77/833- 2 using donor PRLT 2/89-33 and elite inbred maintainer line 841B using donor 863B (Hash et al., 1999). In potato, molecular markers were successfully used to map genetic regions for disease resistance (R7) gene (Leister et al. 1996). MAS was also successful in selecting for increased grain protein in wheat which led to an average increase of 15g kg-1 and was successful in 75% of the materials tested (Chee et al. 2001). Other studies by Edwards and Johnson ((1994) showed that MAS was successful as a selection index for a lot of traits. In rice, root depth was successfully selected for using MAS in 50% of the genotypes through introgression (Shen et al., 2001). Sebolt et al., (2000) used MAS to introgress QTLs for higher protein concentration for wild species into cultivated species.

Research conducted by CIMMYT on the cost- effectiveness of using SSRs in MAS experiments showed that with a small sample size and few markers, the cost is high but the cost goes down when screening several hundreds of genotypes and a large number of molecular markers are used (Dreher et al., 2000).

Mertz et al. (1964) screened a large number of genotypes from a segregating population of maize in order to select for a high protein maize genotype (*opaque 2)* which is found on the short arm of chromosome seven of the maize genome. The *opaque-2* locus has been cloned (Schmidt et al., 1990) and three SSRs were detected within the sequence of the gene itself (phi057, phi112 and umc1066) which CIMMYT has for years used this information to screen thousands of genotypes in different segregating populations to select genotypes which have one copy of the mutant allele (Ribaut et al., 2002).

MAS in maize breeding for drought tolerance

Maize breeders dealing with MAS are in a privileged situation because maize has a diploid genome, high level of polymorphism, large number of DNA markers publicly available, a lot of maize QTL studies published and a large number of genes already characterized. Thus various MAS approaches are available to improve maize. Genes that have been cloned and sequenced can be amplified or hybridized using DNA markers can be used in MAS. Maize improvement (for example drought tolerance) can also be achieved through QTL introgression which requires that a target genome be between two DNA markers that define the QTL (Ribaut et al., 1999).

In maize, Stuber (1994) reported results of introgression of genomic regions from Tx303 into B73 and from Oh73 into Mo17 through marker assisted backcross. The results showed that the crosses derived from converted versions of B73 and Mo17 averaged higher yields than the hybrids from the normal B73 x Mo17 hybrid. These results showed a successful manipulation of polygenic traits using MAS-BC.

Studies conducted at CIMMYT on marker-assisted selection were successful in the improvement of the elite maize line (CML 247) for drought tolerance. This line was improved through marker-assisted backcrossing (BC-MAS) using P1 as a donor line. Data from, the cross, an F_2 population and from the F_3 family evaluations were used to

identify five genomic regions responsible for drought tolerance which were transferred to the recipient line (Ribaut et al., 1999). The same author also reported about population improvement through changes in allelic frequency for drought tolerance in maize using MAS. In this study, 120 genotypes were screened of cycle 0, 4 and 8 using 40 RFLP probes with alleles increasing with each cycle of selection being favorable for drought tolerance. DNA markers were then used to validate the presence of the alleles which were associated with the improvement in drought tolerance. In addition, CIMMYT has been mapping and evaluating a number of populations across environments and years followed by selection based on genetic and phenotypic data since 1994 (Ribaut et al. 1996; 1997). The same, populations were also selected for drought tolerance using conventional methods.

Marker assisted selection also help to save breeding time if the heritability of the trait is high and field evaluation is very costly or simply cannot be done at your location, environmental effects are significant and the classical selection is expensive or slow, or if the conditions for selection are only present occasionally (for example selection for drought tolerance in the rainy season) and if you want to backcross a known gene into an inbred line as rapidly as possible (Banziger et al., 2000 and Ribaut et al., 2002). In addition, molecular markers can contribute to maize improvement through identifying heterotic groups, assigning inbreds to heterotic groups, establishing relationships among cultivars, predicting hybrid performance, choosing parents in a hybrid program, evaluating hybrid performance, assessing genetic change over time, analyzing genomic regions of pedigree-related genotypes, protecting Intellectual Property Rights, increasing intensity of selection while maintaining variability, increasing parental control by selecting before pollination, allowing selection to be conducted when phenotypic evaluation is difficult and reducing the number of seasons by selecting outside the selection environments (Betran at al., 2003; Lee, 1995). In order to maximize the efficiency of marker assisted selection as a tool for selection for drought tolerance, selection should be done for few loci with large phenotypic effects. The genotypes identified must be evaluated in the field under managed drought conditions to quantify the efficiency of the selection technique.

CIMMYT has been mapping genomic regions associated with drought tolerance from a number of populations across seasons and across environments both in Mexico and Africa. These mapping studies have allowed the identification of QTLs consistent across mapping populations and environments (Ribaut, et al., 2004). Hence, it is possible to select genotypes based on genotypes at these QTLs and compare their performance with conventionally selected genotypes.

CHAPTER III MATERIALS AND METHODS

Germplasm

Early generation $F_{2:3}$ lines were developed from four biparental populations, CML440 x COMPE, CML312 x NAW, CML 441 x CML444 and CML444 x K64R by CIMMYT. These populations have been used to map QTLs for grain yield and associated traits under stress and non stress environments. Two polymorphic markers were used for each target region. Over the past ten years, about 4000 drought QTLs have been identified. The stable regions were identified using an output of a combined QTL analysis conducted on each cross. Almost 30% of the combined QTLs identified were included in the selected regions considered for MAS. With the information obtained during the mapping studies, marker assisted selection on these populations was conducted at CIMMYT-Mexico by Dr. Jean-Marcel Ribaut. Markers located at the most relevant and consistent QTLs previously identified were used to select 50 $F_{2:3}$ lines with desirable combination of favorable alleles and 50 $F_{2:3}$ lines with unfavorable combination of alleles. The relative value of alleles at these marker loci was determined during the mapping study using information of performance under drought. The resulting $F_{2:3}$ lines per population were crossed to one single cross tester from the opposite heterotic group. Lines from populations CML440 x COMPE and CML312 x NAW were crossed with tester CML444 x CML395. Lines from populations CML441 x CML444 and CML444 x K64R were crossed with tester CML442 x CML312 (Fig. 2). The 400 testcrosses were evaluated under stress and non stress environments.

 Schematic diagram showing how the test crosses were developed from each population (e.g., CML441 x CML444).

Fig. 2. Production of testcrosses for evaluation.

Environments and stress management

The testcrosses were evaluated in Malawi and Zimbabwe underfour different environments as shown in Table 3a:

Table 3a. continued

An alpha lattice (incomplete block) design (Patterson and Williams, 1976) with two replicates was used for each experiment. Each experimental unit consisted of one row plot. Description of all trials, locations, plot characteristics and management is presented in Table 3b.

Trial	Location	# of	Plot size	# of	Magt	Altitude	Latitude
Code		Entries	(m)	Reps		(masl)	
CML44141	Chitedze	100	5.1 x 0.90	$\overline{2}$	No fert.	1300	13.58E, 33.38S
CML44142	Chitedze	100	5.1 x 0.90	\overline{c}	High N	1300	13.58E, 33.38S
CML44143	Harare	100	4.5×0.75	\overline{c}	High N	1503	31.02E, 17.43S
CML44144	Harare	100	2.1×0.75	\overline{c}	High L	1503	31.02E, 17.43S
CML44145	Chiredzi	100	3.0×0.75	\overline{c}	WW	392	31.57E, 21.03S
CML44146	Chitala	100	5.1 x 0.90	\overline{c}	WW	606	34.40E, 10.40S
CML44147	Chitala	100	5.1 x 0.90	\overline{c}	Drought	606	34.40E, 10.40S
CML44148	Chiredzi	100	3.0×0.75	\overline{c}	Drought	392	31.57E, 21.03S
COMPE4401	Chitedze	102	5.1 x 0.90	\overline{c}	High N	1300	13.58E, 33.38S
COMPE4402	Chitedze	102	5.1 x 0.90	\overline{c}	No fert.	1300	13.58E, 33.38S
COMPE4403	Harare	102	4.5×0.75	\overline{c}	High N	1503	31.02E, 17.43S
COMPE4404	Harare	102	2.1×0.75	\overline{c}	Low N	1503	31.02E, 17.43S
COMPE4405	Chiredzi	102	3.0×0.75	\overline{c}	WW	392	31.57E, 21.03S
COMPE4406	Chiredzi	102	3.0×0.75	\overline{c}	Drought	392	31.57E, 21.03S
COMPE4407	Chitala	102	5.1 x 0.90	\overline{c}	Drought	606	34.40E, 10.40S
COMPE4408	Chitala	102	5.1 x 0.90	\overline{c}	WW	606	34.40E, 10.40S
K64R4441	Chitedze	98	5.1 x 0.90	\overline{c}	No fert.	1300	13.58E, 33.38S
K64R4442	Chitedze	98	5.1 x 0.90	\overline{c}	High N	1300	13.58E, 33.38S
K64R4443	Harare	98	4.5×0.75	\overline{c}	High N	1503	31.02E, 17.43S
K64R4444	Harare	98	2.1×0.75	\overline{c}	Low N	1503	31.02E, 17.43S
K64R4445	Chiredzi	98	3.0×0.75	\overline{c}	WW	392	31.57E, 21.03S
K64R4446	Chiredzi	98	3.0×0.75	\overline{c}	Drought	392	31.57E, 21.03S
K64R4447	Chitala	98	5.1 x 0.90	\overline{c}	Drought	606	34.40E, 10.40S
K64R4448	Chitala	98	5.1 x 0.90	\overline{c}	WW	606	34.40E, 10.40S
NAW3121	Chitedze	102	5.1 x 0.90	$\overline{2}$	No fert.	1300	13.58E, 33.38S
NAW3122	Chitedze	102	5.1×0.90	$\overline{2}$	High N	1300	13.58E, 33.38S

Table 3b. Summary of trials conducted, altitude, latitude, location, type of management and plot siz es.

Magt, management; masl, meters above sea level; #, number; M, meter; WW, well-watered; No fert., no nitrogen fertilization.

Management of drought and low N sites

Depleting the soil of excess nitrogen by growing continuous maize without fertilizers and removing stover after every season for three years developed low nitrogen sites. No nitrogen was applied to these trials. The drought trials were irrigated to field capacity from planting until three weeks before flowering in order to induce drought stress at flowering while the well-watered trials were irrigated up to physiological maturity.

Field measurements

Data were collected on plot basis on the following agronomic traits: emergence count, days to pollen shed (days from planting to 50% pollen shed), days to silking (days from planting to 50% silking), plant height (distance in cm from the ground to where the tassel starts to branch), leaf senescence was determined by visual estimation of the proportion of dead leaves across plants of the whole plot (rating scale from 1 to 10 with 1 being 10% of leaves dead and 10 being 100% of leaves dead), ear height (distance from the base of the plant to where the ear is borne), harvest plant number (all the plants in the plot but excluding those at both sides of the plot), ear number (all the ears that were harvested from the plot), ear and grain weight (weight of all the ears harvested and grains shelled from a plot), grain texture (based on grain hardness of flintnes), root lodging (all plants that were not standing on their roots), percent moisture content (estimated with a Dickey's Grain Moisture Tester) and 100 kernel weight (weight of 100 grains from each plot weighed using a scale).

Statistical analyses

Analysis of variance per and across environments

Analysis of variance per locations was conducted using Remltool, where testcrosses, replications and blocks were considered as random effects. Across locations analysis was done using Proc Mixed in SAS (SAS, 1997). Heritabilities and genotypic and phenotypic correlations per environment were analyzed using Proc Mixed and Proc IML in SAS where both the genotypes and the replications were considered as random effects. Contrasts for the testcross groups were conducted using Proc GLM in SAS (SAS, 1997). Combined analysis of variance across locations was computed using PROC GLM in SAS (SAS, 1997).

Relationships among environments

Additive Main Effects and Multiplicative Interaction (AMMI) analysis of grain yield of testcrosses was carried out to assess the relationship among environments. Single value decomposition biplots were generated with testcross means per location using Excel addin software Biplot v1.1 (Smith, Virginia Tech; <http://www.stat.vt.edu/facstaff/epsmith.html>). Biplots visualize the relationship between environments as well as the relative performance of genotypes on environments. Vectors in the AMMI biplots represent environments. Environments that discriminate genotypes in a similar manner have close vectors in the same direction. Environments that discriminate genotypes in a different manner, which creates GxE interaction, have vectors further apart facing opposite directions.

Broad sense heritability for the different traits per environment and across environments was estimated using the PROC MIXED procedure in SAS® 8.0 (Holland et al., 2002; <http://www4.ncsu.edu/~jholland/homepage.htm>). Heritabilities and its respective standard errors were estimated on genotypic mean basis. As was the case in adjusted means calculations, comparisons between GLM and MIXED heritability estimates were performed to establish if any differences existed between them, and the extent of such differences. Heritability for the different traits by individual environment was estimated as follows:

$$
H = \frac{\sigma_G^2}{\sigma_G^2 + \frac{\sigma_g^2}{r'}}
$$

wh ere,

 σ_G^2 is the genotypic variance,

 σ_{ε}^2 is the error variance, and *r'* is the harmonic mean of replications.

Heritability across environments was calculated as follows:

$$
H = \frac{\sigma_G^2}{\sigma_G^2 + \frac{\sigma_{GE}^2}{r'} + \frac{\sigma_{E}^2}{r'e'}}
$$

where,

 σ_G^2 is the genotypic variance,

 σ_{GE}^2 is the genotype by environment interaction variance, σ_e^2 is the error variance, *r'*is the harmonic mean of replications, *e'* is the harmonic mean of environments.

Phenotypic and genotypic correlation

Phenotypic and genotypic correlation coefficients and their standard errors were estimated using a multivariate restricted maximum likelihood estimation (Holland, et al., 2002). The estimation was done using the PROC MIXED procedure in $SAS^{\otimes} 8.0$ (http://www4.ncsu.edu/~jholland/homepage.htm). The program provides variances and covariances, genotypic correlation coefficient (r_G) , phenotypic correlation (r_P) and their respective standard errors. Genotypic correlation r_G was calculated as follows:

$$
r_G = \frac{Cov_G}{\sqrt{\sigma_{GX}^2 \sigma_{GY}^2}}
$$

where,

Cov_G is the genotypic covariance between traits x and y. σ_{GX}^2 is the genotypic variance of trait x, and $\sigma_{\alpha y}^2$ is the genotypic variance of trait y.

In addition to the genotypic and phenotypic correlations, single value decomposition biplots were generated to visualize the relationship among standardized traits at each in the biplot represent traits. Traits with close vectors are positively correlated and traits environment and across environments using Excel add-in software Biplot v1.1. Vectors with vectors in opposite directions are negatively correlated.

xpected direct and indirect genetic gain to selection E

Expected direct genetic gain to selection for each environment and across environments was estimated for grain yield following Falconer and Mackay (1996):

Genetic gain = $1.75*\sqrt{\sigma_g^2}*\sqrt{h^2}$

where,

 σ_g^2 is the genotypic variance of target trait, and *h*² is its heritability.

Expected indirect genetic gain or correlated response between environments was estimated for grain yield (Falconer and Mackay, 1996) as follows:

$$
CR_y=1.75*\sqrt{h^2}*\sqrt{\sigma^2_g}*\sigma_{xy}
$$

where:

 h^2 is the heritability for target trait in the environment where selection is done, σ_g^2 is the genotypic variance of that same trait in the response environment, and σ_{xy} is the correlation coefficient between the two environments.

reliminary assessment of MAS efficiency in testcrosses P

The relative efficiency of marker assisted selection was assessed in three ways:

- . Comparing the overall mean of the best 50 and worst 50 marker based line 1 testcrosses.
- 2. Comparing the overall drought and low N tolerance indices of these two groups of genotypes.
- 3. Ranking the testcrosses for grain yield at each environment and compare the relative.
- 4. Number of the best and worst marker based testcrosses among the top yielding testcrosses.

Drought tolerance index (*DTI*) measures how much genotypes reduce their performance under drought as compared to their performance in well-watered conditions. The calculation was done as follows:

$$
DTI = ((GYG_{ww} - GYG_{drt})/GYG_{ww}) * 100
$$

where,

 GYG_{ww} = Grain yield under well-watered conditions; GYG_{drt} = Grain yield under drought;

Likewise, the nitrogen tolerance index (*NTI*) was calculated as:

 $NTI = ((GYG_{hn} - GYG_{ln}) / GYG_{hn}) * 100$

where,

GYGhn = Grain yield under high nitrogen conditions;

 GYG_{ln} = Grain yield under low nitrogen;

CHAPTER IV RESULTS AND DISCUSSION

Average grain yield was variable across environments and testcross populations (Table 4). Drought stress environments were the lowest yielding environments and high N the highest yielding environments. Following is presented the results for each of the testcross populations at each environment.

Table 4. Mean, minimum and maximum grain yields per trial for all environments and population of testcrosses evaluated in Malawi and Zimbabwe in 2003 and 2004.

Table 4. continued

Magt, management; No fert., no nitrogen fertilization; WW, well-watered; N., nitrogen.

Population CML441/CML444

Results per environment

Chitedze no nitrogen fertilization

This experiment was conducted under no nitrogen fertilization and rain fed conditions at Chitedze Research Station (Malawi) during the 2003 and 2004 season. The purpose was to induce low N stress, however, the nitrogen content in the soil was higher than expected and no stress was apparent. Grain yield average was $5.43 \text{ Mg} \text{ ha}^{-1}$ (range from 0.45 to 8.03 Mg ha^{-1}) (Table 5). There were significant differences for grain yield, anthesis date, ears per plant, grain moisture content and 100-kernel weight but not for anthesis-silking interval and plant height (Table 5). Heritabilities were 0.47, 0.51, 0.17, 0.22, 0.29, 0.30 and 0.42 for grain yield, anthesis date, anthesis-silking interval, plant height, ears per plant, moisture content and 100 grain weight, respectively. Average grain yield for the first 50 testcrosses was significantly greater than the average for the last 50 testcrosses (Table 5).

Genotypic and phenotypic correlations were estimated only among traits that showed significance differences. Grain yield was negatively correlated with anthesis date, and positively correlated with plant height, ears per plant, 100 kernel weight, ears per plant and grain texture (Table 6, Fig. 3). The magnitudes of genotypic correlations were greater than those of phenotypic correlations. Genotypic correlations ranged from -0.59 to 0.99, while the phenotypic correlations ranged from -0.43 to 0.15. High genotypic correlations were observed between grain yield and plant height and grain texture. Grain yield components such as ears per plant and 100 kernel weight had also a strong correlation with grain yield (Fig. 3). Other strong genotypic correlations were observed between plant height and 100 kernel weight and grain moisture.
Table 5. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML441 x CML444 evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004 season.

36.6
19.3
49.8
9.4
12.2
20.1
37.1
36.2
20.0
7.4
0.42
0.12

***,**,* Significant at $P < 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content; TEX, grain texture; GWT, 100 kernel weight.

Table 6. Genotypic (above diagonal) and phenotypic (below diagonal) correlations among traits and their standard errors (*SE***) for population CML441 x CML444 evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004 season.**

 GYG, grain yield; AD, anthesis date; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; TEX, grain texture; GWT, 100 kernel weight; MOI, moisture content.

Fig. 3. Single value decomposition biplot of standardized traits showing their correlations for population CML441 x CML444 evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004 season. (GYG, grain yield; AD, anthesis date; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; TEX, grain texture; GWT, 100 grain weight; MOI, moisture content).

Harare low nitrogen

This experiment was conducted under low nitrogen conditions in Harare (Zimbabwe) under rain fed conditions during the 2003/2004 season. The trial did not receive any nitrogen fertilization but just 60 kg ha⁻¹ of P_2O_5 . Significant differences were observed for all the traits except grain yield (Table 7). Mean values of the best 50 genotypes and 50 worst genotypes were also not significantly different. Anthesis date, plant height and leaf senescence had relative high heritabilities of 0.53, 0.64 and 0.62, respectively, while

anthesis-silking interval and ears per plant had moderate heritabilities of 0.44 and 0.28, respectively.

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; SEN, leaf senescence.

Anthesis date had a negative genotypic correlation with anthesis-silking interval (-0.63), plant height (-0.25) and ears per plant (-0.67) (Table 8, Figure 4). Anthesis-silking interval had positive correlations with plant height (0.28) and ears per plant (0.29) . Phenotypic correlations ranged from -0.44 to 0.29 and genotypic correlations from -0.92 to 0.95.

Table 8. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) for population CML441 x CML444 conducted under low nitrogen conditions in Harare, Zimbabwe during 2003 and 2004 season.**

	AD	ASI	PH	EPP	SEN
AD		$-0.63(0.19)$	$-0.25(0.03)$	$-0.67(0.39)$	0.41(0.21)
ASI	$-0.44(0.06)$		0.28(0.22)	0.29(0.22)	$-0.92(0.27)$
PН	$-0.25(0.01)$	0.24(0.07)		0.95(30.4)	$-0.46(0.19)$
EPP	$-0.23(0.07)$	0.24(0.07)	0.29(1.23)		$-0.54(0.28)$
SEN	0.14(0.08)	$-0.19(0.08)$	$-0.13(0.08)$	$-0.33(0.07)$	

AD, anthesis date; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; SEN, leaf senescence.

Fig. 4. Single value decomposition biplot of standardized traits showing their correlations for population CML441 x CML444 evaluated under low nitrogen fertilization in Harare, Zimbabwe in 2003 and 2004 season. (GYG, grain yield; AD, anthesis date; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; SEN, leaf senescence).

Chitedze high nitrogen

This experiment was conducted at Chitedze Research Station during the 2003/2004 season under rain fed conditions. This trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. Significant differences among testcrosses were obtained for grain yield, anthesis date, a nthesis-silking interval, plant height, root lodging, grain moisture content and grain texture (Table 9). No significance differences were observed for number of experiment with no fertilization at the same location. ears per plant. Heritabilities for grain yield and anthesis-silking interval were low, moderate for grain moisture and grain texture, and relatively high for anthesis date and plant height. Average grain yield was 4.53 Mg ha⁻¹, which was lower than the

Grain yield was positively correlated with plant height and grain texture, and negatively correlated with anthesis date and root lodging (Table 10, Fig. 5). Genotipic correlation between grain yield and plant height (0.69) and plant height and texture (0.77) were high. Moderate phenotypic correlations were observed between grain yield and plant height (0.38) , grain texture and plant height (0.33) , and between grain yield and grain texture (0.38).

Anthesis-silking interval had negative genotypic correlations with plant height, grain yield, grain texture and grain texture at -0.22, -0.26 and -0.32, respectively. Negative phenotypic correlations were also observed between anthesis-silking interval and grain yield (-0.11).

Table 9. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML441 x CML444 evaluated under high nitrogen fertilization at Chitedze, Malawi in 2003 and 2004 season.

Statistics	GYG	AD	ASI	PH	RL	EPP	MOI	TEX
	Mg ha ⁻¹	d	d	cm		#	$\%$	$1-5$
Mean	4.53	77.0	0.60	198	8.20	1.00	12.7	3.30
Significance	\ast	NS	***	***	***	NS	***	***
Minimum	0.14	72.2	-2.30	108	0.00	0.50	6.40	1.50
Maximum	7.49	80.4	3.30	224	57.3	1.90	15.1	4.50
LSD(5%)	2.88	4.70	2.30	27.0	19.8	0.50	6.29	0.80
CV(%)	32.7	3.07	204.1	6.80	78.5	17.3	130.3	12.2
MSE	2.20	5.60	1.50	181	41.4	0.03	0.64	0.17
Mean $(Ent. 1-50)$	4.88	77.0	0.50	199	5.48	1.0	14.9	3.00
Mean $(Ent. 51-100)$	4.2	77.0	0.70	197	10.7	1.0	1.3	3.00
σ_{c}^{2} e σ_{G}^{2}	2.20	5.60	1.47	192.3	41.4	0.03	0.66	0.16
	0.19	0.00	0.14	187.8	11.03	0.03	0.21	0.09
h^2 (family basis)	0.15	0.00	0.16	0.66	0.35	0.16	0.39	0.51
Standard Error h^2	0.18	0.00	0.17	0.07	0.13	0.17	0.14	0.10
\cdot \sim abada ah abada ah artista di t	0.001	1.0.07 \sim \sim \sim			1.3.70	۰.		

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; RL, root lodging;

EPP, ears per plant; MOI, grain moisture content; TEX, grain texture.

Table 10. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (SE) for population CML441 x CML444 conducted under high nitrogen conditions at Chitedze, Malawi during 2003 and 2004 season.

	GYG	ASI	PH	EPP	TEX	RL	MOI
		-0.22	0.69	0.56	1.28	-1.86	1.06
GYG		(1.05)	(0.02)	(0.59)	(0.96)	(1.96)	(1.25)
	-0.11		-0.26	0.61	-0.32	-0.50	0.09
ASI	(0.07)		(0.02)	(1.02)	(0.49)	(0.39)	(0.56)
	0.38	-0.04		1.26	0.77	-0.66	0.20
PH	(0.04)	(0.01)		(0.63)	(0.16)	(0.25)	(22.3)
	0.70	-0.06	0.36		0.84	-0.75	0.17
EPP	(0.04)	(0.07)	(0.07)		(0.54)	(0.44)	(0.26)
	0.32	-0.06	0.33	0.26		-0.73	0.20
TEX	(0.07)	(0.08)	(0.07)	(0.07)		(0.34)	(0.27)
	-0.17	0.12	-0.19	-0.03	-0.11		-0.93
RL	(0.07)	(0.01)	(0.08)	(0.01)	(0.08)		(0.22)
	0.07	-0.06	0.08	0.03	0.06	-0.10	
MOI	(0.08)	(0.08)	(2.38)	(0.04)	(0.01)	(0.10)	

GYG, grain yield; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; TEX, grain texture.; RL, root lodging, MOI, moisture content.

andardized traits showing their correlations for Fig. 5. Single value decomposition biplot of st population CML441 x CML444 conducted under high nitrogen conditions at Chitedze, Malawi during 2003 and 2004 season. (GYG, grain yield; AD, 50% antheis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; TEX, grain texture.; RL, root lodging, MOI, moisture content).

Harare high nitrogen

This experiment was conducted in Harare (Zimbabwe) under rain fed conditions during the 2003/2004 season. The trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. Significant differences among testcrosses were observed for grain yield, anthesis date, plant height, ears per plant, grain texture and grain moisture, and non significant for anthesis-silking interval (Table 11). Grain yield was high with an average of 9.09 Mg ha⁻ ¹. All traits with significant differences had a range of heritability estimates from 0.33 to 0.69. Heritability estimates were relatively high for grain yield and grain texture, intermediate for anthesis date and plant height, and low for ears per plant and grain moisture.

****** Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; TEX, grain texture; MOI, grain moisture content.

Grain yield had high genotypic correlation with ears per plant and plant height (Table 12, Fig. 6). Generally, phenotypic correlations were lower than genotypic correlations but showed similar trends. There was negative genotypic correlation between grain moisture and plant height.

Table 12. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) for population CML441 x CML444 conducted under high nitrogen conditions in Harare, Zimbabwe during 2003 and 2004 season.**

	GYG	AD	PН	EPP	TEX	MOI
GYG		0.08(0.17)	1.06(0.19)	0.75(62.09)	$-0.22(0.18)$	0.28(0.25)
AD	0.08(0.08)		0.33(0.23)	0.41(0.30)	0.06(0.20)	0.11(0.28)
PН	0.35(0.07)	0.05(0.08)		0.41(0.38)	$-0.38(0.38)$	$-0.44(0.36)$
EPP	0.41(5.41)	0.12(0.08)	0.07(0.08)		0.08(0.24)	0.56(1.09)
TEX	0.04(0.08)	0.02(0.08)	0.03(0.08)	0.09(0.08)		$-0.02(0.29)$
MOI	0.06(0.08)	$-0.04(0.08)$	$-0.02(0.08)$	0.02(0.08)	$-0.02(0.08)$	

GYG, grain yield; AD, 50% anthesis; PH, plant height; EPP, ears per plant; TEX, grain texture; MOI, moisture content.

CML444 conducted under high nitrogen conditions in Harare, population CML441 xZimbabwe during 2003 and 2004 season. (GYG, grain yield; AD, 50% anthesis; PH, plant height; EPP, ears per plant; TEX, grain texture; MOI, moisture content). Fig. 6. Single value decomposition biplot of standardized traits showing their correlations for

Chiredzi well-watered

Thi s experiment was conducted under well-watered conditions at Chiredzi, Zimbabwe during the dry season under irrigation in 2004. Water was applied to the experiment to field capacity from planting up to physiological maturity. The trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. Average grain yield was 6.43 Mg ha⁻¹, however, no significant differences were observed for any trait. This was surprising as no apparent reason was observed that could increase the error or reduce genotypic variance (Table 13).

Genotypic and phenotypic correlations were not estimated because all the traits were not significant. Nevertheless, single value decomposition of standardized traits indicated high correlation between grain yield, plant height and ears per plant (Fig. 7).

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content.

Fig.7. Single value decomposition biplot of standardized traits showing their correlations for population CML441 x CML444 conducted under well-watered conditions at Chiredzi, Zimbabwe in 2004. (GYG, grain yield, AD, 50% anthesis; PH, plant height; EPP, ears per plant; ASI, antheis-silking interval; MOI, moisture content).

Chitala well-watered experiment

This experiment was conducted under irrigation conditions at Chitala (Malawi) during the dry season in 2004. Water was applied to the experiment to field capacity from planting up to physiological maturity. The trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. Significant differences were observed for grain yield, anthesis date, plant height and ears per plant (Table 14). Heritabilities were moderate to high for grain yield (0.45) , anthesis date (0.62) , plant height (0.57) but low for ears per plant (0.29) .

***,**,* Significant at $P < 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content.

There were positive genotypic and phenotypic correlations between grain yield and plant height and between grain yield and ears per plant. Negative correlations were observed between grain yield and 50% anthesis date and between plant height and 50% anthesis date (Table 15 and Fig. 8).

Table 15. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (SE) for population CML441 x CML444 conducted under well-watered conditions at Chitala, Malawi in 2004.

	GYG	AD	PН	EPP	
GYG		-0.07	0.73	0.44	
AD	-0.16		-0.36	0.14	
PН	0.42	-0.20		0.41	
EPP	0.45	-0.04	ገ 17		

GYG, grain yield; AD, 50% an thesis; PH, plant height; EPP, ears per plant

 Single value decomposi Fig. 8. tion biplot of standardized traits showing their correlations for population CML441 x CML444 conducted under well-watered conditions at Chitala, Malawi in 2004. (GYG, grain yield, AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; **EPP, ears per plant; MOI, moisture content).**

Chitala drought experiment

The experiment was conducted during the dry season at Chitala Experimental Station (Malawi) during 2004. Water was applied to the experiment up to field capacity from planting until three weeks before flowering, when irrigation was withdrawn. The intention was to induce drought stress during the flowering period. There were sign ificant different for grain yield, anthesis date, an thesis-silking interval and moisture content but not for ears per plant and between the mean of the best 50 and worst genotypes (Table 16). Heritabilities were 0.15, 0.70, 0.24, 0.63, 0.15 and 0.15 for grain yield, anthesis date, anthesis-silking interval, plant height, ears per plant and moisture content, respectively.

, Significant at $P < 0.001$, 0.01 and 0.05, respectively, and NS = non s

***,* * Significant at $P < 0.001$, 0.01 and 0.05, respectively, and $NS =$ non significant.
GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content.

Grain yield had positive genotypic correlations with plant height (0.70) and moisture content (0.36), and negative correlations with anthesis date (-0.40) and anthesis-silking interval (-0.18) (Table 17, Fig. 9). Phenotypic correlations were positive between plant height and grain yield (0.46) and moisture content (0.40) and between grain yield and moisture content (0.61). The rest were negative.

Table 17. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (SE) for population CML441 x CML444 conducted under drought conditions at Chitala, Malawi during 2003 and 2004 season.

	GYG	AD	ASI	PН	MOI
GYG		$-0.40(0.39)$	$-0.18(0.64)$	0.70(4.80)	0.36(0.68)
AD	$-0.25(0.07)$		$-0.43(0.27)$	$-0.13(0.16)$	$-0.20(0.33)$
ASI	$-0.14(0.07)$	$-0.28(0.07)$		$-0.28(0.26)$	$-0.83(0.73)$
PН	0.46(0.23)	$-0.25(0.08)$	$-0.13(0.08)$		0.67(0.35)
MOI	0.61(0.05)	$-0.22(0.07)$	$-0.17(0.07)$	0.40(0.06)	

 GYG, grain yield, AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; MOI, grain moisture.

Fig. 9. Single value decomposition biplot of standardized traits showing their correlations for population CML441 x CML444 conducted under drought conditions at Chitala, Malawi during 2004. (GYG, grain yield, AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; SL, stem lodging; MOI, grain moisture).

Chiredzi drought experiment

The experiment was conducted during the 2004 dry season at Chiredzi Experimental Station (Zimbabwe). Water was applied to the experiment up to field capacity from planting until three weeks before flowering when irrigation was withdrawn to induce drought stress during the flowering period. Despite that nitrogen fertilizer was applied, the general performance of the experiment was poor because of inherent low fertility of the experimental site. Grain yields were very low with a mean of $0.32 \text{ Mg} \text{ ha}^{-1}$ (range from 0.00 to 1.29 Mg ha^{-1}) (Table 18). Heritabilities were low ranging from 0.18 for grain yield to 0.23 for anthesis-silking interval.

Table 18. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML441 x CML444 evaluated under drought conditions at Chiredzi, Zimbabwe in 2004.

Statistics	GYG	AD	ASI	PH
	Mg ha ⁻¹	d	d	cm
Mean	0.32	98.0	10.3	143
Significance	\ast	NS	NS	NS
Minimum	0.00	93.6	0.86	101
Maximum	1.29	105.2	18.8	173
LSD(5%)	0.55	13.7	10.9	40.0
CV(%)	82.6	6.60	34.9	13.5
MSE	0.07	7.45	12.9	344
Mean (Ent. 1-50)	0.30	98.1	10.6	141
Mean (Ent. 51-100)	0.30	98.8	9.90	145
	0.08	7.45	12.9	333
$\sigma_{\rm c}^2$ $\sigma_{\rm G}^2$	0.01	0.90	1.96	0.00
h^2 (family basis)	0.18	0.19	0.23	0.00
Standard Error h^2	0.18	0.19	0.45	0.00

***,**,* Significant at $P < 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking; PH, plant height.

Genotypic and phenotypic correlations could not be estimated for this experiment because most of the traits expect grain yield were not significant. Single value decomposition biplot shows grain yield positively correlated with ears per plant and negatively correlated with 50% anthesis date (Fig. 10).

Fig. 10. Single value decomposition biplot of standardized traits showing their correlations for population CML441 x CML444 conducted under drought conditions at Chiredzi, Zimbabwe during 2004 season. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking; PH, plant height).

Results across environments

Across sites significant for grain yield

The analysis across environments was conducted for those environments that had significant differences for grain yield in this population. These were no nitrogen

fertilization (Chitedze), high nitrogen (Harare and Chitedze), well watered (Chitala), drought (Chitala and Chiredzi).

Significant differences were observed among all the traits except ears per plant in the analysis across all environments with significant differences for grain yield (Table 19). Average grain yield was $4.63 \text{ Mg} \text{ ha}^{-1}$. Heritability estimates ranged from 0.10 to 0.85. Heritabilities were relatively high for grain texture (0.85) , plant height (0.52) , and 100 kernel weight (0.52) . Heritability for grain yield was moderate (0.50) and low for 50% anthesis date (0.10), anthesis-silking interval (0.14) and grain moisture content (0.21) .

Table 19. Statistics, averages, variance components, heriability and its standard error for experiment CML441 x CML444 across all environments with significant differences for grain yield Malawi and Zimbabwe in 2003 and 2004.

Statistics	GYG	AD	ASI	PН	EPP	TEX	MOI	GWT
	Mg ha ⁻¹	d	d	cm	#	1-5	$\%$	g
Mean	4.63	81.24	2.43	203.65	0.70	3.26	13.64	37.75
Significance	***	\ast	$***$	***	NS	***	***	***
CV	27.01	4.33	69.22	9.93	25.45	0.13	9.31	17.33
$\begin{array}{c} \sigma^2_e \\ \sigma^2_g \\ \sigma^2_{GxE} \end{array}$	1.48	11.02	3.07	355.5	0.0003	0.11	1.51	35.42
	0.18	0.14	0.05	35.78	0.0003	0.07	0.05	3.94
	0.32	2.00	0.09	18.87	0.002	0.02	0.33	4.33
h^2 (family basis)	0.50	0.10	0.14	0.52	0.09	0.85	0.21	0.52
Standard Error h^2	0.08	0.15	0.15	0.08	0.15	0.03	0.15	0.11

****** Significant at $P \le 0.001$, 0.01, and 0.05, respectively, NS = non-significant

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MO, grain moisture; TEX, grain texture; GWT, 100 kernel weight.

MSE, mean square error; h^2 , broad sense repeatability.

Grain yield had positive genotypic and phenotypic correlations with plant height, 100 kernel weight, grain texture and moisture content. Anthesis-silking interval and 50% and thesis date were both negatively correlated with grain yield (Table 20).

	GYG	AD	ASI	PH	TEX	MOI	GWT
GYG			-0.10	0.94	0.59	0.44	0.82
			(0.32)	(0.32)	(0.11)	(0.35)	(0.22)
AD	-0.11		-0.51	$\overline{}$	-0.58	0.44	-0.11
	(0.03)		(0.70)		(0.23)	(0.41)	(0.33)
ASI	-0.09	-0.28		-0.17			-0.73
	(0.03)	(0.03)		(0.30)			(2.97)
PH	0.31	-0.06	-0.03		0.54	0.54	0.80
	(0.03)	(0.03)	(0.03)		(0.12)	(0.34)	(0.22)
TEX	0.21	-0.12	-0.03	0.18		0.15	0.23
	(0.05)	(0.04)	(0.04)	(0.05)		(0.27)	(0.19)
MOI	0.04	0.18	-0.02	0.05	-0.01		0.09
	(0.33)	(0.03)	(0.03)	(0.03)	(0.04)		(0.32)
GWT	0.11	-0.03	0.10	0.10	0.15(0.08	
	(0.04)	(0.04)	(0.04)	(0.04)	0.05)	(0.04)	

Table 20. Genotypic (above) and phenotypic (below) correlations and their sta nvironments ndard errors (SE) for experiment CML441 x CML444 across all e sign ificant for grain yield evaluated in Malawi and Zimbabwe in 2003 and 2004.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; TEX, grain texture; MOI, moisture content; GWT, 100 kernel weight.

Across high N environments

Appendix B). Moderate heritabilities were observed for grain yield (0.55) and plant height (0.57) . Heritabilities for other traits were low. Significant differences were observed for grain yield, plant height, ears per plant and moisture content in analysis across optimal nitrogen fertilization under rain fed conditions in Malawi and Zimbabwe during the 2003/2004 season (Table 21 and

Statistics	GYG	AD	ASI	PH	EPP	MOI	GWT
	Mg ha ⁻¹	d	d	cm	#	$\%$	g
Mean	6.82	74.70	0.84	228.02	0.84	15.81	39.53
Significance	***	NS	NS	***	**	***	NS
CV	21.23	2.83	136.67	6.77	19.00	9.03	15.26
	6.98	5.40	1.44	824.5	0.04	3.41	33.36
	1.24	0.07	0.00	146.09	0.003	0.19	0.74
σ_{e}^{2} σ_{ge}^{2} σ_{GxE}^{2}	0.00	0.38	0.06	0.00	0.00	0.30	1.33
h^2 (family basis)	0.55	0.03	0.00	0.57	0.21	0.14	0.05
Standard Error h^2	0.06	0.11	0.00	0.06	0.08	0.10	0.18
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Table 21. Statistics, averages, variance components, heriability and its standard error for experiment CML441 x CML444 across high nitrogen conditions in Malawi and Zimbabwe in 2003 and 2004.

***,**,* Significant at $P < 0.001$, 0.01, and 0.05, respectively, NS = non-significant

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; TEX, grain texture; GWT, 100 kernel weight.

MSE, mean square error; h^2 , broad sense repeatability.

Across drought environments

No significant differences were observed for any trait except grain moisture and 100 kernel weight in analysis across environments with drought stress (Table 22 and Appendix C). Average grain yield was very low $(1.15 \text{ Mg ha}^{-1})$. In addition, heritabilities were very low and ranged from 0.00 to 0.37.

***,**,* Significant at $P \le 0.001$, 0.01, and 0.05, respectively, NS = non-significant

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; GW T, 100 kernel weight.

MSE, mean square error; h^2 , broad sense repeatability.

Correlations among traits across environments and stresses

Across all environments

There were positive phenotypic correlations between grain yield and ears per plant, 100 kernel weight and plant height across all environments including stressed and non stressed environments (Fig. 11). Flowering time (50 % anthesis date) and grain moisture were also closely correlated.

Fig. 11. Single value decomposition biplot for different traits for experiment CML441 x CML444 **across all environments in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; TEX, grain texture; GWT, 100 kernel weight).**

Correlations across high N environments

Positive phenotypic corrections were observed among grain yield, plant height and ears per plant (Fig. 12). Grain yield was negatively correlated with anthesis-silking interval and anthesis date.

Fig. 12. Single value decomposition biplot across high nitrogen environments for experiment CML441 x CML444 across high nitrogen conditions in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; TEX, grain texture; GWT, 100 kernel weight).

Correlations across drought environments

High positive correlations were observed between grain yield and plant height and ears per plant (Fig. 13). Anthesis-silking interval, grain moisture and anthesis date were negatively correlated with grain yield.

Fig. 13. Single value decomposition biplot for different traits across drought environments for experiment CML441 x CML444 across drought conditions in Malawi and Zimbabwe in 2003 and 2004. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; TEX, grain texture; GWT, 100 kernel weight.

Relationships among environments for grain yield

The AMMI biplot for grain yield showed that low nitrogen, high nitrogen and no environments were also closely related. This scenario was common in both Malawi and Zimbabwe (Fig. 14). fertilizer environments discriminated testcrosses similarly. Drought and well-watered

FERT, no nitrogen fertilization; DRT MLW, drought Malawi; DRT ZM, drought Zimbabwe; **HN** MLW, high nitrogen Malawi; HN ZM, high nitrogen Zimbabwe). **Fig. 14. AMMI biplot for grain yield showing the relationship among environments for experiment CML441 x CML444 across all environments in Malawi and Zimbabwe in 2003 and 2004. (Low N, low nitrogen; WW MLW, well-watered Malawi; WW ZM, well-watered Zimbabwe, NO**

Table 23. Genotypic (above diagonal) and phenotypic (below diagonal) correlations among environments and their standard errors (*SE***) for experiment CML441 x CML444 across all environments in Malawi and Zimbabwe in 2003 and 2004.**

Environment	NOFR	HNZM	HNMLW	HNZM	WWMLW	WWZ	DRTMW	DRTZM
	T					M		
Chitedze no		\mathcal{S}	1.77	0.82	0.27(0.42)		-0.04	-0.39
fertilization			(1.13)	(0.16)			(0.69)	(0.42)
(NOFRT)								
Harare low N	0.03							
(HNZM)	(0.07)							
Chitedze high N	0.18			2.07	-0.06		-2.22	0.48
(HNMLW)	0.07)			(1.21)	(0.80)		(3.93)	(0.86)
Harare high N	0.32		0.37		-0.03		-0.41	-0.64
(HNZM)	(0.07)		(0.06)		(0.31)		(0.81)	(0.37)
Chitala well-watered	0.03	0.05	0.11	0.08			-0.71	-1.56
(WWMLW)	(0.07)	(0.07)	(0.07)	(0.07)			(0.75)	(2.51)
Chiredzi well-								
watered								
(WWZM)								
Chitala drought	0.01	-0.03	0.09	-0.04	-0.01			-0.05
(DRTMW)	(0.07)	(0.07)	0.07)	(0.07)	(0.07)			(1.13)
Chiredzi drought	-0.02		-0.04	-0.13	-0.06		0.04	
(DRTZM)	(0.07)		(0.07)	(0.07)	(0.07)		(0.07)	

[§]No estimable because one or the two traits were non significant at any environment

Expected gene tic gain

Estimates of heritabilities and genetic variances were used to compute genetic gain for both direct (selection in one environment or stress to improve performance in that environment or stress) and indirect (selection in one environment or stress to improve performance in another environment and stress). Genetic gain estimates for direct selection were variable across environments and stresses as consequence of variable heritabilities and genetic variance displayed (Tables 23 and 24). Greater genetic gains were for environments Harare high nitrogen and Chitedze no fertilization. Low and drought stressed environments had low values for expected genetic gain.

Gen., genetic; h^2 , broad sense repeatability.

Expected genetic gain across all environments was 0.54 Mg ha⁻¹ (Table 25). The highest genetic gain corresponded to environments across high nitrogen $(1.45 \text{ Mg haha}^{-1})$.

able 25. Expected genetic gain for grain yield (Mg ha-1) across environments and T stresses for population CML 441 x CML 444 evaluated in Malawi and Zimbabwe in 2003 and 2004 assuming selection of the best 10%.

Gen., genetic; h^2 , broad sense repeatability.

Estimates of correlated response for indirect selection were also variable depending on the genetic correlation between selection and target environments as well as their heritabilities (Table 26). The highest correlated response was for selection under high nitrogen environments to improve environment with no nitrogen fertilization (0.39 Mg ha⁻¹). This response could be misleading as the no nitrogen fertilized environment did not have nitrogen stress, which means selecting under high nitrogen for another high nitrogen environment. A positive correlated response was estimated for selection under drought to improve yield at high nitrogen environments $(0.23 \text{ Mg } \text{ha}^{-1})$. Negative correlated response was estimated when selection was done under well-watered conditions for drought and no nitrogen fertilization $(-0.18$ and -0.02 Mg ha⁻¹, respectively) and very low response when selection was done under well-watered conditions to improve yield under no nitrogen fertilization $(0.02 \text{ Mg ha}^{-1})$. These results suggest that for this population, direct selection is more effective than indirect selection.

Table 26. Correlated response estimates for indirect selection for different environments and stresses for experiment CML441 x CML444 in Malawi and Zimbabwe in 2003 and 2004.

Selection under	Response in	Correlated Response (Mg ha $^{-1}$)
Well-watered	Drought	-0.18
Well-watered	high nitrogen	0.12
Well-watered	no fertilization	-0.02
High nitrogen	no fertilization	0.39
Drought	high nitrogen	0.23
Drought	no fertilization	-0.02

Preliminary assessment of MAS efficiency in testcrosses

In order to assess the efficiency of marker-assisted selection in selecting drought tolerant genotypes, a contrast was conducted between the means of the first 50 testcrosses selected for favorable alleles at consistent QTL and the mean of the last 50 testcrosses selected for unfavorable alleles at the same QTL. There were significant differences between the two groups in few environments (under no nitrogen fertilization, under low nitrogen, and well-watered conditions at Chitala (Malawi) (Table 27). No significant differences between the two groups were observed in other environments or across environments.

Table 27. Grain yield means for the first and last 50 entries, their differences and significances at single environments and across environments for experiment CML441 x CML444 conditions in Malawi and Zimbabwe in 2003 and 2004.

Selection of the best five entries for each environment was conducted based on the highest yielding testcrosses to assess which group of testcrosses (best or worst) contributed most to the 5 highest yielding testcrosses. There were a mixed group of testcrosses from both groups across all the environments. It was surprising to note that under drought conditions at Chiredzi and Chitala the highest yielding test crosses came from the worst group (entries 53 and 85 respectively). However, some test rosses showed some consistency in being among the best high yielding test crosses. These were entry 27 under well-watered conditions, entry 16 under high nitrogen, and entry 30 under drought. All these entries came from the best group of testcrosses (Table 28).

Environment	Best 5 entries for grain yield
Chitedze no fertilization	25, 79, 96, 5, 3
Harare low N	68, 675, 36, 16
Chitedze high N	1, 12, 16, 33, 69
Harare high N	98, 76, 78, 75, 16
Chiredzi well-watered	53, 27, 30, 74, 60
Chitala well-watered	26, 27, 11, 36, 57
Chitala drought	85, 30, 73, 35, 67
Chiredzi drought	53, 27, 30, 74, 61
Average across locations	51, 50, 97, 24, 63
Average High N	16, 1, 76, 79, 69
Average Well-watered	24, 94, 10, 14, 65
Average Drought	13, 11, 92, 9, 81

Table 28. Top 5 entries for grain yield at single environment and across environments for experiments CML441 x CML444 conditions in Malawi and Zimbabwe in 2003 and 2004.

Drought (DTI) and nitrogen (NTI) tolerance indices were estimated in order to identify testcrosses that reduce less their performances under stressed conditions relative to unstressed conditions at the same locations. Testcrosses that maintain a good performance under stress are good sources for drought tolerance genes. The average DTI for the first and last 50 entries was 56.0 and 55.3 in Malawi and 94.7 and 94.9 in Zimbabwe, respectively (Appendix M). The average NTI for the first and last 50 entries was 76.4 and 76.8, respectively (Zimbabwe). The testcrosses with the best DTU and NTI indices came from both groups (Table 29).

ices at two Table 29. Best testcrosses based on drought and nitrogen tolerance ind locations for CML441 x CML444 evaluated in Malawi and Zimbabwe in 2003 **and 2004 season.**

Parameter	Zimbabwe	Malawi
DTI	29, 50, 42, 87, 68	85, 42, 51, 35, 24
NTI	97, 68, 14, 6, 77	$\overline{}$

Population CML440/COMPE

Results per environment

Chitedze no nitrogen fertilization

This experiment was conducted under no nitrogen fertilization and rain fed conditions at Chitedze Research Station (Malawi) during the 2003/2004 season. The purpose was to induce low N stress, however, the nitrogen content in the soil was higher than expected and no stress was apparent. Grain yield average was 3.85 Mg ha⁻¹ (range 2.05 to 6.74 Mg ha⁻¹) (Table 30). There were no significant differences for all the traits except for 100 kernel weight . Heritabilities were 0.09 and 0.30 for moisture content and 100 grain weight while the other traits had zeros. Average grain yield for the first 50 testcrosses was not significantly greater than the average for the last 50 testcrosses (Table 30).

Genotypic correlations were not estimated because of the non significance of the traits. Phenotypic correlations were estimated using single value decomposition of the standardized traits. Grain yield was positively correlated with plant height, root lodging and surprisingly with anthesis-silking interval but was negatively correlated with anthesis date (Fig. 15).

Table 30. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML440 x COMPE evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004.

Statistics	GYG	AD	ASI	PH	EPP	MOI	TEX	GWT
	Mg ha ⁻¹	d	d	cm	#	$\%$	$1-5$	g
Mean	3.85	67.9	1.0	218.0	0.90	15.0	2.9	39.00
Significance	NS	NS	NS	NS	NS	NS	NS	***
Minimum	2.05	65.0	-0.5	192.0	0.70	13.4	2.00	20.8
Maximum	6.74	71.7	3.9	271.0	1.40	16.6	4.00	49.1
LSD(5%)	2.02	4.4	2.2	34.0	0.30	2.00	0.90	11.6
CV(%)	22.8	2.96	105.3	7.40	4.60	3.20	33.6	5.01
MSE	0.77	4.03	1.1	262.0	0.01	0.23	0.95	24.11
Mean (Ent. 1-50)	3.84	67.8	1.0	215.0	1.00	14.90	2.90	39.1
Mean $(Ent. 51-100)$	3.85	68.0	1.0	220.0	0.90	15.10	2.90	5.01
$\sigma_{\rm e}^2$ $\sigma_{\rm e}^2$	0.77	4.03	1.08	245.5	0.01	0.23	0.95	24.10
	0.00	0.00	0.00	0.00	0.00	0.05	0.00	5.09
h^2 (family basis)	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.30
Standard Error h^2	0.00	0.00	0.00	0.00	0.00	0.20	0.00	0.17

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content; TEX, grain texture; GWT, 100 kernel weight.

Fig. 15. Single value decomposition biplot of standardized traits showing their correlations for population CML440 x COMPE evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004 season. (AD; 50% anthesis; ASI, anthesis-silking interval; GYG, grain yield; PH, plant height; EPP, ears per plant; EPO, ear position; RL, root lodging; SL, stem lodging, MOI, moisture content and TEX, grain texture).

Harare low nitrogen experiment

This experiment was conducted under low nitrogen conditions in Harare (Zimbabwe) estimates were generally moderate with grain yield having the highest heritability of under rainfed conditions during the 2003/2004 season. The trial did not receive any nitrogen fertilization but only 60 kg ha⁻¹ P₂O₅. Significant differences were observed for all the traits except anthesis silking interval (Table 31). Mean values of the best 50 genotypes and 50 worst genotypes were not significantly different. Heritabilities 0.35, followed by plant height (0.28), 0.25 for 50% anthesis date and the lowest was from anthesis-silking interval (0.07).

able 31. Statistics, genotypic variance, heritability and their standard errors for T traits in testcrosses from population CML440 x COMPE evaluated under low nitrogen at Harare, Zimbabwe in 2003 and 2004.

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height.

Anthesis date had a positive genotypic correlation with plant height (0.63) while grain yield had negative genotypic correlations with plant height (-0.18) and anthesis date (but negative between grain yield and 50% anthesis date (-0.25) and between plant height0.11). Phenotypic correlations were positive between grain yield and plant height (0.19) and anthesis date (-0.17) (Table 32 and Fig.16). Genotypic correlations ranged from - 0.1 1 to 0.63 while phenotypic correlations were from -0.17 to 0.12.

Table 32. Genotypic (above diagonal) and phenotypic (below diagonal) correlations **and their standard errors (SE) for population CML440 x COMPE conducted under** low nitrogen conditions in Harare, Zimbabwe during 2003 and 2004.

	GYG	AD	PН
GYG		$-0.11(0.56)$	$-0.18(0.51)$
AD	$-0.25(0.07)$		0.63(0.23)
PН	0.19(0.08)	$-0.17(0.01)$	
	CVC grain viald: AD , 50% anthosis: DU plant hoight		

GYG, grain yield; AD, 50% anthesis; PH, plant height

ig. 16. Single value decomposition biplot of standardized traits showing their correlations Ffor population CML440 x COMPE evaluated under low nitrogen fertilization in Harare, Zimbabwe in 2003 and 2004 . (AD; 50% anthesis; GYG, grain yield; ASI, anthesis-silking interval; PH, plant height).

Chitedze high nitrogen fertilization

This experiment was conducted at Chitedze Research Station (Malawi) during the 2003/2004 season under rain fed conditions. The experiment was fertilized with 120 kg N ha⁻¹ and 60 kg P_2O_5 ha⁻¹. Grain yield average was 5.56 Mg ha⁻¹ (range 3.58 to 7.34 Mg ha⁻¹) (Table 33).

Statistics	GYG	AD	ASI	PH	EPP	TEX	GWT
	Mg ha ⁻¹	d	d	cm	#	$1-5$	g
Mean	5.56	73.0	0.4	218.0	0.80	3.20	43.70
Significance	NS	NS	NS	$* *$	NS	NS	NS
Minimum	3.58	69.6	-2.80	181.0	0.30	2.40	38.1
Maximum	7.34	75.8	4.40	249.0	1.10	4.10	51.1
LSD(5%)	2.48	4.5	3.20	26.0	0.30	0.80	7.30
CV(%)	23.20	3.5	38.7	7.10	18.8	6.30	8.20
MSE	1.67	6.5	2.40	245.0	0.02	0.20	12.9
Mean (Ent. 1-50)	5.70	72.5	0.50	217.0	0.80	3.10	43.5
Mean (Ent. 51-100)	5.42	72.8	0.40	219.0	0.70	3.20	43.8
σ_{c}^{2} σ_{G}^{2}	1.47	4.40	2.37	205.5	0.03	0.15	12.57
	0.00	0.00	0.00	12.0	0.00	0.001	0.00
h^2 (family basis)	0.00	0.00	0.00	0.11	0.00	0.02	0.00
Standard Error h^2	0.00	0.00	0.00	0.20	0.00	0.20	0.00

Table 33. Statistics, genotypic variance, heritability and their standard errors for i traits in testcrosses from population CML440 x COMPE evaluated under high **ization hited ala 20 20 nitrogen fertil at C ze, M wi in 03 and 04.**

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, moisture content; TEX, grain texture; GWT, 100 kernel weight.

The mean of the first 50 testcrosses was significantly higher than the mean of the last 50 testcrosses. All the traits were not significantly different except for plant height. Surprisingly, even the heritabilities were also very low. Genotypic correlations were not esti mated because of the non significance of the traits. Phenotypic correlations were estimated using single value decomposition of the standardized traits. These showed that there was a positive correlation between grain texture and 100 grain weight, and between grain yield and ears per plant. There was a negative phenotypic correlation between
anthesis date and anthesis-silking interval and between anthesis-silking interval and grain yieldt (Fig. 17).

Fig. 17. Single value decomposition biplot of standardized traits showing their correlations for population CML440 x COMPE conducted under high nitrogen conditions at Chitedze, Malawi in 2003 and 2004. (AD; 50%anthesis date; ASI, anthesis-silking interval; GYG, grain yield; PH, plant height; EPP, ears per plant; MOI, moisture content ; TEX, grain texture).

Harare high nitrogen fertilization

This experiment was conducted under rain fed conditions in Harare (Zimbabwe) during the 2003/2004 season. It was fertilized with 120 kg N ha⁻¹ and 60 kg P₂O₅ ha⁻¹. Average grain yield was $8.02 \text{ Mg} \text{ ha}^{-1}$ (range 5.73 to 9.77 Mg ha⁻¹). Significant differences were observed for grain yield only but not for the other traits. Heritability for grain yield was 0.33, and very low or 0 for the other traits (Table 34).

Using single decomposition biplots of standardized traits (Fig.18), phenotypic correlations were estimated. This showed that there were weak phenotypic correlations amongst all the traits, which is explained by the non significant differences for the traits.

 ig. 18. Single value decomposition biplot of standardized traits showing their correlations for Fpopulation CML440 x COMPE conducted under high nitrogen conditions in Harare, Zimbabwe during 2003 and 2004. (AD; 50% anthesis; ASI, anthesis-silking interval; GYG, grain yield; PH, plant height; MOI, moisture content).

Table 34. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML440 x COMPE evaluated under high nitrogen fertilization in Harare, Zimbabwe in 2003 and 2004.

Statistics	GYG	AD	ASI	PН	MOI
	Mg ha ⁻¹	d	d	cm	#
Mean	8.02	69.5	1.20	241	12.6
Significance	*	NS	NS	NS	NS
Minimum	5.73	66.0	-1.60	218	8.10
Maximum	9.77	72.8	4.60	267	15.2
LSD(5%)	2.12	3.20	2.50	26.0	3.20
CV(%)	13.02	2.30	105.9	5.30	13.2
MSE	1.09	2.60	1.60	164	2.76
Mean $(Ent. 1-50)$	8.09	69.6	1.10	241	12.5
Mean (Ent. 51-100)	7.96	68.4	1.20	241	12.7
	1.10	2.42	1.54	161.6	2.76
σ_e^2 σ_g^2 h^2 (family basis)	0.27	0.11	0.00	20.4	0.33
	0.33	0.08	0.00	0.20	0.19
Standard Error h^2	0.14	0.19	0.00	0.17	0.17

^{***,**,*} Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; MOI, grain moisture content.

Chitala well-watered experiment

This experiment was conducted under well-watered conditions at Chitala (Malawi) during the dry season under irrigation in 2004. Water was applied to the experiment to field capacity from planting up to physiological maturity. The trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. Significant differences were observed for 50% anthesis date and plant height only and not for the other traits. However, there were no significant differences between the mean of the first 50 and last 50 testcrosses. Heritabilities were moderate for 50% anthesis date (0.46) and plant height (0.42) but low for moisture content (0.26) and 0.01 for grain yield (Table 35).

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GY G, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MO I, moisture content.

Genotypic correlation was conducted for 50% anthesis date and plant height because they were the only traits that were significantly different. Positive genotypic (1.04) and phenotypic correlations (0.01), were observed between the two traits although the phenotypic correlation was weak. Grain yield was positively correlated with eras per plant but these were negatively correlated with anthesis-silking interval and 50% anthesis date (Fig.19).

Fig. 19. Single value decomposition biplot of standardized traits showing their correlations for population CML440 x COMPE conducted under well-watered conditions at Chitala, Malawi in 2004. (AD; 50% anthesis; ASI, anthesis-silking interval; GYG, grain yield; PH, plant height; EPP, ears per plant; MOI, moisture content).

Chiredzi well-watered experiment

This experiment was conducted under well-watered conditions at Chiredzi (Zimbabwe) during the dry season under irrigation in 2004. Water was applied to the experiment to field capacity from planting up to physiological maturity. The trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. Mean grain yield was 4.77 Mg ha⁻¹ (ranged from 3.51 to 6.09 Mg ha⁻¹). There were no significant differences for all the traits except moisture content. The mean of the first 50 testcrosses was also not significantly different from the mean of the other 50 testcrosses. Heritabilities were very low, they ranged from zero to to 0.11 for grain yield (Table 36). This scenario was also observed in the other populations when evaluated at the same environment.

Lack of significant differences for all but one trait resulted in genotypic correlations not being estimated. However, phenotypic correlations were estimated using single value decomposition biplot of standardized traits. There were positive phenotypic correlations between grain yield and ears per plant and surprisingly between grain yield and anthesissilking interval, which are normally negative. Negative correlations were observed between grain yield and 50% anthesis date and between 50% anthesis date and anthesissilking interval (Fig. 20).

Table 36. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML440 x COMPE evaluated under wellwatered conditions at Chiredzi, Zimbabwe in 2004.

Statistics	GYG	AD	ASI	PH	EPP	MOI	SEN
	Mg ha ⁻¹	d	d	cm	#	$\%$	$\%$
Mean	4.77	99.5	-0.81	183.0	1.00	10.5	67.9
Significance	NS	NS	NS	NS	NS	$***$	NS
Minimum	3.51	96.9	-3.33	189.0	0.80	7.80	55.3
Maximum	6.09	101.9	2.76	272.0	1.20	13.4	83.5
LSD(5%)	1.30	3.36	2.89	30.0	0.20	15.6	15.6
CV(%)	30.7	1.70	183.5	47.9	9.2	15.2	10.5
MSE	0.40	3.33	2.21	503.4	0.01	1.70	51.0
Mean $(Ent. 1-50)$	4.75	99.2	-0.50	183.0	1.00	10.6	67.1
Mean $(Ent. 51-100)$	4.79	98.7	-0.80	185.0	1.00	10.5	68.6
$\sigma_{\rm c}^2$ $\sigma_{\rm G}^2$	0.38	3.10	2.21	242.2	0.01	1.82	51.0
	0.02	0.00	0.12	0.00	0.00	0.00	0.00
h^2 (family basis)	0.11	0.00	0.09	0.00	0.00	0.00	0.00
Standard Error h^2	0.19	0.00	0.18	0.00	0.00	0.00	0.00
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***,**,* Significant at $P < 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content; GWT, 100 kernel weight; SEN, leaf senescence.

Fig. 20. Single value decomposition biplot of standardized traits showing their correlations for population CML440 x COMPE conducted under well-watered conditions at Chiredzi, Zimbabwe in 2004. (AD; 50% anthesis; ASI, anthesis-silking interval; GYG, grain yield; PH, plant height; EPP, ears per plant; MOI, moisture content; SEN, leaf senescence).

Chitala drought experiment

The experiment was conducted during the dry season of 2004 at Chitala Experimental Station (Malawi). Water was applied to the experiment up to field capacity from planting until three weeks before flowering. The intention was to induce drought stress during the flowering period. There were significant differences for grain yield, anthesis date, plant height and ears per plant but not for anthesis-silking interval and between the mean of the best 50 and worst testcrosses (Table 37). Heritabilities were 0.26, 0.10, 0.03, 0.25 and 0.41 for grain yield, anthesis date, anthesis silking interval, plant height and ears per plant, respectively.

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant.

Positive genotypic correlations were observed between grain yield and plant height (0.43) and ears per plant (0.65) and between 50% anthesis date and plant height (1.05) and between plant height and ears per plant (0.51) but was negative between grain yield and 50% anthesis date (-0.78). Positive phenotypic correlations were observed between grain yield and ears per plant (0.54) and plant height (0.25), and between plant height and ears per plant (0.30). The rest were negative (Table 38). Genotypic correlations ranged from -1.17 to 1.05 while phenotypic correlations were from -0.27 to 0.54 (Table 38 and Fig. 20).

Table 38. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE)* **for population CML440 x COMPE conducted under drought conditions at Chitala, Malawi during 2003 and 2004.**

	GYG	AD.	PН	EPP
GYG		$-0.78(0.88)$	0.43(2.42)	0.65(0.27)
AD.	$-0.27(0.07)$		1.05(1.60)	$-1.19(1.22)$
PН	0.25(0.22)	$-0.19(0.07)$		0.51(0.41)
EPP	0.54(0.06)	$-0.10(0.08)$	0.30(0.07)	

GYG, grain yield, AD, 50% anthesis; PH, plant height; EPP, ears pr plant.

Fig. 21. Single value decomposition biplot of standardized traits showing their correlations for population CML440 x COMPE conducted under drought conditions at Chitala, Malawi in 2004. (AD; 50% anthesis; ASI, anthesis-silking interval; GYG, grain yield; PH, plant height; EPP, ears per plant).

Chiredzi drought experiment

The experiment was conducted during the dry season of 2004 at Chiredzi Experimental Station (Zimbabwe). Water was applied to the experiment up to field capacity from planting until three weeks before flowering. The intention was to induce drought stress during the flowering period. Despite that nitrogen fertilizers were applied to this experiment, the general performance was poor because of inherent low fertility of the experimental site. Grain yields were very low. Mean yield was 1.81 Mg ha⁻¹ with a range from 0.07 to 3.67 Mg ha⁻¹ (Table 39). Heritabilities were low ranging from 0.02 to 0.30 for grain yield and ears per plant. Estimates of genotypic and phenotypic correlations, showed that there were strong and positive genotypic and phenotypic correlations between grain yield and ears per plant (1.84 and 0.51 respectively) but were negative between grain yield and grain texture (-0.15) and moisture content (-0.06). Moisture content and grain texture had also strong genotypic correlations (0.88). Most traits had negative phenotypic correlations except between grain moisture and texture which was positive (0.05) Table 40 and Fig.21).

Table 39. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML440 x COMPE evaluated under drought conditions at Chiredzi, Zimbabwe in 2004.

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking; PH, plant height; EPP, ears per plant; TEX, grain texture; MOI, moisture content.

Table 40. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) for population CML440 x COMPE conducted under drought conditions at Chiredzi, Zimbabwe in 2004.**

GYG, grain; EPP, ears per plants; TEX, grain texture; MOI, moisture content

Fig. 22. Single value decomposition biplot of standardized traits showing their correlations for population CML440 x COMPE conducted under drought conditions at Chiredzi, Zimbabwe in 2004. (GYG, grain yield; EPP, ears per; plant; MOI, moisture content; TEX, grain texture).

Results across environments

Across all environments significant for grain yield

The analysis across environments was conducted for those environments that had significant differences for grain yield in this population. These were low nitrogen (Harare), high nitrogen (Harare) and drought (Chitala and Chiredzi).

Significant differences were observed only for grain yield and 50% anthesis date but not for the other traits. Average grain yield was $3.64 \text{ Mg} \text{ ha}^{-1}$. Heritability estimates were generally low ranging from 0.00 to 0.37. Heritabilty was 0.19 for grain yield, 0.20 for 50% anthesis date, 0.29 for anthesis-silking interval, 0.37 for plant height, 0.21 for moisture content, 0.19 for 100 kernel weight and 0.00 for ears per plant (Table 41).

Table 41. Statistics, averages, variance components, heritability and its standard error for experiment CML440 x COMPE across all environments with significant differences for grain yield in Malawi and Zimbabwe in 2003 and 2004.

Statistics	GYG	AD	ASI	PH	EPP	MOI	GWT
	Mg ha ⁻¹	d	d	cm	#	$\frac{0}{0}$	g
Mean	3.64	79.18	1.99	199.02	0.82	12.04	30.62
Significance	***	***	NS	NS	NS	NS	NS
CV	28.41	2.74	92.24	8.83	23.99	13.72	9.18
	0.64	0.34	2.84	176.49	0.03	2.25	6.39
$\sigma_{\rm q}^2$ $\sigma_{\rm G}^2$ $\sigma_{\rm GxE}^2$	0.03	0.14	0.15	13.21	0.00	0.08	0.17
	0.13	0.56	0.00	3.52	0.002	0.11	0.00
h^2 (family basis)	0.19	0.20	0.29	0.37	0.00	0.21	0.19
Standard Error h^2	0.15	0.14	0.11	0.12	0.00	0.14	0.37

***,**,* Significant at $P \le 0.001$, 0.01, and 0.05, respectively.

GYG, grain yield; PH, plant height; AD, 50% anthesis; GWT, 100gwt, grain weight; EPP, ears per plant; ASI, anthesis-silking interval; MOI, moisture content.

MSE, mean square error; h^2 , broad sense repeatability.

Across high N environments

No significant differences were observed for any trait except for plant height in the analysis across high nitrogen fertilization in Malawi and Zimbabwe during 2003/2004 season. (Table 42 and Appendix E). Similarly all the traits had zero heritabilities except plant height which had a low heritability estimate of 0.24. The non significance of the traits at the Chitedze Research Station environment might have contributed to the non significance for the traits across high nitrogen sites.

Table 42. Statistics, averages, variance components, heritability and its standard error for experiment CML440 x COMPE across high nitrogen conditions in Malawi and Zimbabwe in 2003 and 2004.

***,**,* Significant at $P \le 0.001$, 0.01, and 0.05, respectively.

GYG, grain yield; PH, plant height; AD, 50% anthesis; GWT, 100gwt, grain weight; EPP, ears per plant; ASI, anthesis-silking interval; MOI, moisture content.

MSE, mean square error; h^2 , broad sense repeatability.

Across drought environments

Significant differences were observed for anthesis date only across drought stress environments (Table 43 and Appendix F). Heritability estimates ranged from 0 to 0.10.

Table 43. Statistics, averages, variance components, heritability and its standard error for experiment CML440 x COMPE across drought stressed environments conducted in Malawi and Zimbabwe in 2003 and 2004.

***,**,* Significant at $P \le 0.001$, 0.01, and 0.05, respectively.

GYG, grain yield; PH, plant height; AD, 50% anthesis; EPP, ears per plant; ASI, anthesis-silking interval; MOI, moisture content.

MSE, mean square error; h^2 , broad sense repeatability.

Correlations among traits across environments and stresses

Across all environments

Positive correlations were observed between grain yield and ears per plant while

negative correlations were observed between grain yield and 50% anthesis date (Fig 23).

Fig. 23. Single value decomposition biplot of standardized traits showing their correlations for population CML440 x COMPE evaluated across all environments in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; EPP, ears per; plant; PH, plant height; MOI, moisture content; TEX, grain texture).

Across high N environments

There was a strong and positive correlation between grain yield and ears per plant but the two were negatively correlated with moisture content and anthesis-silking interval. Strong negative correlations were observed between anthesis-silking interval and 50% anthesis date and between grain yield and moisture content (Fig 24).

Fig. 24. Single value decomposition biplot of standardized traits showing their correlations for population CML440 x COMPE evaluated across high nitrogen environments in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; EPP, ears per; plant; PH, plant height; MOI, moisture content).

Across drought environments

Positive correlations were observed between grain yield and plant height and moisture content. Negative correlations were observed between 50% anthesis date and anthesissilking interval and between grain yield and anthesis-silking interval (Fig.25).

Fig. 25. Single value decomposition biplot of standardized traits showing their correlations for population CML440 x COMPE evaluated across drought environments in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; EPP, ears per; plant; PH, plant height; MOI, moisture content).

Relationships among environments for grain yield

In the AMMI biplot well-watered in Malawi, high nitrogen Zimbabwe and drought environments in Zimbabwe discriminated the testcrosses in a similar manner. No nitrogen fertilization in Malawi and drought conditions in Malawi, and high nitrogen in Malawi and well-watered in Zimbabwe also classified the testcrosses similarly (Fig. 26).

Fig. 26. AMMI biplot for grain yield showing the relationship among environments for population CML440 x COMPE conducted in Malawi and Zmbabwe in 2003 and 2004. (Low N, low nitrogen; WW MLW, well-watered Malawi; WW ZM, well-watered Zimbabwe, NO FERT, no nitrogen fertilization; DRT MLW, drought Malawi; DRT ZM, drought Zimbabwe; HN MLW, high nitrogen Malawi; HN ZM, high nitrogen Zimbabwe).

Expected genetic gain

Expected genetic gain from direct selection was estimated using heritabilities, genetic variance and their standard errors by selecting from the individual environment (direct). An attempt was also made to estimate expected amount of gain one gets by selecting in one environment and the expected response in another environment (indirect selection). These estimates were not conducted because most correlation coefficients could not be estimated from the across site analysis. The results from this study indicate that genetic gains were variable across locations and environments. High genetic gains were observed from Harare high nitrogen environment $(0.52 \text{ Mg} \text{ ha}^{-1})$ and Harare low nitrogen $(0.40 \text{ Mg } \text{ha}^{-1})$ and the lowest were under Chitedze high nitrogen and no nitrogen fertilization (0.00) (Table 44).

Table 44 . Expected genetic gain for grain yield (Mg ha-1) per environment for CML440 x COMPE evaluated in Malawi and Zimbabwe in 2003 and 2004 assuming selection of the best 10%.

Environment	Mean	Error	Genotypic variance	h ²	Genetic Gain (R)
Chitedze no fertilization	3.85	0.77	0.00	0.00	0.00
Harare low N	1.81	0.58	0.15	0.35	0.40
Chitedze high N	5.56	1.47	0.00	0.00	0.00
Harare high N	8.02	1.10	0.27	0.33	0.52
Chitala well-watered	3.80	0.84	0.01	0.01	0.02
Chiredzi well-watered	4.77	0.38	0.02	0.11	0.08
Chitala drought	2.56	0.46	0.08	0.26	0.25
Chiredzi drought	1.81	0.52	0.01	0.02	0.02
Average across					
locations \sim	4.06	0.78	0.01	0.10	0.06

 h^2 , broad sense repeatability.

Expected genetic gain across environments and stresses was very low (Table 45).

Table 45. Expected genetic gain for grain yield (Mg ha-1) across environments for experiment CML 440 x COMPE evaluated in Malawi and Zimbabwe in 2003 and 2004 assuming selection of the best 10%.

Gen., genetic; h^2 , broad sense repeatability.

Preliminary assessment of MAS efficiency in testcrosses

The efficiency of marker assisted selection in selecting drought tolerant testcrosses, was assessed by conducting a contrast between the means of the best 50 testcrosses selected for favorable alleles at consistent QTL and the mean of the worst 50 testcrosses selected for unfavorable alleles at the sam QTL. Significant differences between the two groups were observed under high nitrogen fertilization at Chitedze (Malawi) and under drought conditions at Chiredzi (Zimbabwe) but not at the other environments and across environments (Table 46).

Environment	Mean (Ent. 51-100) Mean (ent. $1-50$)		Difference	Significance
	$(Mg \text{ ha}^{-1})$	$(Mg \text{ ha}^{-1})$		
Chitedze no fertilization	3.84	3.85	-0.01	NS
Harare low N	1.80	1.90	-0.10	NS
Chitedze high N	5.70	5.42	0.28	\ast
Harare high N	8.09	7.96	0.13	NS
Chitala well-watered	3.87	3.74	0.13	NS
Chiredzi well-watered	4.75	4.79	θ	NS
Chitala drought	2.60	2.50	0.10	NS
Chiredzi drought	1.88	1.73	0.18	\ast
Average across locations	4.09	4.04	0.05	NS
Average High N	6.90	6.69	0.21	NS
Average Well-watered	4.31	4.27	0.04	NS
Average Drought	2.17	2.22	0.05	NS

Table 46. Mean grain yields, for the first and last 50 entries, their significances at single and across environments for population CML440 x COMPE conducted in Malawi and Zimbabwe in 2003 and 2004.

* Significant at $P = 0.05$; NS, not significant.

Top five entries for grain yield were selected for each environment by ranking the testcrosses from the highest to the lowest yielding. The aim was to assess which group of testcrosses (best or worst) contributed most to the 5 highest yielding testcrosses. The results showed that both groups of testcrosses contributed almost equally to the list of five most high yielding testcrosses although there were variations amongst environments (Table 47). However some consistency was observed for some testcrosses. For example entries 97 and 36 were consistently among the top 5 high yielding testcrosses under all the high nitrogen and the drought sites, respectively. Entry 83 was among the top five average across all locations, well-watered and drought conditions (Table 47).

Table 47. Top 5 entries for grain yield at single environment and across environments for population CML440 x COMPE evaluated in Malawi and Zimbabwe in 2003 and 2004.

Environment	Best 5 entries for grain yield
Chitedze no fertilization	88, 55, 101, 47, 27
Harare low N	59, 89, 29, 102 18
Chitedze high N	97, 18, 88, 39, 64
Harare high N	97, 73, 59, 84, 24
Chitala well-watered	46, 93, 83, 49, 86
Chiredzi well-watered	33, 84, 66, 64, 15
Chitala drought	20, 67, 38, 22, 36
Chiredzi drought	35, 27, 28, 39, 36
Average across locations	88, 73, 83, 30, 18
Average High N	97, 84, 73, 30, 19
Average Well-watered	83, 17, 7, 68, 71
Average Drought	83, 14, 53, 34, 28

Drought tolerance index (DIT) and nitrogen tolerance index (NTI) were estimated in order to identify testcrosses that reduce their performances under stressed conditions relative to unstressed conditions at the same locations. Testcrosses that maintain good performance under stress are good sources of drought tolerant genes. The average DTI of the first and last 50 entries were 29.7% and 28.2% (Malawi) and 59.7% and 63.65% (Zimbabwe), respectively (Appendix N). The average NTI for the first and last 50 entries were 78.13% and 75.99%, respectively (Zimbabwe). The testcrosses with the best DTI and NTI indices came from both groups (Table 48).

Table 48. Best 5 testcrosses for drought tolerance index (DTI) and nitrogen tolerance index (NTI) for population CML440 x COMPE evaluated in Malawi and Zimbabwe in 2003 and 2004.

Population CML444 x K64R

Results per environment

Chitedze no nitrogen fertilization

This experiment was conducted under no nitrogen fertilization and rain fed conditions at Chitedze Research Station (Malawi) during the 2003/2004 season. The purpose was to induce low N stress, however, the nitrogen content in the soil was higher than expected and no stress was apparent. Grain yield average was $5.32 \text{ Mg } \text{ha}^{-1}$ (range 0.01 to 7.36) Mg ha⁻¹) (Table 49). Significant differences were observed for grain yield, anthesis date, grain texture, moisture content and 100 kernel grain weight (Table 49). Heritabilities were 0.37, 0.34, 0.05 0.11, 0.27, 0.49, 0.54 and 0.31 for grain weight, anthesis date, anthesis-silking interval, plant height, ears per plant, grain texture, moisture content and 100 kernel grain weight, respectively. Average grain yield for the first 50 testcrosses was not significantly greater than the average for the last 50 testcrosses (Table 49).

Genotypic correlations were estimated for only those traits which were significantly different. Positive genotypic correlations were observed between grain yield and grain texture (0.65) and between grain yield and 100 kernel weight (0.46) but was negative with anthesis date (-0.34) and moisture content (-0.54). Phenotypic correlations were positive between 100 kernel weight and grain yield (0.48). The rest of the phenotypic correlations were negative (Table 50 and Fig. 27).

Table 49. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML444 x K64R evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004.

Statistics	GYG	AD	ASI	PH	EPP	MOI	TEX	GWT
	Mg ha ⁻¹	d	d	cm	#	$\%$	$1-5$	g
Mean	5.32	71.4	0.79	214.4	1.10	14.3	3.49	38.7
Significance	***	*	NS	NS	NS	***	***	***
Minimum	0.01	67.8	-2.60	119.0	0.90	11.8	2.00	29.0
Maximum	7.36	75.6	2.30	239.0	1.40	16.9	4.50	47.0
LSD(5%)	1.84	3.10	1.72	38.2	0.29	1.73	1.01	7.99
CV(%)	20.9	2.20	109.6	8.79	13.1	5.60	14.5	11.7
MSE	1.17	2.39	0.77	354.9	0.02	0.65	0.26	20.0
Mean (Ent. 1-50)	5.42	71.4	0.80	215.0	1.10	14.5	3.60	39.7
Mean $(Ent. 51-100)$	5.22	71.4	0.70	214.0	1.10	14.2	3.30	37.9
	1.17	2.33	0.77	354.8	0.02	0.63	0.25	20.0
σ_{c}^{2} σ_{G}^{2}	0.34	0.61	0.02	21.9	0.003	0.37	0.11	4.45
h^2 (family basis)	0.37	0.34	0.05	0.11	0.27	0.54	0.49	0.31
Standard Error h^2	0.14	0.14	0.19	0.20	0.15	0.10	0.11	0.16
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***,**,* Significant at $P < 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content; TEX, grain texture; GWT, 100 kernel weight.

Table 50. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) from population CML444 x K64R evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004.**

GYG, grain yield; AD, 50% anthesis; MOI, grain moisture content; TEX, grain texture; GWT, 100 kernel weight.

Fig. 27. Single value decomposition biplot of standardized traits showing their correlations for population CML444 x K64R evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004. (AD; 50%anthesis date; GYG, grain yield; MOI, moisture content; GWT, 100 kernel weight; TEX, grain texture).

Harare low nitrogen experiment

This experiment was conducted under low nitrogen conditions in Harare (Zimbabwe) under rainfed conditions during the 2003/2004 season. No nitrogen fertilizer was applied but only 60 kg ha⁻¹ P₂O₅. There were significant differences for grain yield, anthesis date and ears per plant (Table 51). Mean maize yield was 0.87 Mg ha^{-1} (range was 0.16 to 1.74 Mg ha-1). The average of the best 50 genotypes and 50 worst genotypes were not significantly different. Heritabilities were generally low to moderate with 0.41 for plant height, 0.31 for ears per plant, 0.28 for 50% anthesis date, 0.15 for grain yield, 0.04 for anthesis-silking interval and 0.00 for moisture content.

Table 51. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML444 x K64R evaluated under low nitrogen at Harare, Zimbabwe in 2003 and 2004.

Statistics	GYG	AD	ASI	PH	EPP	MOI
	Mg ha ⁻¹	d	d	cm	#	$\frac{0}{0}$
Mean	0.87	77.4	3.10	199.0	0.80	10.7
Significance	$***$	*	NS	NS	\ast	NS
Minimum	0.16	73.1	-0.10	128.0	0.20	8.60
Maximum	1.74	85.8	7.00	230.0	0.11	14.9
LSD(5%)	0.72	5.04	3.80	273.0	0.40	3.24
CV(%)	41.4	3.10	60.9	68.8	12.2	12.2
MSE	0.13	5.79	3.57	207.7	0.03	1.79
Mean (Ent. 1-50)	0.82	77.1	3.20	210.0	0.79	10.7
Mean (Ent. 51-100)	0.92	77.6	2.90	199.0	0.79	10.7
$\sigma_{\rm c}^2$ $\sigma_{\rm G}^2$	0.13	5.79	3.57	246.5	0.04	1.62
	0.01	1.12	0.07	86.2	0.01	0.00
h^2 (family basis)	0.16	0.28	0.04	0.41	0.31	0.00
Standard Error h^2	0.18	0.15	0.12	0.14	0.14	0.00

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height, EPP, ears per plant. MOI, grain moisture.

Grain yield had positive genotypic and phenotypic correlations with ears per plant but negative genotypic and phenotypic correlation with 50% anthesis date (Table 52 and Fig. 28).

Table 52. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) from population CML444 x K64R conducted under low nitrogen at Harare, Zimbabwe in 2003 and 2004.**

	GYG	AD.	EPP
GYG		$-0.124(2.46)$	2.23(4.84)
AD	$-0.23(0.07)$		$-0.46(0.55)$
EPP	0.54(0.06)	$-0.23(0.07)$	

GYG, grain yield; AD, 50% anthesis; EPP, ears per plant.

Fig. 28. Single value decomposition biplot of standardized traits showing their correlations for population CML444 x K64R evaluated under low nitrogen fertilization in Harare, Zimbabwe in 2003 and 2004. (AD; 50% anthesis; GYG, grain yield; EPP, ears per plant).

Chitedze high nitrogen fertilization

This experiment was conducted at Chitedze Research Station (Malawi) during the 2003/2004 season under rain fed conditions. The experiment was fertilized with 120 kg N ha⁻¹ and 60 kg P₂O₅ ha⁻¹. Grain yield average was 5.17 Mg ha⁻¹ (range 0.70 to 7.54) Mg ha⁻¹) (Table 53).

Table 53. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses for population CML444 x K64R evaluated under high nitrogen fertilization at Chitedze, Malawi in 2003 and 2004.

Statistics	GYG	AD	ASI	PH	EPP	TEX	MOI	GWT
	Mg ha ⁻¹	d	d	cm	#	$1-5$	$\%$	g
Mean	5.17	76.9	0.50	208.0	0.90	3.60	14.3	43.3
Significance	***	***	NS	***	NS	***	NS	***
Minimum	0.70	71.5	-2.50	166.0	0.50	2.50	12.7	28.5
Maximum	7.54	82.8	2.50	231.0	2.90	4.60	16.0	54.8
LSD(5%)	2.32	4.20	2.40	18.0	0,70	0.80	1.60	10.3
CV(%)	25.78	2.80	228.2	4.29	37.1	10.4	5.70	12.1
MSE	1.78	4.50	1.30	79.5	0.10	0.10	0.70	27.3
Mean (Ent. 1-50)	5.12	76.7	0.47	209.0	0.90	3.70	14.4	44.1
Mean (Ent. $51-100$)	5.22	77.2	0.51	207.0	0.90	3.53	14.3	44.2
$\sigma_{\rm e}^2$ $\sigma_{\rm g}^2$	1.73	4.82	1.41	79.5	0.11	0.14	0.64	26.1
	0.25	1.53	0.06	62.3	0.00	0.08	0.00	8.60
h^2 (family basis)	O.22	0.39	0.08	0.61	0.00	0.54	0.00	0.40
Standard Error h^2	0.17	0.14	0.19	0.08	0.00	0.10	0.00	0.13
$\cdot \sim$	\cdot \cdot \sim \cdot \sim \sim \sim \cdot \sim	\sim \sim 1	1.0.07	\blacksquare	1.3T ₀	\cdot \sim		

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content; TEX, grain texture; GWT, 100 kernel weight.

No significant differences were observed between the mean of the first 50 testcrosses and the mean of the last 50 testcrosses. There were significant differences between grain yield, 50% anthesis date, plant height, grain texture and 100 kernel weight. Heritabilities were 0.22, 0.39, 0.08, 0.61, 0.54, and 0.40 for grain yield, 50% anthesis date, anthesissilking interval, plant height, grain texture and 100 kernel weight, respectively (Table 53).

Positive genotypic correlations were observed between grain yield and 50% anthesis date (0.66) , plant height (2.05) , grain texture (0.36) and 100 kernel weight (0.24) . Phenotypic correlations ranged from -0.21 to 0.12 while genotypic correlations ranged from -0.15 to 2.05. Positive phenotypic correlations were observed between grain yield and plant height and between grain yield and texture (Table 54 and Fig. 29). Negative correlation were between grain yield and 50% anthesis date.

Table 54. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) for population CML444 x K64R conducted under high nitrogen conditions at Chitedze, Malawi in 2003 and 2004.**

	GYG-	AD	PН	TEX	GWT
GYG		0.66(0.82)	2.05(1.87)	0.36(1.87)	0.24(0.49)
AD	$-0.21(0.08)$		$-0.05(0.08)$	0.25(0.29)	0.34(0.27)
PН	0.41(0.07)	$-0.05(0.03)$		0.17(0.22)	0.32(0.22)
TEX	0.20(0.08)	$-0.01(0.8)$	0.04(0.08)		0.23(0.27)
GWT	0.11(0.08)	0.12(0.08)	0.08(0.08)	0.002(0.08)	

GYG, grain yield; AD, 50% anthesis; PH, plant height; TEX, grain texture; GWT, 100 kernel weight

Fig. 29. Single value decomposition biplot of standardized traits showing their correlations forpopulation CML444 x K64R conducted under high nitrogen conditions at Chitedze, Malawi during 2003 and 2004. (AD; 50% anthesis; GYG, grain yield; PH, plant height; GWT, 100 kernel weight; TEX, grain texture).

This experiment was conducted under rain fed conditions in Harare (Zimbabwe) during the 2003/2004 season. The experiment was fertilized with 120 kg N ha⁻¹ and 60 kg P₂O₅ ha⁻¹. Average grain yield was 9.64 Mg ha⁻¹ (range 4.75 to 12.85 Mg ha⁻¹) (Table 55). Significant differences were observed for grain yield, 50% anthesis date and moisture content. Heritabilities were moderate for grain yield (0.49), 0.60 for 50% anthesis date, 0.16 for anthesis-silking interval, 0.23 for plant height and 0.29 for moisture content (Table 55).

Table 55. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML444 x K64R evaluated under high nitrogen fertilization in Harare (Zimbabwe) in 2003 and 2004.

Statistics	GYG	AD	ASI	PH	MOI
	Mg ha ⁻¹	d	d	cm	$\frac{0}{0}$
Mean	9.64	72.8	0.71	270.7	14.7
Significance	***	***	NS	NS	***
Minimum	4.75	68.7	-2.80	232.0	13.3
Maximum	12.91	75.2	2.50	299.5	16.6
LSD(5%)	2.52	2.48	2.43	33.3	1.85
CV(%)	12.85	1.70	169.0	5.92	6.38
MSE	1.54	1.54	1.40	256.4	0.90
Mean (Ent. 1-50)	9.70	72.5	0.81	273.1	14.6
Mean (Ent. 51-100)	9.60	73.0	0.62	268.3	14.8
$\sigma_{\rm e}^2$ $\sigma_{\rm g}^2$ h^2	1.70	1.57	1.54	256.4	0.88
	0.81	1.17	0.15	38.6	0.18
(family basis)	0.49	0.60	0.16	0.23	0.29
Standard Error h^2	0.10	0.09	0.17	0.17	0.14

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; MOI, grain moisture content.

Genotypic correlations were positive but weak between grain yield and 50% anthesis date and moisture content (Table 56 and Fig. 30). Correlation between 50% anthesis date and moisture content was negative. Phenotypic correlations between the traits were also weak ranging from 0.01 to 0.03.

Table 56. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) from population CML444 x K64R conducted under high nitrogen conditions in Harare, Zimbabwe in 2003 and 2004.**

GYG, grain yield; AD, 50% anthesis; MOI, grain moisture content.

Fig. 30. Single value decomposition biplot of standardized traits showing their correlations for population CML444 x K64R evaluated under high nitrogen conditions in Harare, Zimbabwe during 2003 and 2004. (AD; 50% anthesis; GYG, grain yield; MOI, moisture content).

Chitala well-watered experiment

This experiment was conducted under well-watered conditions at Chitala (Malawi) during the dry season under irrigation in 2004. Water was applied to the experiment using sprinkler irrigation to field capacity from planting up to physiological maturity. The trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. There were no significant differences for all the traits. Mean grain yield was 4.66 Mg ha⁻¹ and ranged from 2.89 to 6.56 Mg ha⁻¹. Heritabilities ranged from 0.00 to 0.08 (Table 57).

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; TEX, grain texture; MOI, grain moisture content.

Genotypic correlations were not estimated because the non significance differences of the traits. Phenotypic correlations were estimated using single value decomposition biplot of standardized traits. Positive correlations were observed between grain yield and ears per plant while negative correlation was between grain yield and anthesis date (Fig. 31).

 Fig. 31. Single value decomposition biplot of standardized traits showing correlations for population CML444 x K64R evaluated under well-watered conditions at Chitala, Malawi in 2004. (AD; 50% anthesis; ASI, anthesis-silking interval; GYG, grain yield; PH, plant height; EPP, ears per plant; MOI, moisture content).

Chiredzi well-watered experiment

This experiment was conducted under well-watered conditions at Chiredzi (Zimbabwe) during the dry season under irrigation in 2004. Water was applied to the experiment to field capacity from planting up to physiological maturity. The trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. Grain yields ranged from 2.84 to 6.68 Mg ha⁻¹ with a mean of $5.15 \text{ Mg } \text{ha}^{-1}$. No significant differences were observed for any trait. Similarly, the mean of the first 50 testcrosses was so not significantly different from the mean of the other 50 testcrosses. Most of the traits had 0.00 heritability estimates except for anthesis date (0.09) and moisture content (0.03) (Table 58).

Genotypic correlations were not estimated due to the non significance differences of any trait. However, phenotypic correlations were estimated using single value decomposition biplot of standardized traits. Positive correlations were between grain yield, plant height and ears per plant but these had a negative correlation with anthesis-silking interval, 50% anthesis date, moisture content and leaf senescence (Fig 32).

watel ed conditions at Chiledzi, Zhinbabwe in 2004.							
Statistics	GYG	AD	ASI	PH	EPP	MOI	SEN
	Mg ha ⁻¹	d	d	cm	#	$\%$	$\frac{0}{0}$
Mean	5.15	102.3	0.66	240.0	1.10	9.00	72.5
Significance	NS	NS.	NS	NS	NS	NS	NS
Minimum	2.84	97.3	-1.83	182.0	0.60	8.00	61.0
Maximum	6.68	103.3	4.12	295.0	1.30	11.0	85.3
LSD(5%)	1.76	14.3	3.08	52.2	0.30	1.35	11.1
CV(%)	19.4	2.06	63.4	9.64	89.1	7.80	7.66
MSE	0.99	4.43	2.61	535.3	0.01	0.47	30.9
Mean (Ent. 1-50)	5.10	71.2	1.10	250.0	0.94	8.90	72.1
Mean (Ent. $51-100$)	5.20	70.9	1.10	249.0	0.96	8.90	72.8
σ_{c}^{2} e	0.90	4.43	2.44	535.3	0.02	0.47	30.9
	0.00	0.21	0.00	0.00	0.00	0.01	0.00
h ² (family basis)	0.00	0.09	0.00	0.00	0.00	0.03	0.00

Table 58. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML444 x K64R evaluated under wellwatered conditions at Chiredzi, Zimbabwe in 2004.

***,**,* Significant at $P < 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

Standard Error *h²*

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content; SEN, leaf senescence.

0.00 0.20 0.00 0.00 0.00 0.21 0.00

Fig. 32. Single value decomposition biplot of standardized traits showing their correlations for population CML444 x K64R conducted under well-watered conditions at Chiredzi, Zimbabwe in 2004. (GYG, grain yield; AD; 50% anthesis; ASI, anthesis-silking interval; GYG, grain yield; PH, plant height; EPP, ears per plant; MOI, moisture content; SEN, leaf senescence).
Chitala drought experiment

The experiment was conducted during the dry season of 2004 at Chitala Experimental Station (Malawi). Sprinkler irrigation was applied to the experiment up to field capacity from planting until three weeks before flowering. The intention was to induce drought stress during the flowering period. Average grain yield was $1.84 \text{ Mg} \text{ ha}^{-1}$ and range was from 0.62 to 3.26 Mg ha⁻¹. Significant differences were observed for grain yield only but not for any other trait (Table 59). Estimates of heritabilities were low or zero (Table 59). Heritability for grain yield was 0.28.

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; TEX, grain texture; MOI, grain moisture content.

Grain yield had a positive phenotypic correlation with plant height and grain texture, and negative correlations were between grain yield and anthesis-silking interval and between grain yield and 50% anthesis date (Fig. 33).

Fig. 33. Single value decomposition biplot of standardized traits showing their correlations for population CML444 x K64R evaluated under drought conditions at Chitala, Malawi in 2004. (GYG, grain yield; AD; 50%anthesis date; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; TEX, grain texture; MOI, moisture content).

Chiredzi drought experiment

The experiment was conducted during the dry season of 2004 at Chiredzi Experimental Station (Zimbabwe). Water was applied to the experiment up to field capacity from planting until three weeks before flowering. Despite that nitrogen fertilizers were applied to this experiment, the general performance was poor because of inherent low fertility of the experimental site. Grain yield average was $0.20 \text{ Mg} \text{ ha}^{-1}$ with a range from 0.00 to 1.04 Mg ha⁻¹ (Table 60). Heritabilities were moderately high ranging from 0.13 to 0.63 (Table 60). Heritability for grain yield was 0.52, 0.63 for anthesis date, 0.52 for anthesissilking interval, 0.48 for plant height, 0.50 for ears per plant, and 0.13 for leaf senescence.

Table 60. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML444 x K64R evaluated under drought conditions at Chiredzi, Zimbabwe in 2004.

Statistics	GYG	AD	ASI	PH	EPP	SEN
	Mg ha ⁻¹	d	d	cm	#	$\%$
Mean	0.20	104.3	8.80	156.0	0.20	63.3
Significance	***	***	***	***	***	NS
Minimum	0.00	98.0	0.30	80.0	0.00	51.2
Maximum	1.04	111.0	22.5	179.0	0.60	82.0
LSD(5%)	0.32	4.20	7.40	26.0	0.25	15.4
CV(%)	99.3	2.06	17.6	8.43	70.7	6.20
MSE	0.03	4.60	2.40	140.8	0.02	52.7
Mean (Ent. 1-50)	0.20	104.0	9.20	159.0	62.8	52.7
Mean (Ent. 51-100)	0.20	104.0	8.40	154.0	63.7	62.9
$\sigma_{\rm e}^2$ $\sigma_{\rm q}^2$	0.03	4.42	2.44	141.1	0.02	53.3
	0.02	3.90	8.95	65.3	0.01	4.04
h^2 (family basis)	0.52	0.63	0.52	0.48	0.50	0.13
Standard Error h^2	0.11	0.08	0.36	0.12	0.11	0.20

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking; PH, plant height; EPP, ears per plant; SEN, leaf senescence.

Positive genotypic and phenotypic correlations were observed between grain yield and ears per plant (0.96 and 0.84 respectively) (Table 61 and Fig. 34). Grain yield was both negatively correlated with 50% anthesis date and anthesis-silking interval. Phenotypic correlations were generally smaller than genotypic correlations but they both agreed on sign.

Table 61. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) from population CML444 x K64R conducted under drought conditions at Chiredzi, Zimbabwe in 2004.**

	GYG	AD	ASI	PН	EPP
GYG		$-0.96(0.16)$	$-2.06(7.85)$	0.23(0.23)	0.96(0.06)
AD	$-0.39(0.07)$		0.07(0.43)	$-0.62(0.18)$	$-0.95(0.17)$
ASI	$-0.45(0.10)$	$-0.21(0.17)$		$-0.11(0.37)$	0.32(0.14)
PH	0.27(0.08)	$-0.31(0.07)$	0.09(0.20)		0.34(0.14)
EPP	0.84(0.02)	$-0.36(0.07)$	0.28(29.59)	0.28(29.59)	

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH; plant height; EPP, ears per plant.

Fig. 34. Single value decomposition biplot of standardized traits showing their correlations for population CML444 x K64R evaluated under drought conditions at Chiredzi, Zimbabwe in 2004. (AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; GYG, grain yield; EPP, ears per plant).

Results across environments

Across all environments significant for grain yield

The analysis across environments was conducted for those environments that had significant differences for grain yield in this population. These were no nitrogen fertilization (Chitedze), low nitrogen (Harare), high nitrogen (Chitedze and Harare) and drought (Chitala and Chiredzi).

Significant differences were observed for grain yield, 50% anthesis date, anthesis-silking interval and ears per plant but not for plant height, grain moisture and 100 kernel weight. Average grain yield was 3.82 Mg ha⁻¹. Grain yield, 50% anthesis date, ears per plant, and 100 kernel weight had moderate to high heritability estimates (0.46, 0.36, 0.48 and 0.51, respectively) (Table 62).

Table 62. Statistics, averages, variance components, heritability and its standard error for experiment CML444 x K64R across all environments with significant differences for grain yield in Malawi and Zimbabwe in 2003 and 2004.

Statistics	GYG	AD	ASI	PН	EPP	TEX	MOI	GWT
	Mg ha ⁻¹	d	d	cm	#	1-5	$\frac{0}{0}$	g
Mean	3.82	80.46	2.30	204.38	0.66	3.57	14.26	37.58
Significance	***	***	***	NS	***	***	NS	NS
$CV\%$	27.42	5.42	89.24	29.12	35.91	13.63	9.01	18.90
	0.87	17.32	4.58	3302.45	0.04	0.22	1.81	32.87
	0.09	0.83	0.17	57.66	0.003	0.02	0.00	3.44
$\begin{array}{l} \sigma_{e}^{2} \\ \sigma_{g}^{2} \\ \sigma_{GxE}^{2} \end{array}$	0.18	0.47	0.04	0.00	0.00	0.04	1.16	2.04
h^2 (family basis)	0.46	0.36	0.30	0.17	0.48	0.38	0.00	0.51
Standard Error h^2	0.09	0.11	0.12	0.14	0.09	0.19	0.00	0.11

***,**,* Significant at $P \le 0.001$, 0.01, and 0.05, respectively.

GYG, grain yield; PH, plant height; AD, 50% anthesis; GWT, 100gwt, grain weight; EPP, ears per plant; ASI, anthesis-silking interval; MOI, grain moisture.

MSE, mean square error; h^2 , broad sense repeatability.

Positive genotypic and phenotypic correlations were observed between grain yield and ears per plant but grain yield was negatively correlated with anthesis-silking interval and 50% anthesis date. Phenotypic correlations for the other traits were negative and weak (Table 63).

Table 63. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) from population CML444 x K64R across environments significant for grain yield in Malawi and Zimbabwe in 2003 and 2004.**

	GYG	AD	ASI	EPP	TEX
GYG		$-0.21(0.28)$	$-0.31(0.30)$	0.55(0.25)	0.73(0.54)
AD	$-0.12(0.03)$		$-0.05(0.25)$	$-0.74(0.17)$	$-2.65(2.36)$
ASI	$-0.13(0.03)$	$-0.08(0.03)$		$-0.47(0.29)$	0.87(0.77)
EPP	0.44(0.03)	$-0.31(0.03)$	$-0.18(0.03)$		0.83(0.58)
TEX	0.19(0.04)	$-0.03(0.03)$	$-0.07(0.04)$	0.12(0.04)	

GYG, grain yield; AD, anthesis date; ASI, anthesis-silking interval; EPP, ears per plant; TEX, grain texture.

Across high N environments

Experiments which were conducted under high nitrogen fertilization environments in Malawi and Zimbabwe during 2003/2004 season were used in this analysis. Significant differences were observed for grain yield, 50% anthesis date, plant height and moisture content. Average grain yield was $7.42 \text{ Mg} \text{ ha}^{-1}$ (Table 64 and Appendix H). Heritability estimates were generally moderate or low. Heritability for grain yield was 0.32, 0.18 for anthesis date, 0.39 for plant height, 0.17 for moisture content, and 0.35 for 100 kernel weight.

Statistics	GYG	AD	ASI	PH	EPP	MOI	GWT
	Mg ha ⁻¹	d	d	cm	#	$\%$	g
Mean	7.42	74.8	0.60	239.4	0.91	14.5	42.1
Significance	***	***	NS	***	NS	\ast	NS
$CV\%$	17.89	2.60	205.7	5.88	37.1	6.07	13.6
	0.77	3.20	1.48	167.0	0.11	0.77	21.3
	0.44	0.44	0.00	52.5	0.00	0.08	5.78
$\sigma_{\rm g}^2$ $\sigma_{\rm g}^2$ $\sigma_{\rm GxE}^2$	0.10	0.91	0.10	0.00	0.00	0.00	0.19
h^2 (family basis)	0.32	0.18	0.00	0.39	0.00	0.17	0.35
Standard Error h^2	0.08	0.11	0.00	0.07	0.00	0.08	0.14

Table 64. Statistics, averages, variance components, heritability and its standard error for experiment CML444 x K64R across high N conditions in Malawi and Zimbabwe in 2003 and 2004.

***,**,* Significant at $P \le 0.001$, 0.01, and 0.05, respectively.

GYG, grain yield; PH, plant height; AD, 50% anthesis; GWT, 100 kenrel weight; EPP, ears per plant; ASI, anthesis-silking interval; MOI, grain moisture; MSE, mean square error; *h²* , broad sense repeatability.

Across drought environments

No significant differences across drought stressed environments were observed for all the traits except for anthesis-silking interval (Table 65 and Appendix I). Heritability estimates ranged from 0.00 to 0.19. Mean grain yield was 1.00 Mg ha⁻¹.

Table 65. Statistics, averages, variance components, heritability and its standard error for experiment CML444 x K64R across drought environments in Malawi and Zimbabwe in 2003 and 2004.

Statistics	GYG	AD	ASI	PH	EPP	MOI
	Mg ha ⁻¹			cm	#	$\frac{0}{0}$
Mean	1.00	92.2	5.44	161.5	0.37	16.7
Significance	NS	NS	*	NS	NS	NS
CV	82.5	7.60	65.1	16.5	63.4	14.4
	0.19	44.5	12.0	205.7	0.02	7.05
	0.00	0.00	1.44	0.00	0.001	0.00
$\sigma_{\rm g}^2$ $\sigma_{\rm g}^2$ $\sigma_{\rm GxE}^2$	0.06	1.93	0.00	54.1	0.004	0.00
(family basis)	0.00	0.00	0.19	0.00	0.04	0.00
Standard Error h^2	0.00	0.00	0.13	0.00	0.14	0.00
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***,**,* Significant at $P < 0.001$, 0.01, and 0.05, respectively.

GYG, grain yield; PH, plant height; AD, 50% anthesis; EPP, ears per plant; ASI, anthesis-silking interval; MOI, grain moisture; MSE, mean square error; h^2 , broad sense repeatability.

Correlations among traits across environments and stresses

Across all environments

Positive correlations were observed between grain yield and plant height and ears per plant. Negative correlations were observed between anthesis-silking interval and ears per plant and between 50% anthesis date and grain yield (Fig. 35).

Fig. 35. Single value decomposition biplot of standardized traits showing their correlations for population CML444 x K64R evaluated across all environments in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis date; ASI, anthesis-silking interval; plant;PH, plant height; EPP, ears per plant; MOI, moisture content; TEX, grain texture; GWT, 100 kernel weight).

Across high N environments

There were positive correlations between grain yield and plant height and between 50% anthesis date and 100 kernel weight but these were negatively correlated with anthesissilking interval (Fig. 36).

Fig. 36. Single value decomposition biplot of standardized traits showing their correlations for population CML444 x K64R evaluated across high nitrogen environments in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; EPP, ears per; plant; PH, plant height; MOI, moisture content; GWT, 100 kernel weight; TEX, grain texture).

Across drought environments

Grain yield was positively correlated with ears per plant and plant height. Negative correlations were observed between 50% anthesis date and 100 kernel weight, between grain yield and anthesis-silking interval and between plant height and anthesis-silking interval (Fig. 37).

Fig. 37. Single value decomposition biplot of standardized traits showing their correlations from for population CML444 x K64R evaluated across drought environments in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; EPP, ears per; plant; PH, plant height; GWT, 100 kernel weight).

The AMMI biplot for grain yield showed that both in Malawi and Zimbabwe drought conditions discriminated the testcrosses equally. High nitrogen environments in Malawi and Zimbabwe and the no nitrogen fertilization in Malawi were another group of similar environments while low nitrogen and well-watered environments in Zimbabwe also discriminated testcrosses in similar manner (Fig. 38). The biplot also showed that the high nitrogen environments were completely different from the drought environments.

Fig. 38. AMMI biplot for grain yield showing the relationship among environments for experiment CML444 x K64R evaluated across all environments in Malawi and Zimbabwe in 2003 and 2004. (LN, low nitrogen; WW MLW, well-watered Malawi; WW ZM, well-watered Zimbabwe, NF, no nitrogen fertilization; DRT MLW, drought Malawi; DRT ZM, drought Zimbabwe; HN MLW, high nitrogen Malawi; HN ZM, high nitrogen Zimbabwe).

Expected genetic gain from direct selection was estimated using heritabilities and genetic variance for individual environments (Table 66). Gains for indirect selection were not estimated because most correlation coefficients between environments were not estimable. The results from this study indicate that genetic gains were variable across locations and environments. The highest genetic gains were observed for Harare high nitrogen (1.10 Mg ha⁻¹) and Chitedze no nitrogen fertilization (0.62 Mg ha⁻¹) environments and the lowest genetic gains were for well-watered conditions (0.00) (Table 66).

 h^2 , broad sense repeatability.

Expected genetic gain across environments was $0.29 \text{ Mg} \text{ ha}^{-1}$ while the high nitrogen environment resulted in the highest genetic gain of 0.66 Mg ha⁻¹ (Table 67).

Table 67. Expected genetic gain for grain yield (Mg ha-1) across environments for experiment CML444 x K64R conducted in Malawi and Zimbabwe in 2003 and 2004 assuming selection of the best 10%.

Environment	Mean	Error	Gen. variance	GxE variance	h ²	Genetic Gain (R)
Across all environments	4.09	0.88	0.06	0.26	0.45	0.29
Across high N	7.42	0.77	0.44	0.00	0.32	0.66
Across well-watered	4.9	0.85	0.00	0.00	0.00	0.00
Across drought	.00	0.19	0.00	0.02	0.00	0.00

 h^2 , broad sense repeatability.

Preliminary assessment of MAS efficiency in testcrosses

There were no significant differences for the means of the best 50 testcrosses selected for favorable alleles at consistent QTL and the mean of the worst 50 testcrosses selected for unfavorable alleles at the same QTL either within environments or across environments (Table 68).

Table 68. Mean grain yield, for the first and last 50 entries, their significances at single and across environments for population experiment CML444 x K64R conducted in Malawi and Zimbabwe in 2003 and 2004.

Environment	Mean (ent. $1-50$) $(Mg ha^{-1})$	Mean $(Ent. 51-100)$ $(Mg ha^{-1})$	Difference	Significance
Chitedze no fertilization	5.42	5.22	0.20	NS
Harare low N	0.82	0.92	-0.10	NS
Chitedze high N	5.12	5.22	-0.10	NS
Harare high N	9.70	9.60	0.10	NS
Chitala well-watered	4.68	4.64	0.04	NS
Chiredzi well-watered	5.10	5.20	-0.10	NS
Chitala drought	1.90	1.80	0.10	NS
Chiredzi drought	0.20	0.20	0	NS
Average across locations	4.11	4.06	0.05	NS
Average High N	7.47	7.38	0.09	NS
Average Well-watered	4.88	4.92	-0.04	NS
Average Drought	1.01	0.99	0.02	NS

Top five entries for grain yield were selected for each environment by ranking the testcrosses from the highest to the lowest yielding genotype. The results showed that both groups of testcrosses contributed to the list of five most high yielding testcrosses although more testcrosses came from the group that was selected for less favorable alleles (Table 69). Some consistent performance was observed for some testcrosses. For example entries 46, 29 and 96 were among the top 5 high yielding testcrosses under all the two well-watered environments.

Table 69. Top yielding 5 entries for grain yield at single environment and across environments for population CML444 x K64R evaluated in Malawi and Zimbabwe in 2003 and 2004.

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In order to identify testcrosses that reduce their performances less under stressed conditions relative to unstressed conditions at the same locations, drought tolerance index (DIT) and nitrogen tolerance index (NTI) were estimated. Testcrosses that maintain good performance under stress are good sources of drought and low nitrogen tolerant genes. The testcrosses with the best DTI and NTI indices came from both groups (Table 70). The average DTI of the first and last 50 entries were 50.7% and 60.6% in Malawi, and 95.5% and 96.2% in Zimbabwe, respectively (Appendix O). The average NTI for the first and last 50 entries was 91.4% and 90.3%, respectively in Zimbabwe.

Table 70. Best 5 testcrosses for drought tolerance index (DTI) and nitrogen tolerance index (NTI) for population CML444 x K64R evaluated in Malawi and Zimbabwe in 2003 and 2004.

Population CML312/NAW

Results per environment

Chitedze no nitrogen fertilization

This experiment was conducted under no nitrogen fertilization and rain fed conditions at Chitedze Research Station (Malawi) during the 2003 and 2004 season. The purpose was to induce low N stress, however, the nitrogen content in the soil was higher than expected and no stress was apparent. Grain yield average was 5.47 Mg ha^{-1} (range 2.98) to 9.38 Mg ha-1) (Table 71). Significant differences were observed for grain yield, anthesis date, ears per plant and moisture content but not for anthesis-silking interval, grain texture and plant height (Table 71). Heritability estimates were 0.18, 0.17, 0.21, 0.06, 0.15, 0.16 and 0.24 for grain yield, anthesis date, anthesis-silking interval, plant height, ears per plant, gain texture and moisture content, respectively. Average grain yield for the first 50 testcrosses was not significantly greater than the average for the last 50 testcrosses (Table 71).

Grain yield had a positive genotypic correlation with ears per plant while moisture content was positively correlated with 50% anthesis date (Table 72). Phenotypic correlations were positive between grain yield and 50% anthesis date. Moisture content had also positive correlations with 50% anthesis date (Table 72 and Fig. 39).

Table 71. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML312 x NAW evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004.

Statistics	$\mathrm{GYG}^{\$}$	AD	ASI	PH	EPP	TEX	MOI
	Mg ha ⁻¹	d	d	cm	#	$1-5$	$\%$
Mean	5.47	72.4	1.00	252.0	0.90	2.90	14.5
Significance	**	*	NS	NS.	\ast	NS	*
Minimum	2.98	64.3	-0.50	135.0	0.70	2.00	7.00
Maximum	9.38	77.2	3.50	273.0	1.30	4.00	16.7
LSD(5%)	2.63	10.2	1.72	43.0	0.23	0.90	2.48
CV(%)	24.8	7.10	87.5	8.32	1.28	15.3	8.14
MSE	1.86	26.4	0.77	439.1	0.01	0.19	1.39
Mean (Ent. 1-50)	5.55	72.2	1.00	252.0	0.97	2.90	14.5
Mean $(Ent. 51-100)$	5.38	72.5	1.00	251.0	0.95	3.00	14.4
σ_{c}^{2} e σ_{G}^{2}	1.87	26.4	0.70	440.2	0.02	0.22	1.95
	0.20	2.75	0.09	13.2	0.002	0.02	0.30
h^2 (family basis)	0.18	0.17	0.21	0.06	0.15	0.16	0.24
Standard Error h^2 about the charter also starts \cdot \sim \sim \sim \sim	0.18 0.001001	0.17 1.0.05	0.16	0.21 1.3.70	0.18	0.17 \cdot \sim	0.17

***,**,* Significant at $P < 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content; TEX, grain texture.

Table 72. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) for population CML312 x NAW evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004.**

GYG, grain yield; AD, 50% anthesis; EPP, ears per plant; MOI, moisture content.

Fig. 39. Single value decomposition biplot of standardized traits showing their correlations for population CML312 x NAW evaluated under no nitrogen fertilization at Chitedze, Malawi in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; TEX, grain texture; GWT, 100 kernel weight; MOI, moisture content).

Harare low nitrogen

This experiment was conducted under low nitrogen conditions in Harare (Zimbabwe) under rainfed conditions during the 2003/2004 season. The trial did not receive any nitrogen fertilization, just 60 kg ha⁻¹ of P_2O_5 . There were significant differences for all the traits except ears per plant and moisture content (Table 73). Mean values of the best 50 genotypes were significantly higher than the mean of the 50 worst genotypes. Grain yield, and plant height had moderate heritabilities of 0.38 and 0.49, respectively, while anthesis date was low (0.22) and the other traits were 0.00.

Statistics	GYG	AD	ASI	PH	EPP	MOI
	Mg ha ⁻¹	d	d	cm	#	$\%$
Mean	1.75	79.4	1.73	232.1	0.91	9.46
Significance	**	$***$	\ast	$***$	NS	NS
Minimum	0.47	74.2	-1.63	199.2	0.43	7.44
Maximum	3.24	85.4	5.23	295.8	1.60	11.1
LSD(5%)	1.27	4.52	3.00	32.6	1.70	2.45
CV(%)	87.5	2.90	91.1	7.00	92.9	11.0
MSE	0.44	5.63	2.43	169.18	0.74	0.98
Mean (Ent. 1-50)	1.84	79.4	1.60	264.0	1.00	9.50
Mean (Ent. 51-100)	1.64	79.4	1.90	262.0	0.80	9.40
σ_{c}^{2} σ_{G}^{2}	0.44	5.34	2.27	154.8	0.73	0.87
	0.13	0.75	0.00	52.1	0.00	0.00
h^2 (family basis)	0.38	0.22	0.00	0.40	0.00	0.00
Standard Error h^2	0.13	0.17	0.00	0.13	0.00	0.00

Table 73. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML312 x NAW evaluated under low nitrogen at Harare, Zimbabwe in 2003 and 2004.

***,**,* Significant at $P < 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, moisture content.

Plant height had positive genotypic correlations with grain yield while grain yield was also positively correlated with moisture content (Table 74 and Fig. 40). Negative phenotypic correlations were observed between grain yield and anthesis date and between plant height and anthesis-silking interval. Grain yield and plant height were positively correlated.

Table 74. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) for population CML312 x NAW conducted under low nitrogen conditions in Harare, Zimbabwe during 2003 and 2004.**

GYG, grain yield; AD, 50% anthesis; PH, plant height.

Fig. 40. Single value decomposition biplot of standardized traits showing their correlations for population CML312 x NAW evaluated under low nitrogen fertilization in Harare, Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, moisture content).

Chitedze high nitrogen

This experiment was conducted at Chitedze Research Station during the 2003/2004 season under rainfed conditions. This trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha^{-1} P_2O_5 . The testcrosses were significantly different for grain yield and grain texture only but not for the other traits (Table 75). No significance differences were observed between the means of the first 50 testcrosses and the mean of the second 50 testcrosses. Grain texture had the highest heritability estimate of 0.82, 0.31 for grain yield, 0.19 for

plant height, 0.14 for 50% anthesis date while the other traits had 0.00 heritability estimates. Grain yield averaged $4.54 \text{ Mg} \text{ ha}^{-1}$ and had a range of 1.97 to 7.33 Mg ha⁻¹.

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; RL, root lodging; EPP, ears per plant; MOI, grain moisture content; TEX, grain texture.

Only weak negative genotypic and positive phenotypic correlations were observed between grain yield and grain texture (-0.04 and 0.04, respectively) (Fig. 41).

Fig. 41. Single value decomposition biplot of standardized traits showing their correlations for population CML312 x NAW evaluated under high nitrogen conditions at Chitedze, Malawi during 2003 and 2004. (GYG, grain yield AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; TEX, grain texture; GWT, 100 kernel weight).

Harare high nitrogen

This experiment was conducted in Harare (Zimbabwe) under rainfed conditions during the 2003/2004 season. The trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. Differences among testcrosses were significant for 50% anthesis date, anthesis-silking interval and plant height (Table 76). Grain yield average was 8.74 Mg ha⁻¹ with a range of 5.30 to 11.20 Mg ha⁻¹. All traits with significant differences had a range of heritability estimates from 0.33 to 0.69. Heritability estimates were 0.51 for 50% anthesis date, 0.22 for anthesis-silking interval, 0.20 for grain yield and 0.05 for plant height. Moisture content had 0.00 heritability estimates (Table 76).

Table 76. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML312 x NAW evaluated under high nitrogen fertilization at Harare, Zimbabwe in 2003 and 2004.

Statistics	GYG	AD	ASI	PH	MOI
	Mg ha ⁻¹	d	d	cm	$\%$
Mean	8.74	71.4	1.26	275.6	14.0
Significance	NS	***	\ast	\ast	NS
Minimum	5.30	68.2	-1.52	244.1	11.1
Maximum	11.2	74.6	3.66	295.3	15.5
LSD(5%)	2.92	3.03	2.00	24.3	2.30
CV(%)	17.6	2.21	73.8	5.20	7.70
MSE	2.36	2.50	0.86	204.0	1.15
Mean (Ent. 1-50)	8.50	71.2	1.20	275.0	13.9
Mean (Ent. 51-100)	8.90	71.5	1.30	277.0	13.9
	2.26	2.17	0.98	175.1	1.29
$\sigma_{\rm c}^2$ $\sigma_{\rm c}^2$	0.29	1.12	0.14	5.06	0.00
h^2 (family basis)	0.20	0.51	0.22	0.05	0.00
Standard Error h^2	0.16	0.10	0.18	0.20	0.00

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; MOI, grain moisture content.

Negative phenotypic correlations were observed between 50% anthesis date and anthesis-silking interval and between 50% anthesis date and plant height (Table 77). Positive correlation was observed between grain yield and plant height. (Table 77 and Fig. 42).

Table 77. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) from population CML312 x NAW conducted under high nitrogen conditions at Harare, Zimbabwe during 2003 and 2004.**

	AD	ASI	PН
AD		$-1.03(0.29)$	0.32(0.72)
ASI	$-0.49(0.60)$		$-0.38(0.93)$
PН	$-0.02(0.08)$	0.07(0.08)	

AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height.

Fig. 42. Single value decomposition biplot of standardized traits showing their correlations for population CML312 x NAW evaluated under high nitrogen conditions in Harare, Zimbabwe during 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; PH, plant height; ASI, anthesis silking interval; MOI, moisture content).

Chitala well-watered experiment

This experiment was conducted under irrigated conditions at Chitala Experimental Station (Malawi) during the dry season in 2004. Water was applied to the experiment to field capacity from planting up to physiological maturity. The trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. Grain yield, anthesis-silking interval, plant height and ears per plant had significant differences among the testcrosses (Table 78). Heritabilities were low for all the traits: 0.17 for grain yield, 0.24 for anthesis-silking interval, 0.22 for plant height, 0.01 for moisture content while the rest of the traits had 0.00 heritability estimates. The mean of the first and last 50 testcrosses were not significantly different from each other. Average grain yield was $3.90 \text{ Mg} \text{ ha}^{-1}$ while the range was 1.28 to 6.03 Mg ha⁻¹ (Table 78).

Table 78. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML312 x NAW evaluated under wellwatered conditions at Chitala, Malawi in 2004.

Statistics	GYG	AD	ASI	PH	EPP	TEX	MOI
	Mg ha ⁻¹	d	d	cm	#	$1-5$	$\%$
Mean	3.90	79.6	2.71	202.6	0.66	2.69	13.9
Significance	$***$	NS	*	***	**	NS	NS
Minimum	1.28	76.3	0.86	128.6	0.21	1.95	10.9
Maximum	6.03	84.7	6.71	232,1	9.70	3.50	16.8
LSD(5%)	1.94	3.77	2.35	25.1	0.30	1.07	3.00
CV(%)	24.6	2.40	47.9	6.40	31.6	20.2	9.80
MSE	0.92	3.81	1.70	168.1	0.04	0.30	1.84
Mean (Ent. 1-50)	3.90	79.6	2.80	204.0	0.70	2.70	13.9
Mean (Ent. 51-100)	3.90	79.6	2.60	201.0	0.70	2.70	13.9
$\sigma_{\rm c}^2$ $\sigma_{\rm G}^2$	0.92	3.22	1.40	168.0	0.03	0.28	2.03
	0.09	0.00	0.22	23.9	0.00	0.00	0.01
(family basis) h^2	0.17	0.00	0.24	0.22	0.00	0.00	0.01
Standard Error h^2	0.19	0.00	0.17	0.19	0.00	0.00	0.25

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content; TEX, grain texture.

Grain yield had positive genotypic correlations with plant height and negative correlation with anthesis-silking interval (Table 79). Most phenotypic correlations amongst the traits were positive but in low magnitude (Table 79 and Fig. 43).

Table 79. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) from population CML312 x NAW conducted under well-watered conditions at Chitala, Malawi in 2004.**

GYG, grain yield; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant.

Fig. 43. Single value decomposition biplot of standardized traits showing their correlations for population CML312 x NAW evaluated under well-watered conditions at Chitala, Malawi in 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content, TEX, grain texture.

Chiredzi well-watered

This experiment was conducted under well-watered conditions at Chiredzi, Zimbabwe during the dry season under irrigation in 2004. Water was applied to the experiment to field capacity from planting up to physiological maturity. The trial was fertilized with 120 kg N ha⁻¹ and 60 kg ha⁻¹ P₂O₅. Mean grain yield was 6.06 Mg ha⁻¹, while the range was from 4.23 to 7.65 Mg ha⁻¹. No significant differences were observed for any trait and for the means of the first and last 50 testcrosses (Table 80). This was not expected as no apparent reason was observed that could increase the error or reduce genotypic variance.

Table 80. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML312 x NAW evaluated under wellwatered conditions at Chiredzi, Zimbabwe in 2004.

Statistics	GYG	AD	ASI	PH	EPP	MOI
	Mg ha ⁻¹	d	d	cm	#	$\frac{0}{0}$
Mean	6.06	101.0	0.75	256.2	0.95	9.65
Significance	NS	NS	NS	NS	NS	NS
Minimum	4.23	97.5	-1.91	217.6	0.69	7.88
Maximum	7.65	103.4	2.59	286.3	1.17	12.6
LSD(5%)	2.08	2.44	2.38	39.0	0.26	2.17
CV(%)	17.3	0.50	0.70	6.81	15.5	11.0
MSE	1.09	1.39	1.29	304.1	0.02	1.13
Mean (Ent. 1-50)	6.00	100.9	0.80	257.0	0.93	9.67
Mean (Ent. 51-100)	6.10	101.1	0.70	256.0	0.96	9.64
$\sigma_{\rm e}^2$	1.07	1.40	1.39	304.1	0.02	1.12
	0.004	0.20	0.03	0.59	0.00	0.11
h^2 (family basis)	0.01	0.22	0.05	0.004	0.00	0.17
Standard Error h^2	0.21	0.17	0.20	0.23	0.00	0.18

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content.

Single value decomposition biplot of standardized traits was done to estimate phenotypic correlations among the traits. Strong phenotypic correlations were observed between grain yield and ears per plant, between plant height and anthesis-silking interval, and between moisture content and 50% anthesis (Fig. 44). The pairs of positive correlations were negatively correlated.

Fig. 44. Single value decomposition biplot of standardized traits showing their correlations for population CML312 x NAW conducted under well-watered conditions at Chiredzi, Zimbabwe in 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content).

Chitala drought experiment

The experiment was conducted during the dry season at Chitala Experimental Station (Malawi) in 2004. Water was applied to the experiment up to field capacity from planting until three weeks before flowering, when irrigation was withdrawn. The intention was to induce drought stress during the flowering period. No significant differences were observed for any trait (Table 81). All the traits had 0.00 heritability estimates due to the non significance of the traits and subsequent estimates for genotypic variance equal to 0.00. Grain yield averaged 1.29 Mg ha⁻¹ and ranged from 0.57 to 2.19 Mg ha⁻¹.

Statistics	GYG	AD	ASI	PH	EPP	TEX	MOI	GWT
	Mg ha ⁻¹	d	d	cm	#	$1-5$	$\frac{0}{0}$	g
Mean	1.29	80.7	3.83	175.3	0.52	2.55	20.1	35.2
Significance	NS	NS	NS	NS	NS	NS	NS	NS
Minimum	0.57	75.2	-1.40	50.7	0.08	1.44	13.5	24.6
Maximum	2.19	87.3	17.4	200.0	0.80	3.50	25.8	48.5
LSD(5%)	1.10	6.22	4.47	27.0	0.38	1.26	6.70	11.6
CV(%)	41.3	3.69	53.3	7.89	33.3	24.3	16.2	16.8
MSE	0.28	8.89	4.13	191.1	0.03	0.38	10.6	34.8
Mean (Ent. 1-50)	1.33	80.7	3.60	175.0	0.50	2.50	20.0	35.1
Mean (Ent. 51-100)	1.25	80.7	4.10	176.0	0.50	2.60	20.2	35.2
	0.25	8.89	6.23	191.1	0.02	0.33	9.59	31.3
σ_{c}^{2} e	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
h^2 (family basis)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Standard Error h^2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Table 81. Statistics, genotypic variance, heritability and their standard errors for traits in testcrosses from population CML312 x NAW evaluated under drought conditions at Chitala, Malawi in 2004.

***,**,* Significant at $P \le 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture content, TEX, grain texture.

Phenotypic correlations among traits were estimated using single value decomposition of standardized traits. Negative correlations were observed between grain yield and anthesis-silking interval, between ears per plant and 50% anthesis date, and between grain yield and 50% anthesis. Positive correlations were observed between grain yield and ears per plant and between 100 kernel weight and 50% anthesis date (Fig. 45).

Fig. 45. Single value decomposition biplot of standardized traits showing their correlations for population CML312 x NAW conducted under drought conditions at Chitala, Malawi in 2004. (GYG, grain yield, AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; SEN, leaf senescence; GWT, 100 kernel weight; TEX, grain texture; MOI, moisture content).

Chiredzi drought experiment

This experiment was conducted during the 2004 dry season at Chiredzi Experimental Station (Zimbabwe). Water was applied to the experiment up to field capacity from planting until three weeks before flowering when irrigation was withdrawn to induce drought stress during the flowering period. Despite that nitrogen fertilizer was applied, the general performance was poor because of inherent low fertility of the experimental site. Grain yields were very low with a mean of 0.20 Mg ha^{-1} (range was from 0.00 to 0.93 Mg ha⁻¹) (Table 82). Significance differences were observed for all traits. Estimates

of heritabilities were moderate ranging from 0.26 for grain yield and was the highest for anthesis date with 0.52. The mean of the best 50 and the mean of the worst 50 testcrosses were not significantly different.

***,**,* Significant at $P < 0.001$, 0.01 and 0.05, respectively, and NS = non significant.

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant.

Single value decomposition biplot of standardized traits showed grain yield was positively correlated with ears per plant and negatively correlated with anthesis-silking interval and 50% anthesis date (Fig. 46).

Fig. 46. Single value decomposition biplot of standardized traits showing their correlations for population CML312 x NAW evaluated under drought conditions at Chiredzi, Zimbabwe in 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant).

Results across environments

Across all environments significant for grain yield

The analysis across environments was conducted for those environments that had significant differences for grain yield in this population. These were no nitrogen fertilization (Chitedze), low nitrogen (Harare), high nitrogen (Chitedze), well-watered (Chitala) and drought (Chiredzi).

There were significant differences for grain yield, 50% anthesis date, plant height, moisture content and 100 kernel weight (Table 83). Average grain yield was 3.19 Mg ha⁻¹. Heritability estimates were generally low for all the traits with 0.04 for grain yield, 0.32 for 50% anthesis date, 0.04 for anthesis-silking interval, 0.27 for plant height, 0.45 for moisture content, 0.21 for grain texture, 0.37 for 100 kernel weight and 0.00 for ears per plant.

Table 83. Statistics, averages, variance components, heritability and its standard error for experiment CML312 x NAW across all environments with significant differences for grain yield in Malawi and Zimbabwe in 2003 and 2004.

***,**,* Significant at $P \le 0.001$, 0.01, and 0.05, respectively, NS = non-significant

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; TEX, grain texture; GWT, 100 kernel weight.

MSE, mean square error; h^2 , broad sense repeatability.

Positive genotypic correlations were observed between grain yield and plant height and between grain yield and 100 kernel weight while negative correlations were between grain yield and 50% anthesis date (Table 84).

Table 84. Genotypic (above diagonal) and phenotypic (below diagonal) correlations and their standard errors (*SE***) from population CML312 x NAW across environments significant for grain yield evaluated in Malawi and Zimbabwe in 2003 and 2004.**

	GYG	AD.	PН	MOI	GWT
GYG		0.21(0.93)	1.59(2.07)	$-1.94(3.73)$	5.63(106.9)
AD	$-0.07(0.03)$		0.05(0.40)	0.84(0.83)	$\overline{}$
PН	0.37(0.03)	0.19(0.03)		1.17(1.05)	0.67(0.57)
MOI	0.15(0.04)	0.38(0.03)	0.26(0.03)		$-0.45(0.83)$
GWT	0.27(0.03)	$\overline{}$	0.26(0.03)	0.22(0.04)	

GYG, grain yield; AD, 50% an thesis date; PH, plant height; MOI, moisture content; GWT, 100 kernel weight.

Across high N environments

Experiments conducted under high nitrogen environments in Malawi and Zimbabwe during the 2003/2004 were used in this analysis. Significant differences were observed for grain yield, 50% anthesis date and grain texture in analysis across optimal nitrogen fertilization under rain fed conditions in Malawi and Zimbabwe during the 2003/2004 season (Table 85 and Appendix K). Heritability estimates were 0.84 for grain texture, 0.46 for 100 kernel weight, and 0.28 for grain yield. The rest of traits including anthesissilking interval, ears per plant and moisture content had 0.00 heritability estimates.
Statistics	GYG	AD	ASI	PН	EPP	MOI	TEX	GWT
	Mg ha ⁻¹	d	d	cm	#	$\%$	1-5	g
Mean	6.62	75.6	0.99	249.6	0.66	14.8	3.06	41.6
Significance	**	**	NS	NS	NS	NS	***	NS
$CV\%$	21.1	2.32	128.2	6.20	28.2	6.20	7.80	11.1
	1.77	2.67	1.61	212.8	0.67	0.68	0.05	14.6
	0.19	0.06	0.00	13.7	0.00	0.00	0.10	3.10
σ_{e}^{2} σ_{g}^{2} σ_{GxE}^{2}	0.08	0.64	0.00	3.51	0.00	0.00	0.01	0.00
h^2 (family basis)	0.28	0.05	0.00	0.20	0.00	0.00	0.84	0.46
Standard Error h^2	0.15	0.20	0.00	0.17	0.00	0.00	0.04	0.11

Table 85. Statistics, averages, variance components, heritability and its standard error for experiment CML312 x NAW across high nitrogen conditions in Malawi and Zimbabwe in 2003 and 2004.

***,**,* Significant at $P < 0.001$, 0.01, and 0.05, respectively, NS = non-significant

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; TEX, grain texture; GWT, 100 kernel weight.

MSE, mean square error; h^2 , broad sense repeatability.

Across drought environments

This is a combined analysis of two experiments that were conducted under drought stress in Malawi and Zimbabwe in 2004. No significant differences were observed for all traits except anthesis-silking interval (Table 86 and Appendix L). Average grain yield was very low $(0.74 \text{ Mg ha}^{-1})$. In addition, heritabilities estimates ranged from 0.00 to 0.31.

Statistics	GYG	AD	ASI	PН	EPP	MOI	GWT
	Mg ha ⁻¹	d		cm	#	$\%$	g
Mean	0.74	91.3	4.06	180.0	0.32	20.2	35.3
Significance	NS	NS	**	NS	NS	NS	NS
CV	72.7	3.36	56.6	11.7	57.5	16.1	17.0
$\sigma_{\gamma^e}^2$	0.15	6.21	6.69	206.4	0.02	9.59	31.3
	0.001	0.17	0.75	14.0	0.001	0.00	0.00
σ_{GxE}^2	0.00	0.27	0.00	14.5	0.001	0.00	0.00
h^2 (family basis)	0.02	0.09	0.31	0.19	0.17	0.00	0.00
Standard Error h^2	0.18	0.21	0.17	0.19	0.19	0.00	0.00
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Table 86. Statistics, averages, variance components, heritability and its standard error for experiment CML312 x NAW across drought environments in Malawi and Zimbabwe in 2003 and 2004.

***,**,* Significant at $P \le 0.001$, 0.01, and 0.05, respectively, NS = non-significant

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; GWT, 100 kernel weight.

MSE, mean square error; h^2 , broad sense repeatability.

Correlations among traits across environments and stresses

Across all environments

Positive phenotypic correlations were observed between grain yield and ears per plant, 100 kernel weight and plant height across all stressed and non stressed environments (Fig. 47). Flowering time (50 % anthesis date) and grain moisture were also closely correlated. Anthesis-silking interval was negatively correlated with grain yield, plant height and 100 kernel weight.

Fig. 47. Single value decomposition biplot for different traits showing their correlations for for population CML312 x NAW evaluated across all environments in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; TEX, grain texture; GWT, 100 kernel weight).

Across high N environments

There were positive phenotypic corrections between grain yield and plant height, and 100 kernel weight and ears per plant. Negative correlation was observed between 50% anthesis date and anthesis-silking interval and between ears per plant and grain texture (Fig. 48).

Fig. 48. Single value decomposition biplot across high nitrogen environments for population CML312 x NAW evaluated in Malawi and Zimbabwe in 2003 and 2004. GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; TEX, grain texture; GWT, 100 kernel weight.

Correlations across drought environments

Positive correlations were observed between grain yield and plant height and ears per plant while 50% anthesis date was negatively correlated with plant height, grain yield and ears per plant (Fig. 49). Grain yield was negatively correlated with anthesis-silking interval and 50% anthesis date.

Fig. 49. Single value decomposition biplot for different traits showing their correlations for population CML312 x NAW evaluated across drought environments in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; TEX, grain texture; GWT, 100 kernel weight).

Relationships among environments for grain yield

The AMMI biplot for grain yield showed that in both Malawi and Zimbabwe, wellwatered environments discriminated the testcrosses equally. High nitrogen environments also classified the genotypes in a similar manner. However, drought environments in Malawi and Zimbabwe discriminated the genotypes differently. No nitrogen fertilization and low nitrogen environments were closely related to high nitrogen environments (Fig. 50 and Table 87).

- **Fig. 50. AMMI biplot for grain yield showing the relationship among environments for experiment CML312 x NAW evaluated in Malawi and Zimbabwe in 2003 and 2004. (ZMLN, Zimbabwe low nitrogen; MLWWW, well-watered Malawi; ZMWW, well-watered Zimbabwe, MLWNF, Malawi no nitrogen fertilization; MLWDRT, drought Malawi; ZMDRT, drought Zimbabwe; MLWHN, high nitrogen Malawi; ZMHN, high nitrogen Zimbabwe).**
- **Table 87. Genotypic (above diagonal) and phenotypic (below diagonal) correlations among environments and their standard errors (***SE***) for population CML312 x NAW evaluated in Malawi and Zimbabwe in 2003 and 2004.**

ZMLN, Zimbabwe low nitrogen; MLWWW, well-watered Malawi; MLWNF, Malawi no nitrogen fertilization; ZMDRT, drought Zimbabwe; MLWHN, high nitrogen Malawi.
No estimable because one or the two traits were non significant at any environment

Expected genetic gain

Estimates of heritabilities and genetic variances were used to compute genetic gain for both direct (selection in one environment or stress to improve performance in that environment or stress) and indirect (selection in one environment or stress to improve performance in another environment and stress). Estimates of genetic gain for direct selection were variable across environments and stresses as consequence of variable heritabilities and genetic variance display (Table 88). Greater genetic gains were from Chitedze and Harare high nitrogen environments $(0.52 \text{ and } 0.42 \text{ Mg ha}^{-1})$, respectively) while the lowest genetic gain was observed under drought stressed environment at Chitala (0.00).

			Gen.		Genetic Gain
Environment	Mean	Error	variance	h ²	(R)
Chitedze no fertilization	5.47	1.87	0.20	0.18	0.33
Harare low N	1.75	0.44	0.13	0.38	0.39
Chitedze high N	4.54	1.27	0.29	0.31	0.52
Harare high N	8.74	2.26	0.29	0.2	0.42
Chitala well-watered	3.9	0.92	0.09	0.17	0.22
Chiredzi well-watered	6.06	1.07	0.004	0.01	0.01
Chitala drought	1.29	0.25	0.00	0.00	0.00
Chiredzi drought	0.2	0.05	0.01	0.26	0.09
Average across locations	4.00	1.03	0.02	0.18	0.11

Table 88. Expected genetic gain for grain yield (Mg ha-1) across environments and stresses for population CML312 x NAW conducted in Malawi and Zimbabwe in 2003 and 2004 assuming selection of the best 10%.

 h^2 , broad sense repeatability.

Expected genetic gain across all environments was 0.11 Mg ha⁻¹ (Table 89). The highest genetic gain corresponded to environments under high nitrogen.

Gen., genetic; h^2 , broad sense repeatability.

Estimates of correlated response for indirect selection were also variable depending on the genetic correlation between selection and target environments as well as their heritabilities (Table 90). The highest correlated response was for selection under low nitrogen environments to improve environment with high nitrogen fertilization (0.44 Mg ha⁻¹). Positive correlated responses were estimated for selection under well-watered environment to improve yield at high nitrogen environments $(0.21 \text{ Mg ha}^{-1})$ and for selection under no nitrogen fertilization to improve yield under high nitrogen (0.30 Mg ha $^{-1}$). Negative correlated responses were estimated when selection was done under well-watered conditions for low nitrogen and no nitrogen fertilization (-0.11 and -0.14 Mg ha⁻¹, respectively) and very low response when selection was done under no nitrogen fertilization conditions to improve yield under low nitrogen $(0.02 \text{ Mg ha}^{-1})$. These results suggest that for this population, direct selection is more effective than indirect selection.

Preliminary assessment of MAS efficiency in testcrosses

Well-watered low nitrogen -0.11 Well-watered high nitrogen 0.21 No fertilization low nitrogen 0.02 No fertilization high nitrogen 0.30 Low nitrogen high nitrogen 0.44

There were significant differences between the means of two groups of testcrosses in only under low nitrogen environment in Zimbabwe but not for all other individual environments and across (Table 91).

Table 91. Grain yield means for the first and last 50 entries, their differences and significances at single and across environments for population CML312 x NAW evaluated in Malawi and Zimbabwe in 2003 and 2004.

Selection of the best five entries for each environment was conducted based on the highest yielding testcrosses to assess which group of testcrosses (best or worst) contributed most to the 5 highest yielding testcrosses. Best 5 testcrosses came from both groups (Table 92). It was observed that entry 10 was among the best 5 under no nitrogen fertilization, low nitrogen, across all environments, across high nitrogen environments and across drought environments. Entry 23 was among the best 5 under high nitrogen, across all environments and across high nitrogen environments while entry 32 was among the best 5 entries under high nitrogen, under drought stress and across all drought environments. This indicates that there are potential genotypes that can perform across environments and for specific environments.

Table 92. Top 5 entries for grain yield at single environment and across environments for population CML312 x NAW evaluated in Malawi and Zimbabwe in 2003 and 2004.

Environment	Best 5 entries for grain yield
Chitedze no fertilization	40,53, 17, 10, 75
Harare low N	10, 44, 83, 26, 16
Chitedze high N	74, 71, 76, 23, 56
Harare high N	90, 65, 32, 43, 85
Chitala well-watered	6, 98, 45, 74, 68
Chiredzi well-watered	88, 36, 89, 38, 55
Chitala drought	32, 26, 35, 18, 94
Chiredzi drought	16, 96, 36, 85, 101
Average across locations	10, 23, 44, 40, 32
Average High N	10, 23, 85, 73, 25
Average Well-watered	98, 6, 38, 3, 99
Average Drought	32, 10, 24, 25, 26

Drought (DTI) and nitrogen (NTI) tolerance indices were estimated in order to identify testcrosses that reduce less their performances under stressed conditions relative to unstressed conditions at the same locations. Testcrosses that maintain a good performance under stress are good sources for drought tolerance genes. The average DTI

for the first and last 50 entries was 63.5% and 64.2% (Malawi) and 96.4% and 96.9% (Zimbabwe), respectively (Appendix P). The average NTI for the first and last 50 entries was 77.9% and 81.6%), respectively. The testcrosses with the best DTU and NTI indices came from both groups (Table 93).

Table 93. Best testcrosses based on drought and nitrogen tolerance indices at two locations for population CML312 x NAW evaluated in Malawi and Zimbabwe in 2003 and 2004 season.

Summary results across populations

Grain yield and its components

For selection, each environment served a different purpose. Low nitrogen environments would help select cultivars which are superior in the utilization of available nitrogen while high nitrogen and well-watered environments allowed for monitoring yield potential under optimal conditions. Drought environments were meant to identify cultivars which would do well under drought. The results from all the populations showed that there was variability in these populations for grain yield, its components and other agronomic traits. Highest average grain yields across populations and environments were obtained from CML444 x K64R and lowest from CML440 x COMPE. Generally, high yields were obtained from the high nitrogen environments which was expected and lowest under drought.

The no nitrogen environment in Malawi produced grain yields which were comparable and in some cases even higher than high nitrogen fertilization (a site meant to be a low nitrogen site). This observation demonstrated the need for proper management of test environments otherwise wrong conclusions can be drawn. Therefore, this site should no longer be used as a low N site until further depletion is done to reduce the nitrogen content of the soil. Malawi and Zimbabwe well-watered environments were consistently non significant. This was very surprising because these locations had high grain yields and more variability among testcrosses was expected. A possible reason to this could be because the magnitude of the error was high. Another possible reason would be due to the effect of single row plots which have been reported to reduce performance of individual genotypes such as height, aggressive rooting and lax leaves which may provide little or no advantage in well bordered plots and may be disadvantageous under drought (Bolanos and Edmeades, 1996). This could hold true because this was under well-watered conditions where plants are more vigorous. Banziger, et al., (1995)

observed that small plots were not a major source of environmental error during selection under low nitrogen.

Grain yield was associated with plant height, ears per plant, anthesis-silking interval and anthesis date in populations CML441 x CML444, CML444 x K64R and CML312 x NAW (Figures 51 and 52). No relation was observed between grain yield and ears per plant in population CML440 x COMPE. This shows that as selection tools, some traits can be more important in one population than another. Across environments, low nitrogen, high nitrogen and drought environments were responsible for most of the variation in all populations but well-watered environments were not significant (Table 94).

		Population CML441 X CML444								Population CML440 X COMPE			
ENVT	GYG	AD	ASI	PH	EPP	TEX	GY G	AD	ASI	PH	EPP	TEX	MOI
MLW NF	$***$	$***$	NS	NS	$***$	$***$	NS	NS	NS	NS	NS	NS	NS
ZM LN MLW	NS	$***$	***	***	***	NA	\star	**	NS	\ast	NA	ΝA	NA
HN	\star	NS	***	***	NS	$***$	NS	ΝS	NS	NS	NS	NS	NS
ZM HN MLW	$***$	$***$	NS	$***$	\star	***	*	NS	NS	*	NS	ΝA	NA
WW ΖM	NS	NS	NS	NS	NS	NS	NS	***	NS	$***$	NS	NS	NS
WW MLW	$***$	$***$	NS	$***$	$***$	NA	NS	NS	NS	NS	$***$	NS	NS
DRT ZM	\star	$***$	***	$***$	NS	NA	$***$	***	NS	$***$	$***$	NA	NA
DRT	\star	NS	NS	NS	NS	NA	$***$	NS	NS	NS	$***$	NA	NA

Table 94. Significances for grain yield and secondary traits across populations and environments evaluated in Malawi and Zimbabwe in 2003 and 2004.

Table 94. continued

GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MOI, grain moisture; GWT, 100 kernel weight.

ZMLN, Zimbabwe low nitrogen; MLWWW, well-watered Malawi; ZMWW, well-watered Zimbabwe, MLWNF, Malawi no nitrogen fertilization; MLWDRT, drought Malawi; ZMDRT, drought Zimbabwe; MLWHN, high nitrogen Malawi; ZMHN, high nitrogen Zimbabwe.

Fig. 51. Relationship between grain yield and ears per plant across populations evaluated in Malawi and Zimbabwe in 2003 and 2004.

Fig. 52. Relationship between grain yield and anthesis-silking interval (ASI) across populations and stresses evaluated in Malawi and Zimbabwe in 2003 and 2004.

Heritabilities across populations

Estimates of heritability for the different traits were variable across environments and populations. Testcrosses from CML441 x CML444 and CML444 x K64R had higher heritability estimates for grain yield, 50% anthesis date, ears per plant and plant height compared to the other two populations, CML440 x COMPE and CML312 x NAW.

Heritabilities were generally larger for grain yield, anthesis date, ears per plant and plant height under high nitrogen and drought environments in both Malawi and Zimbabwe across all populations (Fig. 53). While it has been observed that heritability of grain yield declines under drought (Blum, 1988), the results of the current study indicate that similar progress can be made for grain yield under both drought and low N conditions.

This is in agreement with what was reported by Lafitte and Edmeades (1994) especially when grain yield is significantly different (Table 94 and Fig 54). The observed low values of heritability estimates under well-watered conditions was due to non significant differences for the traits, which resulted in genetic variance estimates being estimated to zero.

Fig. 53. Relationship between grain yield and heritability estimates across different environments and populations evaluated in Malawi and Zimbabwe in 2003 and 2004.

CML 440 x COMPE CML 312 x NAW

Fig. 54. Heritability estimates for grain yield, anthesis date, anthesis-silking interval, plant height and ears per plant in four testcross populations across single environments. (ZMLN, Zimbabwe low nitrogen; MLWWW, well-watered Malawi; ZMWW, well-watered Zimbabwe, MLWNF, Malawi no nitrogen fertilization; MLWDRT, drought Malawi; ZMDRT, drought Zimbabwe; MLWHN, high nitrogen Malawi; ZMHN, high nitrogen Zimbabwe).

Relationships between environments across populations

The AMMI analysis biplot highlights the behavior of environments in discriminating the genotypes. In case of grain yield, drought and well-watered environments behaved similarly, as well as high nitrogen and no nitrogen fertilization environments. This was consistent for populations CML441 x CML444, CML444 x K64R and CML312 x NAW. Apparently populations behaved in a similar manner across testing environments. Population CML 440 x COMPE reacted to environments differently. Different populations then can have different response to environmental variation (Fig. 54a, b, c, and d).

 Fig. 55a. AMMI biplots for grain yield showing the relationship among environments for population CML441 x CML 444 evaluated in Malawi and Zimbabwe in 2003 and 2004. (ZMLN, Zimbabwe low nitrogen; MLWWW, well-watered Malawi; ZMWW, well-watered Zimbabwe, MLWNF, Malawi no nitrogen fertilization; MLWDRT, drought Malawi; ZMDRT, drought Zimbabwe; MLWHN, high nitrogen Malawi; ZMHN, high nitrogen Zimbabwe).

Fig. 55b. AMMI biplots for grain yield showing the relationship among environments for populations CML440 x COMPE evaluated in Malawi and Zimbabwe in 2003 and 2004. (ZMLN, Zimbabwe low nitrogen; MLWWW, well-watered Malawi; ZMWW, well-watered Zimbabwe, MLWNF, Malawi no nitrogen fertilization; MLWDRT, drought Malawi; ZMDRT, drought Zimbabwe; MLWHN, high nitrogen Malawi; ZMHN, high nitrogen Zimbabwe).

Fig. 55c. AMMI biplots for grain yield showing the relationship among environments for CML312 x NAW testcross populations evaluated in Malawi and Zimbabwe in 2003 and 2004. (ZMLN, Zimbabwe low nitrogen; MLWWW, well-watered Malawi; ZMWW, well-watered Zimbabwe, MLWNF, Malawi no nitrogen fertilization; MLWDRT, drought Malawi; ZMDRT, drought Zimbabwe; MLWHN, high nitrogen Malawi; ZMHN, high nitrogen Zimbabwe).

Fig. 55d. AMMI biplots for grain yield showing the relationship among environments for population CML444 x K64R evaluated in Malawi and Zimbabwe in 2003 and 2004. (ZMLN, Zimbabwe low nitrogen; MLWWW, well-watered Malawi; ZMWW, well-watered Zimbabwe, MLWNF, Malawi no nitrogen fertilization; MLWDRT, drought Malawi; ZMDRT, drought Zimbabwe; MLWHN, high nitrogen Malawi; ZMHN, high nitrogen Zimbabwe).

Expected genetic gain for selection and usefulness

Yield under low N was reduced by over 60 % compared to yield under high nitrogen experiments across all the populations. Yield under drought was reduced by over 90% in Zimbabwe and about 50% in Malawi compared to yield under well-watered environments. High nitrogen environments had the highest genetic gain across all the populations while drought conditions had the lowest genetic gain. Banziger et al. (1997) that reported that selection under high nitrogen was less efficient for performance under low N when yield was reduced by more than 40%. Across all populations, higher expected genetic gain was associated with high heritability estimates (Fig. 56).

Correlated responses were variable among the populations. Tescrosses from CML441 x CML444 had the highest correlated response when selection was done under drought conditions to improve yield under high nitrogen conditions $(0.23 \text{ Mg} \text{ ha}^{-1})$. Population CML312 x NAW had the highest correlated response when selection was done under low nitrogen to improve yield under high nitrogen conditions $(0.44 \text{ Mg ha}^{-1})$. Negative correlated responses means that direct selection is more beneficial than indirect selection and also that testcrosses had to be selected for each environment separately.

Heritability estimates showed a positive correlation with genetic gain (Fig 56). The higher the heritability, the higher the genetic gain. This correlation showed that the possibility of making progress during selection is higher for traits or populations with higher heritability estimates. For our populations, more progress could be achieved in populations CML441 x CML444 and CML444 x K64R than with CML440 x COMPE and CML312 x NAW. **S**election for plant height, ears per plant, 50%, anthesis silking interval and grain yield had greater expected genetic gain than other traits moisture content, 100 kernel weight and root lodging.

Fig. 56. Relationship between expected genetic gain (Mg ha-1) for grain yield and heritability estimates in four testcross populations evaluated in Malawi and Zimbabwe in 2003 and 2004 assuming a selection intensity of 10%.

Correlation among traits across populations

Correlations between grain yield and secondary traits were variable across populations (Fig. 56a and 56b). Positive correlations were observed between grain yield and ears per plant, and grain yield and plant height in three of the populations (CML440 x COMPE, CML444 x K64R and CML312 x NAW). Population CML441 x CML444 had positive correlations between grain yield and ears per plant but not with between grain yield and plant height. All populations had negative correlations between anthesis-silking interval and grain yield, grain yield and 50% anthesis date and between anthesis-silking interval and ears per plant (Fig 57) although the magnitudes were different. In addition, the data also reveals that genotypic and phenotypic correlations of grain yield and ears per plant were apparently higher across all the populations than the other traits suggesting that this relationship is ubiquitous in maize. Ears per plant is one of the key traits that could be used for indirect selection for grain yield in these populations and environments. The negative correlation between grain and anthesis silking interval should also account for the increased number of ears per plant as short anthesis silking interval is associated with increased partitioning of assimilates to the growing ear and reduced number of barren ears (Bolanos and Edmeades, 1996).

Genotypic and phenotypic correlations between grain yield and the rest of traits were very small and inconsistent. Genotypic and phenotypic correlations generally agreed in sign and magnitude although some exceptions existed.

Fig. 57a. Single value decomposition biplot for different traits across environments for populations CML441 x CML44 (above) and CML440 x COMPE (below) evaluated in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MO, grain moisture; TEX, grain texture; GWT, 100 kernel weight).

Fig. 57b. Single value decomposition biplot for different traits across environments and populations CML444 x K64R (above) and CML312 x NAW (below) evaluated in Malawi and Zimbabwe in 2003 and 2004. (GYG, grain yield; AD, 50% anthesis; ASI, anthesis-silking interval; PH, plant height; EPP, ears per plant; MO, grain moisture; TEX, grain texture; GWT, 100 kernel weight).

Fig. 58. Correlation between anthesis-silking interval and ears per plant across populations evaluated in Malawi and Zimbabwe in 2003 and 2004.

Preliminary assessment of MAS

A comparison of the best and worst entries for grain yield showed that there were significant differences among the best 50 and the worst 50 testcrosses in few cases across the environments and populations (Table 95). Population CML441 x CMM444 had a large number of significant differences between the two groups than the other populations. Population CML444 x K64R did not have any differences between the two groups across all the environments. There was variability in the efficiency of MAS among the different populations. Bernardo et al. (2002) indicated that lack of correlation between QTLs and their correlated responses in the field are due to false positives which account for 10 to 30 times more exaggerated. It was therefore recommended that in order to improve efficiency of MAS, a 0.0001 probability level should be used compared to

Environment	CML441 x	CML440x CML444x		CML312x
	CML444	COMPE	K64R	NAW
Chitedze no fertilization	\ast	NS	NS	NS
Harare low N	\ast	NS	NS	\ast
Chitedze high N	\ast	\ast	NS	NS.
Harare high N	NS	NS	NS	NS
Chiredzi well-watered	NS	NS	NS	NS
Chitala well-watered	\ast	NS	NS	NS
Chitala drought	NS	NS	NS	NS
Chiredzi drought	NS	*	NS	NS
Average across	NS	NS	NS	NS.
locations				
Average High N	NS	NS	NS	NS
Average Well-watered	NS	NS	NS	NS
Average Drought	NS	NS	NS	NS

Table 95. Grain yield significances for the first and last 50 entries, at single environments, across environments and across populations evaluated in Malawi and Zimbabwe in 2003 and 2004.

0.10 which is currently used by most researchers. This Marker assisted selection for drought tolerance was not efficient in these populations. There are several possible reasons for this outcome: (1) QTL mapping and MAS were conducted based on inbred progeny performance when here selected inbreds were evaluated as testcrosses with representative testers; (2) difference in environmental conditions between QTL mapping and testcross evaluations could affect the results; and (3) MAS for several traits and QTLs is difficult and complex. could be because we tested testcross and not the actual inbred lines which were selected for MAS, too many QTLs and differences in testing environments which affected MAS. However, the non-sisgnificance was also a good indication that the one hundred genotypes tested were a good representation of each population.

Using drought tolerance index and nitrogen tolerance index for in comparing the two groups, also showed no differences. Recommended testcrosses for different environments were also mixed from both the best and the worst group. The current results suggests that more work needs to be done in order to fine tune the use of markerassisted selection in selecting drought and low N tolerant genotypes because the current

study has not identified the difference between the best and the worst group of testcrosses.

CHAPTER V CONCLUSIONS

There were significant differences among the populations for grain yield. Highest grain yields were obtained from population CML444 x K64R and the lowest grain yields were obtained from CML440 x COMPE. Across the test environments, high nitrogen sites had the highest yields while the lowest were for drought conditions. The site which has been used for low nitrogen experimentation at Chitedze in Malawi has accumulated a lot of nitrogen, therefore it should be depleted further before any low N work is conducted on this site.

Heritability estimates were variable across populations and environments. Testcrosses from CML441 x CML444 and CML444 x K64R had higher heritability estimates for grain yield, 50%anthesis date, ears per plant, and plant height compared to CML440 x COMPE and CML312 x NAW. Across the test environments, drought and high nitrogen environments had higher heritability estimates for grain yield, 50%anthesis date and ears per plant. More progress during selection can be achieved in some populations and less in others because if differences in heritability of the traits.

Environments discriminated testcrosses differently. Drought and well-watered environments discriminated testcrosses in a similar manner as one group while high and low nitrogen environments were also another group which discriminated the genotypes equally. This discrimination was consistent for two populations CML441 x CML444 and CML444 x K64R but different for populations CML440 x COMPE and CML312 x NAW.

Correlations between grain yield and secondary traits were variable. All populations had negative correlations between grain yield and anthesis silking interval while positive correlations were observed between grain yield and ears per plant for all populations. So

for these populations, these two traits could be used for more useful for indirect selection for grain yield. However, genotypic and phenotypic correlations for the other traits were very small and inconsistent but they generally agreed in sign and magnitude.

Marker-assisted selection was not efficient in this study possibly because we tested testcross instead of the inbred lines which were selected for drought tolerance and also because of differences in testing environments.

All populations had highest direct genetic gain from high nitrogen environments and lowest gains were realized under drought. Correlated responses due to selection under one environment to improve yield in another environment were different among the populations. Grain yield were improved under high nitrogen environments when selection was done under drought (CML441 x CML444) and under low nitrogen (CML132 x NAW). But in general, direct selection was more beneficial than indirect selection.

Results from the no nitrogen fertilization site at Chitedze and well-watered environments have taught us the need for proper experimental management and good data collection as pre-requisites to production of meaningful results from field experiements.

REFERENCES

- Atlin, G.N., and K.J Frey. 1990. Predicting the relative effectiveness of direct vs indirect selection for oat yield in three types of stress environments. Euphytica 44: 137-142
- Badu-Apraku, B., M.A. B. Fakorede, A. Menkir, A.Y. Kamara, and A. Adam. 2004. Effects of drought screening methodology on genetic variances and covariances in Pool 16 DT maize population. Journal of Agricultural Sciences 142: 445-452.
- Banziger, M., F.J. Betran, and H.R. Lafitte. 1997. Efficiency of high-nitrogen selection environment for improving maize for low-nitrogen environments. Crop Sci. 37:1103-1109.
- Banziger, M., and H.R. Lafitte. 1997. Efficiency of secondary traits for improving maize for low N target environments. Crop Sci. 37: 1110-1117.
- Banziger, M., G.O. Edmeades, and H.R. Lafitte. 1999. Selection for drought tolerance increases maize yields across a range of nitrogen levels. Crop Sci. 39:1035- 1040.
- Banziger, M., G.O. Edmeades, D. Beck, and M. Bellon. 2000. Breeding for Drought and Nitrogen Stress Tolerance in Maize. From Theory to Practice. CIMMYT, Mexico City.
- Banziger, M. 2002. Drought relief, seed relief in sight, CIMMYT, Harare.
- Bennetzen, J.L. 2000. Comperative genomics approaches to the study of drought tolerance. *In* Ribaut, J. M., and D. Poland (eds.). Molecular Approaches for the Genetic Improvement of Cereals for Stable Production in Water Limited-Environments. A Strategic Planning Workshop held at CIMMYT, Mexico City.
- Bernardo, R. 2002. Breeding for Quantitative Traits in Plants. Stemma Press, Woodbury, Minnesota.
- Betrán, F.J., D. Beck, M. Banziger, and G.O. Edmeades. 2003. Genetic analysis of inbred grain yield under stress and nonstress environments in tropical maize. Crop Sci. 43: 807-817.
- Blum, A., 1988. Plant Breeding for Stress Environments. CRC Press, Boca Raton, Florida.
- Bolaños, J., and G.O. Edmeades. 1993. Eight cycles of selection for drought tolerance to lowland tropical maize.I. Responses in grain yield, biomass, and radiation utilization. Field Crops Res. 31:233-252.
- Bolaños, J., and G.O. Edmeades. 1993. Eight cycles of selection for drought tolerance to lowland tropical maize.II. Response in yield, biomass and radiation utilization. Field Crops Res. 31:253-268.
- Bolaños, J., G.O. Edmeades, and L. Martinez. 1993. Eight cycles of selection for drought tolerance to lowland tropical maize.III. Responses in drought-adaptive physiological and morphological traits. Field Crops Res. 31:269-286.
- Bolaños, J., and G.O. Edmeades. 1996. The importance of anthesis-silking interval in breeding for drought stress in tropical maize. Field Crops Res. 45:65-80.
- Byrne, P.F., J. Bolaños, G.O. Edmeades, and D.L. Eaton. 1995. Gains from selection under drought vs multilocation testing in related tropical maize populations. Crop Sci. 35: 63-69.
- Chee, P.W., E.M. Elias, J.A. Anderson, and S.F. Kianian. 2001. Evaluation of a high protein grain protein QTL from *Triticum turgidum* L. var. *dicoccoides* in an adapted durum wheat background. Crop Sci. 41:295-301.
- CIMMYT. 1988. Change for the Better: CIMMYT 1988 Annual Report. CIMMYT, Mexico City.
- CIMMYT, 1990. 1989/90 CIMMYT Maize World Facts and Trends: Realizing the Potential of Maize in Sub-Saharan Africa. CIMMYT, Mexico City.
- CIMMYT, 1992. 1991-92 CIMMYT World Maize Facts and Trends: Maize Research Investment and Impacts in Developing Countries. CIMMYT, Mexico City.
- CIMMYT, 1998. Change for the Better: CIMMYT 1998 Annual Report. CIMMYT, Mexico City.

CIMMYT-Zimbabwe, 2000. CIMMYT-Zimbabwe: 2000 Research Highlights.

CIMMYT, Harare.

- Claassen, M.M., and R.H.Shaw. 1970. Water deficit effects on corn. II. Grain components. Agronomy Journal. 62:652-655.
- Cregan, P.B., J. Mudge, E.W. Fickus, D. Danesh, R. Denny and N.D. Young. 1999. Two simple sequence repeat markers to select for soybean cyst nematode resistance conditioned by the *rhg* 1 locus. Theor. Appl.Genet. 99:811-818.
- Deday, H.P., E. Biner, A. Grassia, and J.W. Peak. 1973. Effect of heritability and predicted selection response to *Medicago sativa.* Heredity 31:293-296.
- Dreher, K., M.L. Morris, J.M. Ribaut, M. Khairallah, S. Pandey and G. Srinivasan. 2000. Is marker assisted selection cost-effective compared to conventional plant breeding methods? The case of quality protein maize. Conference paper, Third Annual Conference of the International Consortium for Agricultural Biotechnology Research. Ravello, Italy.
- Edmeades, G.O., J. Bolaños, and H.R. Lafitte. 1992. Progress of breeding for drought tolerance in maize. *In* Wilkinson, D. (ed.), Proceedings of the $47th$ Annual Corn and Sorghum Ind. Res. Conf., ASTA, Washington DC.
- Edmeades, G.O., J. Bolaños, S.C. Chapman, H.R. Lafitte, and M. Banziger. 1999. Selection improves tolerance in tropical maize populations: I. Gains in biomass, grain yield, and harvest index. Crop Sci. 39: 1306-1315.
- Edwards, M., and L. Johnson. 1994. RFLPs for rapid recurrent selection. *In* Analysis of Molecular Marker Data Joint Plant Breeding Symposium Ser., Ame. Soc. Hort. Sci., Crop Sci. Soc. Amer. Madison, Wisconsin.
- Falconer, D.S. 1989. Introduction to Quantitative Genetics. Longman, New York.
- Falconer, D.S., and T.F.C. Mackay. 1996. Introduction to Quantitative Genetics. 4th ed. Longman, London.
- FAO, 1989. FAOSTAT Statistical Database of the Food and Agriculture Organization of the United Nations. World-wide Web:www.fao.org
- FAO 1998. FAO agricultural statistics on the World-wide Web:www.fao.org
- Fehr, W.R. 1993. Principles of Cultivar Development Vol. 1: Theory and Technique, Iowa State University Press, Ames.
- Feil, B., R. Thiraporn, and P. Stamp. 1993. *In vitro* nitrate reductase activity of laboratory-grown seedlings as an indirect selection criterion for maize. Crop Sci. 33: 1280-1286.
- Finne, M.A., O.A. Rognli, and I. Schjelderup. 2000. Genetic variation in a Norweigian germplasm collection of white clover (*Trifolium repens* L.). Euphytica. 112: 57- 68.
- Fischer, K.S., E.C. Johnson, and G.O. Edemeades. 1983. Breeding and selection for drought resistance in tropical maize. CIMMYT, Mexico City.
- Gouesnard, B. and A. Gallais. 1992. Genetic variance components estimation in a nested mating design with positive assortative mating and application to maize. Crop Science 32: 1127-1132.
- Grant, R.F., B.S. Jackson, J.R. Kiniry and G.F. Arkin. 1989. Water deficit timing effects on yield components in maize. Agronomy Journal. 81:61-65.
- Hallauer, R.A., and J.B. Miranda. 1988. Quantitative Genetics in Maize Breeding. Iowa State University Press, Ames.
- Hash, C.T., S. Rattan, P. G. Cavan, J. C. Howarth, A. Sharma, M.AF.R. Bidinger, and J.R. Witcombe. 1999. Marker-assisted backcrossing to improve terminal drought tolerance in pearl millet. *In* Ribaut, J.M. and D. Poland (eds.). Molecular Approaches for Genetic Improvement of Cereals for Stable Production in Water Limited Environments. A Strategic Planning Workshop held at CIMMYT, Mexico City.
- Heisey, P.W., M.L. Morris, D. Byerlee, and M.A. Lopez-Pereira. 1998. Economics of hybrid maize adoption. *In* Morris M.L. (ed). Maize Seed Industries in Developing Countries. Lynne Reinner Publishers, Boulder, Colorado.
- Heisey, P.W., and G.O. Edmeades. 1999. Part 1. Maize production in drought stressed environments: technical options and research resource allocation. *In* CIMMYT (ed.) World Maize Facts and Trends 1997/98. CIMMYT, Mexico City.
- Holland, J.B., W.E. Nyquist, and C.T. Cervantes-Martinez. 2002. Estimating and interpreting heredity for plant breeding: an update. Plant Breeding Rev. 22: 9- 111.
- Hurd, E.A. 1976. Plant Breeding for drought resistance. *In* T.T. Kolzlowski (ed.). Water Deficits and Plant Growth. Academic 4:317-353.
- Lafitte, H.R., and G.O. Edmeades. 1988. An update of selection under stress: selection criteria. In: B. Gelaw (ed.). Towards Self-sufficiency. A Proceeding of the Second Eastern , Central and Southern Africa Regional Maize Workshop. The College Press, Harare.
- Lafitte, H.R., and G.O. Edmeades. 1994. Improvement of tolerance to low soil nitrogen in tropical maize.II. Grain yield, biomass accumulation, and N accumulation. Field Crops Res. 39: 15-25.
- Lee, M. 1995. DNA markers and plant breeding programs. Advanced Agronomy 55:265-344.
- Leister, D., A. Ballvora, F. Salamini, and C. Gebhardt. 1996. A PCR-based approach for isolating pathogen resistance genes from potato with potential for wide adaptation in plants. Nature Genetics 14:421-429.
- McCown, R.L., B.A. Keating, M.E. Probert, and R.K. Jones. 1992. Strategies for sustainable crop production in semi-arid Africa. Outlook Agric. 21:21-31.
- Mertz, E.T., L.S. Bates and O.E. Nelson. 1964. Mutant that changes protein composition and increases lysine content of maize endosperm. Science 145:279-280.
- Mohan, M., S. Nair, A. Bhagwat, T.G. Krishna, M.Yano, C.R. Bhatia, and T. Sasaki. 1997. Genome mapping, molecular markers and marker-assisted selection in crop plants. Molecular Breeding 3:87-103.
- Morris, M.L. 1998. Overview of the world maize economy. *In* Morris M.L. (ed) Maize Seed Industries in Developing Countries, Lynne Rienner, London.
- Nhlane, W.G. 1990. Breeding flint maize hybrids (hard endosperm grain) in Malawi in response to smallholder processing needs. *In* Gebrekidan, B. (ed.). Maize Improvement, Production and Protection in Eastern and Southern Africa.

Proceedings of the Third Eastern and Southern Africa Regional Maize Workshop. CIMMYT, Nairobi.

- Oppenheimer, H.R. 1961. Adaptation to drought. *In* C.J. Bucher (ed.). Plant Water Relationships in Arid and Semi-Arid Conditions, UNESCO, Switzland.
- Patterson, H.D, and E.R. William. 1976. A new class of resolvable incomplete block designs. Biometrika 63: 83-89.
- Quizenberry, J.E. 1982. Breeding for drought resistance and plant water use efficiency. *In* M.N. Christiansen and C.F. Lewis (eds.). Breeding Plants for Less Favorable Environments. John Wiley and Sons, Brisbane, Australia.
- Ragot, M., P.H. Sisco, D.A. Hoisington and C.W. Stuber. 1995. Molecular-markermediated characterization of exotic alleles at quantitative trait loci in maize. Crop Sci. 35:1306-1315.
- Reader, J. 1997. Africa: A Biography of the Continent. Hamish Hamilton, London.
- Ribaut, J.M., D.A. Hoisington, J.A. Deutsch, C. Jiang, and D. Gonzalez-de-Leon. 1996. Identification of quantitative trait loci under drought conditions in tropical maize. 1. Flowering parameters and anthesis-silking interval. Theor. Appl. Genet. 92:905-914.
- Ribaut, J.M., D.G. Leon, C. Jiang, X. Hu, J. Betran, and D. Hoisington. 1997. Markerassisted Selection for Improving Drought Tolerance in Tropical Maize Lines. CIMMYT, Mexico City.
- Ribaut, J.M., G.O. Edmeades, E. Perotti, and D. Hoisington. 1999. QTL analysis, MAS results and perspectives for drought tolerance improrvement in tropical maize. *In* Ribaut, J.M. and D. Poland (eds.). Molecular Approaches for Genetic Improvement of Cereals for Stable Production in Water Limited Environments. CIMMYT, Mexico City.
- Ribaut, J.M., M. Banziger, J. Betran, G.O. Edmeades, K. Dreher and D. Hoisington. 2002. Use of molecular markers in plant breeding: drought tolerance improvement in tropical maize. *In* M.S. Kang (ed.). Quantitative Genetics, Genomics and Plant Breeding, CAB International, Wallingford.
- Ribaut, J.M., M.C. Sawkins, M. Banziger, M. Vargas, E. Huerta, C. Martinez, and M. Moreno. 2004. Marker-assisted selection in tropical maize based on consensus map, perspectives, and limitations. *In* Poland, D., M. Sawkins, J-M. Ribaut, and D. Hoistington. Resilient Crops for Water Limited Environments: Proceedings of a Workshop Held at Quernavaca, Mexico.
- SAS Institute. 1997. SAS/STAT. Guide for Personal Computers. Version 8.0 Cary NC: SAS Institute, Inc.
- Schmidt, R.J., F.A. Burr, M.J. Aukermen and B. Burr. 1990. Maize regulatory gene opaque-2 encodes a protein with a "leucine zipper" that binds to zein DNA. Proceedings of the National Academy of Sciences 87:46-50.
- Sebolt, A.M., R.C. Shoemarker, and B.W. Diers. 2000. Analysis of quantitative trait loci allele from wild soybean that increases the seed protein concentration in soybean. Crop Sci. 36:1676-1683.
- Shen, L., Courtois, K.L. McNally, S. Robin, and Z. Li. 2001. Evaluation of near-isogenic lines of rice introgressed with QTLs for root depth through marker-aided selection. Theor. Appl. Genet. 103:75-83.
- Shull, G.H. 1908. The composition of a field of maize. Rep. Amer. Breeders Assoc. 4:296-301.
- Smale, M., Z.H.W. Kaunda, H.L. Makina, and M.M.K. Mkandawire. 1994. Farmers, Evaluation of Newly Released Maize Cultivars in Malawi: A Comparison of Local Maize, Semi-flint and Dent hybrids. CIMMYT, Mexico City.
- Stuber, C.W. 1994. Enhancement of grain yield in maize hybrid using marker-facilitated introgression of QTLs. *In* Analysis of Molecular Marker Data. ASHS and CSSA Symposium, Corvalis, Oregon.
- Stuber, C.W., and R.H. Moll. 1996. Epistasis in maize (*Zea mays* L.). 2: comparison of selected with unselected populations. Genetics 67: 137-149.
- Vasal, S.K., H. Cordova, D. Beck, and G.O. Edmeades. 1997. Choices among breeding procedures and strategies for developing stress tolerant maize germplasm. *In* G.O. Edmeades, M. Banziger, H.R. Mickleson, and C.B. Peň-Valdivia (eds.). Developing Drought and Low-N Tolerant Maize. CIMMYT, Mexico City.
- Visser, B. 1994. Technical aspects of drought tolerance. Biotechnology and Development Monitor 18:5.
- Vivek, B., M. Banziger, and K.V. Pixley. 2004. Characterization of maize germplasm grown in Eastern and Southern Africa: results of the 2003 regional trials coordinated by CIMMYT, Harare.
- Weinmann, H. 1975. Agricultural Research and Development in Southern Rhodesia: 1924-1950. Series in Science, No 2. University of Rhodesia, Salisbury.
- Westgate, M.E. 1997. Physiology of flowering in maize: identifying avenues for improving kernel set during drought. *In* G.O. Edmeades, M. Banziger, H.R. Mickelson and C.B. Pena-Valdivia (eds.). Developing Drought and Low N-Tolerant Maize Proceedings of a Symposium. CIMMYT, Mexico City.
- Young, N.D. 1999. A cautiously optimistic vision for marker assisted breeding. Molecular Breeding. 5:505-510.
- Zaidi, P.H. 2004. Drought Tolerance in Maize: Theoretical Considerations and Practical Implications, Maize Program. CIMMYT, Mexico City.
- Zambezi, B.T. 1997. Characteristics of Maize Cultivars Released in Some Selected Countries of the Southern Africa Development Community. CIMMYT, Harare.
- Zhang, J., U. Schurr, and W.J. Davis. 1987. Control of stomatal behaviour by abscisic acid which apparently originates from the roots. Journal of Experimental Botany 38:1174-1181.

APPENDIX A

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML441 x CML444 EVALUATED ACROSS ALL ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2003 AND 2004

 Anth date, 50% anthesis date; ASI, anthesis-silking interval; EPP, ears per plant

APPENDIX B

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML441 x CML444 EVALUATED ACROSS HIGH N ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2003 AND 2004

ASI, anthesis-silking interval; Anth date, anthesis date; EPP, ears per plant; MOI, moisture content

APPENDIX C

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML441 x CML444 EVALUATED ACROSS DROUGHT ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2004

anth date, anthesis date; ASI, anthesis-silking interval, EPP, ears per plant

APPENDIX D

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML440 x COMPE EVALUATED ACROSS ALL ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2003 AND 2004

Anth date, anthesis date; ASI, anthesis-silking interval, EPP, ears per plant

APPENDIX E

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML440 x COMPE EVALUATED ACROSS HIGH N ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2003 AND 2004

Anth date, anthesis date; ASI, anthesis-silking interval; EPP, ears per plant

APPENDIX F

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML440 x COMPE EVALUATED ACROSS DROUGHT ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2004

Anth date, anthesis date; ASI, antheis silking interval; EPP, ears per plant

APPENDIX G

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML444 x K64R EVALUATED ACROSS ALL ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2003 AND 2004

Anth date, anthesis date; ASI, anthesis-silking interval; EPP, ears per plant

APPENDIX H

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML444 x K64R EVALUATED ACROSS HIGH N ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2003 AND 2004

APPENDIX I

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML444 x K64R EVALUATED ACROSS DROUGHT ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2004

APPENDIX J

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML312 x NAW EVALUATED ACROSS ALL ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2003 AND 2004

Anth date, anthesis date; ASI, anthesis silking interval; EPP, ears per plant

APPENDIX K

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML312 x NAW EVALUATED ACROSS HIGH N ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2003 AND 2004

Anth date, anthesis date; ASI, anthesis-silking interval; EPP, ears per plant

APPENDIX L

GRAIN YIELD AND ITS COMPONENTS FOR POPULATION CML312 x NAW EVALUATED ACROSS DROUGHT ENVIRONMENTS IN MALAWI AND ZIMBABWE IN 2004

Anth date, anthesis date; ASI, anthesis-silking interval; EPP, ears per plant.

APPENDIX M

DROUGHT TOLERANCE INDEX FOR GRAIN YIELD FOR CML441 x

CML444 GROWN IN MALAWI AND ZIMBABWE IN 2004

DTI, drought tolerance index

APPENDIX N

DROUGHT TOLERANCE INDEX FOR GRAIN YIELD FOR CML440 x COMPE GROWN IN MALAWI AND ZIMBABWE IN 2004

DTI, drought tolerance index

APPENDIX O

DROUGHT TOLERANCE INDEX FOR GRAIN YIELD FOR CML444 x K64R

GROWN IN MALAWI AND ZIMBABWE IN 2004

DTI, drought tolerance index

APPENDIX P

DROUGHT TOLERANCE INDEX FOR GRAIN YIELD FOR CML312 x NAW GROWN IN MALAWI AND ZIMBABWE IN 2004

DTI, drought tolerance index
VITA

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He attended Bunyenga and Mzuzu CCAP Primary Schools from 1973 to 1983. He then went to Ntcheu Secondary School from 1983-1987. He was enrolled at Natural Resources College from 1987-1989 where he obtained a Certificate in Agriculture. In 1989, the Ministry of Agriclture Research Department employed him as a Technical Assistant. In 1991, he was enrolled at the University of Malawi, Bunda College of Agriculture where he obtained a Diploma in agriculture in 1993 and then graduated with a Bachelor of Science degree majoring in crop science in 1995.

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