GENETIC VARIABILITY AND PREDICTED RESPONSES TO SELFED PROGENY SELECTION IN THREE MAIZE (*Zea mays* L.) POPULATIONS FOR TOLERANCE TO LOW SOIL NITROGEN

BY

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MSc./AGRIC/04773/2010-11

A THESIS SUBMITTED TO THE SCHOOL OF POSTGRADUATE STUDIES, AHMADU BELLO UNIVERSITY, ZARIA, NIGERIA

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF A

MASTER DEGREE IN PLANT BREEDING

DEPARTMENT OF PLANT SCIENCE

FACULTY OF AGRICULTURE

AHMADU BELLO UNIVERSITY ZARIA
NIGERIA

SEPTEMBER, 2014

DECLARATION

I declare that the work in the thesis entitled *"*GENETIC VARIABILITY AND PREDICTED RESPONSES TO SELFED PROGENY SELECTION IN THREE MAIZE (*Zea mays* L.) POPULATIONS FOR TOLERANCE TO LOW SOIL NITROGEN*"* has been performed by me in the Department of Plant Science under the supervision of Prof. S.G. Ado, Dr S.O. Ajala and Dr. S.M. Bugaje. The Information derived from the literature has been duly acknowledged in the text and a list of references provided. No part of this thesis was previously presented for another degree or Diploma at this or any other University.

AFOLABI Samson Oluwaseun _____ _____
Signature Date

CERTIFICATION

This thesis entitled "GENETIC VARIABILITY AND PREDICTED RESPONSES TO SELFED PROGENY SELECTION IN THREE MAIZE (*Zea mays* L.) POPULATIONS FOR TOLERANCE TO LOW SOIL NITROGEN" by Afolabi Samson O. meets the regulations governing the award of the Degree of M.Sc. of Ahmadu Bello University and is approved for its contribution to knowledge and literary presentation.

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DEDICATION

This thesis is dedicated to God who gave me all that I needed to complete this work; my parents (Mr. and Mrs. Afolabi S. A.) who encouraged and taught me the dignity and value of work and also to my siblings for their love and support during the period of this study.

ACKNOWLEDGEMENTS

I wish to express my profound gratitude to God Almighty for His provision, protection and support during the course of this work. To Him is all glory (Amen). My thanks go to my supervisors; Prof. S.G. Ado, Dr S.O. Ajala and Dr. S.M. Bugaje for their critical analysis, useful advice and the sharing of academic and technical skills at all stages of this work. God bless you all for supervising this research work.

I am deeply grateful to my parents Mr. and Mrs. S.A. Afolabi who were instrumental in all aspects towards my enrolment for this programme and the success of this work. Thank you all and God bless you. My gratitude also goes to my friends, colleagues and all the academic and technical staff of the Department of Plant Science, A.B.U Zaria as well as the field supervisors of International Institute for Tropical Agriculture (IITA) for their technical support.

The cooperation and financial assistance of Mr. Opeyemi Afolabi, Mrs. O. O. Benson, Mrs. Deola Lamidi, Mrs. Nike Iyanda, Mr. and Mrs. Deborah Adejugbe and my lovely wife, Mrs Morounranti Afolabi is highly acknowledged and appreciated. My thanks also go to Prof. A.O. Ogungbile (MD/CEO, Premier Seed Nigeria Limited) for his fatherly advice and love. God bless you sir.

ABSTRACT

Low soil nitrogen is a major constraint to maize production in the West African savanna. The development of maize cultivars with better performance under low soil nitrogen level is of great significance. In this study, S_1 (Selfed) progeny recurrent selection method was employed to improve three different maize populations (DMR ESR-W, TZE COMP. 3DT and ACR 9331 DMRSR) for tolerance to low soil nitrogen. S_1 progenies were generated from each of the three maize populations and evaluated under both low and high soil nitrogen levels in Mokwa (9˚18´N and 5˚04´E, 457m above sea level, 1100mm annual rainfall) and Zaria (9˚16´N and 7˚20´E, 686m above sea level, 1040mm annual rainfall) during the rainy season of 2011. Analysis of variance for grain yield and other agronomic traits evaluated under both fertility levels across the two locations showed significant differences ($p<0.05$) among the S_1 progenies. These indicate the presence of wide genetic variability amongst the genotypes. Genotypic variances were generally large enough for effective selection to take place in each of the population. Low to moderate heritability estimates of 25.50% for DMR ESR-W, 36.54% for ACR 9331 DMRSR and 40.59% for TZE COMP. 3DT were obtained for grain yield under low soil nitrogen level across the two locations. Grain yield was improved by 15.97% for DMR ESR, 23.0% for TZE COMP. 3DT and by 24.97% for ACR 9331 DMRSR. Positive genotypic correlations were observed for grain yield with plant height, ear height, and number of ears per plant and stay green in all the three maize populations. This indicates the usefulness of these traits for indirect selection purposes in improving grain yield. About 30% yield reduction was observed for all the genotypes evaluated under low nitrogen level as compared to those evaluated under high nitrogen level. However, some of the genotypes exhibited relatively high mean grain yield under both fertility levels across the two locations. Genotypes with better performance under both

fertility levels were selected from each of the three populations based on a selection index that combines grain yield, number of ears per plant, stay green and anthesis-silking interval. Grain yield was found to be improved by 15.97% for DMR ESR, 23.0% for TZE COMP. 3DT, and 24.97% for ACR 9331 DMRSR under low soil nitrogen level. Appreciable genetic gains were also obtained for plant height, ear height, ASI and stay green across the three populations. The results obtained from this study confirmed the effectiveness of the S_1 family selection scheme as a population improvement procedure capable of improving the performance of maize population for tolerance to low soil nitrogen.

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ABBREVIATIONS

Anthesis Silking Interval	ASI
Analysis of Variance	ANOVA
Days to 50% Pollen Shed	D.Pollen
Days to 50% Silking	D.Silk
Ear Aspect	E/Apect
Ear Height	EHT
Error Variance	σ^2_e
Genotypic Variance	σ^2_g
Genotype x Location Variance	σ^2_{gl}
Grain Yield (kg/ha)	GY
Heritability for the Trait under Consideration	h^2
International Institute for Tropical Agriculture	IITA
Nitrogen	N
Number of ears per Plant	E/Plant
Number of Locations	l
Number of Replications	r
Observed Mean Square for Genotypes	M_g
Observed Mean Square for Genotypes x Location Interaction	M_{gl}
Observed Mean Square for E	M_e
Parental Control	c
Phenotypic Standard Deviation	σ_{ph}
Phenotypic Variance	σ^2_{ph}

Plant Aspect	PASP
Plant Height	PLHT
Self Progeny	S_1
Standardized Selection Differential often Referred to as K	i
Stay Green	S.Green

CHAPTER ONE

1.0 INTRODUCTION

Maize (*Zea mays* L.) is one of the oldest food grains. It belongs to the grass family Poaceae (Gramineae), tribe Maydeae, and is the only cultivated species of economic importance in the genus (Paliwal, 2000). It is an economically important crop and is the third most important cereal grain in the world economy after wheat and rice (FAO, 1992). Maize is primarily a provider of calories supplying almost 20% of the world's calories, it also provides about 15% of all food crop protein (National Research Council, 1988). It is a source of food for human consumption; feed for livestock and raw materials for agro-based industries. It is the world's most widely distributed crop from the tropics to the temperate zones and is cultivated at latitudes ranging from the equator to approximately 50° North and South, at altitudes ranging from sea level to more than 3,000m elevation (Morris, 2001). Plant physiologists reported that of the six classes of cereals (wheat, rye, rice, oats, sorghum and maize), only maize and sorghum have the "C-4 path way" with more efficient CO_2 fixation package which leads to greater potential for increased productivity, especially in the tropics.

The origin of maize is still controversial. The oldest evidence of maize as human food comes from archeological sites in Mexico, where small cobs of maize estimated to be more than 5,000 years old were found in the caves of ancient inhabitants (Wilkes, 1979; 1985). Three major theories which summarize the origin of maize are:

Asian origin, which suggest that maize originated in Asia, probably in the Himalayan region, (Anderson, 1945), *Andean origin* suggesting that maize originated in the Andean

highlands of Peru, Bolivia and Ecuador (Mangelsdorf and Reeves, 1959) based on the presence of pop maize in South America and the wide genetic diversity present in Andean maize and finally the *Mexican origin* that implies that maize originated in Mexico, where maize and teosinte have coexisted since ancient times where both species have a wide biodiversity (Iltis, 1983; Wilkes, 1989). The Andean hypothesis has since been discarded because no known wild relative of maize, including teosinte, is found in these highlands (Wilkes, 1989).

Maize is one of the most important cereal crops in Sub-Saharan Africa (SSA) and serves as a major component in the diet of the people of West and Central Africa (WCA) especially in the northern Guinea Savanna (NGS) and southern Guinea savanna (SGS). It is one of the five major crops accounting for 7 to 70% of the total cereal production in 11 countries of West and Central Africa (CIMMYT, 1994; Manyong *et al*. 1996). Maize is especially important in the NGS where the grain yield potential is high and it is one of the two major crops in about 40% of the area under agricultural production (Smith *et al*., 1997). The production and utilization potential of maize have increased greatly in recent times and it is now dominating the farming systems in the NGS zone. In the past two decades, it has spread rapidly into the savannas, replacing traditional cereal crops like sorghum [*Sorghum bicolor* (L.) Moench] and millet [*Pennisetum americanum* (L.) Leeke], particularly in areas with good access to fertilizer and markets (Alabi *et al*., 2003). Fakorede *et al*. (2003) reported that although land areas cultivated to maize, sorghum and millet were about equal from 1990 to 1995 in WCA, average annual increase in total production of maize (0.43 million tons) from 1980 to 2001 was much

larger than the annual increase for millet and sorghum (0.23 and 0.30 million tons, respectively). Average grain yield for maize in the West African sub-region increased from 0.9 tons/ha in 1980 to about 1.3 tons/ha in 2001, an annual increase of 0.02 tons/ha. Grain yield of millet and sorghum remained more or less unchanged throughout this period.

In Nigeria, maize has a wider range of uses than any other cereal crop. It is a major staple food and makes an important contribution to the diet of majority of the people, constituting about 80-90% of the dietary profile of adults and over 80% of that of infants (Dowswell *et al*., 1996). Apart from its value as a major staple food, it is also an important cash crop (Kim *et al*., 1998). The major maize producing areas of Nigeria are located in the Guinea Savanna agro-ecology. This zone has great potential for maize production because of higher radiation levels, lower night temperature, and reduced incidence of pests and diseases, particularly in areas with access to fertilizer (Kassam *et al*., 1975). Nigeria accounted for about 15% of Africa's production with an average yield of 2.27 tons/ha, a level considered low when compared to the other parts of the world. Several constraints including drought (Bellon, 2001), parasitic and perennial weeds (Berner *et al*., 1995; Weber *et al*., 1996) and low soil fertility especially low soil N has been reported as the most important factors limiting maize yields in the savanna (Clark, 1990; Kling *et al*., 1997b). Soils in most parts of West and Central Africa are inherently low in nitrogen, they are mainly kaolinitic Alfisols that are generally low in organic matter and cation exchange capacity (Jones and Wild, 1975) resulting in low N availability.

Nitrogen stress affects cell and tissue growth thereby influencing leaf area and photosynthetic capacity, hence reducing maize yield by as much as 40% (Banziger *et al.*, 1997). Although, resource-poor farmers rely on shifting cultivation or bush fallow for soil fertility maintenance, but because of increasing population pressure in recent times, it has become increasingly difficult to sustain the system. Nutrients and organic matter in the soil are depleted with a corresponding decrease in yield. Considering the low soil N level of the savanna soils and the tremendous capacity of the zone for maize production, developing maize cultivars that are tolerant to low soil N would increase the productivity of maize in the region. Genetic variation in response to N supply of inbred lines (Balko and Russell, 1980) and maize populations (Lafitte and Edmeades, 1994) have been observed and this suggest that it is possible to breed varieties or hybrids with tolerance to low soil N.

Recurrent selection, a cyclic procedure that involves the identification and intermating of superior genotypes in a population to form a new and improved population from which further selection can be practiced (Ajala *et al*., 1995) has been used to improve maize populations for tolerance to different environmental stresses. It is an efficient method for increasing the frequency of desirable genes (Hallauer *et al*., 1988). Several intra-population recurrent selection schemes have been proposed for the improvement of maize yield and other important traits including tolerance to low soil nitrogen in maize breeding populations. Vasal *et al.* (1997) and Banziger *et al.* (2000) observed that different selection methods including half-sib, full-sib and selfed progeny selection can be used for

the improvement of maize population for low-N tolerance. However, reports from several works have indicated that methods which are effective in improving one population may not be so for another, furthermore various selection schemes differ in effectiveness when applied to the same population.

1.1 JUSTIFICATION

Low soil nitrogen is common in farmers' fields in Sub-Saharan Africa and this can be attributed to several factors. In seasons with adequate rainfall, soil nitrogen can be leached below the root zone and the crops suffer nitrogen deficiency. Soil nitrogen deficiency is further worsened by the wide spread removal of crop residues for use as animal feed and fuel (Zambezi and Mwambula, 1997). Furthermore, the high cost of nitrogen fertilizer and poor weed control increase the incidence of nitrogen stress in many instances (Lafitte and Edmeades, 1994). Due to the high prices of inorganic fertilizer, most farmers apply nitrogen at sub-optimal levels (McCown *et. al*., 1992). The estimated annual loss of maize grain yield to low N stress alone varies from 10% to 50% (Wolfe *et al.*, 1988). Therefore, the development of maize genotypes tolerant to low N stress is crucial to increase productivity of maize in Sub-Saharan Africa. Developing maize genotypes with high nitrogen use efficiency and high yield potential is one effective strategy to reduce fertilizer cost. Genotypes with high yield potential under both low and optimal N levels are needed to support the rapidly growing population and may provide incentives to farmers who are trying to make modest increase in N-fertilizer application in their maize fields.

Considering the low soil N levels of the Nigerian savanna and the tremendous capacity of these zones in maize production, developing low-N tolerant maize varieties capable of fully exploiting available nutrients or that can be productive under low soil N levels would broaden the cultivation of maize and also offer economic and environmental benefits to small-holder farmers.

1.2 OBJECTIVES

The present study was conducted to evaluate the genetic variability and predict response to selfed progeny selection in three maize populations under low and high soil nitrogen across the climatic conditions of Zaria and Mokwa.

The specific objectives of the study therefore are to:

1. Determine the level of genetic variability of traits associated with yield and tolerance to low-N in three maize populations using the S_1 family selection method.
2. Measure the association between grain yield and other agronomic traits in the maize populations under low-N stress condition.
3. Predict responses to S_1 family selection under both low and high N levels.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Low Soil Nitrogen and its Constraint to Maize Production

Nitrogen stress is the major nutrient constraint to maize productivity in the northern guinea savanna of West and Central Africa. It is the mineral element required in greatest quantity by maize, thus efficient N uptake and use by maize plants is of fundamental importance to maize production systems in Africa (Muza *et al*., 2004). Ma and Dwyer (1998) identified N fertilizer as the most energy consuming component of maize grain production. N is the most limiting nutrient as it is the most mobile in the soil and the nutrient needed in largest quantities by the crop (Laegreid *et al*., 1999). Inorganic fertilizer use in sub-Saharan Africa is constrained by high cost, inaccessibility and lack of credit faced by small holders even in the high potential moist mid-altitude eco-zones (Kamara *et al*., 2005; Diallo *et al*., 2004; Banziger and Diallo, 2004; Banziger *et al*., 2006). Where there is a high risk of crop failure, especially due to drought, recommended N fertilizer rates are often lower than N rates that give maximum yields under optimum conditions (McCown *et al*., 1992). Poor weed control additionally increases the incidence of N stress in many instances. Together, these constraints result in low N being a frequent characteristic of maize-growing environments in the tropics (Banziger and Lafitte, 1997).

Variation in N supply affects both growth and development of maize plants (McCullough *et al.,* 1997). Nitrogen affects photosynthetic rate, leaf area, size of the sink and thus yield (Dass *et al*., 1997). The onset of grain filling is a critical phase of nitrogen supply within the maize plant (Christensen *et al*., 1981).When N supply is limiting, leaves become the main source of mobilized N to the ear (Below, 1997). Chlorophyll

concentration reduction and leaf yellowing are good indicators of N remobilization (Dwyer *et al*., 1995). N deficiency accelerates leaf senescence by reducing chlorophyll concentration (Monneveux *et al*., 2005). Stay green can reflect N balance in cereals during grain filling (Borrell *et al*., 2001), but greenness can also be cosmetic rather than functional (Thomas and Howarth, 2000). Lack of N enhances kernel abortion (Pearson and Jacob, 1987) and reduces final grain number (Lemcoff and Loomis, 1986; Uhart and Andrade, 1995; Monneveux *et al*., 2005) and grain yield (Monneveux *et al*., 2005). Reduction of grain weight under low N condition is more attributable to reduction in grain filling period than in growth rate (Monneveux *et al*., 2005). Cultivars yield differently in different N environments due to genetic differences (Smalberger and DuToit, 2004). Relative grain yield reduction due to N stress also depends on the type of progeny and N-stress intensity (Banziger *et al*., 1997). Smalberger and DuToit (2004) recorded a grain yield ranging from 0.65 - 3.85 tons/ha under low N and 4.17 - 6.93tons/ha under optimum N for South African cultivars. They observed that the cultivar that gave the best yield (6.93 tons/ha) under optimum N gave as low a yield as 0.98 tons/ha under low N. Betran *et al*. (2003) compared maize hybrid yield under low and high N environments and found that grain yield for hybrids in the low N environment was 33% of grain yield in the high N environment. In low-input agriculture, cultivar/varieties with better grain yield under low-N conditions are recommended as one of the key elements for sustainable agriculture (Sattelmacher *et al*., 1994). The performance of most commercial maize hybrids and varieties under low N and small holder farmer's conditions is limited because they were developed under very high N levels on good soils found on research stations (Muza *et al*., 2004). This indicates a need

for developing cultivars that will give good yields under both optimum and low N conditions. Diallo *et al*. (2004) evaluated 63 single crosses along with seven local checks under low N and optimal conditions and observed grain yields ranging from 1.2 - 3.5 tons/ha under low N and from 3.1 - 7.4 tons/ha under optimal conditions. Banziger *et al*. (1997) observed a relative grain yield reduction of 37 to 78% in different experiments conducted under low N in tropical maize. Similarly, Banziger *et al*. (1997), and Banziger *et al*. (1999) reported a relative grain yield reduction ranging from 37 to 89% and from 20 to 50%, respectively. Monneveux *et al*. (2005) noted an average yield reduction of 67.4% for maize hybrids under low N conditions as compared to optimum management. Experiments under low N, yielding on average 25 – 35% (1.5 – 3.5 tons/ha) of the yields obtained under recommended agronomic management/high rainfall conditions (6.0 – 9.0 tons/ha) is regarded as optimal for expressing N stress tolerance in tropical maize (Banziger *et al*., 1997). Banziger *et al*. (1997) also observed a significant reduction in plant height (27.1%), ear height (42.2%), ears per plant (11.2%), grains per ear (47.8%) and grain weight (30.7%) under low N. The authors also observed an average of less than one ear per plant, which reflects bareness rather than prolificacy. Monneveux *et al.* (2005) reported that on average anthesis silk interval increased from 0.33 days under optimal to 2.42 days under low N conditions, which is more than seven fold that of the optimal conditions. Low N stress also increases the incidence of ear rot disease (Banziger *et al*., 2006).

2.2 Breeding Maize for Tolerance to Low Soil Nitrogen

Maize has a strong positive response to N supply and inadequate soil nitrogen is second to drought as a constraint to maize production (Lafitte and Banziger, 1997). Also, weeds aggravate N deficiency as they are always in competition with the crops for nutrient uptake. Shortage of nitrogen normally results to reduced growth of leaves and grain since it is required for the formation of both structural and enzymatic proteins. Low soil N will continue to be a major constraint to maize production in WCA as long as continuous, intensive and unsustainable farming practices continue to prevail (Banziger *et al*., 1997). Nitrogen is by far the most transitory of all fertilizer nutrients, being subject to losses from both leaching and gaseous evolutions. Most N is absorbed into maize roots through mass flow of NO_3^-, a highly soluble ion that moves in the direction of moisture flow. It has become the major energy and cost input among production requisites, as well as a significant contributor to ground water NO_3^- pollution (Pratt, 1984; CAST, 1985). Yield loss due to low soil N is in the range of 10 – 15% (Banziger *et al*., 1997; Wolfe *et al*., 1988). Thus, it is of utmost importance that N fertilizer be used in the most efficient manner possible for economic, environmental, and energy conservation reasons (Olson and Kurtz, 1982).

Lafitte and Banziger (1997) reported that while breeding efforts to address the issue of low soil N are less advanced than the work on drought, the data available suggest that progress can be made in improving yields under fertility stress as well. Genetic studies evaluating N response in breeding lines and maize hybrids suggested polygenic inheritance (Eghball and Maranville, 1993). An exploratory study using a mixture of

tropical germplasm showed that yield under low N was improved after a cycle of half-sib selection at low N (Muruli and Paulsen, 1981). Several studies have shown genetic variation among varieties in nitrogen uptake, partitioning and yield response to N supply. This encouraged Lafitte and Edmeades (1994) to initiate improvement of yield of a lowland tropical maize variety (Across 8328) under low N. There has also been considerable interest in the possibility of directly evaluating inbred lines in low N nurseries to identify lines that will perform better in hybrid combinations for low N target environments. Lafitte and Edmeades (1995) reported that traits such as plant height and maturity measured in S_2 or S_3 lines under low N were correlated with the same traits measured in the hybrid, but no association was found between line and hybrid yields at low N. After three cycles of selection in Acr. 8328, and some variations on the ideotype approach used, the average yield gain per cycle was 4.5 percent at low N and 2.3 percent at high N (Lafitte *et al*., 1997). Some maize genotypes are also capable of utilizing absorbed N more efficiently for grain production (Chevalier and Schrader, 1977). There may be potential for developing cultivars that accumulate large amounts of N during the vegetative phase and redistribute efficiently during grain production. Certain maize inbreds were also identified that responded well to the ammonium form of nitrogen (Moll *et al*., 1982). Horst *et al*. (2003) found significant differences among maize cultivars in grain yield under conditions of low N supply. It was reported that N efficiency was related more closely to N uptake efficiency (N accumulation at a given N supply) than utilization efficiency (dry matter yield per unit N taken up by the plant). Akintoye *et al.* (1999) also established a positive relationship between N efficiency and N-uptake and N utilization efficiency. Moll *et al*. (1982) reported that differences among maize hybrids

for nitrogen use efficiency (NUE) are largely due to variation in utilization of accumulated N before anthesis, especially under low N supply. Gass *et al.* (1971) reported that residual nitrates is readily used by maize to depths as 180cm in deep soils developed on mantle rock, providing that substantial available N does not exist at shallower depths. Schepers *et al.* (1986) also projected that a measure of residual mineral N along with an estimate of the soil's N mineralization capacity in any deep, medium to fine textured, and well-drained soil will be needed for meeting current and future economic and environmental requirements.

The efficiency of selection for yield in low-N environments may be improved by selection for correlated secondary traits (Blum, 1979). Traits related to efficient N uptake and metabolism have been suggested as selection parameters. Among these traits are high plant nitrate content (Mollaretti *et al*., 1987) and improved N uptake characteristics by seedlings. The selection criteria identified by CIMMYT (International Maize and Wheat Improvement Center) for maize tolerance to low N include (1) grain yield at high and low N, (2) plant height under low N, and (3) ear leaf area under low N (Edmeades *et al*., 1999). The usefulness of secondary traits that could be used in selection of tolerance to low N was examined in a number of populations grown under low N at Poza Rica, Mexico by genetic analysis (Banziger *et al*., 1997). The number of ears per plant and leaf senescence rate was found to be valuable traits in identifying superior genotypes.

2.3 Genetic Variability for Adaptive Traits

Genetic variation is a prerequisite for any crop improvement. The most important factor influencing selection and gains over contrasting environments is the amount of available genetic variation for traits necessary for improvement under specific constraints or stress (Blum, 1979; Ceccarelli, 1989; Vasal *et al.,* 1997a). It has been indicated that selection cannot create variability but can act on heritable variability already existing in the population (Singh and Chaudhary, 1985; Hallauer and Miranda, 1988). It is considered best to start selection on high performing and agronomically desirable germplasm exhibiting large variation for stress tolerant traits (Vasal *et al*., 1997b).

The knowledge of genetic variation and relationships between accessions or genotypes is important to understand the genetic variability present and its potential use in breeding programs (Thormann *et al.,* 1994; Yoseph *et al*., 2005). An insight into the magnitude of variability is of utmost importance as it provides the basis for effective selection (Singh, 2005). The composition of the phenotype (the observable properties of an organism), is simply expressed as the outcome of three major sources of variation: the genotype, the environment which includes all factors external to the plant that affect development and growth, and interactions of all kinds (Lee, 2006). Falconer (1989) and Banziger and Cooper (2001) described genetic variance as a measure of the extent of genetic differences among the germplasm units (individuals or families) evaluated. The choice of breeding methods for genetic improvement of a crop depends upon the nature and magnitude of genetic variability present (Singh and Chaudhary, 1985; Hallauer and Miranda, 1988). Besides, estimated genetic variance refers to a specific population from

which the experimental material is a sample for a specific set of environmental conditions (Dudley and Moll, 1969; Hallauer and Miranda, 1988).

The primary goal of any plant breeding program is to develop and identify high yielding transgressive segregants. Kisha *et al*. (1997) indicated that populations with greater genetic variance are expected to produce higher yielding transgressive segregants than populations having lower genetic variance. Genetic variation can be created by domestication, germpasm collection, plant introduction, hybridization (intervarietal, distant, somatic), mutation, polyploidy, somaclonal variation and genetic engineering (Singh, 2005). Different mating designs are used in the estimation of genetic variability and other components of variance.

2.4 Recurrent Selection

Recurrent selection is a plant breeding procedure designed to change the mean of a trait in a population of plants by increasing the frequency of favourable alleles. The procedure is especially suited for improving quantitatively inherited traits, and it provides population with high percentage of superior genotypes that can be useful as parents in breeding programme or as potential cultivars (Hallauer and Miranda, 1988). Recurrent selection not only improves the performance of the populations but also the performance of lines derived from them, because genetic variability is maintained by inter mating the selected individuals for further cycles of selection. Recurrent selection has been effective in gradually improving population performance as well as the performance of the hybrids developed from the succeeding cycles of selection in maize (Vassal *et al*., 1997b).

Population improvement by recurrent selection is done through increasing the frequency of favorable alleles within the population (Hallauer and Miranda, 1988). Many different recurrent selection procedures have been developed in maize, and each method's effectiveness depend on the population undergoing selection, the selected trait, and the objective and stage of the breeding program (Hallauer and Miranda, 1988; Vasal *et al*., 1997b). Intra-population improvement methods have been more effective than inter-population methods for improving population means *per se* for all traits (Pandey and Gardner, 1992). They have been also effective for improving the drought tolerance of source populations and have increased the probability of developing superior drought tolerant inbred lines from those populations (Edmeades *et al*., 1999). Family based recurrent selection methods result in greater gains when traits under selection are complex and of low heritability (Hallauer and Miranda, 1988; Vasal *et al*., 1997a). The selfed progeny selection (S_1 or S_2), compared with other recurrent selection procedures, increase genetic variability among families and selects against undesirable recessive genes, thus it is more suitable particularly for low heritability traits (Hallauer and Miranda, 1988). Although there is no selection method that is best under all circumstances, selfed progenies are preferred over non inbred progenies because variability and heritabilities increase with levels of inbreeding (Bolaños and Edmeades, 1996; Vasal *et al*., 1997b). It significantly improves tolerance to inbreeding over time and generates superior inbred progenies that may be the progenitors of advanced lines (Beck and Betran, 1997; Vasal *et al*., 1997b).

2.5 Selfed Progeny (S_1) Selections

Population improvement by recurrent selection is an important component of breeding programmes with naturally cross-fertilizing plants, whether the aim is open-pollinated, synthetic or hybrid cultivars. With characters of low heritability, improvement is faster with family selection than with single plant selection because replicated trials allow the effects of environment and genotype x environment interaction variation to be reduced. In plant species, such as maize, which can be easily selfed by the breeder, S_1 family selection is possible. The S_1 method utilizes all the additive genetic variance in a population, whereas, only half of the additive variance appears in genetic variance among the full-sib family (Hallauer and Miranda, 1988). It involves the evaluation of large number of genotypes from the population, identification and selection of desirable genotypes, and recombination of the selected genotypes to form a new population from which further selection can be made (Fakorede and Obilana, 1979). All intra-population improvement schemes, except mass selection, rely on progeny testing as a means to distinguish among single plants whose superiority is environmentally induced and those whose superiority stems from superior genotypes (Allard, 1960).

Maize population improvement for low N stress has been accomplished in source population by recurrent selection using full-sib and S_1 family selection methods (Lafitte and Edmeades, 1994; Sallah and Geadelmann, 1997). The S_1 progeny selection provides 50% greater annual gains than full sib selection, with additional advantages in promoting superior progenies more rapidly to inbred lines in pedigree breeding programs (Edmeades *et al*., 1999). Bolaños and Edmeades (1996) found higher phenotypic correlations

between GY and ASI across S_1 than full-sib progenies reported by Fischer *et al*. (1987). Progenies obtained by this approach can be utilized for development of synthetics, which is one way of concentrating specific traits in one cultivar (Falconer, 1989; Edmeades *et al*., 1999). Thus S_1 recurrent selection is the best alternative to assess the variability in traits related to drought and low nitrogen tolerance in elite local populations as well as to improve tolerance to these stresses. Similarly, intercrossing drought tolerant lines with high general combining ability may intensify the degree of tolerance to multiple stresses. However, it takes longer to complete a cycle if there is no off-season facility. In recent years, as a result of theoretical and computer simulation studies, a number of authors have advocated S_1 family selection in preference to other forms of family selections (Wricke and Weber, 1986). However, before using this method on a particular population of interest, a breeder would wish to estimate the predicted response to selection, and to compare it with those of other possible methods, such as full-sib (FS) and half-sib (HS) family selection.

2.6 Heritability

Success of breeders in changing the characteristics of a population depends on the degree of correspondence between phenotypic and genotypic values (Dabholkar, 1992; Singh and Ceccarelli, 1995). In crop improvement, only the genetic component of variation is important since only this component is transmitted to the next generation. The extent of contribution of genotype to the phenotypic variation for a trait in a population is ordinarily expressed as the ratio of genetic variance to the total variance, i.e., phenotypic variance, for the trait; this ratio is known as heritability (Singh, 2005). Thus heritability

denotes the proportion of phenotypic variance that is due to genotype. According to Falconer and Mackay (1996), the relative importance of heredity in determining phenotypic values is called the heritability of the character. The term heritability has been further divided into broad sense and narrow sense, depending whether it refers to the genotypic value or breeding value, respectively (Falconer, 1989; Holland *et al.*, 2003). Heritability expresses the extent to which individual phenotypes are determined by the genotypes. A large percentage for a character is regarded as highly heritable whereas if it is smaller, some environmental agency is considered responsible for phenotypic manifestation of the character (Dabholkar, 1992). On the other hand, the ratio of additive variance to phenotypic variance is called heritability in the narrow sense and expresses the extent to which phenotypes are determined by the genes transmitted from the parents. The ratio also expresses the magnitude of genotypic variance in the population, which is mainly responsible for changing the genetic composition of a population through selection (Falconer, 1989; Dabholkar, 1992; Holland *et al*., 2003). Estimates of heritability serve as a useful guide to breeders. The knowledge of the relative heritability of the various traits and their genotypic and phenotypic correlations can aid in the design of efficient breeding systems where many traits need to be improved simultaneously (Jones and Wild, 1975). The breeder is able to appreciate the proportion of variation that is due to genotypic (broad sense heritability) or additive (narrow sense heritability) effects, that is, the heritable proportion of variation in the first case, and the proportion of genetic variation that is fixed in pure lines in the latter case (Singh, 2005). A broad sense heritability estimate based on various components of variance provides information on the relative magnitudes of genetic and environmental variation in the germplasm (Dudley

and Moll, 1969). However, the type of gene action involved in the expression of a character has a significant role in determining heritability values. Characters that are controlled largely by genes acting in an additive fashion have higher heritability than characters governed by genes with large non-additive effects (Hanson, 1963; Falconer, 1989; Dabholkar, 1992). According to Dabholkar (1992), it is important to note that heritability is a property not only of the character being studied, but also the population being sampled and the environmental circumstances to which individuals have been subjected. More variable environmental conditions reduce the magnitude of heritability while more uniform conditions increase it (Rosielle and Hambling, 1981). If heritability of a character is high, for example, 0.8 or more, selection for the character should be fairly easy (Singh, 2005). This is because there would be a close correspondence between the genotype and the phenotype due to a relatively smaller contribution of the environment to the phenotype. A high heritability implies that the genetic variation for a trait can be precisely assessed from phenotypic observations (broad-sense) and that the trait can be easily transmitted to the offspring of the selected genotypes (narrow sense) (Falconer, 1989; Banziger and Cooper, 2001). But for a character with low heritability, say less than 0.4, selection may be difficult or impractical due to the masking effect of the environment on genotypic effects (Singh, 2005). Even the unit used in reporting, influences the magnitude of heritability (Hanson, 1963). Furthermore, predicting response to selection, heritability estimates are used to identify optimum environments for selection (Singh and Ceccarelli, 1995).

2.7 Selection Response and Predicted Responses in Maize Population

The critical task of a plant breeder after generating variability amongst populations is to advance the populations to subsequent generations through selection. Selection entails discriminating among genetic variations (heterogeneous population) to identify and choose a number of individuals to establish the next generation. The consequence of this is differential reproduction of genotypes in the population such that gene frequencies are altered and subsequently the genotypic and phenotypic values of the targeted traits. Response to selection is the difference between the mean phenotypic value of the offspring of selected parents and the whole of the parental generation before selection. It is simply the change of population mean between generations following selection. Similarly, selection differential is the mean phenotypic value of the individuals selected as parent expressed as a deviation from the population mean (Banziger and Lafitte 1997).

Falconer (1960) pointed out that the magnitude of change in gene frequency in a population due to selection depends on both the intensity of selection and the initial gene frequency. This change was expected to be greater at higher selection intensities and at intermediate initial gene frequency, while at low selection intensity with either large or small initial gene frequency, the change in gene frequency was observed to be least (Hallauer and Miranda, 1988). This follows that the greater the rate of change in gene frequency, the more effective is the selection. Hence, selection is most effective at intermediate gene frequency and at higher selection intensities, while it is least at lower selection intensities with either large or small gene frequencies. Falconer (1960) indicated that changes in gene frequency could not in practice be followed for frequency of

selection to be measured. However, since changes in gene frequency result in changes in the observable properties of metric characters, these observable properties (means, variance and covariance) are used to describe the effectiveness of selection.

The difference between the population mean after selection i.e. the population generated from the selected parents and the mean of the population before selection describes the response to selection or the observed gains from selection (Hallauer and Miranda, 1988). Various workers have reported observed gain (G) from selection. Lafitte and Edmeades, (1994) conducted three cycles of selection for low-N tolerance in the experimental variety Across 8328BN. Progress was evaluated after three cycles of selection. The gain in Across 8328BN was 2.8%/cycle at low-N and 2.3%/cycle at higher-N for grain yield. Lafitte and Edmeades (1994) used a linear regression between grain yield and cycles of selection as a measure of progress after three cycles of full-sib recurrent selection for Across 8328 BN. There was an increase in mean grain yield of 70kg/ha/cycle corresponding to 2.8% gain/cycle relative to the original population at low-N and 137kg/ha/cycle corresponding to 2.3%/cycle at high-N environment. Similarly, Lafitte and Banziger (1997) evaluated five cycles of full-sib family selection for grain yield of maize at low-N and high-N conditions. Their study, showed that yield gain under N stress resulted in 85kg/ha/cycle (4.5%/cycle) and 120kg/ha/cycle (2.2%/cycle) at high-N. In another study by Banziger *et al*. (1997), after four cycles of selection, they found that yield increased by 100kg/ha per year (3.4%/year) at low-N and 75kg/ha/year (1.2%/year) under high and low-N environments.

Pandey *et al.* (1986) obtained a gain of 180kg/ha/cycle corresponding to 3.6%/cycle in the population Across 28 after three cycles of full-sib recurrent selection at low N environment. Sallah and Geadelmann (1997) evaluated three cycles of full-sib recurrent selection for yield and other agronomic traits under high and low N environments. They reported a gain of 4.6%/cycle for grain yield, 2.4%/cycle for mid silk, 2,8%/cycle for plant height, and 8.4%/cycle for grain moisture at low N environment. On the other hand, the gains at high N environment were 5.0%/cycle for grain yield, 1.9%/cycle for mid-silk, 1.4%/cycle for plant height and 5.4%/cycle for moisture content.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Genetic Background of Experimental Materials

Three open-pollinated maize varieties developed for grain yield and adaptation to abiotic and biotic stresses were used for the experiment. The materials are medium to early maturing white grained cultivars sourced from the maize improvement programme of the International Institute for Tropical Agriculture (IITA) Ibadan, Nigeria. The origin, genetic background, breeding emphasis and ecological adaptation of the maize parents are shown in Table 1. The materials were selected because they were initially bred for drought tolerance which has similar genetic effects with low-N tolerance.

3.2 Location of Experiments

The experiments were conducted at Mokwa (9˚18' N and 5˚04' E, 457 m above sea level, 1100 mm annual rainfall), and Zaria (11˚16' N and 7˚20' E, 686 m above sea level, 1040 mm annual rainfall) in the rainy season of 2011. The fields were established on 10th to 14th July 2011 across the two locations. Mokwa is located in the southern guinea savanna (SGS) and Zaria in the northern guinea savanna (NGS) of the agro-ecological zones of Nigeria (Geographical coordinates).

3.3 Land Preparation

The land in both sites was ploughed, harrowed and ridged two weeks before planting. Soil samples were taken at random on the different N level plots before land preparation for analysis at the Department of Soil Science, Ahmadu Bello University (ABU), Zaria.

Table 3.1: Origin and Genetic Background of the Experimental Materials

S/N	Variety	Origin and genetic background	Breeding emphasis	Ecological adaptation
1	SAMMAZ 20 (TZE COMP 3 DT)	Early, white, flint cultivar derived from diverse sources of early mid-altitude germplasm with drought tolerant cultivars, intermated with TZER-W and DMR-ESRW at IITA.	Drought tolerance	Forest and Savannah
2	DMR ESR-W	Early maturing white-grained cultivar derived by intermating downy mildew resistant (DMR) sources from the Philippines with TZSR (tropical Zea streak Resistant) from IITA (Fajemisin, 1985).	Maize streak virus and Downy mildew resistance	Forest and Savannah
3	Acr 9931 DMRSR	Early, white, flint cultivar derived from diverse sources of early mid-altitude germplasm with drought tolerant cultivars	Maize streak virus and Downy mildew resistance	Forest and Savannah

Source: IITA Archival Report 1988-1992

3.4 Experimental Design and Layout

The base populations of the three tropically adapted early maturing maize varieties were sourced from IITA, Ibadan and used for this study. At least 500 plants were established for each of the populations from a bulked seed, these plants were referred to as the S_0 plants. Large number of S_1 families were developed by selfing some of the S_0 plants at random. At harvest, the S_1 plants with well filled cobs and representative of each population were carefully selected and used as S_1 lines for the evaluations. A total of 125 S_1 lines were developed for DMR ESR, 225 S_1 lines for TZE COMP. 3DT and 247 S_1 lines for ACR 9331 DMR SR. These S_1 progenies were evaluated under 30 kg Nha^{-1} (low N) and 90 kg Nha^{-1} (high N) at the low N screening sites in Institute For Agricultural Research (IAR), Samaru and IITA field in Mokwa. In order to avoid N spill-over, each N level was considered as a separate field trial planted adjacent to each other. The plot size for each entry was two rows of 3.0 m length spaced 0.75 m apart, with intra-row spacing of 0.25 m to give a plant population of approximately 53,333 plants ha^{-1}. The experiments were laid out in an incomplete block design with two replications. Two maize seeds were sown per hill in each location and later thinned to one plant per hill at two weeks after planting (WAP). Basal dressing with phosphorus and potassium were applied at 60 kg P_2O_5 ha^{-1} and 40kg K_2O ha^{-1} to all plots as triple super phosphate and muriate of potash, respectively prior to planting. Nitrogen was applied at 30 kg Nha^{-1} for the low N and 90 kg Nha^{-1} for high N fields, as Urea (46%N) band applied in two equal spilt doses at two and five WAP across the two locations. There were four days difference between the operations in Zaria and those in Mokwa. A formulated mixture of

metolachlor plus atrazin at 1.6 kg ai ha^{-1} and paraquat at 1.0 kg ai ha^{-1} was applied as pre-emergence herbicide and supplemented by hoe weeding at three and six WAP.

3.5 Data Collection

Agronomic traits data were collected during the experiment. They include both crop and yield parameters.

3.5.1 Crop Parameters

***3.5.1.1 Maize plant count*:** This is the number of plants in each plot. This count was carried out at two to three WAP and at harvest. The count at harvest represents the actual number of plants per plot, counted just before harvest.

***3.5.1.2 Plant height (PLHT)*:** This is the distance from the base of the plant to base of the tassel. Five to ten representative plants were measured per plot and the mean calculated to represent the value for the plot. This was done at 12 WAP on all plots.

***3.5.1.3 Ear height (EHT)*:** This is the distance from the base of the plant to the node that had the top most ears. Five representative plants were measured per plot and the mean calculated to represent the value for the plot. This was also done at 12 WAP.

***3.5.1.4 Plant aspect (PASP)*:** This is the general look of the plants in a plot, on the relative plant and ear height, uniformity of the stand, reaction to diseases, insects and lodging. This was scored on a scale of 1-9 (1=excellent and 9=very poor).

***3.5.1.5 Days to 50% Pollen shed (D.Pollen)*:** This is the number of days from planting to when 50% of the plants in a plot had shed pollen.

***3.5.1.6 Days to 50% silking (D.Silk)*:** This is the number of days from planting to when 50% of the plants in a plot had emerged silks.

***3.5.1.7 Anthesis silking interval (ASI)*:** This was calculated as the days to 50% silking minus days to 50% pollen shed for each plot.

***3.5.1.8 Stay green (S.Green)*:** This was determined for the plants on the low-N plots on a scale of 0-10 with 0 = 0%, where leaves below the ear remain green and 10 =100% of all the leaves below the ear are dead.

3.5.2 Yield parameters

***3.5.2.1 Ear number and weight (E/Plant)*:** At maturity, maize cobs were harvested from each plot, counted and weighed. The total number of ears with kernels was divided by the total number of plants that survived up till harvest to determine the number of ears per plant in each plot.

***3.5.2.2 Ear aspect (E/Aspect)*:** The general appeal of the harvested ears of each plot. It was scored based on a scale of 1 to 9 where 1 = excellent and 9 = very poor. The factors that were considered in the score include ear size, uniformity of ears, uniformity of color and texture, grain fill, insect and disease damages.

***3.5.2.3 Moisture content (MC)*:** Grain moisture was measured with moisture tester at harvest using grains from three to five randomly picked ears from each plot.

3.5.2.4 Grain yield (kg/ha) adjusted to 14% moisture (GY): This was calculated using the formula given by Lauer (2002).

$$\frac{Field\ weight\ \times \left(1-(\%\ Moisture)\right)\times Shelling\ \%}{86}\times\frac{10{,}000}{4.5}$$

3.6 Statistical Analysis

The data collected was subjected to statistical analysis using SAS ver. 9.1 (SAS, 2004). Analysis of variance (ANOVA) was done to test for significance between the means for various agronomic traits using PROC SAS (2004). The PROC GLM procedure was used to estimate variances for all the traits. The differences among the genotypes were tested by 'F' test as given in Table 2

3.6.1 Estimation of Genetic Parameters

Genetic variability among the genotypes was estimated as follows:

3.6.1.1 Variance components

Phenotypic and genotypic variances were estimated using the formula given by Lush (1990) and Chaudhary and Pradsad (1968).

$\sigma^2_{ph} = \sigma^2_g + \sigma^2_e$

Where:

σ^2_{ph} = Phenotypic variance

σ^2_g = Genotypic variance

σ^2_e = Error variance

For across locations:

Phenotypic variance (σ^2_{ph}) = $\sigma^2_g + \frac{\sigma^2_{gl}}{r} + \frac{\sigma^2_e}{rl}$

Genotypic variance (σ^2_g) = $\frac{M_g - M_{gl}}{rl}$

Genotype x Location Variance (σ^2_{gl}) = $\frac{M_{gl} - M_e}{r}$

Error variance (σ^2_e) = M_e ($\sigma^2_e = \frac{M_e}{r}$, *On genotypic mean basis*) (Allard, 1960)

Where:

M_g = Observed mean square for genotypes

M_{gl} = Observed mean square for genotypes x location interaction

M_e = Observed mean square for error

r = Number of replications

l = Number of Locations

Table 3.2: Form of ANOVA for one location

Source of variation	df	MS	EMS
Replication	(r-1)	M_l	
Genotype	(g-1)	M_g	$\sigma_e^2 + r\sigma_g^2$
Error	(g-1) (r-1)	M_e	σ_e^2
Total	(rg-1)		

Significance of the differences among the genotypes was tested by 'F' test using the error variance.

Table 3.3: Form of ANOVA for combined locations in one year

Source of variation	df	MS	EMS
Location	(l-1)		
Replication in location	1(r-1)	M_l	
Genotype	(g-1)	M_g	$\sigma_e^2 + r\sigma_{gl}^2 + rl\sigma_g^2$
Genotype X location	(g-1)(l-1)	M_{gl}	$\sigma_e^2 + r\sigma_{gl}^2$
Error	l(g-1)(r-1)	M_e	σ_e^2
Total	(lgr-1)		

Significance of the differences among the genotypes was tested by 'F' test using the error variance.

3.6.1.2 Heritability (h^2)

Heritability in broad sense was computed as the ratio of genotypic variance to the total phenotypic variance as suggested by Hanson (1963) and expressed as percentage.

Heritability (h^2) = $\frac{\sigma_g^2}{\sigma_{ph}^2} \times 100$

Where, σ_g^2 = Genotypic variance

σ_{ph}^2 = Phenotypic variance

The heritability percentage was categorized as low, moderate and high as given by Robinson *et al.* (1949) where 0-30% is considered low, 31-60% is moderate and >60% is high.

3.6.1.3 Correlation Coefficient

Correlation coefficient was computed from variance and covariance components as suggested by Wright (1968). Phenotypic and genotypic correlation estimates were used to determine the level of association between the agronomic traits and grain yield and was computed according to the formula by Singh and Chaudhary (1985).

Genotypic correlation $r_{gxy} = \frac{\sigma_{gxgy}}{\sqrt{\sigma_{gx}^2 \text{ x } \sigma_{gy}^2}}$

r_{gxy} = genotypic correlation of characters X and Y

σ_{gxgy}= genotypic covariance of characters X and Y

σ_{gx}^2= genotypic variance of character X

σ_{gy}^2= genotypic variance of character Y

Phenotypic correlation coefficient was computed using mean squares and mean cross products as follows:

Phenotypic correlation $r_{ph} = \frac{M_{gxgy}}{\sqrt{M_{gx} \times M_{gy}}}$

Where: r_{ph}= phenotypic correlation coefficient of characters X and Y

M_{gxgy} = entry mean product of characters X and Y

M_{gx} = entry mean square of character X

M_{gy} = entry mean square of character Y

3.6.2 Predicted Response to Selection

Predicted response to selection was determined using the formula given by Lush (1990).

ΔG = i.c. σ_{ph}. h^2

Where: i = Standardized selection differential often referred to as K
c = Parental control
σ_{ph} = Phenotypic standard deviation
h^2 = Heritability for the trait under consideration

CHAPTER FOUR

4.0 RESULTS

4.1 Results of Soil Analysis

The result of the physico-chemical analysis of the soil at both sites before land preparation showed that the soils were sandy loam with relatively low level of nitrogen and organic carbon. All the experimental plots had similar percentages of available phosphorus except for the high-N plot in Mokwa which was a little higher (Table 4.1).

Table 4.1: Pre-planting soil physical and chemical properties at the experimental sites

Parameters (%)	Low-N Plot		High-N Plot	
	Zaria	Mokwa	Zaria	Mokwa
Clay	12	10	10	11
Silt	20	21	26	20
Sand	68	69	68	70
Organic carbon	0.72	0.74	0.61	0.78
Texture class	Sandy Loam	Sandy Loam	Sandy Loam	Sandy Loam
Total nitrogen	0.140	0.180	0.21	0.290
Average phosphorus	10.50	10.56	10.50	11.01

4.2 Population Means

The results obtained for the 10 traits of the 125 S_1 lines of DMR ESR evaluated under both low N and high N levels in the individual locations and across the two locations are given in Tables 4.2 and 4.3, respectively.

Grain yield ranged from 151.55 kg/ha to 2444.44 kg/ha with an average of 608.62 kg/ha in Zaria and from 177.78 kg/ha to 2466.67 kg/ha with an average of 1798.4 kg/ha in Mokwa under low N. Average of the two locations ranged from 151.55 kg/ha to 2466.67 kg/ha with a mean of 1203.51 kg/ha under low N. The Coefficient of variation (CV) of the combined data for the population ranged from 11.69% for days to 50% silking to 77.54% for Anthesis-Silking interval (ASI) under low N level (Table 4.2).

Under high N level, grain yield ranged from 248.87kg/ha to 4960.00kg/ha with an average of 1181.37 kg/ha in Zaria and from 177.78kg/ha to 3022.59kg/ha with an average of 2922.80kg/ha in Mokwa while for the combined data, grain yield ranged from 177.78kg/ha to 4960.00kg/ha with an average of 1736.50kg/ha. The CVs ranged from 10.04% for days to 50% Silking to 70.53% for ears per plant under high N level across the two locations (Table 4.3). High CVs were also obtained for ASI in Zaria under both fertility levels. Generally, wide ranges were observed for ear height, stay green, days to 50% Silking, days to 50% pollen and anthesis-silking interval under both low and high-N levels**.** The highest grain yield obtained for this population was 2466.67kg/ha under low-N level and 4960kg/ha under high-N level across the two locations. The average yield reduction due to low N stress for this population was 30.69% across the two locations.

Table 4.2: Mean, Standard Error of the Mean (S.E.M), Range (Min. and Max. values) and Coefficient of Variation (CV) for the 10 Traits of 125 S_1 Lines of DMR ESR Population Evaluated under Low-N in Zaria, Mokwa and Combined Locations

	Zaria				Mokwa				Combined			
Traits	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)
D.Silk	69.04 ± 0.2297	59.00	77.00	5.26	55.48 ± 0.6163	50.00	59.00	1.75	62.26±0.3258	50.00	77.00	11.69
D.Pollen	67.59 ± 0.1901	59.00	75.00	4.44	54.00 ± 0.0671	56.00	56.00	1.96	60.79±0.3205	50.00	75.00	11.79
ASI	1.44 ± 0.0851	-2.00	6.00	93.03	1.48 ± 0.5814	-4.00	5.00	61.78	2.18±0.3332	-2.00	6.00	77.54
PLHT	116.90 ± 1.3059	67.00	197.00	17.66	163.32 ± 1.1924	110.00	230.00	11.54	140.11±1.3638	67.00	230.00	21.77
EHT	44.38 ± 0.8144	20.00	90.00	29.01	72.13 ± 0.8985	40.00	130.00	19.69	58.26±0.8676	20.00	130.00	33.30
HUSK	4.07 ± 0.0520	2.00	6.00	20.21	3.74 ± 0.0390	2.00	5.00	14.91	3.91±0.0322	2.00	6.00	18.46
S. Green	5.52 ± 0.5529	4.00	8.00	15.83	4.41 ± 0.0168	3.00	8.00	13.96	4.97±0.0419	3.00	8.00	18.46
E/Plant	0.54 ±0.0144	0.67	1.10	42.09	1.01 ± 0.0168	0.46	2.20	26.42	0.77±0.0152	0.67	2.2	43.84
E/Aspect	5.44 ± 0.0785	3.00	8.00	22.79	4.38 ± 0.5659	1.00	8.00	20.39	4.91±0.0539	1.00	8.00	24.49
GY kg/ha	608.62 ± 31.5141	151.55	2444.44	81.87	1798.40 ± 51.11	177.78	2466.67	44.93	1203.51±40.11	151.55	2466.67	74.52

D.Silk=Days to 50% silking, D.Pollen=Days to 50% pollen shed, ASI=Anthesis-Silking interval, PLHT=Plant height, EHT=Ear height, HUSK=Husk cover, S.Green=Stay green, E/Plant=Ears per plant, E/Aspect=Ear aspect, GY kg/ha=Grain yield per

Table 4.3: Mean, Standard Error of the Mean (S.E.M), Range (Min. and Max. values) and Coefficient of Variation (CV) for the 9 Traits of 125 S_1 Lines of DMR ESR Population Evaluated under High-N in Zaria, Mokwa and Combined Locations

	Zaria				Mokwa				Combined			
Traits	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ±S.E.M	Min. Values	Max. Values	C.V (%)
D.Silk	68.02±0.2215	58.00	76.00	5.14	57.15±0.1752	53.00	68.00	4.85	62.58±0.2212	53.00	76.00	10.04
D.Pollen	66.84±0.1845	58.00	75.00	4.3	54.91±0.1653	51.00	63.00	4.76	60.88±0.1782	51.00	75.00	10.80
ASI	1.18±0.0793	0.00	6.00	85.90	2.23±0.0524	-1.00	6.00	37.07	1.71±0.0453	-1.00	6.00	69.31
PLHT	117.50±1.0985	70.00	168.00	14.78	152.91±0.9218	100.00	189.00	9.35	135.21±1.0345	70.00	189.00	17.67
EHT	46.09±0.7311	20.00	84.00	25.08	67.16±0.8812	13.00	100.00	20.74	56.63±0.7121	13.00	100.00	29.27
HUSK	3.83±0.0552	2.00	6.00	22.79	3.06±0.0330	2.00	6.00	17.01	3.45±0.0498	2.00	6.00	23.57
E/Plant	0.69±0.0176	0.07	2.14	40.28	1.00±0.0485	0.20	4.00	46.68	0.85±0.0732	0.67	4.00	70.53
E/Aspect	5.70±0.0667	3	9.00	18.48	4.13±0.0349	3.00	6.00	13.37	4.91±0.0773	3.00	9.00	23.42
GY kg/ha	1181.37±38.66	248.87	4960.00	51.74	2922.80±40.54	177.78	3022.59	49.59	1736.5±49.88	177.78	4960.00	50.78

D.Silk=Days to 50% silking, D.Pollen=Days to 50% pollen shed, ASI=Anthesis-Silking interval, PLHT=Plant height, EHT=Ear height, HUSK=Husk cover, S.Green=Stay green, E/Plant=Ears per plant, E/Aspect=Ear aspect, GY kg/ha=Grain yield per hectare.

Similar results were obtained for the for the 225 S_1 lines of TZE COMP.3DT evaluated under both fertility levels (Tables 4.4 and 4.5). Grain yield ranged from 200 kg/ha to 2686.67 kg/ha with an average of 651.23 kg/ha in Zaria and from 177.77 kg/ha to 2642.22 kg/ha with an average of 2023.00 kg/ha in Mokwa under low N level. The combined data under low N revealed that grain yield ranged from 177.77kg/ha to 2686.67kg/ha with an average of 1337.36 kg/ha across the two locations. The coefficient of variation for the population ranged from 11.21% for days to 50% pollen to 73.36% for grain yield/ha across the two locations under low-N level (Table 4.4).

Under high N level, grain yield ranged from 188.45 kg/ha to 4266.67kg/ha with an average of 1309.06 kg/ha and from 177.78 kg/ha to 5155.56 kg/ha with an average of 2527.46 kg/ha in Zaria and Mokwa, respectively. The combined data showed that grain yield ranged from 177.78 kg/ha to 5155.56 kg/ha with an average of 1912.00 kg/ha across the two locations. The coefficient of variation ranged from 10.30% for days to 50% silking to 80.53% for ASI across the two locations under high-N level (Table 4.5). Wide ranges were observed for ear height and anthesis-silking interval. The highest grain yield of the S_1 lines for this population was 2686.67 kg/ha and 5155.56 kg/ha under low and high N levels, respectively. The average yield reduction due to low N stress for this population was 30.05% across the two locations.

Table 4.4: Mean, Standard Error of the mean (S.E.M), Range (Min. and Max. values) and Coefficient of Variation (CV) for the 10 Traits of 225 S_1 Lines of TZE COMP. 3DT Population Evaluated under Low-N in Zaria, Mokwa and Combined Locations

	Zaria				Mokwa				Combined			
Traits	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)
D.Silk	67.91±0.1858	56.00	75.00	5.81	55.18±0.0408	52.00	57.00	1.57	61.54±0.2326	52.00	75.00	11.34
D.Pollen	66.46±0.1605	56.00	74.00	5.13	53.93±9.0461	50.00	56.00	1.81	60.20±0.2249	50.00	74.00	11.21
ASI	1.44±0.0549	0.00	5.00	80.13	1.24±0.0285	0.00	4.00	48.74	1.34±0.0311	0.00	5.00	69.60
PLHT	125.25±0.8328	85.00	197.00	14.11	164.74±0.9832	105.00	220.00	12.67	144.99±0.9210	85.00	220.00	19.06
EHT	49.67±0.5419	20.00	84.00	23.15	75.15±0.7953	30.00	120.00	22.44	62.41±0.6417	20.00	120.00	30.85
HUSK	3.64±0.0390	0.00	6.00	22.77	3.76±0.0257	2.00	6.00	14.49	3.70±0.0235	0.00	6.00	19.01
S. Green	5.53±0.0459	3.00	9.00	17.60	3.66±0.0257	2.00	5.00	14.69	4.59±0.0408	2.00	9.00	26.66
E/Plant	0.59±0.0175	0.67	4.30	62.01	1.09±0.0138	0.30	0.30	26.77	0.85±0.0139	0.67	4.31	49.18
E/Aspect	5.58±0.0557	0.00	9.00	21.17	4.21±0.0849	2.00	2.0	42.86	4.89±0.0557	0.00	40.0	34.16
GY kg/ha	651.23±0.00	200.00	2686.67	69.92	2023±41.54	177.77	2642.22	43.57	1337.36±32.70	177.78	2686.67	73.36

D.Silk=Days to 50% silking, D.Pollen=Days to 50% pollen shed, ASI=Anthesis-Silking interval, PLHT=Plant height, EHT=Ear height, Husk=Husk cover, S.Green=Stay green, E/Plant=Ears per plant, E/Aspect=Ear aspect, GY kg/ha=Grain yield per hectare.

Table 4.5: Mean, Standard error of the mean (S.E.M), Range (Min. and Max. values) and Coefficient of Variation (CV) for the 9 traits of 225 S_1 lines of TZE COMP 3DT Population established and studied under High-N in Zaria, Mokwa and Combined Location

	Zaria				Mokwa				Combined			
Traits	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)

D.Silk	65.51±0.1799	56.0	76.00	5.83	54.51±0.0558	52.00	63.00	2.17	60.01±0.2061	52.00	76.00	10.30
D.Pollen	64.42±0.1557	56.0	76.00	5.13	52.84±0.0569	50.00	60.00	2.28	58.63±0.2101	50.00	76.00	10.75
ASI	1.09±0.0586	-2.00	5.00	113.88	1.67±0.0412	-2.00	4.00	52.33	1.38±0.0371	-2.00	5.00	80.53
PLHT	133.67±0.7611	100.00	187.00	12.07	166.97±0.8662	100.00	218.00	11.00	150.32±0.8003	100.00	218.00	15.97
EHT	54.31±0.5013	25.00	87.00	19.58	76.18±0.7276	40.00	122.00	20.26	65.24±0.5727	25.00	122.00	26.33
HUSK	3.20±0.0340	2.00	5.00	22.57	2.72±0.0278	1.00	5.00	21.62	2.96±0.0234	1.00	5.00	23.66
E/Plant	0.89±0.0134	0.14	2.25	34.73	1.18±0.0207	0.22	3.67	37.25	1.00±0.0137	0.14	3.67	41.11
E/Aspect	5.2±0.0407	2.00	8.00	16.58	4.15±0.0289	2.00	7.00	14.79	4.67±0.0305	2.00	8.00	19.56
GY kg/ha	1309.06±30.068	188.45	4266.67	48.62	2527.46±43.73	177.78	5155.56	45.76	1912.00±29.08	177.78	5155.56	52.31

D.Silk=Days to 50% silking, D.Pollen=Days to 50% pollen shed, ASI=Anthesis-Silking interval, PLHT=Plant height, EHT=Ear height, HUSK=Husk cover, S.Green=Stay green, E/Plant=Ears per plant, E/Aspect=Ear aspect, GY kg/ha=Grain yield per hectare.

The 257 S_1 lines of ACR 9331 DMRSR also showed variation within the genotypes for all the traits measured under both fertility levels. Under low N condition, grain yield ranged from 144.44 kg/ha to 2155.56 kg/ha with an average of 420.96 kg/ha and from 177.77 kg/ha to 2444.44 kg/ha with an average of 1424.99 kg/ha in Zaria and Mokwa, respectively. The combined data revealed that grain yield ranged from 144.44 kg/ha to 2444.44 kg/ha with an average of 922.97 kg/ha across the two locations. The Coefficient of variation for the population ranged from 11.37% for days to 50% pollen shed to 82.01% for grain yield/plot across the two locations under low-N level (Table 4.6).

Under high N levels, grain yield ranged from 106.67 kg/ha to 3555.56 kg/ha with an average of 593.76 kg/ha and from 177.78 kg/ha to 4777.78kg/ha with an average of 2144.66 in Zaria and Mokwa, respectively. The combined data showed that the yield ranged from 106.67 kg/ha to 4777.78 kg/ha with an average of 1369.21 kg/ha. The CVs ranged from 12.27% for days to 50% silking to 78.25% for ASI across the two locations under high-N level (Table 4.7). Wide ranges were also observed for ear height (23.00-110.00cm) and anthesis-silking interval (ASI) (2.00-6.00 days)**.** The highest grain yield of the S_1 lines for this population was 2444.44 kg/ha and 4777.78kg/ha across the two locations under low-N level and high-N levels, respectively. The average yield reduction due to low N stress for this population was 32.59% across the two locations.

Table 4.6: Mean, Standard Error of the Mean (S.E.M), Range (Min. and Max. values) and Coefficient of Variation (CV) for the 10 Traits of 257 S_1 Lines of ACR 9331 DMR SR Population Evaluated under Low-N in Zaria, Mokwa and Combined Locations

	Zaria				Mokwa				Combined			
Traits	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)
D.Silk	66.65±0.1681	58.00	75.00	5.72	54.13±0.0614	49.00	66.00	2.57	60.39±0.2148	49.00	75.00	11.41
D.Pollen	65.33±0.1415	56.00	75.00	4.90	52.85±0.0652	48.00	63.00	2.80	59.09±0.2096	48.00	75.00	11.37
ASI	1.31±0.0517	0.00	3.00	89.35	1.27±0.0288	-1.00	3.00	51.48	1.29±0.0295	-1.00	3.00	73.48
PLHT	105.15±0.6699	75.00	164.00	14.44	142.610.85177	95.00	200.00	13.54	123.88±0.7967	75.00	200.00	20.62
EHT	38.72±0.4089	24.00	80.00	23.94	58.43±0.6729	25.00	110.00	26.11	48.58±0.4994	24.00	110.00	32.96
HUSK	3.93±0.1504	0.00	4.00	21.42	3.91±0.0322	0.00	4.00	18.72	3.92±0.0246	0.00	4.00	20.11
S. Green	6.01±0.0353	1.00	8.00	13.32	3.66±.0253	2.00	5.00	15.68	4.83±0.0426	1.00	8.00	28.26
E/Plant	0.59±0.2272	0.06	4.00	8738	1.08±0.2230	1.00	6.00	46.96	0.83±0.0176	0.07	10.00	67.85
E/Aspect	6.05±0.0462	3.00	8.00	17.37	4.35±0.2681	10.0O	14.00	30.93	5.20±0.0460	0.90	14.00	28.35
GY kg/ha	420.96±11.54	144.44	2155.56	62.19	1424.99±33.397	177.77	2444.44	53.14	922.97±23.6067	144.44	2444.44	82.01

D.Silk=Days to 50% silking, D.Pollen=Days to 50% pollen shed, ASI=Anthesis-Silking interval, PLHT=Plant height, EHT=Ear height, HUSK=Husk cover, S.Green=Stay green, E/Plant=Ears per plant, E/Aspect=Ear aspect, GY kg/ha=Grain yield per hectare.

Table 4.7: Mean, Standard Error of the Mean (S.E.M), Range (Min. and Max. values) and Coefficient of Variation (CV) for the 9 Traits of 257 S_1 Lines of ACR 9331 DMR SR Population Evaluated under High-N in Zaria, Mokwa and Combined Locations

	Zaria				Mokwa				Combined			
Traits	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)	Mean ± S.E.M	Min. Values	Max. Values	C.V (%)
D.Silk	66.26±0.2116	49.00	76.00	7.24	53.66±	49.00	71.00	4.46	59.96±0.2311	49.00	76.00	12.27
D.Pollen	64.85±0.1933	46.00	74.00	6.76	51.99±	46.00	67.00	4.54	58.42±0.1871	46.00	74.00	12.54
ASI	1.42±0.0652	-1.00	6.00	94.23	1.67±	-2.00	6.00	50.19	1.54±0.0871	-2.00	6.00	78.25
PLHT	104.13±0.8398	60.00	165.00	18.29	155.77±	54.00	220.00	12.27	129.94±0.9421	57.00	221.00	24.71
EHT	37.71±0.4727	20.00	103.00	28.43	67.64±	26.00	110.00	20.49	52.67±0.4320	23.00	110.00	36.89
HUSK	3.82±0.0341	2.00	5.00	20.26	2.98±	0.00	5.00	20.89	3.39±0.0291	0.00	5.00	24.06
E/Plant	0.71±0.0231	0.09	4.00	73.68	1.13±	0.90	4.00	48.69	0.92±0.0311	0.09	4.00	62.65
E/Aspect	5.98±0.0383	3.00	9.00	14.49	4.46±	3.00	9.00	43.74	5.22±0.0387	3.00	9.00	32.37
GY kg/ha	593.76±19.2194	106.67	3555.56	73.39	2144.66±	177.78	4777.78	40.27	1369.21±18.99	106.67	4777.78	75.52

D.Silk=Days to 50% silking, D.Pollen=Days to 50% pollen shed, ASI=Anthesis-Silking interval, PLHT=Plant height, EHT=Ear height, HUSK=Husk cover, S.Green=Stay green, E/Plant=Ears per plant, E/Aspect=Ear aspect, GY kg/ha=Grain yield per hectare.

4.3 Population Variability

The mean squares for the 125 S_1 lines of DMR ESR population were highly significant ($P<0.01$) for most of the traits studied under low N levels, except for ASI which was not significant in both locations. The mean squares for plant height and ear height were only significant ($P<0.05$) in Mokwa. The combined ANOVA showed that the mean squares for the genotypes were significant for grain yield and husk cover, while they were highly significant for other traits. The mean squares for genotype x locations were highly significant for all the traits except for stay green which was only significant ($P<0.05$), whereas mean square for ASI was not significant (Table 4.8).

The mean squares were highly significant for almost all the traits studied under high N level except for ear aspect which was not significant in both locations. Also the mean squares for number of ear per plant and husk cover were not significant in Zaria and Mokwa respectively. The combined ANOVA showed that the mean squares for the genotypes and genotype x location were highly significant for all the traits studied (Tables 4.9).

Table 4.8: Mean Squares for the 10 Traits of 125 S_1 Lines of the DMR ESR-W Population Evaluated under Low-N in Zaria, Mokwa and across the two Locations

*= Significant difference at 5% level of probability ; **= Significant at 1% level of Probability

Sources of variation	df	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	S. Green	E/Plant	E/Aspect	Yield
					ZARIA						
Rep	1	0.7840	0.2560	0.1440	391.8760	462.4000	2.7040	0.3240	13.4560	5.1840	1488930.84
Genotypes	124	17.25**	11.56**	2.33	578.77**	204.97**	0.90**	0.97**	11.92**	1.41**	248759.20**
Error	124	9.2356	6.5866	1.3134	274.2954	124.2790	0.4378	0.5578	11.0931	1.6437	237805.99
Total	249										
					MOKWA						
Rep	1	4.6232	0.5760	1.9360	1695.2040	1048.5760	0.0160	3.6000	0.0023	0.0360	1140938.30
Genotypes	124	1.01**	1.12**	0.80	408.87*	258.04*	0.41**	0.39**	0.09**	0.78**	931615.71**
Error	124	0.8578	1.1325	0.8795	291.3249	138.8018	0.2176	0.3419	0.0572	0.8263	370695.30
Total	249										
					COMBINED						
Loc	1	22957.0	23092.8	0.20	269398.47	96271.69	13.45	153.46	26.86	140.45	1769463.10
Rep(Loc)	2	4.60	0.80	1.57	1858.59	1451.80	1.15	0.88	0.02	3.04	2618306.40
Genotypes	124	10.05**	7.21**	1.49**	625.47**	268.58**	0.81*	0.74**	0.09**	1.18**	680218.50*
Genotypes x Loc	124	8.21**	5.47**	1.64	362.17**	194.43**	0.50**	0.62*	0.06**	1.02**	50016.50**
Error	249	5.02	3.84	1.09	282.59	131.25	0.33	0.46	0.049	1.29	303075.20
Total	499										

Table 4.9: Mean Squares for the 9 Traits of 125 S_1 Lines of the DMR ESR-W Population Evaluated under High-N in Zaria,

Sources of variation	df	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	E/Plant	E/Aspect	Yield

Mokwa and across the two Locations

					ZARIA					
Rep	1	40.80	24.96	1.94	298.12	84.10	8.10	0.10	7.39	127037.95
Genotypes	124	17.95**	12.78**	2.16**	494.11**	203.89**	0.94**	0.10	1.53	525298.09**
Error	124	6.34	4.12	0.98	109.31	63.77	0.52	0.05	0.64	223993.74
Total	249									
					MOKWA					
Rep	1	5.77	15.88	2.50	1281.42	191.84	0.68	0.002	0.40	5469424.20
Genotypes	124	11.32*	9.93**	0.72**	329.09**	213.81**	0.32	0.84**	0.34	551685.61**
Error	124	4.04	3.66	0.64	87.17	174.44	0.22	0.35	0.40	229376.40
Total	249									
					COMBINED					
Loc	1	14764.18	17760.80	138.34	156751.22	55503.65	72.20	11.88	308.90	1552111.57
Rep/ Loc	2	38.64	40.32	0.18	1407.84	10.95	6.73	0.54	2.18	3631792.36
Genotypes	124	21.66**	17.19**	1.57**	523.54**	253.54**	0.82**	0.47**	1.90**	765480.66**
Genotypes x Loc	124	7.61**	5.52**	1.31**	299.66**	164.17**	0.45**	0.46**	0.78**	311503.04**
Error	249	5.20	3.87	0.83	98.54	119.69	0.38	0.19	0.47	233664.90
Total	499									

*= Significant difference at 5% level of probability ; **= Significant at 1% level of Probability

The analysis of variance for the S_1 lines of TZE COMP. 3DT evaluated across the two locations at each fertility level demonstrated highly significant differences ($P<0.01$) among the genotypes in each of the two locations except for number ears per plant and ear aspect in Zaria and husk cover and ear aspect in Mokwa under low-N. The combined mean squares for the genotypes evaluated under low-N environment across the two locations showed significant differences for all the traits, while the mean squares for genotype x location were highly significant for all traits except for ear height, stay green, ears per plant and ear aspect under low N which are only significant (Table 4.10).

Similar results were observed for the same genotypes evaluated under high-N, the mean squares were significant for all the traits across the two locations. The combine ANOVA showed that the mean squares are significant for most of the traits except for plant height, ear aspect and grain yield which are highly significant (Table 4.11).

Table 4.10: Mean Squares for 10 Traits of 225 S_1 Lines of the TZE COMP. 3DT Population Established under Low-N in Zaria, Mokwa and across the two Locations

*= Significant difference at 5% level of probability ; **= Significant at 1% level of Probability

Sources of variation	df	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	S. Green	E/Plant	E/Aspect	Yield kg/ha
					ZARIA						
Rep	1	30.68	12.64	3.93	594.00	324.67	1.8	0.57	2.47	3.05	2438100.39
Genotypes	224	23.28**	17.19**	1.59**	378.27**	146.48*	0.81**	0.83*	0.13	1.32	256307.92**
Error	224	7.84	6.04	1.12	246.26	117.91	0.56	1.07	0.14	1.48	158550.75
Total	449										
					MOKWA						
Rep	1	10.58	2.88	2.42	1658.88	921.63	9.38	0.06	0.27	2.42	6662383.00
Genotypes	224	0.86**	1.12**	0.39**	476.32**	286.39*	0.28	0.33*	0.09**	3.27	625159.90**
Error	224	0.63	0.80	0.34	394.04	282.81	0.31	0.25	0.08	3.23	928406.30
Total	449										
					COMBINED						
Loc	1	36295.7	35175.0	8.79	350681.57	145920.12	3.48	792.19	55.69	426.48	422772880.9
Rep/ Loc	2	38.63	13.79	6.11	134.24	1170.61	1.53	0.49	2.21	0.02	8583861.50
Genotypes	224	13.36**	10.34**	0.94*	497.24**	247.04**	0.62**	0.87**	0.13**	2.53**	743729.7**
Genotypes x Loc	224	10.72**	7.91**	1.04**	357.66*	185.19*	0.48**	0.53*	0.09*	2.22*	441876.7*
Error	449	4.24	3.42	0.73	320.15	200.36	0.44	0.54	0.11	2.27	391855.3
Total	899										

Table 4.11: Mean Squares for the 9 Traits of 225 S_1 Lines of the TZE COMP. 3DT Population Established under High-N in Zaria, Mokwa and across the two Locations

Sources of variation	df	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	E/Plant	E/Aspect	Yield
					ZARIA					
Rep	1	117.56	32.54	26.40	560.01	628.94	2.13	1.43	12.84	13686291.9
Genotypes	224	21.39**	16.10**	1.93**	366.82**	145.37**	0.62*	0.09*	0.97**	475334.6**
Error	224	7.79	5.74	1.16	155.04	81.02	0.43	0.08	0.52	335342.6
Total	449									
					MOKWA					
Rep	1	13.52	9.10	0.44	190.78	47.37	5.56	0.09	0.06	25115671.9
Genotypes	224	1.49*	1.35*	0.83**	376.42**	244.11**	0.37*	0.22**	0.43**	1190037.5**
Error	224	1.31	1.56	0.70	298.99	232.37	0.33	0.17	0.33	532929.5
Total	449									
					COMBINED					
Loc	1	27203.0	30148.5	75.69	249500.25	107584.0	51.36	28.85	248.59	116120898.8
Rep/ Loc	2	25.67	3.61	10.02	702.25	165.56	7.29	0.40	5.60	37941219.7
Genotypes	224	12.35**	9.76**	1.28**	491.05**	244.05**	0.59*	0.15**	0.94**	1144513.8**
Genotypes x Loc	224	10.52*	7.70*	1.48*	252.19**	145.42*	0.39*	0.15*	0.46**	520858.4**
Error	449	4.55	3.65	0.93	227.02	156.69	0.38	0.12	0.42	434136.0
Total	899									

*= Significant difference at 5% level of probability ; **= Significant at 1% level of Probability

The analysis of variance demonstrated highly significant differences ($P<0.01$) among the 257 S_1 lines of ACR 9931 DMR SR in each location except for ears per plant and ear aspect in both locations under low N level. However, the combined ANOVA for the genotypes evaluated under low-N environment across the two locations showed that mean squares for the genotypes were highly significant for all the traits. The G×L mean squares were significant for all the traits under low N condition (Table 4.12).

Highly significant differences for genotypes were also observed for most of the traits except which is only significant under high N level at both locations. G×L mean squares were also highly significant for all the traits except for husk cover and ear aspect which are significant at $P<0.05$ under high-N condition (Table 4.13).

Table 4.12: Mean Squares for the 10 Traits of 257 S_1 lines of the ACR 9331 DMR SR Population Established under Low-N in Zaria Mokwa and across the two Locations

*= Significant difference at 5% level of probability ; **= Significant at 1% level of Probability

Sources of variation	df	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	S. Green	E/Plant	E/Aspect	Yield
						ZARIA					
Rep	1	67.31	47.35	1.75	870.74	275.05	0.00	4.67	0.93	1.22	57622.15
Genotypes	256	19.97**	14.05**	1.57**	331.02**	109.93**	0.90**	0.74**	0.44	1.27	84552.58**
Error	256	8.89	6.38	1.18	127.91	61.21	0.52	0.53	0.08	0.92	52574.50
Total	453										
						MOKWA					
Rep	1	106.94	75.79	2.53	667.58	1355.25	5.90	0.86	0.02	0.07	1826172.6
Genotypes	256	1.86**	2.33**	0.43*	459.19**	264.72**	0.61**	0.36*	0.27	1.81	754472.6**
Error	256	1.62	1.76	0.42	284.87	196.65	0.44	0.30	0.24	1.82	385855.2
Total	453										
						COMBINED					
Locations	1	40189.3	39952.4	0.39	360383.28	100403.33	0.08	1421.58	60.90	739.99	258639381.9
Rep/Loc	2	2.25	1.64	0.04	1542.46	1424.64	2.95	0.76	0.61	0.93	1264561.6
Genotypes	256	11.90**	8.82**	1.02**	514.76**	216.13**	0.95**	0.62**	0.41**	1.63**	513976.6**
Genotypes x Loc	256	9.88**	7.53**	0.97**	275.47**	159.28**	0.56**	0.47**	0.31**	1.45*	326160.4**
Error	453	5.59	4.30	0.81	205.84	128.94	0.49	0.42	0.16	1.37	219670.7
Total	907										

Table 4.13: Mean Squares for the 9 traits of 257 S_1 Lines of the ACR 9331 DMRSR Population Established under High-N in Zaria Mokwa and across the two Locations

*= Significant difference at 5% level of probability ; **= Significant at 1% level of Probability

Sources of variation	df	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	E/Plant	E/Aspect	Yield kg/ha
					ZARIA					
Rep	1	125.50	116.69	0.16	283.88	4.75	0.33	1.28	0.19	6498.38
Genotypes	256	27.87**	23.59**	2.46**	437.13**	134.00**	0.71*	0.35**	0.92**	266511.76**
Error	256	17.78	14.44	1.92	287.29	96.07	0.48	0.19	0.58	113344.84
Total	453									
					MOKWA					
Rep	1	56.37	44.47	0.70	0.22	71.91	1.15	4.08	55.05	1482370.5
Genotypes	256	8.69**	8.74**	0.76**	505.32**	262.74**	0.53*	0.33**	3.97**	1208648.7**
Error	256	2.72	2.43	0.64	233.04	124.89	0.25	0.26	3.47	301592.0
Total	453									
					COMBINED					
Loc	1	39586.11	41169.14	15.52	655397.04	226319.19	176.60	45.34	568.33	599042211.10
Rep/Loc	2	174.82	152.39	0.77	133.18	57.02	0.13	0.41	24.50	847409.60
Genotypes	256	19.89**	17.86**	1.63**	586.39**	226.92**	0.77**	0.30**	2.39**	861407.1**
Genotypes x Loc	256	16.73**	14.41**	1.64**	350.84**	166.15**	0.47*	0.38**	2.46*	576319.3**
Error	453	10.14	8.35	1.27	259.59	110.49	0.37	0.24	2.10	209578.0
Total	907									

4.4 Estimates of Genetic Variance Components

Estimates of genetic variance components obtained for each location are presented in Tables 4.14 to 4.15. In nearly all the cases, phenotypic (σ_{ph}^2) and environment (σ_e^2) variances exceeded their respective standard errors at both N levels. In some cases, the estimates of genetic (σ_g^2) variance and genotype x environment interaction variances (σ_{gl}^2) were either negative or smaller than their standard errors. Phenotypic variance (σ_{ph}^2) was largest for all the traits amongst the three population sets, however, it was lower than the error variance (σ_e^2) for the combined analysis for the three maize populations. The estimated genetic variances for days to 50% silking, plant height, ear height, stay green and grain yield were large enough for effective selection.

The 125 S_1 lines of DMR ESR-W evaluated under low-N level across the two locations showed positive genotypic variance (σ_g^2) for most of the traits except for ASI and days to 50% pollen shed at Mokwa and ear aspect at both location which were negative. Phenotypic variance (σ_{ph}^2) and error variance (σ_e^2) were positive for all the traits (Table 4.14). The major component that contributed to the expression of the phenotypic variance for most of the traits was attributable to the genotypic variance (σ_g^2). The estimate of σ_{gl}^2 were relatively lower compared to those of σ_{ph}^2 and σ_e^2 for all the traits while it was slightly higher than the σ_g^2 for days to 50% silking, days to 50% pollen shed and ASI under low N condition. Plant height, ear height and grain yield per hectare had the largest estimates for σ_{ph}^2, σ_e^2 and σ_{gl}^2 across the two locations (Table 4.15).

Under high N level, the genotypes showed positive σ_g^2 for all the traits in each location. Phenotypic variance (σ_{ph}^2) and error variance (σ_e^2) were also positive for all the traits in both locations. The estimate of σ_{gl}^2 were relatively lower compared to those of σ_{ph}^2 and σ_e^2 for most of the traits except for plant height (Tables 4.16 and 4.17).

Table 4.14: Estimates of Genotypic Variance(σ_g^2), Phenotypic Variance (σ_{ph}^2) and Error Variance(σ_e^2), for the 10 Traits of the 125 S_1 Lines of DMR ESR-W Population Established under Low-N in Mokwa and Zaria

	ZARIA			MOKWA		
Traits	σ_g^2	σ_e^2	σ_{ph}^2	σ_g^2	σ_e^2	σ_{ph}^2
D.Silk	4.0096±0.11	4.6178±3.98	8.6274±3.45	0.0770±0.01	0.4289±0.32	0.5059±0.26
D.Pollen	2.4865±0.05	3.2933±2.34	5.7798±1.23	-	0.5663±0.45	0.5606±1.59
ASI	0.5079±0.12	0.6567±0.54	1.1646±0.12	-	0.4397±0.12	0.4011±1.10
PLHT	152.2394±35.50	137.1477±103.45	289.3871±134.90	58.7700±18.98	145.6625±123.67	204.4325±131.89
EHT	40.3449±12.34	62.1395±45.87	102.4844±45.89	59.6208±23.76	69.4009±56.87	129.0217±56.00
HUSK	0.2315±0.03	0.2189±0.12	0.4504±0.28	0.0953±0.002	0.1088±0.23	0.2041±0.13
S. Green	0.2084±0.12	0.2789±0.24	0.4873±0.34	0.0255±0.011	0.1709±0.14	0.1964±0.38
E/Plant	0.0103±0.03	0.0209±0.01	0.0312±0.01	0.0136±0.001	0.0286±0.01	0.0422±0.01
E/Aspect	-0.1169±0.12	0.8218±0.78	0.7049±0.68	-	0.4132±0.31	0.3906±0.24
Yield	5971.665±0.3	117529.16±345689.0	123500.825±23478.0	280460.2000±456789.12	185347.65±123456.90	465807.5000±345678.20

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=$\sigma^2_{ph;}$

Table 4.15: Estimate of Genotypic Variance(σ_g^2), Phenotypic Variance(σ_{ph}^2), Error Variances (σ_e^2) and Genotype X Environment Interaction Variance (σ_{gl}^2) for the 10 Traits of the 125 S_1 Lines of DMR ESR-W Population Established under Low-N across the two Locations (Mokwa and Zaria)

Traits	σ_g^2	σ_e^2	σ_{gl}^2	σ_{ph}^2
D.Silk	0.4602±0.14	5.0297±2.13	1.5917±0.34	2.5134±0.34
D.Pollen	0.4355±0.17	3.8442±0.34	0.8126±0.21	1.8028±0.73
ASI	-	1.0941±0.01	0.2707±0.11	0.3740±0.23
PLHT	65.8270±29.01	282.5920±24.45	39.7868±0.24	156.3684±24.56
EHT	18.5361±6.57	131.2498±23.45	31.5921±4.32	67.1446±32.89
HUSK	0.0750±0.10	0.3327±0.23	0.0859±0.001	0.2011±0.10
S. Green	0.0303±0.01	0.4603±0.12	0.0815±0.01	0.1861±0.10
E/Plant	0.0060±0.010	0.0494±0.01	0.0060±0.01	0.0213±0.01
E/Aspect	0.0405±0.02	1.2388±0.50	-	0.2941±0.01
Yield	45004.1250±10000.0	301670.4000±23445.87	98815.0000±2345.0	169829.2250 ±30000.0

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=σ^2_{ph}; Genotype x Location Variance=σ^2_{gl}

Table 4.16: Estimate of Genotypic Variance(σ_g^2), Phenotypic Variance(σ_{ph}^2) and Error Variances (σ_e^2) for the 9 traits of the 125 S_1 Lines of DMR ESR-W Population Established under High-N in Mokwa and Zaria

	ZARIA
MOKWA	

Traits	σ_g^2	σ_e^2	σ_{ph}^2	σ_g^2	σ_e^2	σ_{ph}^2
D.Silk	5.8093±2.34	3.1681±2.12	8.9774 ±3.43	3.6371±0.56	2.0210±1.78	5.6581±1.45
D.Pollen	4.3316±1.90	2.0586 ±1.65	6.3902±2.32	3.1375±1.23	1.8291±0.98	4.9666±2.43
ASI	0.5866±0.23	0.4922±0.86	1.0788±0.32	0.0426±0.01	0.3185±0.23	0.3611±0.34
PLHT	192.4017±24.56	54.6548±23.78	247.0565±45.10	120.9576±31.45	43.5870±23.10	164.5440±54.45
EHT	70.0645±21.13	31.8847±21.12	101.9492±35.09	19.6819±3.67	87.2244±34.56	106.9863±43.23
HUSK	0.2125±0.01	0.2597±0.02	0.4722±90.21	0.0465±0.23	0.1122±0.01	0.1587±0.22
E/Plant	0.0238±0.01	0.0269±0.02	0.0507±0.01	0.2460±0.01	0.1729±0.02	0.4187±0.34
E/Aspect	0.44720.12	0.3189±0.13	0.7661±0.31	0.0415±0.01	0.13145±0.10	0.1729±0.01
Yield	150652.17±20000	111996.87±12345.	262649.04±123.			275842.80±23456.
	.1	56	78	161154.60±12455.45	14688.20±12777.00	78

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=σ^2_{ph}

Table 4.17: Estimate of Genotypic Variance(σ_g^2), Phenotypic Variance (σ_{ph}^2), Error Variances (σ_e^2) and Genotype X Environment Interaction Variance (σ_{gl}^2) for the 9 Traits of the 125 S_1 Lines of DMR ESR-W Population Established under High-N across the two Locations (Mokwa and Zaria)

Traits	σ_g^2	σ_e^2	σ_{gl}^2	σ_{ph}^2
D.Silk	3.5111±1.21	5.2002±1.98	1.2066±0.11	5.4144±1.90
D.Pollen	2.9176±1.01	3.8742±1.23	0.823±80.23	4.2980±1.87

ASI	0.0671±0.01	0.8252±0.31	0.2403±0.11	0.3935±0.12
PLHT	55.9718±18.90	98.5368±39.23	100.5604±34.54	130.8862±40.90
EHT	22.3416±10.09	119.6950±46.90	22.2386±8.90	63.3847±23.54
HUSK	0.0924±0.03	0.3786±0.12	0.0337±0.23	0.2039±0.10
E/Plant	0.0011±0.01	0.1990±0.01	0.1342±0.04	0.1179±0.01
E/Aspect	0.0790±0.02	0.4712±0.02	0.1549±0.05	0.2743±0.11
Yield	113494.4050±10008.98	233664.9000±98667.01	38919.0700±12678.34	191370.1650±12222.32

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=$\sigma^2_{ph;}$ Genotype x Location Variance=σ^2_{gl}

Similar results were obtained for the 11 traits of the 225 S_1 lines of TZE COMP. 3DT evaluated under low-N and high-N levels in Mokwa and Zaria. The genotypes showed positive σ_g^2 for most of the traits studied under low-N level except for number of ears per plant in Zaria and husk cover in Mokwa, while Phenotypic variance (σ_{ph}^2) and error variance (σ_e^2) were positive for all the traits in the two locations (Table 4.18). Days to 50% silking, days to 50% pollen shed, ear aspect, plant height, ASI, husk cover and grain yield all showed positive σ_{gl}^2, while stay green, number of ears per plant, ear height and ear aspect revealed negative σ_{gl}^2 (Table 4.19).

Under the high-N level, the genotypes revealed positive σ_g^2 for all the traits in each location except for days to 50% pollen shed in Mokwa which showed negative σ_g^2 estimate. The phenotypic and error variances were relatively large and positive for all the traits (Table 4.20). Positive σ_{gl}^2 estimates were obtained for most of the traits except for ear height which showed a negative estimate. Plant height, ear height and grain yield per hectare had large estimates for σ_{ph}^2, σ_e^2 and σ_{gl}^2 estimates (Tables 4.21).

Table 4.18: Estimate of Genetic Variance (σ_g^2), Phenotypic Variance(σ_{ph}^2), and Error Variances(σ_e^2) for the 10 Traits of the 225 S_1 Lines of TZE COMP. 3DT Population Established under Low-N in Mokwa and Zaria

	ZARIA			MOKWA		
Traits	σ_g^2	σ_e^2	σ_{ph}^2	σ_g^2	σ_e^2	σ_{ph}^2
D.Silk	7.7219±2.78	3.9192±2.45	11.6411±5.10	0.1133±0.01	0.3189±0.31	0.4322 ±0.24.50
D.Pollen	5.5727±2.12	3.0215±1.89	8.5942±2.32	0.1580±0.012	0.4000±0.23	0.5380±0.12
ASI	0.2369±0.02	0.5622±0.21	0.7991±0.45	0.0222±0.01	0.1722±0.023	0.1944±0.02
PLHT	66.0035±12.45	123.1304±65.89	189.1339±89.10	41.1408±12.23	197.0178±87.08	283.1584±78.98
EHT	14.2885±3.45	58.9537±34.56	73.2422±68.74	1.7882±0.23	141.4045±90.98	143.1927±89.09
HUSK	0.1239±0.19	0.2811±0.21	0.4050±0.12	-	0.1566±0.46	0.1487±0.01
S. Green	0.1179±0.01	0.4155±0.11	0.5334±0.30	0.0421±0.001	0.1233 ±0.01	0.16545±0.02
E/Plant	-	0.0713±0.01	0.0666±0.01	0.0110±0.001	0.0375±0.001	0.0485±0.06
E/Aspect	0.0795±0.001	0.6589±0.23	0.7384±0.03	0.0223±0.01	1.6144±1.23	1.6367±0.98
Yield	48878.58±12001.1			151623.20±45987.		
	0	79275.38±9099.0	128154.00± 89761.98	1	312580.00±9087.34	464203.20±1323.90

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=σ^2_{ph}

TABLE 4.19: Estimate of Genotypic Variance(σ_g^2), Phenotypic Variance(σ_{ph}^2), Error Variances (σ_e^2) and Genotype X Environment Interaction variance (σ_{gl}^2) for the 10 Traits of the 225 S_1 Lines of TZE COMP. 3DT Population Established under Low-N across the two Location (Mokwa and Zaria)

Traits	σ_g^2	σ_e^2	σ_{gl}^2	σ_{ph}^2
D.Silk	0.6610±0.13	4.2382±1.98	3.2395±1.23	3.3403±1.23
D.Pollen	0.6059±0.17	3.4215±1.43	2.2460±0.67	2.5842±0.93
ASI	-	0.7344±0.23	0.1542±0.01	0.2355±0.05
PLHT	34.8947±8.98	320.1481±79.90	18.7563±4.21	124.3098±45.89
EHT	15.4617±4.98	200.3581±45.67	-	61.7605±18.98
HUSK	0.0350±0.01	0.4378±0.13	0.0188±0.01	0.1539±0.01
S. Green	0.0851±0.01	0.5389±0.19	-	0.2173±0.02
E/Plant	0.0094±0.01	0.1089±0.20	-	0.03360.01
E/Aspect	0.0766±0.03	2.273±0.33	-	0.6322±0.23
Yield	75463.2500±12345.09	391855.3000±123456.09	25010.7000±64454.09	185932.4250±68970.01

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=$\sigma^2_{ph;}$ Genotype x Location Variance=σ^2_{gl}

Table 4.20: Estimate of Genotypic Variance(σ_g^2), Phenotypic Variance(σ_{ph}^2) and Error Variances (σ_e^2) for the 9 Traits of the 225 S_1 Lines of TZE COMP. 3DT Population Established under High-N in Mokwa and Zaria

	Zaria			Mokwa		
Traits	σ_g^2	σ_e^2	σ_{ph}^2	σ_g^2	σ_e^2	σ_{ph}^2

D.Silk	6.7996±2.45	3.8933 ± 2.90	10.6929±3.23	0.0886±0.01	0.6555±0.02	0.7441±0.48
D.Pollen	5.1838±1.98	2.8678±1.23	8.0516±1.23	-	0.7778±0.04	0.6756 ±0.34
ASI	0.3871±0.12	0.5789±0.89	0.9660±0.23	0.062±60.02	0.3511±0.28	0.4137±0.43
PLHT	105.8893±30.34	77.5222±28.90	183.4115±65.89	38.7157±7.98	149.4945±78.94	188.2020±28.09
EHT	32.1746±9.89	40.5089±20.98	72.6836±20.34	5.8693±1.80	116.1845±83.23	122.0538±67.34
HUSK	0.0938±0.01	0.2144±0.12	0.0387±0.17	0.0182±0.01	0.1644±0.19	0.1826±0.11
E/Plant	0.0040±0.001	0.0387±0.011	0.0427±0.02	0.0276±0.01	0.0827±0.05	0.1103±0.01
E/Aspect	0.2244±0.01	0.2600±0.18.	0.4844±0.20	0.0499±0.01	0.1633±0.02	0.2132±0.11
Yield	69996.0±20890.1					
	0	16671.30±145091..01	237667.00±120012.01	328554.0±154452.12	266464.80±11111.2	595018.80±120111.12

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=σ^2_{ph}

Table 4.21: Estimate of Genotypic Variance(σ_g^2), Phenotypic Variance(σ_{ph}^2), Error Variances(σ_e^2) and Genotype X Environment Interaction Variance $\left(\sigma_{gl}^2\right)$ for the 9 Traits of the 225 S_1 Lines of TZE COMP. 3DT Population Established under High-N across the two Location (Mokwa and Zaria)

Traits	σ_g^2	σ_e^2	σ_{gl}^2	σ_{ph}^2
D.Silk	0.4574±0.13	4.5489±1.89	2.9867±0.98	3.0880±0.23
D.Pollen	0.5165±0.18	3.6456±1.78	2.0248±0.84	2.4403±0.94
ASI	-	0.9300±0.23	0.2729±0.01	0.3209±0.14

PLHT	59.7148±21.34	227.0167±89.09	12.5877±3.67	122.7628±32.34
EHT	24.6577±10.21	156.6933±45.52	-	61.0131±19.08
HUSK	0.0504±0.01	0.3789±0.15	0.0056±0.00	0.1479±0.01
E/Plant	0.0009±0.00	0.1214±0.01	0.0148±0.001	0.0387±0.001
E/Aspect	0.1208±0.01	0.4233±0.05	0.0164±0.001	0.2348±0.01
Yield	155913.8±89761.34	434136.0±98765.78	43361.2±987.90	286128.4±97543.34

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=$\sigma^2_{ph;}$ Genotype x Location Variance=σ^2_{gl}

The 257 S_1 lines of ACR 9331 DMR ESR evaluated under both low-N and high-N levels revealed positive genotypic variances for all the traits studied in the two locations except for ear aspect in Mokwa under low N level. Phenotypic variance (σ_{ph}^2) and error variance (σ_e^2) estimates were larger than the genotypic variance (σ_g^2) estimate under both fertility levels in the two locations (Table 4.22). Positive σ_{gl}^2 estimates were obtained for all the traits and were greater than the corresponding σ_g^2 estimate for most of the traits except for plant height and stay green which had values lower than the corresponding σ_g^2 estimates (Tables 4.23).

Under high-N level, the genotypes revealed positive σ_g^2 and σ_{ph}^2 estimates for all the traits in both location. The phenotypic and error variances were in most cases relatively large and positive for all the traits (Table 4.24). Positive σ_{gl}^2 estimates were obtained for all the traits in both Zaria and Mokwa (Table 4.25).

Table 4.22: Estimate of Genotypic Variance(σ_g^2), Phenotypic Variance (σ_{ph}^2) and Error Variances(σ_e^2) for the 10 Traits of the 257 S_1 Lines of ACR 9331 DMRSR Population Established under Low-N in Mokwa and Zaria

	Zaria			Mokwa		
Traits	σ_g^2	σ_e^2	σ_{ph}^2	σ_g^2	σ_e^2	σ_{ph}^2
D.Silk	5.5407±1.98	4.4427±2.46	9.9834±5.34	0.1163±0.01	0.8118±0.23	0.9281±0.13
D.Pollen	3.8355±1.76	3.1888±2.13	7.0243±3.34	0.2833±0.02	0.8817±0.37	1.1650±0.89
ASI	0.1952±0.02	0.5884±0.25	0.7836±0.23	0.0024±0.00	0.2107±0.19	0.2131±0.18
PLHT	101.5598±34.23	63.9526±34.31	165.5125±42.13	87.1637±12.45	142.4332±56.98	229.5969±56.76
EHT	24.3590±8.90	30.6053±10.34	54.9643±20.56	34.0363±8.90	98.3240±39.89	132.3603±45.78
HUSK	0.1904±0.10	0.2597±0.01	0.4501±0.23	0.0839±0.01	0.2207±0.12	0.3046±0.19.76
S. Green	0.1027±0.01	0.2653±0.12	0.3680±0.13	0.0278±0.001	0.1502±0.98	0.1780±0.19
E/Plant	0.1798±0.001	0.0422±0.01	0.2220±0.11	0.0142±0.001	0.1209±0.10	0.1351±0.13
E/Aspect	0.1754±0.01	0.4615±0.30	0.6369±0.43	-	0.9122±0.48	0.9045±0.34
Yield	15989.00±3498.1			184308.70±3876.2		
	4	26287.25±10765.32	42276.29±20134.34	9	192927.60±78765.78	377236.30±100897.23

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=σ^2_{ph}

Table 4.23: Estimate of Genotypic Variance (σ_g^2), Phenotypic Variance(σ_{ph}^2), Error Variances(σ_e^2) and Genotype X Environment Interaction Variance (σ_{gl}^2) for the 10 Traits of the 257 S_1 Lines of ACR 9331 DMRSR Population Established under Low-N across two Locations (Mokwa and Zaria)

Traits	σ_g^2	σ_e^2	σ_{gl}^2	σ_{ph}^2
D.Silk	0.5063±0.21	5.5874±1.89	2.1439±1.12	2.9751±0.32
D.Pollen	0.3216±0.15	4.3044±0.98	1.6134±0.98	2.2044±0.89
ASI	0.0134±0.01	0.8066±0.12	0.0811±0.01	0.2556±0.09
PLHT	59.8214±18.09	205.8409±34.45	34.8164±10.23	128.6898±21.56
EHT	14.2132±2.47	128.9470±29.90	15.1672±3.90	54.0335±18.89
HUSK	0.0985±0.01	0.4855±0.12	0.0357±0.01	0.2377±0.10
S. Green	0.0382±0.01	0.4243±0.23	0.0221±0.01	0.1553±0.01
E/Plant	0.0258±0.01	0.1633±0.01	0.0709±0.01	0.1021±0.01
E/Aspect	0.0467±0.01	1.3708±0.65	0.0382±0.01	0.4085±0.12
Yield	46954.00 ±10232.12	219670.70±67811.34	53244.85±9345.12	128494.15±24231.01

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=σ^2_{ph}; Genotype x Location Variance=σ^2_{gl}

Table 4.24: Estimate of Genotypic Variance(σ_g^2), Phenotypic Variance (σ_{ph}^2), and Error Variances(σ_e^2) for the 9 Traits of the 257 S_1 Lines of ACR 9331 DMR SR Population Established under High-N in Mokwa and Zaria

ZARIA MOKWA

Traits	σ_g^2	σ_e^2	σ_{ph}^2	σ_g^2	σ_e^2	σ_{ph}^2
D.Silk	5.0406±1.09	8.9916±4.98	13.9322±4.98	2.988±0.67	1.3576±0.87	4.3456±1.34
D.Pollen	4.5785±0.98	7.2202±2.46	11.7987±3.45	3.1566±1.02	1.2147±0.12	4.3713±1.22
ASI	0.2701±0.10	0.9590±0.23	1.2291±0.23	0.0588±0.01	0.3207±0.02	0.3795±0.21
PLHT	74.9178±13.89	143..6488±57.90	218.5666±34.74	136.1428±34.21	116.5204±12.34	252.6632±65.09
EHT	18.9685±4.34	48.0348±38.09	67.0033±19.90	68.9246±10.09	62.4448±23.45	131.3695±234.98
HUSK	0.1150±0.01	0.2415±0.01	0.3565±0.14	0.13905±0.14	0.1250±0.01	0.2641±0.11
E/Plant	0.0768±0.01	0.0981±0.01	0.1749±0.11	-	0.1737±0.03	0.1661±0.09
E/Aspect	0.1772±0.03	0.2903±0.04	0.4675±0.12	0.2473±0.21	1.7355±0.69	1.9828±1.29
Yield	76583.46±1234.34	56672.42±25767.10	133255.90±14567.12	453528.40±34564.09	150796.00±75666.09	604524.40±67809.09

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=σ^2_{ph}

TABLE 4.25: Estimate of Genotypic Variance (σ_g^2), phenotypic variance (σ_{ph}^2), Error Variances (σ_e^2) and Genotype X Environment Interaction Variance (σ_{gl}^2) for the 9 Traits of the 257 S_1 Lines of ACR 9331 DMRSR Population Established under High-N across two Locations (Mokwa and Zaria)

Traits	σ_g^2	σ_e^2	σ_{gl}^2	σ_{ph}^2
D.Silk	0.7936±0.28	10.1412±1.65	3.2911±1.23	4.9745±1.39
D.Pollen	0.8631±0.23	8.3545±1.33	3.0273±0.95	4.4654±0.98

ASI	-	1.2688±0.34	0.1851±0.03	0.4066±0.02
PLHT	58.8869±11.04	259.59±24.98	45.6231±14.98	146.5964±13.09
EHT	15.1918±2.34	110.4990±13.94	27.8256±5.67	56.7294±8.32
HUSK	0.0732±0.02	0.3669±0.11	0.0531±0.01	0.1915±0.01
E/Plant	-	0.2398±0.03	0.0714±0.02	0.0751±0.02
E/Aspect	-	2.1009±0.78	0.1816±0,01	0.5981±0.11
Yield	71271.95±12341.09	209578.00±56783.09	183370.7±4556.98	215351.80±23456.90

*Error Variance= σ^2_e; Genotypic Variance= σ^2_g; Phenotypic Variance=$\sigma^2_{ph;}$ Genotype x Location Variance=$\sigma^2_{gl;}$

4.5 Heritability Estimates

The broad sense heritability estimates obtained for the 125 S_1 lines of DMR ESR-W evaluated under low-N level were low to moderate ranging from 16.38% for number of ears per plant to 52.61% for plant height in Zaria and from 1.01 % for days to 50 % pollen shed to 60.20% for grain yield in Mokwa. The combined analysis gave heritability estimates ranging from 9.33 % for ASI to 42.10 % for plant height. Moderate heritability estimates (31% - 60%) were obtained for plant height, ear height, stay green and grain yield in each location. Grain yield showed heritability estimate of 33.69 % in Zaria, 60.20 % in Mokwa and an average of 26.50 % across the two locations. The highest estimate across the two locations was obtained for plant height (42.10 %) and the lowest for ASI (9.33 %).

For the same genotypes evaluated under high-N, the heritability estimates range from 45.00% for husk cover to 77.88 % for plant height in Zaria, while it ranged from 11.79 % for ASI to 73.51 % for plant height in Mokwa. Days to 50 % pollen shed showed the highest heritability estimate (67.88 %) across the two locations. Grain yield per hectare showed heritability estimates of 57.36% in Zaria, 58.42 % in Mokwa and an average of 59.31% across the two locations. Generally the heritability estimates for some of the traits such as Days to 50 % pollen shed, Days to 50 % silking, ASI, plant height, ear height and grain yield evaluated under low-N were considerably lower than those evaluated under high-N level (Table 4.26).

Table 4.26: Heritability estimates (h^2) for the 10 characters of the 125 S_1 lines of the DMR ESR-W population evaluated in Zaria, Mokwa and across the two locations under Low-N and High-N levels

	Low-N Level		High-N Level	

Traits	Zaria	Mokwa	Combined	Zaria	Mokwa	Combined
D.Silk	46.48	15.21	18.31	64.71	64.28	64.85
D.Pollen	43.02	-	24.16	67.79	63.17	67.88
ASI	43.61	-	-	54.38	11.79	17.05
PLHT	52.61	28.74	42.10	77.88	73.51	42.76
EHT	39.37	46.20	27.61	68.72	18.41	35.25
HUSK	51.39	46.69	37.30	45.00	29.30	45.33
S. Green	42.76	12.98	16.26	++	++	++
E/Plant	33.01	32.22	27.95	46.90	58.75	0.89
E/Aspect	16.38	5.78	13.77	58.37	23.99	28.81
Yield	33.69	60.20	26.50	57.36	58.42	59.31

++ = Data not collected under High N level; - = Negative variance was obtained

Low to high heritability estimates were also obtained for the 10 traits of the 225 S_1 lines of TZE COMP. 3DT evaluated under both fertility levels. The estimates appeared to be higher in Zaria compared to Mokwa. Under low soil N, the heritability estimates ranged from 7.05 % for number of ear per plant to 66.33 % for days to 50 % silking in Zaria, while the estimates ranged from 1.24 % for ear height to 32.66 % for grain yield in

Mokwa. Grain yield showed heritability estimates of 38.14 % in Zaria, 32.66% in Mokwa and 40.59% across the two locations.

The trend under high-N was similar to that obtained under low-N (Table 4.27). Grain yield and days to 50 % pollen shed had moderate to high heritability estimates (31% - 60%), while ear height, ASI and ear aspect had low estimates (0% - 30%) estimates in the two locations.

Table 4.27: Heritability estimates (h^2) for the 10 characters of the 225 S_1 lines of the TZE COMP. 3DT population evaluated in Zaria, Mokwa and across the two locations under Low-N and High-N levels

	Low-Level			High-N Level		
Traits	Zaria	Mokwa	Combined	Zaria	Mokwa	Combined
D.Silk	66.33	26.21	19.79	63.59	11.90	14.81
D.Pollen	64.84	28.31	23.44	64.38	-	21.17
ASI	29.65	11.41	-	40.07	15.13	-
PLHT	34.90	17.27	28.07	57.73	20.57	48.64
EHT	19.51	1.24	25.03	44.27	4.80	40.41
HUSK	30.59	-	22.77	30.43	9.96	34.07
S. Green	22.10	25.44	39.19	++	++	++
E/Plant	-	22.65	28.08	9.37	25.01	2.43

E/Aspect	10.77	1.36	12.12	46.33	23.39	51.44
Yield	38.14	32.66	40.59	29.45	55.21	54.49

++ = Data not collected under High N level; - = Negative variance was obtained

The 257 S_1 lines of ACR 9331 DMRSR evaluated under low-N showed low (0% - 30%) to moderate (31% - 60%) heritability estimates for most of the traits studied. The heritability estimates ranged from 24.91% for ASI to 80.99 % for number of ears per plant in Zaria and from 1.12 % for ASI to 48.85 % for grain yield in Mokwa. The combined analysis gave heritability estimates ranging from 5.24 % for ASI to 46.89 % for husk cover. Moderate heritability estimates (31% - 60%) were obtained for plant height and grain yield in each location and across the two locations. Grain yield per hectare showed heritability estimate of 37.82 % in Zaria, 48.85 % in Mokwa and 36.54 % across the two locations.

Similar estimates were obtained under high-N level. The heritability estimates ranged from 21.98% for ASI to 57.47 % for grain yield in Zaria and from 4.57 % for number of

ears per plant to 75.05 % for grain yield in Mokwa. Grain yield per hectare showed heritability estimates of 57.47 % in Zaria, 75.05 % in Mokwa and 33.10 % across the two locations. The highest heritability estimate was obtained for plant height (46.48% under low-N and 40.17 % under high-N) across the two locations. Grain yield had heritability estimates of 36.54 % under low N and 33.10% under high-N level across the two locations. Generally, the estimates across locations ranged from 14.59 % for days to 50 % pollen to 46.48 % for plant height under low-N and from 0.79 % for ASI to 40.17 % for plant height under high-N level (Table 4.28)

Table 4.28: Heritability estimates (h^2) for the 10 characters of the 257 S_1 lines of the ACR 9331 DMRSR population evaluated in Zaria, Mokwa and across the two locations under Low-N and High-N levels

	Low-N Level			High-N Level		
Traits	Zaria	Mokwa	Combined	Zaria	Mokwa	Combined
D.Silk	55.50	12.53	17.02	36.18	68.76	15.95
D.Pollen	54.60	24.31	14.59	38.81	72.21	19.33
ASI	24.91	1.12	5.24	21.98	15.21	-
PLHT	61.36	37.96	46.48	34.28	53.88	40.17
EHT	44.32	25.71	26.30	28.31	52.47	26.78
HUSK	42.30	27.53	46.89	32.26	52.65	38.22
S. Green	27.91	15.61	41.44	++	++	++
E/Plant	80.99	10.51	24.58	43.91	4.57	-
E/Aspect	27.54	8.50	25.28	37.90	12.47	-
Yield	37.82	48.85	36.54	57.47	75.05	33.10

++ = Data not collected under High N level; - = Negative variance was obtained

4.6 Genotypic and Phenotypic Correlations

The correlation of traits under both low-N and high-N levels for the three maize populations evaluated at the two locations (Zaria and Mokwa) showed the association between grain yield and other traits. In general, the phenotypic and genotypic correlations were significant under both low-N level and high-N levels.

The 125 S_1 lines of DMR ESR-W evaluated under low-N showed that grain yield had significant positive genotypic correlation with plant height (r=0.756), stay green (r=0.652) and ears per plant (r=0.816). Significant negative genotypic correlations were obtained between grain yield and days to 50 % silk (r=-0.659), days to 50 % pollen (r=-0.245), ASI (r=--0.360), ear height (r=-0.599), husk cover (r=-0.521) and ear aspect (r=-0.503). Grain yield also showed significant positive phenotypic correlations with ears per plant (r=0.542), plant height (r=0.648) and ear height (r=0.542) while it showed significant negative phenotypic correlations with other traits such as days to 50% pollen, days to 50 % silking and ASI. The correlations obtained among other traits showed that ear aspect had significant positive genotypic correlation with days to 50 % silk (r=0.607), days to 50 % pollen (r=0.476), husk cover (r=0.521) and stay green (r=0.836); while it showed negative genotypic correlation with plant height, ear height and number of ears per plant (Table 4.29).

Under high-N condition, grain yield showed significant positive genotypic correlation with days to 50 % silking (r=0.309), plant height (r=0.453) and ear height (r=0.635), while it showed significant negative genotypic correlation with days to 50 % pollen (r=-

0.256), ASI (-0.36), husk cover (r=-0.152) and are aspect (r=-0.1712). Significant positive phenotypic correlations were observed between grain yield and days to 50 % silking (r=0.485), plant height (r=0.741), number of ears per plant and ear aspect (r=0.389). Significant negative phenotypic correlations were observed between grain yield and days to 50 % pollen (r=-0.512), ASI (r=-0.130), ear height (r=-0.716) and husk cover (r=-0.275) (Table 4.30).

Table 4.29: Phenotypic (Upper diagonal) and Genotypic (Lower diagonal) Correlations Obtained from the Evaluation of S_1 Families from DMR ESR-W Maize Population under Low-N in two Locations (Mokwa and Zaria)

	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	S.Green	EAR/P	EASP	Yield
D.Silk		0.930	0.569	-0.429	-0.391	0.183	0.294	-0.528	0.493	-0.623*
D.Pollen	0.947		0.229	0.495	-0.460	0.210	0.374	-0.593	0.560	-0.68*
ASI	0.711	0.447		-0.031	-0.004	0.007	-0.057	-0.069	0.052	-0.13*
PLHT	-0.207	-0.19	-0.161		0.687	-0.276	-0.573	0.554	-0.651	0.648*
EHT	-0.045	-0.043	-0.032	0.581		-0.186	-0.404	0.451	-0.469	0.542*
HUSK	0.133	0.076	0.210	-0.129	-0.357		0.398	-0.22	0.401	-0.227*
S. Green	-0.394	-0.606	0.233	0.239	-0.175	0.122		-0.551	0.663	-0.639*
EAR/P	0.388	0.587	-0.213	-0.116	0.068	-0.129	-0.106		-0.668	0.542*
EASP	0.607*	0.476*	0.068	-0.743*	-0.391	0.521*	0.836*	-0.783*		-0.76*
Yield	-0.659*	-0.245*	-0.360*	0.756*	-0.599*	-0.521*	0.652*	0.816*	-0.503*	

* = Significant at P=0.05 level of probability

Table 4.30: Phenotypic (Upper diagonal) and Genotypic (Lower diagonal) Correlations Obtained from the Evaluation of S_1 families from DMR ESR-W Maize Population under High-N in two Locations (Mokwa and Zaria).

	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	EAR/P	EASP	Yield
D.Silk		0.975	0.569	-0.435	-0.303	-0.281	-0.935	0.392	0.485*
D.Pollen	0.258		0.229	-0.557	-0.296	0.361	-0.654	0.470	-0.513*
ASI	0.680	0.337		-0.031	-0.004	0.007	-0.069	0.052	-0.130*
PLHT	-0.130	-0.116	-0.161		-0.904	-0.525	0.292	-0.844	0.741*
EHT	-0.164	-0.137	-0.032	0.664		-0.595	-0.854	0.630	-0.716*
HUSK	0.080	0.091	0.213	-0.292	-0.361		-0.645	0.428	-0.275*
EAR/P	0.123	0.382	-0.213	0.121	-0.717	0.464		-0.276	0.295*
EASP	0.311	0.230	0.078	-0.537	-0.425	0.242	-0.193		0.389*
Yield	0.309*	-0.256*	-0.360*	0.453*	0.635*	-0.152*	-0.127*	-0.171*	

* = Significant at P=0.05 level of probability

For the second population (TZE COMP. 3DT) under low-N condition, grain yield showed significant positive genotypic correlations with plant height (r=0.965), ear height (r=0.107) and ear aspect (r=0.310), while it showed significant negative genotypic correlation with days to 50 % silk (r=-0.54), days to 50 % pollen (r=-0.61), husk cover (r=-0.521), stay green (r=-0.652) and number of ears per plant (r=-0.593). Significant positive phenotypic correlations were observed between grain yield and days to 50% silk (r=0.638), days to 50 % pollen shed (r=0.981), ASI (r=0.127), plant height (r=0.987), ear height (r=0.107), husk cover (r=0.535), number of ears per plant (r=0.987), and ear aspect (r=0.984). Furthermore, plant height had significant positive genotypic and phenotypic correlations with ear height and ASI. ASI also had significant positive genotypic correlations with days to 50% pollen and days to 50 % silk (Table 4.31).

Under high-N condition, grain yield had significant positive genotypic correlation with plant height (r=0.401), ear height (r=0.526) and number of ears per plant (r=0.82); while it had negative genotypic correlation with days to 50 % silk (r=-0.313), days to 50 % pollen (r=-0.311), ASI (-0.226), husk cover (r=-0.072) and ear aspect (-0.668). Grain yield also showed significant positive phenotypic correlation with days to 50 % pollen (r=0.393), plant height (r=0.453), ear height (r=0.587), ears per plant (r=0.959) and ear aspect (r= 0.792). Significant negative genotypic correlation was observed between grain yield and ear aspect (r=-0.668) (Table 4.32).

Table 4.31: Phenotypic (Upper diagonal) and Genotypic (Lower diagonal) Correlations obtained from the Evaluation of S_1 Families from TZE COMP. 3DT Maize Population under Low-N in two Locations (Mokwa and Zaria).

	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	S.Green	EAR/P	EAS	Yield
D.Silk		0.996	0.561	0.868	0.432	0.489	0.342	0.432	0.709	0.638*
D.Pollen	0.982		-0.508	0.429	-0.667	0.183	0.294	-0.528	0.998	0.981*
ASI	0.636	0.471		0.523*	0.188*	0.21	0.374	-0.593	0.061	0.127*
PLHT	0.988	0.899	0.789*		0.896*	0.007	-0.057	-0.069	0.987	0.987*
EHT	-0.376	0.516	0.164	0.675*		-0.276	-0.573	0.554	-0.888	0.107
HUSK	0.133	0.076	0.210	-0.129	-0.357		-0.404	0.451	0.590	0.535*
S. Green	-0.394	-0.606	0.233	0.239	-0.175	-0.129		0.687	-0.458	-0.458*
EAR/P	0.388	0.587	-0.213	-0.116	0.068	0.392	0.519		0.987	0.987*
EASP	-0.605	-0.793	-0.037	0.897*	-0.778	-0.488	0.274	-0.678		0.984*
Yield	-0.536*	-0.611*	-0.062	0.965*	0.107*	-0.5210*	-0.652*	-0.593*	0.310*	

* = Significant at P=0.05 level of probability

Table 4.32: Phenotypic (Upper diagonal) and Genotypic (Lower diagonal) Correlations obtained from the Evaluation of S_1 Families of TZE COMP. 3DT maize population under High-N across the two locations (Mokwa and Zaria)

	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	EAR/P	EASP	Yield
D.Silk		0.869	-0.213	0.335	0.191	0.263	0.781	0.183	-0.473
D.Pollen	0.980		-0.161	-0.427	0.139	0.289	0.234	0.493	0.393*
ASI	0.711	0.447		-0.031	-0.004	0.007	-0.057	0.052	0.052
PLHT	-0.138	-0.211	-0.032		0.838	-0.280	0.526	-0.651	0.453*
EHT	0.040	-0.022	0.21	0.756		-0.530	0.812	-0.469	0.587*
HUSK	-0.255	-0.207	0.233	-0.157	-0.455		-0.637	0.401	-0.077
EAR/P	-0.113	-0.166	-0.213	0.362	0.599	-0.389		0.663	0.959*
EASP	-0.156	0.256*	0.061	-0.313	-0.519	0.392*	0.519*		0.792*
Yield	-0.313	-0.311	-0.226	0.401*	0.526*	-0.072	0.828*	-0.668*	

* = Significant at P=0.05 level of probability

The 257 S_1 of Acr 9331 DMR SR evaluated under low-N level showed that grain yield had significant positive genotypic and phenotypic correlations with plant height, ear height, number of ears per plant and ear aspect. Grain yield also had significant but negative genotypic correlation with days to 50% silking (r=-0.179), days to 50 % silking (r=0.223), ASI (r=-0.232), and stay green (r= -0.5799) under the low-N level. Plant height, ear height and husk cover also exhibited both positive correlations with one another; significant positive genotypic (r= 0.76) and phenotypic (r=0.86) correlations were observed between plant height and ear height. Negative genotypic and phenotypic correlations were also observed between grain yield and 50 % days to pollen shed as well as days to 50 % silk. Stay green also had negative genotypic and phenotypic correlations with days to 50 % pollen shed and days to 50 % silking (Table 4.33).

Under high-N level, grain yield had significant positive genotypic correlation with plant height and ear height. Grain yield showed non-significant negative genotypic correlations with days to 50% pollen shed and days to 50 % silk. However, days to 50 % pollen shed was highly correlated with days to 50 % silk, while ears per plant correlate positively with most of the traits both genotypically and phenotypically except days to 50 % pollen shed (Table 4.34).

Table 4.33: Phenotypic (Upper diagonal) and Genotypic (Lower diagonal) Correlations obtained from the Evaluation of S_1 Families from ACR 9331 DMRSR Maize Population under Low-N in two Locations (Mokwa and Zaria).

	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	S.Green	EAR/P	EASP	Yield
D.Silk		0.876	0.343	0.342	0.144	0.518	0.734	0.986	0.786	-0.302
D.Pollen	0.792		-0.568	0.316	-0.192	-0.578	-0.837	0.322	0.763	-0.332
ASI	-0.138	-0.211		-0.340	-0.031	-0.004	0.007	-0.057	-0.069	0.052
PLHT	0.260	0.243	-0.126		0.860	0.229	-0.743	-0.228	-0.453	0.387*
EHT	0.066	0.060	-0.032	0.761		-0.236	-0.865	-0.252	-0.987	0.257*
HUSK	-0.359	-0.349	0.213	-0.145	-0.073		-0.424	-0.548	0.334	0.265*
S. Green	-0.537	-0.560	0.233	-0.553	-0.592	0.120		-0.399	0.818	-0.651
EAR/P	-0.069	-0.035	-0.213	-0.129	-0.200	-0.336	-0.199		-0.579	0.345*
EASP	0.492	0.581	0.071	-0.338	-0.524	0.055	0.480	-0.241		0.942*
Yield	-0.179	-0.223	-0.236	0.383*	0.364*	0.146	-0.579	0.160	0.870*	

* = Significant at P=0.05 level of probability

Table 4.34: Phenotypic (Upper diagonal) and genotypic (lower diagonal) correlations obtained from the evaluation of S_1 families from ACR 9331 DMRSR maize population under Low-N in two locations (Mokwa and Zaria).

	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	EAR/P	EASP	Yield/ha
D.Silk		0.985	-0.206	0.143	-0.938	0.433	0.454	0.7510	0.197*
D.Pollen	0.785		-0.614	-0.159	-0.374	0.601	-0.697	0.9277	-0.235
ASI	0.875	-0.127		-0.248	-0.244	-0.226	0.634	0.489	0.579*
PLHT	0.025	-0.064	0.641		0.879	-0.540	0.471	-0.7386	0.526*
EHT	-0.111	-0.227	0.538	0.710		0.276	0.298	0.7795	0.456*
HUSK	0.341	0.401	-0.221	-0.274	-0.198		0.068	0.4811	0.086
EAR/P	0.433	-0.540	0.371	0.392	0.279	0.030		0.9873	0.346
EASP	0.694*	0.764*	0.705*	-0.656	-0.218	0.399*	0.899*		0.062
GWT/P	-0.137	-0.151	-0.758	0.341	0.298	0.044	0.018	-0.407	

* = Significant at P=0.05 level of probability

4.7 Changes in Mean Performance from S_1 Progeny Selection

The observed changes in mean performance combined across the two locations for each of the three maize populations in respect of grain yield and other agronomic traits are presented in Tables 38-40. To facilitate the identification of superior families for possible recombination, a base selection index that combines ear aspect, stay green, anthesis-silking interval, ears per plant, grain yield under low-N (30 kg N/ha) together with grain yield under high-N (90 kg N/ha) was used. Genotypes with good performance under both low-N and high-N levels in the two locations were selected using 10 % selection intensity. A total of 16 genotypes were selected from the 125 genotypes of DMR ESR-W evaluated across the two locations under both low and high N-levels. The selected genotypes showed improvement over the original population for the traits. The selected genotypes silked earlier with a significant reduction of about 10.23 %. Stay green was significantly increased by 4.83 %. The mean grain yield was also changed by selection by up to 29.40 % under low N-level and 2.02 % under high N-level (Table 4.35).

GENOTYPE	D.Silk	ASI	S. Green	EARS/P	EASP	Yield kg/ha	
						30 kgN/ha	90 kgN/ha

Table 4.35: Change in Mean Performance for DMR ESR-W S_1 Progeny Selection for Grain Yield and other Agronomic Traits under low N across Two Locations (Zaria and Mokwa)

DMR ESR-W S1-49	55	2	4	0.8	3	2411	3351
DMR ESR-W S1-19	57	3	5	1.0	5	1755	1733
DMR ESR-W S1-8	57	2	5	0.8	4	1450	1893
DMR ESR-W S1-93	57	2	6	0.7	4	1433	1671
DMR ESR-W S1-15	55	3	5	0.7	5	1766	1529
DMR ESR-W S1-5	56	2	5	1.0	3	1694	1422
DMR ESR-W S1-95	56	1	6	0.8	4	1477	2311
DMR ESR-W S1-119	55	1	6	0.7	3	1558	2071
DMR ESR-W S1-60	56	2	5	0.8	5	1405	1733
DMR ESR-W S1-59	55	2	6	0.6	3	1311	1582
DMR ESR-W S1-80	56	2	5	1.0	4	1933	1689
DMR ESR-W S1-112	55	2	5	0.8	5	1816	1796
DMR ESR-W S1-70	56	3	5	0.7	4	1600	924
DMR ESR-W S1-50	56	2	5	0.8	2	1522	1884
DMR ESR-W S1-89	56	2	5	0.9	3	1022	1778
DMR ESR-W S1-124	56	1	5	0.8	3	1544	2000
Population mean	62.26	2.18	4.97	0.77	4.91	1203.51	1736.50
Mean of S_1 lines selected	55.89	2.00	5.21	0.82	3.63	1557.42	1771.63
Selection differential (%)	-10.23	-8.25	4.83	6.49	-26.07	29.40	2.02

From the 225 S_1 lines of TZE COMP. 3DT evaluated across the two locations under both low and high N-levels, a total of 26 genotypes were selected. The selected genotypes showed improvement over the original population for the traits. Days to 50% silking was improved by -3.2 %, while stay green was reduced by 2.8 %. Ears per plant were

increased by 135.29 %. Mean grain yield was improved by selection by 43.45 % under

GENOTYPES	DYSK	ASI	S. Green	EARS/	EASP	Yield kg/ha	
						30 kgN/ha	90 kgN/ha

low N-level and 16.01 % under high N-level (Table 4.36).

TZE COMP 3 DT S1-155	58	0	5	2	5	1872	1848
TZE COMP 3 DT S1-192	59	2	5	2	4	1927	2266
TZE COMP 3 DT S1-169	61	2	5	2	8	1911	1635
TZE COMP 3 DT S1-62	62	3	5	2	8	1866	1697
TZE COMP 3 DT S1-61	60	-1	5	2	6	1722	1555
TZE COMP 3 DT S1-225	59	-1	4	2	5	1611	1768
TZE COMP 3 DT S1-51	61	-1	5	2	4	1916	1706
TZE COMP 3 DT S1-105	63	4	4	2	5	2255	1875
TZE COMP 3 DT S1-96	62	0	4	2	4	2072	1417
TZE COMP 3 DT S1-9	58	0	4	2	5	1566	2604
TZE COMP 3 DT S1-188	57	-2	4	2	5	1755	1422
TZE COMP 3 DT S1-26	60	-1	5	2	5	1516	2648
TZE COMP 3 DT S1-65	59	1	4	2	5	1422	2186
TZE COMP 3 DT S1-114	57	-1	4	2	3	1983	1262
TZE COMP 3 DT S1-176	59	-1	4	2	4	1800	2151
TZE COMP 3 DT S1-172	60	2	4	2	4	2033	2266
TZE COMP 3 DT S1-78	62	0	4	2	6	1711	2488
TZE COMP 3 DT S1-224	62	3	5	2	6	1916	3333
TZE COMP 3 DT S1-18	60	1	5	2	5	1727	2337
TZE COMP 3 DT S1-210	62	1	5	2	5	2200	2373
TZE COMP 3 DT S1-223	57	-1	4	2	5	1638	3013
TZE COMP 3 DT S1-221	57	-2	5	2	4	2255	2640
TZE COMP 3 DT S1-81	57	-2	4	2	3	1833	2266
TZE COMP 3 DT S1-70	58	-1	5	2	5	2500	1608
TZE COMP 3 DT S1-158	59	2	4	2	3	2400	3022
TZE COMP 3 DT S1-165	59	4	4	2	5	2472	4284
Population mean	61.54	1.34	4.59	0.85	4.89	1337.36	1912.00
Mean of S_1 lines selected	59.54	0.42	4.46	2.00	4.88	1918.42	2218.08
Selection differential (%)	-3.25	-68.43	-2.80	135.29	0.20	43.45	16.01

Table 4.36: Change in Mean Performance for TZE COMP. 3DT S_1 Progeny Selection for Grain Yield and other Agronomic Traits under low N across two Locations (Zaria and Mokwa)

A total of 25 genotypes were selected from the 257 genotypes of ACR 9331 DMRSR evaluated across the two locations under both low and high-N levels. The selected genotypes showed improvement over the original population. They silked earlier with

reduction of 1.34 %. ASI was reduced by 3.10% and ear aspect by 9.42 %. Number of ears per plant increased by 126.0 %. The mean grain yield was improved by up to 67.07

GENOTYPES	DYSK	ASI	S. Green	EARS/P	EASP	Yield kg/ha	
						30 kgN/ha	90 kgN/ha

% under low-N level and 43.62 % under high-N level (Table 4.37).

Acr 9931 DMRSR S1-136	60	1	5	2	5	1283	1822
Acr 9931 DMRSR S1-222	57	1	5	2	5	1250	1658
Acr 9931 DMRSR S1-116	59	1	4	2	5	1439	1573
Acr 9931 DMRSR S1-14	61	2	5	2	5	1439	1618
Acr 9931 DMRSR S1-189	59	1	5	2	5	1389	1600
Acr 9931 DMRSR S1-48	58	1	5	2	5	1461	1556
Acr 9931 DMRSR S1-159	61	1	5	2	5	1300	1876
Acr 9931 DMRSR S1-30	59	2	5	2	5	1294	2164
Acr 9931 DMRSR S1-40	60	1	5	1	5	1506	1524
Acr 9931 DMRSR S1-200	62	2	5	1	5	1467	1969
Acr 9931 DMRSR S1-162	62	1	5	2	5	1361	1964
Acr 9931 DMRSR S1-214	59	1	5	2	4	1400	1769
Acr 9931 DMRSR S1-117	61	2	5	2	4	1611	1733
Acr 9931 DMRSR S1-13	57	1	5	2	4	1272	2280
Acr 9931 DMRSR S1-87	59	1	5	2	5	1633	1564
Acr 9931 DMRSR S1-97	59	2	4	1	5	1300	3067
Acr 9931 DMRSR S1-39	63	2	5	2	5	1650	2373
Acr 9931 DMRSR S1-74	59	0	5	2	5	1511	1760
Acr 9931 DMRSR S1-230	60	1	5	2	4	1783	2000
Acr 9931 DMRSR S1-2	59	1	4	2	4	1944	1867
Acr 9931 DMRSR S1-55	58	1	4	2	5	1994	1444
Acr 9931 DMRSR S1-146	61	1	5	2	5	1761	2107
Acr 9931 DMRSR S1-11	57	1	4	2	4	1772	2480
Acr 9931 DMRSR S1-257	60	2	4	2	4	2189	3426
Acr 9931 DMRSR S1-248	58	1	4	2	4	2383	2978
Population mean	60.39	1.29	4.83	0.83	5.20	922.97	1369.21
Mean of S_1 lines selected	59.58	1.25	4.75	1.88	-4.71	1542.04	1966.42
Selection differential (%)	-1.34	-3.10	-1.66	126.51	9.42	67.07	43.62

Table 4.37: Change in Mean Performance for ACR 9331 DMRSR S_1 Progeny Selection for Grain Yield and other Agronomic Traits under low N across two Locations (Zaria and Mokwa)

4.8 Predicted Response to Selection

The predicted responses to selection for the three populations evaluated under low-N and high-N levels for all traits assuming the highest 10 % of the families are selected for grain yield are shown in Tables 41 to 43 for the data obtained from the two locations. The

standardized selection differential (k) for selecting the upper 10 % was 1.76. For each of the maize populations, the predicted gains for Zaria and Mokwa were quite different probably due to the differences in performance of the S_1 lines caused by environmental differences. The results also showed that selection under low-N level could lead to increase in grain yield, plant height and other traits. However, some of the traits were not drastically changed.

The 125 S_1 lines DMR ESR-W evaluated under low-N condition showed that the expected gain from selection for the traits measured ranged from 0.03 for number of ears per plant to 208.37 kg/ha for grain yield in Zaria, while it ranged from 0.013 for days to 50 % pollen shed to 223.12 kg/ha for grain yield in Mokwa. The combined data showed that the expected gain ranged from -0.1002 days for ASI to 192.2024 kg/ha for grain yield, which corresponds to 15.97 % increase for grain yield. Plant height was increased by 15.74 cm in Zaria, 7.22 cm in Mokwa and by 9.26 cm across the two locations. Ear height and grain yield were increased by 7.01 cm in Zaria, 9.20 cm in Mokwa and by 3.97 cm across the two locations. Ear aspect was improved by 0.23 in Zaria, 0.06 in Mokwa and 0.13 across the two locations. Under high-N condition, the expected gains from selection ranged from 0.18 for number of ear per plant to 517.37 kg/ha for grain yield in Zaria, while it ranged for 0.12 for ASI to 540kg/ha for grain yield in Mokwa. Plant height was increased by 21.53 cm in Zaria, 16.58 cm in Mokwa and by 8.57 cm across the two locations. Ear height and grain yield were increased by 4.93 cm and 456.63 kg/ha, respectively across the two locations. Ear aspect was improved by 0.89 in Zaria, 0.17 in Mokwa and 0.26 across the two locations (Table 4.38).

Table 4.38: Predicted Response (ΔG) to Selection for the 10 Characters of the 125 S_1 Lines of the DMR ESR-W Population Evaluated in Zaria and Mokwa under Low-N and High-N Levels.

	LOW-N LEVEL			HIGH-N LEVEL		
Traits	ZARIA	MOKWA	COMBINED	ZARIA	MOKWA	COMBINED
D.Silk	2.3969	0.1901	5.0916	3.4053	2.6812	2.6480
D.Pollen	1.8172	0.0132	0.5698	3.0066	2.4682	2.4730
ASI	0.8213	0.1069	-0.1002	0.9858	0.1245	0.2881
PLHT	15.7409	7.2282	9.2620	21.5335	16.5862	8.5794
EHT	7.0123	9.2045	3.9798	12.2036	3.3503	4.9384
HUSK	0.6060	0.3616	0.2889	0.5386	0.2011	0.3590
S. Green	0.5193	0.1005	0.1231	++	++	++
EARS/P	0.0320	0.1134	0.0689	0.1816	0.6618	0.0053

E/Aspect	0.2393	0.0631	0.1309	0.8938	0.1731	0.2637
Yield kg/ha	208.3724	723.1224	192.2034	517.3771	540.0064	456.6348

++=Data not collected under high N

For the second population (225 S_1 lines of TZE COMP. 3DT), the expected gain from selection range from 0.0310 for number of ears per plant to 240.29kg/ha for grain yield in Zaria, while it ranged from 0.0303 for number of ears per plant to 391.63kg/ha for grain yield in Mokwa. The combined data ranged from 0.0903 days for ASI to 308.03 kg/ha for grain yield, which corresponds to 23.0% increase for yield under low-N. Plant height and ear height were improved by 5.5035cm and 3.4581cm, respectively across the two locations. The expected gains under high-N level ranged from 0.0346 for number of ears per plant to 252.6862kg/ha for grain yield in Zaria, while it ranged from 0.0736 for husk cover to 749.5371kg/ha for grain yield in Mokwa. The combined data showed that the expected gain ranged from 0.0081 for number of ears per plant to 512.9819kg/ha for grain yield. Plant height and ear height were increased by 9.4766cm and 5.5545cm respectively across the two locations (Table 4.39).

Table 4.39: Predicted Response (ΔG) to Selection for the 10 Characters of the 225 S_1 Lines of the TZE COMP. 3DT Evaluated in Zaria, Mokwa and across the two Locations under Low-N and High-N Levels.

	LOW-N LEVEL			HIGH-N LEVEL		
Traits	ZARIA	MOKWA	COMBINED	ZARIA	MOKWA	COMBINED
D.Silk	3.9808	0.2998	0.6339	3.6485	0.1801	0.4561
D.Pollen	3.3436	0.3637	0.6600	3.2066	0.2157	0.5812
ASI	0.4644	0.0883	-0.0903	0.6911	0.1704	-0.1475
PLHT	8.4458	5.1124	5.5035	13.7572	4.9634	9.4766
EHT	2.9358	0.2610	3.4581	6.6383	0.9326	5.5545
HUSK	0.3391	0.0755	0.1562	0.1017	0.0736	0.2278
S. Green	0.2839	0.1790	0.3172	++	++	++
EARS/P	0.0310	0.0877	0.0889	0.0346	0.1452	0.0081
E/Aspect	0.1611	0.0303	0.1685	0.5626	0.1893	0.4345
Yield kg/ha	240.2991	391.6336	308.0352	252.6862	749.5371	512.9819

++=Data not collected under high N

The expected gain from selection for the 227 S_1 lines of ACR 9331 DMR SR evaluated under low-N ranged from 0.2947 for stay green to 136.8606kg/ha for grain yield in Zaria, while it ranged from 0.0090 days for ASI to 528.0560kg/ha for grain yield in Mokwa. The combined data ranged from 0.0470 days for ASI to 230.5271kg/ha for grain yield, which corresponds to 24.97% increase in yield under low-N level. Plant height was improved by 13.8879 in Zaria, 10.1216cm in Mokwa and 9.2766cm across the two locations. Ear height was improved by 5.7800cm in Zaria, 5.2037 in Mokwa and 3.4021cm across the two locations. The expected gains under high-N level ranged from 0.3168 for number of ears per plant to 526.997kg/ha for grain yield in Zaria, while it ranged from 0.0321 for number of ears per plant o 549.5371kg/ha for grain yield in Mokwa. The combined data showed that the expected gain ranged from 0.0087 for ASI to 270.3428kg/ha for grain yield. Plant height and ear height were increased by 8.5546cm and 3.5545cm respectively across the two locations (Table 4.40).

Table 4.40: Predicted Response (ΔG) to Selection for the 10 Characters of the 257 S_1 Lines of the ACR 9331 DMR SR population evaluated in Zaria, Mokwa and across the two locations under Low-N and High-N levels.

	LOW-N LEVEL			HIGH-N LEVEL		
Traits	ZARIA	MOKWA	COMBINED	ZARIA	MOKWA	COMBINED
D.Silk	3.0769	0.2117	0.5152	2.3751	2.5171	0.6260
D.Pollen	2.5465	0.4578	0.3800	2.3428	2.6561	0.7178
ASI	0.3858	0.0090	0.0470	0.4255	0.1632	-0.0087
PLHT	13.8879	10.1216	9.2766	8.9171	15.0683	8.5546
EHT	5.7800	5.2037	3.4021	4.0757	10.5829	3.5491
HUSK	0.4988	0.2664	0.3961	0.3349	0.4725	0.2892
S. Green	0.2947	0.1153	0.2844	++	++	++
EARS/P	0.6699	0.0665	0.1341	0.3168	0.0321	-0.1303
E/Aspect	0.3829	0.1421	0.2803	0.4535	0.307261	-0.0405
Yield kg/ha	136.8606	528.056	230.5271	369.2277	1026.997	270.3428

++=Data not collected under high N

CHAPTER FIVE

5.0 DISCUSSION

Recurrent selection is a cyclical procedure designed to increase the frequency of favourable alleles in a population. It has been efficiently used by various workers to improve maize performance for drought (Bolanos and Edmeades 1993; Menkir and Kling, 1999), *Striga* resistance (Menkir and Kling 2007; Badu-Apraku *et al*., 2008), downey mildew resistance (Ajala *et al.*, 2003) and stem borer resistance (Ajala *et al.*, 1995). Vasal *et al.* (1997a) and Banziger *et al.* (2000) observed that different selection methods including half sib, full sib and selfed progeny selections can be used for the improvement of maize populations for low-N tolerance. Low nitrogen fertility stress in maize results from several factors including leaching of soil nitrogen below the root zone due to torrential rainfall (Bennet *et al.,* 1989), sub-optimal application of inorganic fertilizer due to high price (McCown *et al.,* 1992) when available, poor weed control thereby increasing the incidence of N deficiency (Lafitte and Edmeades, 1994) and widespread removal of crop residues for use as animal feed and fuel (Zambezi and Mwambula, 1997) especially in the savanna of West and Central Africa. Therefore, development of maize cultivars adapted to low soil nitrogen will increase maize productivity in the region (Betran *et al.,* 2003).

5.1 Soil Analysis

The results obtained from the soil physico-chemical analysis of the individual plots at the two experimental sites indicate that the soils at both sites are deficient in both organic matter and available soil nitrogen and are therefore suitable for the evaluation of genotypes under nitrogen

stress and optimal conditions by artificially controlling the amount of nitrogen available for the plants at different growth stages.

5.2 Mean Performance

The mean performance of the genotypes at the two locations indicates that the three populations have diverse genetic backgrounds and could serve as sources of reliable genetic materials for improvement for tolerance to low soil nitrogen. The wide ranges and CVs for most of the traits measured are indication of substantial genetic variability in the three maize populations to allow good progress from selection for grain yield and tolerance to low soil nitrogen. Mean grain yield under the low-N level was low compared to the mean grain yield under high-N level in each of the three populations. Plant height and grain yield were significantly reduced under the low-N condition by 30-40 % of that evaluated under the high-N level at the two locations. This falls within the range of the yield reductions recorded under stress levels applied during the development of hybrids and inbred lines for tolerance to low-N by other workers (Lafitte and Edmeades, 1994; Betran *et al.*, 2003). The mean yields under low-N condition were lower in all the trials compared to the high-N conditions. About 30 % yield reduction was observed for all the genotypes under low N level across the two locations. Maize has a strong positive response to nitrogen (N) supply, and inadequate N is second only to drought as a constraint to tropical maize production (Lafitte, 2000). Nitrogen stress reduces photosynthesis by reducing leaf area development and accelerating leaf senescence. The pattern of nitrogen stress is usually similar across locations. At the beginning of the season and especially with fertilizer applied, N supply usually exceeds the N demand by the crop. As the season progresses N is used, leading to N depletion in the soil. Consequently N becomes scarce and N stress develops. The usual scenario

is that N stress becomes increasingly severe over time (Banziger *et al.*, 1997). Depending on the timing of N stress in the growing plant parts, different yield determining factors are affected. When there is ample nitrogen available during the growing period, N stress may develop during grain filling only, affecting kernel weight. If stress develops during flowering stage, kernel abortion increases. Nitrogen stress before flowering reduces leaf area development, photosynthetic rate and number of potential kernel ovules. Severe N stress delays both shedding of pollen and emerging of silks, but the delay in silking is relatively more, such that anthesis-silking interval (ASI) becomes longer (Banziger *et al*., 2000). The effect of low soil nitrogen on grain yield was similar across the two locations for the three maize populations.. Selected genotypes could be used to constitute an improved population which can further be used in breeding programmes to develop superior genotypes (lines and hybrids).

In the present study, some of the progenies such as DMR ESR S1-49, S1-80, S1-50 and S1-112 for DMR ESR $S_{1;}$ TZE COMP.3DT S1-192, S1-70, S1-158 and S1-221 for TZECOMP. 3DT S_1 as well as Acr 9331 DMR SR S1-39, S1-248 and S1-257 exhibited relatively high mean grain yield under both fertility levels across the two locations and this is indicative of increased tolerance to low-N level by the progenies. These results agree with the report of Ransom *et al.* (1993) who stated that nitrogen efficient genotypes are those genotypes which have high yield *per se* at both high and low N levels. Higher grain yields, were obtained in Mokwa with heavier kernels, earlier extrusion of incipient silk, earlier anthesis, taller plants and more ears per plant compared to Zaria. This result was not unexpected since there was an even distribution of rain in Mokwa during the growing season while Zaria experienced a short period of drought spell for 14 days within the same growing season at the seedling stage. The average grain yield of the S_1 lines

of TZE COMP. 3DT was found to be higher compared to those of the DMR ESR and ACR 9331 DMRSR under both fertility levels. This indicated, as expected, that the population (TZE COMP. 3DT) is a better source of low nitrogen tolerant genotypes. The population was originally developed for tolerance to drought, a stress factor having similar physiological manifestation as low-N. Kamara *et al*. (2005) evaluated maize genotypes with tolerance to drought under low-N to determine whether the relationship between drought tolerance and low-N is consistent with maize genotypes having different genetic background developed for the sub-region and observed that the drought tolerant varieties were similar or better than some low-N varieties in low-N environment. ACR 9331 DMRSR had the lowest mean yield under both fertility levels. Similar observations were made for most of the other agronomic traits measured in this investigation. TZE COMP. 3DT was indicated as the best performing population under both N-levels followed by DMR ESR and then ACR DMRSR. It was noted that some of the progenies such as TZE COMP. 3DT S1-51 and -155; DMR ESR S1-19 and -112; and ACR 9331 DMRSR S1-40 had good performance under low-N but were less responsive to the improved fertility condition. This indicates existence of genetic variations for efficiency in nutrient utilization among the progenies. The result also implied that the alleles controlling high grain yield in low-N conditions were at least partially different from those alleles controlling high grain yield under high-N condition. This may result in low yield in one of the fertility environments if only one of the fertility environments is used for screening purpose. It also indicates the possibility of selecting lines with high grain yield under a range of soil fertility levels when the data from low-N is combined with grain yield data from high-N. Ceccarelli (1989) stated that differences for grain yield observed in the absence of stress are largely unrelated with differences observed in the presence of stress.

In general, larger CVs were obtained for most of the traits under low-N compared to high-N levels. Badu-Apraku *et al*. (2005) reported similar result under drought stress and suggested that CVs are usually higher under stressed conditions. Large CVs in this type of study was reported by Obilana and Hallauer (1974) to be strictly a function of mean values and also an indication of substantial amount of variability amongst the tested materials. The CVs for ASI, stay green and grain yield were high probably because the data were derived from other traits or based on proportions. This corroborates the findings of Ajala *et al.* (2009) who reported that the CVs of traits derived from other traits are usually higher than the ones measured directly. Days to 50 % pollen shed and days to 50 % silking showed low magnitude of CVs (between 10 % and 11 %) for the three maize populations under both low N and high N. CVs are used to measure variability in genetic populations, to determine the best plot size in uniformity trials, to measure stability of phenotypes, or measure variation in individual or population attributes. It was coined as a measure of relative variability by Karl Pearson in 1895 (Kendall and Stuart, 1977) and as such, CVs can be used to indicate variability among populations, stability of phenotypes, variability of individual plot sizes in uniformity trials, or similar situations in which individual variability is measured.

5.3 Population Variability

Genetic variability is a prerequisite for effective selection in any breeding programme. Analysis of variance (ANOVA) for most of the traits studied showed highly significant differences ($P<0.01$) among the genotypes for most of the traits studied in the three maize populations under both fertility levels and across locations suggesting that good progress can be made in selecting

for improved grain yield and other traits under low-N and high-N levels. It also shows that the genotypes possess differential yield potential under nitrogen stress. Highly significant differences for the combined ANOVA across the two locations for the genotype x environment interactions ($G \times L$) for all the traits evaluated under both fertility levels indicate the need to test the genotypes over different locations or across years to ascertain their stability for use as reliable genetic materials for population improvement. The above findings are in line with the report of Mosisa *et al*. (2004) and Oikeh *et al*. (1997) who reported that different genotypes performed differently across different fertility levels.

5.4 Estimate of Variance Components

Genotype and G × L components of variance were smaller in magnitude compared to those of the environmental components for most of the traits in the population. However, large estimates of genotypic and phenotypic variances were obtained for days to 50% silk and stay green under low-N for each of the three maize populations. These results are in agreement with those reported by Banziger and Cooper (2001); Bouzerzour and Dekhili (1995) and Sallah and Geadelmann (1997). The genotypic variances of days to 50% silk and stay green were also larger than their respective environmental variances. This indicates that the traits are heritable and amenable to improvement through breeding. The low genotypic variance estimates obtained for grain yield under low N level in this study is in close agreement with the earlier findings of Sallah *et al*. (1997) who reported low genetic variance estimates for grain yield under low N environments. Negative genetic variance estimates were obtained for days to 50% pollen shed and ASI in Mokwa and ear aspect across the two locations for DMR ESR under low-N level while no negative estimates were obtained under the high-N level for the same population. For

TZE COMP. 3DT, negative estimates were obtained for number of ears per plant and husk cover in Zaria and Mokwa, respectively, under low-N, while no negative estimate was obtained under high-N level for the same population. Negative estimate was only obtained for ear aspect in Mokwa under low-N level for ACR 9331 DMR SR. It is not uncommon to obtain negative values for genetic variance components (Singh and Chaudhary, 1985; Bridges and Knapp, 1985) and there are several factors that may be responsible for the negative estimates. According to Comstock and Robinson (1952), the most important factors are the presence of linkage effects and assortative mating, deficiency in the genetic model and sampling as well as sample size. In general, negative variances are equated to zero and could have occurred in the present investigation through sampling error.

5.5 Heritability Estimates

The success of selection in any breeding programme depends upon the genetic variation in the materials being studied and also on the extent to which it can be transferred from one generation to the next. Estimates of broad sense heritability for grain yield and other agronomic traits were low for some traits but low to moderate for others in the three maize populations. This indicates presence of considerable amount of genetic variation in the total phenotypic variation. Previous studies by Sallah and Geadelmann (1997) and Banziger and Cooper (2001) reported low heritability of about 0.3 for grain yield, 0.5 for days to 50% anthesis and 0.7 for plant height. The low to moderate heritability estimates (25.50% for DMR ESR, 36.54% for ACR 9331 DMR SR and 40.59% for TZE COMP. 3DT) obtained for grain yield in the three populations under low-N is not unexpected since grain yield is the product of many different component

interactions and thus, highly influenced by environmental factors. It has also been reported that heritability and genetic variances for grain yield usually decrease under abiotic stress as yield levels fall (Banziger *et al*., 2000). Heritability estimates for days to 50% silk, ASI, stay green under low-N and days to 50% pollen shed, days to 50% silk and ASI were high for DMR ESR and TZE COMP. 3DT. Similar findings have been reported by Bolanos and Edmeades (1993) and Lafitte and Banziger (1997). Moderate to high heritability estimates imply that the genetic variation for such traits can be precisely assessed from phenotypic observation and that the trait can be easily transmitted to the offspring of the selected genotypes. Falconer (1960) pointed out that higher heritability estimates might be obtained for traits which could be considered as least important determinant of natural fitness while lower estimates may be obtained for traits that are most closely associated with it. Thus, lower heritability estimates obtained in the present study for ear aspect for the three populations and number of ears per plant for DMR ESR and TZE COMP.3DT, which are strong determinants of high yield under low-N, is therefore not surprising. Obilana and Fakorede (1979), in a critical review of heritability stated that if a trait is strongly influenced by some environmental variations, its heritability would be low in a population in which those environments vary widely. On the other hand, in another population in which the environment is rigidly controlled so that those variations do not occur, the same trait would tend to have high heritability. This statement explains the different heritability estimates obtained for the different N levels for the three maize populations. The estimates were higher for the high-N condition than for the low-N condition for each of the three maize populations.

5.6 Predicted Response to Selection

The difference between the mean of any population after selection, i.e the population generated from the selected parents, and the mean of the population before selection, is the response to selection or the observed gains from selection (Hallauer and Miranda, 1988). Expected genetic gain for grain yield under low-N for this study was 15.97 % for DMR ESR, 23.0 % for TZE COMP. 3DT, and 24.97 % for ACR 9331 DMRSR. Similar genetic gains were obtained by Lafitte and Banziger (1997) for tolerance to low N in other maize populations. Secondary plant characteristics are important as selection criteria for better performance under stress and are often used by breeders to hasten progress from selection. Among the secondary traits evaluated in this study, selections increased stay green by 2.5 % and number of ears per plant by 8.5 % for DMR ESR. This was similar for the other two populations. Considerable high genetic gain was obtained for plant height, ear height and stay green (a relative measure of chlorophyll N content in leaves and stem). Similar results have been reported by Lafitte and Banziger (1997) for plant and ear height under N stress. Increases in plant and ear heights with selection for yield are a common trend (Lafitte and Banziger, 1997; Sallah and Geadelmann, 1997) although undesirable in tropical maize. High yielding tropical maize tends to be too tall, an undesirable situation that causes stalk breakage under windy weather (Ajala *et al.*, 1995; Banziger and Cooper, 2001). Walulu *et al*. (1994) studied the inheritance of stay green in sorghum populations and reported a single dominant gene for the trait with a high genetic variance in relation to the phenotypic variance. They concluded that selection for the trait will result in fast progress. Plants with good stay green attribute have longer grain filling period because of rapid and efficient translocation and remobilization of N from leaves and stem sources to support growth and grain filling under stressed condition. Kamara *et al*. (2005) reported a strong correlation between stay green and grain yield of some maize genotypes under N stress condition.

The genetic gain for ASI in DMR ESR is -0.1005 which is equivalent to 8 %, -0.0914 in TZE COMP. 3DT equivalent to 6.7 % and 0.5056 in Acr 9331 DMR SR equivalent to 3.9 %. The top yielding genotypes under both fertility environments had relatively reduced anthesis-silking intervals. In effect, reduction in ASI, a trait known to affect stability under stressed conditions, will ensure longer duration of grain filling and better grain yield.

5.7 Genotypic and Phenotypic Correlation Coefficient

Generally in this investigation, grain yield had significant positive correlations with plant height, ear height, stay green, ears per plant and ear aspect for the three populations, especially for TZE COMP. 3DT and ACR 9931 DMR ESR under low-N. These results agree with the earlier findings of Banziger and Lafitte (1997) and Kling *et al*. (1997a) who reported strong association between grain yield and number of ears per plant, plant height and 300-kernels weight. The identification of traits that relate or correlate well with high yield under low N conditions, offers prospect for the exploitation of such traits in maize breeding programme aimed at developing N efficient genotypes. ASI and stay green had negative correlations with grain yield under low-N level for TZE COMP. 3DT and ACR 9331 DMRSR, but exhibited positive significant correlation with grain yield for DMR ESR, a case of genotypic difference being exhibited.

The significant and positive correlation of grain yield with plant height and ear height under high N conditions are undesirable because tall plants with relatively higher ear placement tend to be highly susceptible to lodging, especially under high N conditions. Similar results have earlier been reported by Adeyemo (1986) and Lafitte and Banziger (1997). Yield is always positively

correlated with height thus suggesting the use of a restricted index that put a ceiling on height for selection purposes. However, the negative correlations observed between grain yield and days to 50 % pollen and days to 50 % silk are in line with the result of Eckebil (1974) and desirable as it indicates that earlier mating progenies within the three populations under investigation will tend to be higher yielding. This is not unexpected since the populations were previously selected for earliness to maturity.

Commercial acceptability of improved population is an important consideration in plant breeding. Grain yield is a complex trait resulting from less complex traits in the plant. Some of these less complex traits normally display both desirable and undesirable association with grain yield thus suggesting need for appropriate selection indices.. Although, the use of selection indices may reduce expected progress form selection because the superiority of some traits are negated by the inferiority of others used in constructing the index, the resultant genotype is usually gradually improved in the desired direction.

CHAPTER 6

6.0 SUMMARY, CONCLUSION AND RECOMMENDATIONS

6.1 SUMMARY

One hundred and twenty five (125) S_1 lines of DMR ESR, two hundred and twenty five (225) S_1 lines of TZE COMP. 3DT and two hundred and fifty seven (257) S_1 lines of ACR 9331 DMRSR were established at Samaru and Mokwa in 2011 rainy season for population evaluation under low and high N levels. Randomized incomplete block design with two replications was used for the study. Each plot consisted of two rows spaced at 0.25 m and 0.75 m within and between rows, respectively. Data was collected for 10 quantitatively inherited traits: days to 50 % flowering, days to 50 % silking, plant height, ear height, husk cover, stay green, number of ears per plant, ear aspect, grain yield as well as ASI for the genotypes evaluated under low-N. The same set of data was collected under the high-N level except for stay green. Analysis of variance was done on collected data for all the traits for each N level, each location and also for the combined locations.

Generally, the performance of the three maize populations under both fertility conditions showed the existence of genetic variations among the tested materials for most of the traits measured. Significant variations were observed for most of traits among the genotypes of each population under both N levels. These indicate the presence of wide variability amongst the genotypes. Significant variation was also observed for $G \times L$ for the three populations across the two locations. However, environmental influence was more on the expression of the following

characters: plant heights, ear height, stay green, number of ears per plant and grain yield. Large Coefficient of variations were obtained for most of the traits except for days to 50 % pollen shed and days to 50 % silk under both fertility levels. The CVs were higher under low-N levels compared to high-N levels for the three populations. This also indicates the wide variability that exists among the genotypes.

Genetic variance estimates among the traits were all positive except for ACR 9331 DMRSR which had negative genetic variance for ASI, ears per plant and ear aspect as well as TZE COMP 3DT which also showed negative genetic variance for ASI under both low-N and high-N. In most cases, the genotypic variances and genotype x location variances were smaller in magnitude than the variance due to environment under low-N level, while they are slightly higher under high-N level. Broad sense heritability estimates for the studied traits were low to moderate. The low estimates observed were due to low genetic variances obtained for the traits. The study revealed that traits such as days to 50 % flowering, plant height, ear height, stay green and ear aspect are highly heritable. Grain yield showed positive correlation with plant height and ear height across the two locations. Significant negative correlations were observed on grain yield with stay green and ASI in the three populations. Predicted gains from selection were quite moderate for each of the populations under low-N due to the moderate heritability of some of the traits. However, the reliability of the prediction will not be known until the results of the selection scheme are observed in planned experiment for comparing original and improved population cycles. Knowledge of genetic variability is important in determining breeding methods to adopt and gains from selection.

6.2 CONCLUSION

The means, wide ranges, moderate to large CVs for all the traits evaluated under both low-N and high-N levels in this investigation are indication of presence of substantial genetic variability in the three maize populations (DMR ESR, TZE COMP. 3DT and ACR 9331 DMRSR S1 ESR). This indicates good progress from selection for grain yield and other agronomic traits under low-N and high-N levels.

The significant correlations of some secondary traits with grain yield under low-N for the three populations indicate the usefulness of these traits for indirect selection purposes in improving grain yield for low soil fertility. Also, the significant and negative correlation of stay green with grain yield under low-N coupled with the little increase in yield as well as the positive response of reducing days to ASI tend to support the S_1 selection scheme as a good option for improving maize under low-N.

Considerable expected genetic gain was obtained for plant height, ear height, ASI and stays green. These traits were also well associated with grain yield and can be implicated or employed for indirect selection in the three populations. This also confirms the effectiveness of the S_1 family selection scheme as a population improvement procedure capable of improving the performance of maize population for low N tolerance.

6.3 RECOMMENDATIONS

The performance of the three maize populations under both fertility conditions showed existence of wide genetic variation among the materials for most of the traits measured. This aided the selection of superior genotypes that could be recombined for further breeding work such as development of synthetics, inbred lines, hybrids, and new population for continuous improvement for low-N tolerance. It also indicates that the S_1 family selection scheme is very suitable for improving maize population for stress tolerance. The three maize populations are therefore recommended as sources of genotypes with better performance under both low and high soil fertility. Furthermore, TZE COMP. 3DT was found to be more suitable as the genotypes exhibited higher yield potential and stability across the different locations compared to DMR ESR and ACR 9331 DMRSR.

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Appendix i: Mean Values for the 10 traits of the 125 S_1 lines of DMR ESR evaluated under low-N in Zaria and Mokwa

Genoypes	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	S.Green	EAR/P	EASP	GY
DMR ESR-W S1-9	56	54	2	175	65	3	4.5	0.69	3.5	888.89
DMR ESR-W S1-36	56	54.5	1.5	161	60	4	4	1.5	4.5	2133.33
DMR ESR-W S1-70	56	53.5	2.5	162	55.5	4.5	4	1	4	2488.89
DMR ESR-W S1-37	55.5	54.5	1	179.5	66.5	4.5	4	1.03	4	1866.67
DMR ESR-W S1-68	56	54	2	179.5	54.5	4	4.5	0.92	4	1688.89
DMR ESR-W S1-75	55.5	54	1.5	149.5	65	4	4	0.78	4	1600
DMR ESR-W S1-48	55.5	54.5	1	145	57	4	4.5	1.15	4	2222.22
DMR ESR-W S1-62	53	54.5	-1.5	160	60	4.5	4	0.94	4	2577.78
DMR ESR-W S1-80	55.5	52.5	3	169	70	4.5	4.5	1.23	4	2577.78
DMR ESR-W S1-39	56	54.5	1.5	184	75.5	3.5	4.5	1.37	4.5	2488.89
DMR ESR-W S1-65	56	53.5	2.5	150	70	4	4	0.94	4.5	1244.44
DMR ESR-W S1-94	55	52.5	2.5	174.5	65.5	4	4	0.99	4.5	2044.44
DMR ESR-W S1-106	57.5	55.5	2	157.5	66	4	5	1.29	5	888.89
DMR ESR-W S1-28	56.5	54	2.5	159	76.5	3.5	5	1.04	4.5	2488.89
DMR ESR-W S1-125	56	54.5	1.5	179.5	65.5	4	3.5	0.9	3.5	2488.89
DMR ESR-W S1-99	56	54.5	1.5	151	78	3	4.5	0.97	3.5	2488.89
DMR ESR-W S1-86	55	53.5	1.5	159	63.5	3	5	0.79	4.5	1244.44
DMR ESR-W S1-31	55	54	1	152	55	4	3.5	0.96	4.5	2222.22
DMR ESR-W S1-121	56	55	1	144.5	65	4.5	4.5	0.85	4.5	1688.89
DMR ESR-W S1-118	55.5	54.5	1	140.5	45	4	4.5	0.97	6	1600
DMR ESR-W S1-2	55	52.5	2.5	173	86	3.5	4	1.06	4	1777.78
DMR ESR-W S1-113	55.5	54.5	1	185	91.5	3	5	1.04	4.5	1866.67
DMR ESR-W S1-59	55.5	54.5	1	187.5	77.5	4.5	6.5	0.73	2.5	1866.67
DMR ESR-W S1-53	54.5	53.5	1	129	61	4	4.5	1	4	2400
DMR ESR-W S1-78	55.5	54	1.5	157.5	65	4.5	4	1.02	4.5	1866.67
DMR ESR-W S1-34	55.5	53.5	2	150	72.5	3.5	4.5	0.81	3.5	1777.78
DMR ESR-W S1-119	54.5	53	1.5	142	60.5	4	4.5	0.92	4	2222.22
DMR ESR-W S1-17	54	54.5	-0.5	170	80.5	3.5	4	1.17	4.5	2933.33
DMR ESR-W S1-110	55.5	54	1.5	172.5	80	3.5	4.5	1.09	3.5	1777.78
DMR ESR-W S1-23	56.5	55.5	1	138.5	92.5	3	4	0.58	4	266.67
DMR ESR-W S1-122	55.5	54.5	1	197	100	4	4	1.25	4	2666.67
DMR ESR-W S1-19	56.5	55	1.5	165	65	4	4.5	1.23	4.5	2844.44
DMR ESR-W S1-77	56	54	2	158	56	4	4.5	0.94	4.5	711.11
DMR ESR-W S1-24	56	54	2	148	75	4.5	4.5	0.96	4	977.78
DMR ESR-W S1-102	56	54.5	1.5	157	75	4	4.5	1	4	1155.56

DMR ESR-W S1-56	55	53	2	167	86	3.5	4.5	0.79	4.5	1155.56
DMR ESR-W S1-111	55	53	2	164.5	71.5	4	4.5	0.83	4	2133.33
DMR ESR-W S1-73	55	54	1	174.5	90	4	4	0.75	3.5	1777.78
DMR ESR-W S1-83	55.5	55.5	0	182.5	75.5	3.5	4.5	1.08	5	2488.89
DMR ESR-W S1-100	56	55	1	157.5	69	3.5	4	0.83	4	1777.78
DMR ESR-W S1-88	55	53.5	1.5	162.5	79	3	4	1.28	4.5	2577.78
DMR ESR-W S1-101	56	54.5	1.5	145	72.5	4	4	0.87	3.5	2400
DMR ESR-W S1-15	54.5	52.5	2	155	73	3.5	4.5	0.92	3.5	2666.67
DMR ESR-W S1-18	55.5	54	1.5	200.5	108.5	3	4	1.21	4.5	2666.67
DMR ESR-W S1-5	56	54	2	204.5	105	4	4.5	1.33	4	2755.56
DMR ESR-W S1-112	55	51.5	3.5	160	67	3.5	4.5	1.03	4.5	2933.33
DMR ESR-W S1-50	56	54.5	1.5	155	71.5	4	5	1.15	4.5	2577.78
DMR ESR-W S1-43	55.5	54	1.5	152.5	56.5	3	4.5	0.94	5	1688.89
DMR ESR-W S1-82	57	55	2	174.5	75	3.5	4	1.59	4	1600
DMR ESR-W S1-103	55.5	54	1.5	165	79.5	4	5	1.09	4.5	1600
DMR ESR-W S1-60	55.5	53	2.5	162.5	77	3.5	5	1	4.5	2133.33
DMR ESR-W S1-29	55	53	2	167.5	66	3.5	5	1.13	5	1511.11
DMR ESR-W S1-7	54	53	1	161.5	55	3	4.5	1.29	5	1155.56
DMR ESR-W S1-33	56	53.5	2.5	176.5	66.5	3	4.5	0.82	5	1600
DMR ESR-W S1-92	56	55.5	0.5	170	66	4	4	0.92	4.5	1422.22
DMR ESR-W S1-3	56	54.5	1.5	180	73	3.5	4.5	1	6	888.89
DMR ESR-W S1-124	55	53	2	142.5	53	4	5	0.96	4.5	1777.78
DMR ESR-W S1-25	56	54.5	1.5	149.5	75.5	3.5	4.5	0.6	5.5	977.78
DMR ESR-W S1-93	55	53	2	171.5	88.5	3.5	4.5	0.93	4.5	2133.33
DMR ESR-W S1-95	55	53.5	1.5	150.5	61.5	4.5	4.5	0.97	4.5	1955.56
DMR ESR-W S1-67	56	55	1	145.5	54.5	4	5	1.06	5	1333.33
DMR ESR-W S1-20	56.5	54	2.5	183	71.5	4	4.5	1	4.5	1333.33
DMR ESR-W S1-8	56.5	54.5	2	165	80	3	4.5	1.22	5.5	2222.22
DMR ESR-W S1-89	56	55	1	155	66.5	3.5	5	1.04	4.5	1244.44
DMR ESR-W S1-66	56	54	2	159	61.5	4	4.5	0.69	5.5	800
DMR ESR-W S1-52	55	53	2	160	76.5	4	4.5	1.13	5.5	1422.22
DMR ESR-W S1-123	56	55	1	154	66	3.5	4.5	0.99	4	977.78
DMR ESR-W S1-117	55.5	54.5	1	162.5	66	3.5	4.5	1.03	4.5	1688.89
DMR ESR-W S1-32	55.5	54.5	1	164.5	80	3.5	5	0.8	4.5	1511.11
DMR ESR-W S1-98	55.5	54.5	1	170	75	3	4.5	0.91	5	1600
DMR ESR-W S1-84	55	53.5	1.5	170	80	3.5	4.5	1.02	4.5	1777.78
DMR ESR-W S1-81	55.5	54	1.5	159.5	70	4.5	4.5	0.97	4.5	1777.78

DMR ESR-W S1-27	56	54.5	1.5	157.5	75	4	5	0.73	4	1422.22
DMR ESR-W S1-21	55.5	53.5	2	173.5	85.5	4	4.5	0.81	5.5	1955.56
DMR ESR-W S1-64	58	56	2	164.5	62.5	3.5	5	1	5.5	177.78
DMR ESR-W S1-87	55.5	54	1.5	155	65	4	4.5	1.04	5.5	1866.67
DMR ESR-W S1-96	55.5	53.5	2	154.5	62.5	4	4.5	0.88	5	1422.22
DMR ESR-W S1-12	55	53.5	1.5	175	66.5	3.5	5	1.17	4.5	1333.33
DMR ESR-W S1-45	55.5	54.5	1	147.5	56.5	4	4.5	0.89	4	2044.44
DMR ESR-W S1-120	55.5	54	1.5	135	69	4	5	0.85	4.5	2133.33
DMR ESR-W S1-44	56	54.5	1.5	164.5	66.5	3.5	4.5	0.81	5	1422.22
DMR ESR-W S1-26	55	53.5	1.5	166	74.5	3.5	4	1.08	4	1600
DMR ESR-W S1-79	55	53	2	162	71.5	3.5	4.5	0.8	4	888.89
DMR ESR-W S1-41	55	53.5	1.5	160	80	3.5	4	0.88	4.5	2044.44
DMR ESR-W S1-51	55.5	54	1.5	165.5	81	4.5	4	0.88	5	2133.33
DMR ESR-W S1-69	55	53.5	1.5	150	61.5	4	5	0.93	5	888.89
DMR ESR-W S1-114	55.5	54	1.5	154	60	3.5	4.5	0.81	5	1422.22
DMR ESR-W S1-6	55.5	54	1.5	157	67	3.5	4.5	1.07	3.5	1866.67
DMR ESR-W S1-107	54.5	54	0.5	182.5	86.5	4.5	4	0.88	3.5	2666.67
DMR ESR-W S1-4	55.5	54	1.5	177.5	66.5	4	4	0.92	4.5	2133.33
DMR ESR-W S1-11	54.5	53.5	1	177	69.5	3	5	1.23	5	1244.44
DMR ESR-W S1-71	55.5	54.5	1	157	56.5	4	4.5	1.23	4	2400
DMR ESR-W S1-97	56	55	1	158	80	5	5	0.94	5	2400
DMR ESR-W S1-16	55	54	1	145	70	4	5	1.12	4.5	1955.56
DMR ESR-W S1-1	56.5	55	1.5	139	68.5	3.5	4.5	1.34	5	1866.67
DMR ESR-W S1-10	56	53.5	2.5	165	67.5	3.5	4	0.9	4.5	2311.11
DMR ESR-W S1-30	55.5	54	1.5	160	70.5	4	4.5	1.38	5.5	533.33
DMR ESR-W S1-40	54	52.5	1.5	165	82	3.5	4	1.02	5.5	1422.22
DMR ESR-W S1-42	56	54.5	1.5	161	79	4	5	0.88	4.5	1244.44
DMR ESR-W S1-61	55	53.5	1.5	170	67.5	4	4.5	1.06	4.5	1066.67
DMR ESR-W S1-72	56.5	55	1.5	146.5	73	4	4	1.18	5	888.89
DMR ESR-W S1-74	55	54	1	155	61.5	4	4	1.15	4.5	1866.67
DMR ESR-W S1-63	56	54	2	166.5	71.5	3	4	1.17	4	3111.11
DMR ESR-W S1-35	55.5	54.5	1	172.5	70	3.5	4.5	0.79	4	1244.44
DMR ESR-W S1-116	55.5	54.5	1	163.5	66.5	4	4	0.94	4	1688.89
DMR ESR-W S1-22	56	55	1	154	64	3	4.5	1.07	5	977.78
DMR ESR-W S1-104	56	55	1	175	72.5	4	4	1.18	4.5	1511.11
DMR ESR-W S1-57	54.5	53.5	1	162.5	75.5	4	3.5	0.75	4.5	266.67
DMR ESR-W S1-54	56	54	2	159	90	3.5	4.5	1.67	4	2222.22

DMR ESR-W S1-91	55.5	54.5	1	163	80.5	3.5	4	0.93	3.5	2933.33
DMR ESR-W S1-85	55	54	1	175	90.5	3	4.5	1.32	2.5	2222.22
DMR ESR-W S1-49	55	53.5	1.5	177.5	77.5	3.5	3	0.93	3	3822.22
DMR ESR-W S1-14	55.5	53.5	2	200	90	4	4	0.7	4.5	1688.89
DMR ESR-W S1-55	54.5	53.5	1	152.5	60	3.5	5	0.85	4.5	888.89
DMR ESR-W S1-76	54	53	1	169.5	75	4	4.5	1.36	4.5	2577.78
DMR ESR-W S1-46	54	53.5	0.5	144	65	3.5	4.5	0.67	4.5	1066.67
DMR ESR-W S1-109	56	54.5	1.5	162.5	67.5	4	4	0.86	3.5	1333.33
DMR ESR-W S1-58	56	54	2	197	98	3	4	0.84	4	1422.22
DMR ESR-W S1-108	54.5	54	0.5	190	80	3.5	4.5	0.79	4	2133.33
DMR ESR-W S1-13	54.5	53	1.5	140	70	2.5	5	0.81	4	1688.89
DMR ESR-W S1-90	54.5	53	1.5	188	100	3.5	4.5	0.82	3.5	2133.33
DMR ESR-W S1-105	55.5	53.5	2	150	72	4	4	1.08	3.5	2933.33
DMR ESR-W S1-115	56	54	2	173	92	4	3.5	1.11	4.5	3911.11
DMR ESR-W S1-38	55	53.5	1.5	168	87	4	4.5	1.15	4.5	1422.22
DMR ESR-W S1-47	56	54.5	1.5	150	73	4	4	1.75	4.5	888.89

Appendix ii: Mean Values for the 9 traits of the 125 S_1 lines of DMR ESR evaluated under High-N in Zaria and Mokwa

GENOTYPES	DYSK	POLLEN	ASI	PLHT	EHT	HUSK	EARS/P	EASP	GWT/HA
DMR ESR-W S1-9	56.50	54.50	2.00	168.00	66.50	3.00	1.08	3.50	2222.22
DMR ESR-W S1-36	61.50	59.00	2.50	132.50	50.00	3.50	1.10	4.50	1066.67
DMR ESR-W S1-70	55.00	57.00	-2.00	124.50	45.50	3.00	1.14	4.00	1244.44
DMR ESR-W S1-37	55.50	53.50	2.00	156.50	63.50	3.50	0.68	4.00	1600.00
DMR ESR-W S1-68	56.00	53.50	2.50	132.00	45.00	3.50	1.03	3.50	2044.44
DMR ESR-W S1-75	54.50	52.00	2.50	137.50	66.50	3.00	0.91	5.00	800.00
DMR ESR-W S1-48	57.00	55.50	1.50	145.50	74.50	3.50	0.83	4.50	1333.33
DMR ESR-W S1-62	58.00	56.50	1.50	110.00	50.00	3.50	0.68	5.00	1244.44
DMR ESR-W S1-80	56.00	54.00	2.00	156.00	71.50	3.50	0.81	4.00	1688.89
DMR ESR-W S1-39	57.00	54.50	2.50	140.00	52.50	3.00	0.61	4.50	1066.67
DMR ESR-W S1-65	57.50	55.50	2.00	142.50	63.00	3.00	0.90	4.00	800.00
DMR ESR-W S1-94	57.00	55.00	2.00	165.50	72.00	3.00	0.82	4.00	1511.11
DMR ESR-W S1-106	54.50	52.50	2.00	145.50	60.00	3.50	0.84	4.00	1244.44
DMR ESR-W S1-28	59.50	57.00	2.50	155.00	70.00	3.00	0.65	4.00	1066.67
DMR ESR-W S1-125	57.00	55.00	2.00	179.00	67.00	3.50	0.95	3.50	1688.89
DMR ESR-W S1-99	55.00	53.50	1.50	145.50	66.50	3.00	0.72	4.00	1422.22
DMR ESR-W S1-86	56.50	54.50	2.00	150.00	60.50	3.00	0.94	4.00	1511.11
DMR ESR-W S1-31	57.00	54.50	2.50	148.00	55.50	3.00	1.00	4.00	1600.00
DMR ESR-W S1-121	56.00	55.50	0.50	150.50	68.50	3.00	1.15	4.50	1066.67
DMR ESR-W S1-118	59.50	59.00	0.50	152.00	54.00	2.50	0.58	4.50	355.56
DMR ESR-W S1-2	56.00	55.00	1.00	157.00	72.50	3.00	0.80	4.00	1422.22
DMR ESR-W S1-113	59.50	56.00	3.50	111.50	78.50	3.00	0.79	5.00	622.22
DMR ESR-W S1-59	58.50	56.00	2.50	168.00	79.50	3.00	0.97	4.00	1955.56
DMR ESR-W S1-53	55.00	53.50	1.50	135.50	61.00	3.50	0.91	4.00	2222.22
DMR ESR-W S1-78	57.00	54.00	3.00	148.00	60.00	3.50	1.03	3.50	1688.89
DMR ESR-W S1-34	56.00	54.00	2.00	151.00	79.00	3.00	0.93	4.00	1777.78
DMR ESR-W S1-119	55.50	54.00	1.50	138.00	66.50	2.50	1.24	4.00	1600.00
DMR ESR-W S1-17	58.00	56.50	1.50	160.50	74.00	3.00	0.92	4.00	977.78
DMR ESR-W S1-110	57.50	55.50	2.00	156.50	73.00	3.00	0.82	3.00	1688.89
DMR ESR-W S1-23	58.00	56.00	2.00	160.00	95.00	2.00	0.80	4.00	355.56
DMR ESR-W S1-122	57.50	55.50	2.00	168.50	87.50	3.00	0.96	4.00	1333.33
DMR ESR-W S1-19	57.00	55.00	2.00	165.50	67.00	3.00	0.98	4.00	1511.11
DMR ESR-W S1-77	61.50	58.50	3.00	152.00	62.50	3.00	1.00	4.50	622.22
DMR ESR-W S1-24	55.50	53.50	2.00	148.00	57.00	3.50	1.21	4.00	444.44
DMR ESR-W S1-102	56.50	53.50	3.00	133.00	56.50	3.00	1.00	4.00	444.44
DMR ESR-W S1-56	55.50	53.50	2.00	140.50	67.00	3.00	0.76	4.50	1333.33

DMR ESR-W S1-111	54.50	53.50	1.00	160.00	59.00	3.00	0.91	4.00	1866.67
DMR ESR-W S1-73	56.00	52.50	3.50	145.00	70.00	2.50	1.02	4.50	1600.00
DMR ESR-W S1-83	57.50	55.50	2.00	148.00	65.00	3.00	2.23	4.00	1244.44
DMR ESR-W S1-100	62.00	59.00	3.00	149.00	63.00	2.50	0.57	3.50	1422.22
DMR ESR-W S1-88	56.00	53.50	2.50	149.00	80.00	3.00	0.90	4.00	1777.78
DMR ESR-W S1-101	55.50	53.00	2.50	161.00	80.50	3.00	0.83	4.00	1688.89
DMR ESR-W S1-15	56.50	54.50	2.00	160.00	76.50	3.00	0.75	4.00	1777.78
DMR ESR-W S1-18	57.00	54.50	2.50	183.50	90.00	3.00	1.11	4.50	977.78
DMR ESR-W S1-5	57.00	54.00	3.00	121.50	90.00	3.00	0.79	4.00	1866.67
DMR ESR-W S1-112	55.50	53.50	2.00	156.00	70.00	3.00	0.87	4.00	1688.89
DMR ESR-W S1-50	57.50	55.00	2.50	149.00	59.50	3.00	0.83	4.00	1777.78
DMR ESR-W S1-43	65.50	61.50	4.00	154.00	75.50	3.00	1.36	4.50	977.78
DMR ESR-W S1-82	55.50	53.00	2.50	168.00	77.00	3.00	0.95	4.00	1155.56
DMR ESR-W S1-103	55.50	53.50	2.00	154.00	70.00	3.50	1.09	3.50	2133.33
DMR ESR-W S1-60	55.00	52.00	3.00	157.50	73.50	2.50	1.03	4.00	2044.44
DMR ESR-W S1-29	54.00	52.50	1.50	155.00	60.00	3.00	0.81	4.50	1333.33
DMR ESR-W S1-7	63.50	60.50	3.00	162.00	72.00	2.50	0.50	4.00	1422.22
DMR ESR-W S1-33	57.00	54.50	2.50	156.00	59.00	2.50	0.76	4.00	1422.22
DMR ESR-W S1-92	55.50	53.00	2.50	160.50	66.50	4.00	2.53	4.00	1244.44
DMR ESR-W S1-3	58.00	55.50	2.50	164.00	73.50	3.00	0.99	4.00	1866.67
DMR ESR-W S1-124	55.50	53.00	2.50	142.00	64.50	3.00	1.00	4.00	1600.00
DMR ESR-W S1-25	56.00	54.00	2.00	150.50	66.50	3.50	0.90	4.50	1600.00
DMR ESR-W S1-93	54.50	52.00	2.50	161.00	71.00	3.00	0.76	3.50	1777.78
DMR ESR-W S1-95	54.00	52.00	2.00	151.00	60.50	3.00	1.07	4.00	2488.89
DMR ESR-W S1-67	55.50	52.50	3.00	147.50	56.50	3.00	0.96	3.50	1688.89
DMR ESR-W S1-20	56.00	54.00	2.00	167.00	69.50	2.50	0.82	4.50	1333.33
DMR ESR-W S1-8	57.00	55.00	2.00	158.00	71.00	3.00	0.85	3.50	2044.44
DMR ESR-W S1-89	58.00	55.50	2.50	153.50	69.50	3.00	1.04	4.00	2400.00
DMR ESR-W S1-66	54.00	51.50	2.50	151.00	64.00	3.00	0.66	4.50	800.00
DMR ESR-W S1-52	55.50	53.50	2.00	140.00	65.00	3.00	0.86	5.00	711.11
DMR ESR-W S1-123	54.00	51.50	2.50	143.00	53.00	4.00	0.72	4.00	1155.56
DMR ESR-W S1-117	56.50	54.00	2.50	120.50	65.00	3.00	0.56	4.50	711.11
DMR ESR-W S1-32	55.50	53.50	2.00	117.00	32.50	4.00	0.25	5.00	977.78
DMR ESR-W S1-98	56.00	54.00	2.00	158.50	61.50	3.00	1.13	3.50	2933.33
DMR ESR-W S1-84	54.50	54.50	0.00	150.00	55.00	3.00	0.83	4.00	1422.22
DMR ESR-W S1-81	60.50	58.00	2.50	119.00	60.00	3.00	1.30	4.00	1511.11
DMR ESR-W S1-27	58.00	56.00	2.00	93.00	59.50	3.00	1.63	4.00	1155.56
DMR ESR-W S1-21	58.00	55.50	2.50	155.00	70.50	2.50	0.78	3.50	1422.22

DMR ESR-W S1-64	66.00	63.00	3.00	167.00	57.00	4.00	1.00	5.00	177.78
DMR ESR-W S1-87	56.50	54.00	2.50	140.00	52.50	4.50	0.83	5.00	622.22
DMR ESR-W S1-96	56.50	55.00	1.50	151.00	54.00	3.00	1.00	4.50	1244.44
DMR ESR-W S1-12	55.50	58.50	-3.00	170.00	65.50	3.00	1.10	4.00	1422.22
DMR ESR-W S1-45	56.50	54.00	2.50	151.50	60.50	3.00	0.82	4.00	800.00
DMR ESR-W S1-120	57.50	56.00	1.50	138.00	62.50	3.00	3.04	4.50	977.78
DMR ESR-W S1-44	56.50	54.00	2.50	155.00	63.00	3.00	2.57	4.00	1422.22
DMR ESR-W S1-26	55.00	53.50	1.50	106.00	73.50	3.00	0.57	5.00	711.11
DMR ESR-W S1-79	54.00	52.50	1.50	140.00	58.00	3.50	0.77	4.00	622.22
DMR ESR-W S1-41	56.00	54.00	2.00	151.50	73.00	3.00	1.13	4.00	1244.44
DMR ESR-W S1-51	61.00	58.00	3.00	160.00	76.00	4.00	0.96	4.00	977.78
DMR ESR-W S1-69	56.50	54.00	2.50	160.50	60.50	3.50	0.80	4.00	800.00
DMR ESR-W S1-114	56.50	54.50	2.00	147.50	67.50	2.50	0.85	4.00	1155.56
DMR ESR-W S1-6	63.00	60.00	3.00	145.50	58.00	3.00	0.56	4.50	711.11
DMR ESR-W S1-107	56.50	54.00	2.50	171.50	75.00	2.50	7.00	4.00	2044.44
DMR ESR-W S1-4	56.50	52.50	4.00	164.50	75.00	3.00	0.57	4.50	711.11
DMR ESR-W S1-11	54.50	54.00	0.50	163.50	71.50	3.00	0.68	4.00	711.11
DMR ESR-W S1-71	55.00	52.50	2.50	156.50	76.00	3.50	0.98	4.00	1422.22
DMR ESR-W S1-97	53.50	53.50	0.00	154.50	71.00	3.50	0.90	4.50	1600.00
DMR ESR-W S1-16	55.50	53.00	2.50	142.00	62.00	3.00	0.83	5.00	1333.33
DMR ESR-W S1-1	59.50	57.00	2.50	139.50	64.50	3.50	0.88	4.00	1422.22
DMR ESR-W S1-10	57.00	55.00	2.00	171.50	64.00	2.50	0.69	4.00	888.89
DMR ESR-W S1-30	56.50	54.00	2.50	158.00	70.00	3.00	1.10	4.00	711.11
DMR ESR-W S1-40	55.50	53.00	2.50	157.50	80.50	3.00	1.10	4.50	1600.00
DMR ESR-W S1-42	58.00	55.50	2.50	128.00	53.00	3.00	0.76	4.50	1155.56
DMR ESR-W S1-61	56.00	54.00	2.00	130.00	60.00	2.50	1.34	4.00	1422.22
DMR ESR-W S1-72	60.00	60.50	-0.50	138.50	67.50	3.00	1.17	4.50	1066.67
DMR ESR-W S1-74	56.50	54.00	2.50	145.50	60.50	3.00	0.90	4.00	1066.67
DMR ESR-W S1-63	59.00	56.00	3.00	169.00	77.50	2.50	0.91	3.50	2133.33
DMR ESR-W S1-35	59.50	57.50	2.00	160.00	64.00	3.50	2.77	4.00	977.78
DMR ESR-W S1-116	57.00	56.50	0.50	165.00	73.00	3.00	0.95	3.50	1777.78
DMR ESR-W S1-22	56.50	54.50	2.00	161.50	61.50	3.00	5.00	4.50	533.33
DMR ESR-W S1-104	59.50	56.50	3.00	157.00	43.00	2.50	0.81	4.50	800.00
DMR ESR-W S1-57	57.00	56.00	1.00	143.00	52.00	4.00	1.00	4.00	177.78
DMR ESR-W S1-54	57.00	54.50	2.50	107.50	73.50	2.50	0.70	4.00	1333.33
DMR ESR-W S1-91	58.50	55.50	3.00	157.50	77.00	3.00	1.04	4.00	1777.78
DMR ESR-W S1-85	59.50	58.50	1.00	163.00	85.50	3.00	0.60	4.50	888.89
DMR ESR-W S1-49	60.50	58.50	2.00	181.50	85.00	3.50	1.09	3.00	2844.44

DMR ESR-W S1-14	59.00	56.50	2.50	177.00	83.00	3.00	0.80	4.00	1244.44
DMR ESR-W S1-55	58.00	55.50	2.50	167.00	67.00	2.50	0.77	4.50	711.11
DMR ESR-W S1-76	59.00	57.00	2.00	160.00	69.00	4.00	0.88	4.00	1155.56
DMR ESR-W S1-46	57.00	55.00	2.00	145.00	65.00	3.00	0.85	4.00	1244.44
DMR ESR-W S1-109	63.50	61.00	2.50	155.50	74.50	2.50	1.65	4.50	622.22
DMR ESR-W S1-58	60.50	61.00	-0.50	167.50	76.50	3.00	0.88	4.00	800.00
DMR ESR-W S1-108	56.00	53.00	3.00	168.50	81.50	3.00	0.73	4.00	711.11
DMR ESR-W S1-13	56.00	54.00	2.00	157.50	77.00	2.50	1.35	4.50	1066.67
DMR ESR-W S1-90	57.00	55.00	2.00	172.50	90.00	3.50	1.20	3.50	1688.89
DMR ESR-W S1-105	55.00	52.00	3.00	159.00	71.00	3.00	1.00	4.50	1155.56
DMR ESR-W S1-115	61.00	58.00	3.00	168.00	63.00	3.00	1.16	3.50	1600.00
DMR ESR-W S1-38	56.00	54.00	2.00	161.50	81.00	3.00	0.88	4.50	533.33
DMR ESR-W S1-47	62.50	60.00	2.50	156.00	68.50	1.50	0.98	5.00	800.00

Appendix iii: Mean Values for the 10 traits of the 225 S_1 lines of TZE COMP. 3DT evaluated under Low-N in Zaria and Mokwa

Genotypes	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	STAY GREEN	EARS/P	EASP	GY
TZE COMP 3 DT S1-36	55	54	1	182.5	80	3.5	3.5	0.95	3.5	2222.22
TZE COMP 3 DT S1-134	55	54.5	0.5	162.5	75	3	3.5	0.96	3.5	1688.89
TZE COMP 3 DT S1-203	54	53.5	0.5	169.5	66.5	3.5	3.5	0.81	3.5	1688.89
TZE COMP 3 DT S1-133	55.5	54.5	1	162	82	3.5	4	1.47	4.5	1777.78
TZE COMP 3 DT S1-111	56	54.5	1.5	163.5	85	4	4	0.95	3.5	1600
TZE COMP 3 DT S1-144	55.5	54.5	1	184.5	86	3	4	1.13	4	2666.67
TZE COMP 3 DT S1-146	56	54.5	1.5	185.5	89.5	3.5	3.5	0.82	5	1066.67
TZE COMP 3 DT S1-68	56	54.5	1.5	148.5	90	3	3.5	1.12	4	2044.44
TZE COMP 3 DT S1-225	54.5	53.5	1	174.5	90	4	3.5	1.41	3	2666.67
TZE COMP 3 DT S1-107	55.5	54	1.5	166.5	80	3.5	4	0.91	4	2044.44
TZE COMP 3 DT S1-37	55.5	54.5	1	149.5	84	3.5	4	0.79	4.5	1155.56
TZE COMP 3 DT S1-94	56.5	55.5	1	164	77	3	3	1.25	4.5	2755.56
TZE COMP 3 DT S1-176	55.5	53	2.5	165.5	97	3.5	3	1.06	5	2666.67
TZE COMP 3 DT S1-178	55.5	54	1.5	165.5	80	3	4	1.04	4	2400
TZE COMP 3 DT S1-39	55.5	54.5	1	163.5	71.5	3.5	3.5	1.48	5	1155.56
TZE COMP 3 DT S1-129	55	54	1	160	85	3.5	4	1.2	4.5	2488.89
TZE COMP 3 DT S1-11	54	52.5	1.5	135	72.5	3.5	4	0.92	4	1777.78
TZE COMP 3 DT S1-220	54.5	55	-0.5	150.5	70.5	3.5	3	0.95	5	1955.56
TZE COMP 3 DT S1-126	55.5	54.5	1	153.5	71	3.5	3.5	1.45	5	2488.89
TZE COMP 3 DT S1-208	55.5	54	1.5	158.5	69	3	3	1.25	3.5	2844.44
TZE COMP 3 DT S1-157	55.5	54	1.5	180	90	3.5	3.5	1	4	1866.67
TZE COMP 3 DT S1-199	54.5	53	1.5	187	101	3.5	4	1.12	3.5	2844.44
TZE COMP 3 DT S1-33	55	54	1	170	72.5	3	4	1.08	4	1777.78
TZE COMP 3 DT S1-10	55.5	54.5	1	147.5	80	3.5	3	1.15	3.5	2488.89
TZE COMP 3 DT S1-158	55	53	2	177.5	93	3.5	3.5	1.43	3	3466.67
TZE COMP 3 DT S1-67	55	53.5	1.5	195	92.5	3.5	4	1.57	4.5	1777.78
TZE COMP 3 DT S1-61	55	54	1	165	60	4	4	1.49	3.5	3111.11
TZE COMP 3 DT S1-103	54	53.5	0.5	162	82.5	3.5	4	1.16	3.5	2666.67
TZE COMP 3 DT S1-42	55	53.5	1.5	170.5	82.5	3	3	1.42	3.5	2133.33
TZE COMP 3 DT S1-28	54.5	53.5	1	150	78	3.5	3	1.17	3	2666.67
TZE COMP 3 DT S1-25	55	53	2	174.5	56.5	3.5	3.5	1.05	3.5	1866.67
TZE COMP 3 DT S1-221	56	54.5	1.5	160	75	3.5	4	1.46	3.5	3200
TZE COMP 3 DT S1-118	56	53	3	175	81.5	3.5	4	1.01	4	2400
TZE COMP 3 DT S1-8	55	53.5	1.5	165	56.5	4	2.5	1.26	3.5	2400
TZE COMP 3 DT S1-74	54	52.5	1.5	185	93	4	3.5	1.04	4	2044.44
TZE COMP 3 DT S1-31	55.5	54.5	1	162.5	66.5	3.5	1.5	1.22	4.5	1688.89
TZE COMP 3 DT S1-185	56	55	1	165	65	3.5	4	0.81	6.5	711.11
TZE COMP 3 DT S1-131	54	53	1	155	53.5	3	4	0.94	4.5	2133.33
TZE COMP 3 DT S1-180	56	54	2	168	90	4	3.5	1.06	3.5	3200
TZE COMP 3 DT S1-150	56	54	2	185	85.5	3.5	4	1.29	4.5	1511.11

TZE COMP 3 DT S1-40	56	54.5	1.5	182	86.5	3	3.5	0.89	4	2400
TZE COMP 3 DT S1-85	55	54	1	152.5	75	3.5	3.5	1	4	2577.78
TZE COMP 3 DT S1-191	55	53	2	170.5	83	3.5	3	1.21	4	1777.78
TZE COMP 3 DT S1-89	56	55	1	198	92.5	3.5	3	1.12	4	2666.67
TZE COMP 3 DT S1-162	56	55	1	160	76.5	3.5	4	1.06	4.5	1777.78
TZE COMP 3 DT S1-212	55	54	1	152.5	71.5	3.5	3.5	1.03	5	1955.56
TZE COMP 3 DT S1-182	55.5	54.5	1	179	71.5	3.5	4	0.85	4	1600
TZE COMP 3 DT S1-187	54.5	53.5	1	185	81.5	4	3	1.3	3.5	3822.22
TZE COMP 3 DT S1-95	55	53.5	1.5	167.5	79.5	3.5	3.5	1.41	4.5	1511.11
TZE COMP 3 DT S1-64	54.5	53.5	1	180	90.5	4	4	1.14	3.5	2311.11
TZE COMP 3 DT S1-194	54	52.5	1.5	189.5	86.5	4	3	1.16	4	2488.89
TZE COMP 3 DT S1-81	54.5	53.5	1	140	85	4	3.5	1.15	3.5	3288.89
TZE COMP 3 DT S1-91	55	54	1	164.5	78	3.5	4	1.19	3.5	2755.56
TZE COMP 3 DT S1-149	56	55	1	177.5	87.5	3.5	3.5	1.88	4	2133.33
TZE COMP 3 DT S1-142	55.5	54	1.5	135	88.5	4	3.5	1.12	4	1777.78
TZE COMP 3 DT S1-96	56	55	1	177.5	95	4	3	1.24	4	3022.22
TZE COMP 3 DT S1-23	56	55	1	204.5	80	3.5	3.5	1.17	4	2400
TZE COMP 3 DT S1-140	54.5	53.5	1	141.5	80.5	3.5	4	0.9	4	1333.33
TZE COMP 3 DT S1-174	55	53.5	1.5	154.5	70	3.5	3.5	0.89	4.5	1422.22
TZE COMP 3 DT S1-128	56	54	2	133	76.5	3.5	4	1.27	4	2488.89
TZE COMP 3 DT S1-13	56	54.5	1.5	179.5	72.5	3.5	3.5	1.04	4	2222.22
TZE COMP 3 DT S1-183	55.5	53	2.5	174.5	90	3	3.5	1.2	4	1600
TZE COMP 3 DT S1-145	55.5	54.5	1	160.5	85	3.5	4	1.1	4.5	2044.44
TZE COMP 3 DT S1-58	54	53	1	171.5	86.5	3.5	3.5	1.4	4.5	2488.89
TZE COMP 3 DT S1-172	55	54	1	177	61.5	3.5	4	1.17	4	2222.22
TZE COMP 3 DT S1-206	56	55	1	193	85	3.5	4	1.04	4	2222.22
TZE COMP 3 DT S1-51	56	52.5	3.5	187.5	62.5	4	3.5	1.32	3.5	3288.89
TZE COMP 3 DT S1-173	56	56	0	152.5	54.5	4	3	1.12	4.5	2133.33
TZE COMP 3 DT S1-87	56	54.5	1.5	162.5	77.5	3.5	4	1.58	4.5	2133.33
TZE COMP 3 DT S1-152	55.5	54	1.5	130	60	3.5	3.5	1.04	4.5	977.78
TZE COMP 3 DT S1-90	54.5	53	1.5	144.5	56.5	3.5	3.5	1.04	4.5	2133.33
TZE COMP 3 DT S1-204	55	54	1	176.5	63.5	4	3.5	1.52	3.5	3111.11
TZE COMP 3 DT S1-137	54	53	1	170	91	3	3	1	4	177.78
TZE COMP 3 DT S1-211	56	53	3	145	90	4	5	1	4	177.78
TZE COMP 3 DT S1-77	55	53	2	147.5	59.5	4	4	0.67	4.5	888.89
TZE COMP 3 DT S1-166	55.5	54	1.5	162	77.5	3	4	0.59	4.5	800
TZE COMP 3 DT S1-184	54	52	2	167.5	80	3.5	4	0.93	4	1688.89
TZE COMP 3 DT S1-122	54	53	1	165	63	4	3	1	4	177.78
TZE COMP 3 DT S1-15	55.5	55	0.5	157.5	71.5	3.5	3.5	0.8	4	1777.78
TZE COMP 3 DT S1-41	55.5	54.5	1	137.5	70	3.5	4	1.16	4	2222.22
TZE COMP 3 DT S1-115	56	54	2	152	60.5	4	3.5	1.52	22	2577.78
TZE COMP 3 DT S1-100	55	53.5	1.5	174	81	3.5	4	1.43	4	2666.67
TZE COMP 3 DT S1-198	54	53	1	188	85	4.5	4	1.12	4	2222.22

TZE COMP 3 DT S1-216	54.5	53.5	1	144.5	72	3	3.5	1	4.5	2133.33
TZE COMP 3 DT S1-197	55	54	1	144	50.5	4	4.5	0.88	4	888.89
TZE COMP 3 DT S1-175	54.5	54.5	0	154	67.5	3.5	4	0.77	4.5	1422.22
TZE COMP 3 DT S1-201	55.5	54.5	1	158	65	4	3.5	1.26	4.5	1777.78
TZE COMP 3 DT S1-210	55	53.5	1.5	163.5	65.5	4	3.5	1.05	3	3733.33
TZE COMP 3 DT S1-132	54.5	53.5	1	175.5	79	4	4	1.16	5.5	2666.67
TZE COMP 3 DT S1-171	56	55	1	150	70	3.5	4	0.93	3	2044.44
TZE COMP 3 DT S1-101	55.5	53.5	2	164	71.5	3.5	4	0.74	5	711.11
TZE COMP 3 DT S1-79	55	53.5	1.5	155.5	82	3.5	4	0.71	4	1688.89
TZE COMP 3 DT S1-164	55	54	1	143.5	66.5	3.5	4	1.02	4	1600
TZE COMP 3 DT S1-193	55.5	54.5	1	150.5	70.5	3.5	4	1.02	4.5	1866.67
TZE COMP 3 DT S1-75	56	55	1	160	70	4	4	1	4.5	1777.78
TZE COMP 3 DT S1-5	55	53.5	1.5	172.5	75	3.5	4	0.87	5	1600
TZE COMP 3 DT S1-190	54	53	1	195	90	3.5	3.5	1.43	4	1511.11
TZE COMP 3 DT S1-16	55	53	2	170	66.5	4	3.5	1.04	4	1244.44
TZE COMP 3 DT S1-18	55	54	1	159	66.5	4	4	1.13	4	2844.44
TZE COMP 3 DT S1-7	55	54	1	169.5	60	3	3.5	1.42	4	2311.11
TZE COMP 3 DT S1-97	56	55	1	180	100	4.5	4	0.84	4	1777.78
TZE COMP 3 DT S1-60	55.5	54	1.5	160	80	4	4	1.25	4	2044.44
TZE COMP 3 DT S1-222	55.5	53.5	2	144.5	58	3.5	4	1.14	4.5	711.11
TZE COMP 3 DT S1-48	55	52.5	2.5	154.5	63	3.5	3.5	1.02	4	2044.44
TZE COMP 3 DT S1-125	55	53.5	1.5	170	85	4	4	0.62	4	1155.56
TZE COMP 3 DT S1-167	54.5	53	1.5	169.5	71.5	3.5	4	1.18	4.5	2044.44
TZE COMP 3 DT S1-1	55.5	54.5	1	159.5	81.5	3.5	3.5	0.8	4	2044.44
TZE COMP 3 DT S1-106	54.5	54	0.5	135	61.5	4	3.5	0.99	5	1600
TZE COMP 3 DT S1-92	54.5	53.5	1	185	85.5	4	4	0.91	4	977.78
TZE COMP 3 DT S1-35	56	55	1	140	51.5	4	4	0.81	4.5	1511.11
TZE COMP 3 DT S1-29	56	54.5	1.5	177	74	4	3.5	1.15	4	1600
TZE COMP 3 DT S1-71	55.5	53	2.5	143	61	4.5	3.5	0.92	4.5	622.22
TZE COMP 3 DT S1-72	56	54	2	165	81.5	4	4	0.78	4	1422.22
TZE COMP 3 DT S1-138	55.5	54.5	1	161	66.5	3.5	4	1.11	4.5	1422.22
TZE COMP 3 DT S1-124	54.5	53.5	1	172.5	71.5	4	3.5	1.11	4	1866.67
TZE COMP 3 DT S1-195	55	54	1	150.5	60	3.5	4	0.93	4	1688.89
TZE COMP 3 DT S1-189	54.5	54.5	0	170	75.5	3.5	4	1.07	4.5	1955.56
TZE COMP 3 DT S1-214	56	54	2	161.5	76.5	4.5	3.5	0.96	4.5	1688.89
TZE COMP 3 DT S1-104	55	54	1	171.5	73	4	4	0.97	4	1244.44
TZE COMP 3 DT S1-153	55	54	1	155.5	70.5	4	4.5	0.96	4	1600
TZE COMP 3 DT S1-20	54.5	53.5	1	145	42.5	4	3.5	0.93	4.5	1511.11
TZE COMP 3 DT S1-53	55.5	53.5	2	142.5	40	3.5	3	0.87	4.5	1866.67
TZE COMP 3 DT S1-159	55	54	1	142	65	3.5	4	0.64	4.5	2044.44
TZE COMP 3 DT S1-2	54.5	52.5	2	153	65	4	4	1.39	4.5	3022.22
TZE COMP 3 DT S1-52	55.5	54	1.5	155	77	4.5	3.5	1.19	5	2666.67
TZE COMP 3 DT S1-155	55.5	53.5	2	146	71.5	4	4	1.3	4.5	2488.89

TZE COMP 3 DT S1-213	56	55	1	157	75.5	4	4.5	1.29	4.5	1777.78
TZE COMP 3 DT S1-160	54.5	53.5	1	150.5	73	4	4	1.01	4.5	1866.67
TZE COMP 3 DT S1-34	56	55	1	157.5	87.5	4	3.5	0.93	4.5	1511.11
TZE COMP 3 DT S1-49	56	55	1	155	82.5	4	3.5	0.93	4	2488.89
TZE COMP 3 DT S1-59	55.5	54.5	1	179	86.5	4	3.5	0.92	4	1688.89
TZE COMP 3 DT S1-192	54	53	1	175	83	4	4	1.15	3.5	2755.56
TZE COMP 3 DT S1-209	55.5	54.5	1	157.5	60	4	3	0.89	4	2488.89
TZE COMP 3 DT S1-14	54.5	52.5	2	164.5	80	4	4	1.04	4	2488.89
TZE COMP 3 DT S1-151	54.5	53.5	1	170	85	3.5	3.5	0.91	4.5	2488.89
TZE COMP 3 DT S1-154	56	55	1	178	71.5	3.5	4.5	1.21	4.5	2044.44
TZE COMP 3 DT S1-12	55	54	1	170	80	4	4	0.83	5	888.89
TZE COMP 3 DT S1-19	56	55	1	150	65	3.5	4	0.81	3.5	1066.67
TZE COMP 3 DT S1-141	55.5	53.5	2	149	60	3.5	4	1.05	3.5	2488.89
TZE COMP 3 DT S1-186	55.5	54.5	1	147.5	62	4	4	0.91	4.5	2133.33
TZE COMP 3 DT S1-105	54.5	52.5	2	174	83	4	3.5	1.21	3.5	3377.78
TZE COMP 3 DT S1-179	55.5	54.5	1	150	65	4	3	1.12	5	2400
TZE COMP 3 DT S1-6	55.5	54.5	1	194	110	3.5	4	1.03	3.5	2311.11
TZE COMP 3 DT S1-24	55.5	54.5	1	177.5	68	4	3.5	1.21	4	2133.33
TZE COMP 3 DT S1-9	55	54	1	185	74.5	3.5	3	1.06	3.5	2044.44
TZE COMP 3 DT S1-196	54	52.5	1.5	180	65	3.5	3.5	1.13	4	1688.89
TZE COMP 3 DT S1-38	55	54	1	152.5	60	4	4	1.08	5	1244.44
TZE COMP 3 DT S1-165	53.5	52.5	1	185.5	90	4	3.5	1.07	4	3466.67
TZE COMP 3 DT S1-143	54.5	53.5	1	158.5	72.5	4	3.5	1.16	4	1955.56
TZE COMP 3 DT S1-50	55	54	1	165	70	4	4	1.11	4	1600
TZE COMP 3 DT S1-139	55	54	1	145.5	87.5	4	4	0.98	4	1244.44
TZE COMP 3 DT S1-69	55.5	54.5	1	194.5	90	4	3	1.3	4.5	2577.78
TZE COMP 3 DT S1-80	55.5	54.5	1	135	91.5	4	4	0.89	4	2400
TZE COMP 3 DT S1-82	54.5	53.5	1	137.5	62.5	4.5	4	0.97	4	2577.78
TZE COMP 3 DT S1-161	55.5	54.5	1	133.5	45	4	4	0.89	4	1422.22
TZE COMP 3 DT S1-43	54.5	53.5	1	170	70	3.5	4	1.42	4	2844.44
TZE COMP 3 DT S1-30	55.5	54.5	1	174.5	61.5	3.5	3.5	0.82	4.5	2044.44
TZE COMP 3 DT S1-112	55.5	54.5	1	165	65	3.5	3.5	0.83	4.5	1777.78
TZE COMP 3 DT S1-65	54.5	53	1.5	141	64	4.5	3	1.56	4	2311.11
TZE COMP 3 DT S1-170	54	52.5	1.5	174.5	70	4	4	0.91	4.5	622.22
TZE COMP 3 DT S1-156	55	55	0	165	71.5	4.5	3.5	0.88	4	1600
TZE COMP 3 DT S1-62	54	52.5	1.5	160	67.5	3.5	4	1.13	4.5	3288.89
TZE COMP 3 DT S1-99	55.5	54.5	1	160	61.5	4	3	1.59	4	2488.89
TZE COMP 3 DT S1-93	55.5	54.5	1	135	72.5	4.5	4	1.32	4	2311.11
TZE COMP 3 DT S1-135	54.5	53.5	1	170	62.5	3.5	4	1.07	4	1066.67
TZE COMP 3 DT S1-136	55.5	54.5	1	149	75	3.5	3.5	1.03	4	1600
TZE COMP 3 DT S1-202	56	55	1	154.5	60	4	4	1.14	4	2222.22
TZE COMP 3 DT S1-188	54	52.5	1.5	175	75.5	4	3.5	1.22	3.5	2755.56
TZE COMP 3 DT S1-57	55.5	54.5	1	187.5	80	4	3.5	1.1	3.5	1955.56

TZE COMP 3 DT S1-3	54	52.5	1.5	155	70	4	4	1.17	4	2044.44
TZE COMP 3 DT S1-22	56	55	1	175	100	4	2.5	1.48	4.5	1866.67
TZE COMP 3 DT S1-168	56	55	1	182	95	4	4	1.08	4	2222.22
TZE COMP 3 DT S1-63	55	54	1	199.5	96.5	4	4	0.85	4	2311.11
TZE COMP 3 DT S1-217	54.5	53.5	1	159.5	80.5	4.5	4	1.16	3.5	1688.89
TZE COMP 3 DT S1-163	54.5	53.5	1	157.5	75	4	4	1.02	4	1955.56
TZE COMP 3 DT S1-84	55	54	1	189.5	87	4	4	1.62	4.5	1866.67
TZE COMP 3 DT S1-54	55.5	54	1.5	137	70	3.5	3	0.6	4	1422.22
TZE COMP 3 DT S1-200	55	54	1	172.5	75.5	4	3.5	0.9	4	2755.56
TZE COMP 3 DT S1-117	55	56	-1	177.5	72	4	4	1.5	4.5	800
TZE COMP 3 DT S1-223	53.5	52	1.5	160	75.5	3	3.5	1.04	4	2577.78
TZE COMP 3 DT S1-121	54	53	1	164.5	79	4	4	0.85	4.5	2666.67
TZE COMP 3 DT S1-66	54.5	53.5	1	170	67.5	4	4	1.13	5	1688.89
TZE COMP 3 DT S1-116	55	54	1	166.5	61	3.5	3.5	1.32	4	2755.56
TZE COMP 3 DT S1-86	55	54	1	159.5	59	4	3.5	1.36	4	3022.22
TZE COMP 3 DT S1-219	55	54	1	166.5	78	4	4	0.95	4	1511.11
TZE COMP 3 DT S1-21	55	54	1	163	77	3.5	3.5	1.47	4	2400
TZE COMP 3 DT S1-127	55.5	54	1.5	162.5	92.5	4.5	4	1.08	4	2311.11
TZE COMP 3 DT S1-224	55.5	54.5	1	175	86.5	4	3.5	1.13	4.5	2933.33
TZE COMP 3 DT S1-98	54.5	53	1.5	160	71.5	3.5	3	0.79	4	711.11
TZE COMP 3 DT S1-148	56	55	1	153.5	66	4	3	1.52	4.5	1600
TZE COMP 3 DT S1-113	56	55	1	155	60	4	4	1.17	4	2044.44
TZE COMP 3 DT S1-123	56	55	1	155	70.5	4	4	1.19	4	2666.67
TZE COMP 3 DT S1-181	55	54	1	157.5	58	4	4	1.15	4	1955.56
TZE COMP 3 DT S1-46	55	53.5	1.5	153.5	66.5	4	3.5	0.87	4	1955.56
TZE COMP 3 DT S1-130	56	55	1	151	87	3.5	3.5	0.93	4	800
TZE COMP 3 DT S1-55	56	55	1	137.5	51.5	3.5	4	0.61	4.5	800
TZE COMP 3 DT S1-17	55.5	54.5	1	174.5	81.5	4	3	0.8	4	622.22
TZE COMP 3 DT S1-27	55	54	1	175	95	4	3.5	0.96	4	1688.85
TZE COMP 3 DT S1-44	54.5	53.5	1	150	61.5	4	3	0.88	4	1600
TZE COMP 3 DT S1-78	56	55	1	142.5	85.5	4	3	1.31	4	2844.44
TZE COMP 3 DT S1-32	55	54	1	152	71	4	3	0.87	4	2133.33
TZE COMP 3 DT S1-45	55	54	1	155	86	4	4	1.09	4.5	1333.33
TZE COMP 3 DT S1-215	54	52.5	1.5	182.5	55.5	4	4	1.23	4	2488.89
TZE COMP 3 DT S1-177	55	53	2	175	80.5	4	3.5	1	4.5	1511.11
TZE COMP 3 DT S1-218	56	55	1	174.5	70	4.5	3.5	1.06	4	2400
TZE COMP 3 DT S1-76	56	54	2	164.5	60	3.5	3.5	1.21	4	2133.33
TZE COMP 3 DT S1-110	56	55	1	195	95.5	4	3.5	1.09	4.5	1866.67
TZE COMP 3 DT S1-83	56.5	55.5	1	159.5	67.5	3.5	3.5	1.5	5	977.78
TZE COMP 3 DT S1-205	55.5	54	1.5	195	102.5	3.5	3.5	1.12	4.5	1955.56
TZE COMP 3 DT S1-119	56	54.5	1.5	170	75	5	4	0.83	4	2222.22
TZE COMP 3 DT S1-56	55	54	1	158	72	4	3	0.87	3.5	2222.22
TZE COMP 3 DT S1-108	55	54	1	179.5	72	4	3.5	1.14	4	1333.33

TZE COMP 3 DT S1-169	54.5	53.5	1	169.5	76.5	4	4	1.33	4	3377.78
TZE COMP 3 DT S1-109	55.5	54	1.5	188	75	4	4	1.24	4	2488.89
TZE COMP 3 DT S1-70	54.5	53	1.5	185.5	78.5	4	3.5	1.25	3.5	4444.44
TZE COMP 3 DT S1-88	55	54	1	185	80.5	4	3	1.13	3.5	2222.22
TZE COMP 3 DT S1-26	54.5	53.5	1	151.5	80.5	4.5	3.5	1.09	3.5	2400
TZE COMP 3 DT S1-47	56	53.5	2.5	170.5	61.5	3.5	3.5	1.3	4	2666.67
TZE COMP 3 DT S1-73	55.5	54.5	1	183.5	85	4	3.5	1.64	4.5	2311.11
TZE COMP 3 DT S1-147	56	54	2	175	80	3.5	3.5	1.13	4.5	1600
TZE COMP 3 DT S1-4	54.5	53.5	1	192.5	100	5	3	1.2	4	2755.56
TZE COMP 3 DT S1-102	56	55	1	175	76.5	3.5	2.5	1.22	4.5	2133.33
TZE COMP 3 DT S1-120	56	55	1	179	80	4	3.5	1.08	4	2488.89
TZE COMP 3 DT S1-207	55	54	1	180	89.5	4	3	1.38	4.5	2311.11
TZE COMP 3 DT S1-114	54	53	1	181	70	4	3.5	1.09	4	2844.44

Appendix iv: Mean Values for the 9 traits of the 225 S_1 lines of TZE COMP. 3DT evaluated under High-N in Zaria and Mokwa

Genotypes	DYSK	P0LLEN	ASI	PLHT	EHT	HUSK	EAP	GY
TZE COMP 3 DT S1-36	54.5	52.5	2	185.5	80	2.5	4	2044.44
TZE COMP 3 DT S1-134	55	53.5	1.5	167	60	3	4	1688.89
TZE COMP 3 DT S1-203	53	53	0	174.5	85	3	4.5	1866.67
TZE COMP 3 DT S1-133	55	53	2	174	82.5	3	4.5	1333.33
TZE COMP 3 DT S1-111	55.5	53.5	2	173.5	89	3	4	1333.33
TZE COMP 3 DT S1-144	55	53.5	1.5	190	75	3	4.5	2044.44
TZE COMP 3 DT S1-146	54.5	53	1.5	175.5	96.5	3	4.5	1244.44
TZE COMP 3 DT S1-68	53.5	52.5	1	170	127.5	2.5	4.5	1244.44
TZE COMP 3 DT S1-225	53	59.5	-6.5	164.5	69	2.5	4	1777.78
TZE COMP 3 DT S1-107	54.5	52.5	2	170	65	3	4.5	1066.67
TZE COMP 3 DT S1-37	53	53.5	-0.5	151.5	75	2	4.5	1866.67
TZE COMP 3 DT S1-94	55	53.5	1.5	170.5	90	2	3	3555.56
TZE COMP 3 DT S1-176	54.5	52	2.5	174.5	91	2.5	3	2933.33
TZE COMP 3 DT S1-178	55	53.5	1.5	165.5	71.5	2.5	4	1333.33
TZE COMP 3 DT S1-39	54.5	53	1.5	154	74	3	4.5	888.89
TZE COMP 3 DT S1-129	54	52.5	1.5	183	86	3	4	2400
TZE COMP 3 DT S1-11	53.5	52	1.5	152.5	65.5	2.5	5	977.78
TZE COMP 3 DT S1-220	55	53.5	1.5	163.5	71.5	3	4.5	1422.22
TZE COMP 3 DT S1-126	55	53	2	163	75.5	3	4.5	2311.11
TZE COMP 3 DT S1-208	54.5	53	1.5	164.5	67.5	3	4.5	1422.22
TZE COMP 3 DT S1-157	54	51	3	173	62.5	2.5	4.5	1777.78
TZE COMP 3 DT S1-199	54	52.5	1.5	170.5	80.5	3	4	2044.44
TZE COMP 3 DT S1-33	53.5	53	0.5	185	82.5	3.5	4.5	1777.78
TZE COMP 3 DT S1-10	54	53.5	0.5	157.5	68	3	4	2933.33
TZE COMP 3 DT S1-158	54	53	1	159.5	81	3	3.5	3644.44
TZE COMP 3 DT S1-67	54	53	1	167	77	3	4.5	1244.44
TZE COMP 3 DT S1-61	56	53	3	149.5	61.5	3	4	1777.78
TZE COMP 3 DT S1-103	55.5	52.5	3	153	69	2.5	4	1688.89
TZE COMP 3 DT S1-42	54	54	0	175	71.5	2.5	4.5	800
TZE COMP 3 DT S1-28	53.5	53	0.5	145	60.5	3	4	2133.33
TZE COMP 3 DT S1-25	56	54.5	1.5	163	62	3	4.5	1511.11
TZE COMP 3 DT S1-221	55	53	2	165	92	3	3.5	3466.67
TZE COMP 3 DT S1-118	56	53	3	160.5	88	3	3.5	2311.11
TZE COMP 3 DT S1-8	56	54	2	171	66.5	3	4	3288.89
TZE COMP 3 DT S1-74	54.5	52.5	2	165.5	73.5	3	4	2844.44

TZE COMP 3 DT S1-31	54.5	53	1.5	159	78.5	2.5	4	3733.33
TZE COMP 3 DT S1-185	55	52.5	2.5	162.5	71.5	2.5	4.5	800
TZE COMP 3 DT S1-131	53	54	-1	151	60	2.5	4	1955.56
TZE COMP 3 DT S1-180	55	53	2	171.5	93	2.5	3.5	1688.89
TZE COMP 3 DT S1-150	53.5	54	-0.5	152	97	2.5	4	1155.56
TZE COMP 3 DT S1-40	55	52.5	2.5	175.5	80	3	4	2400
TZE COMP 3 DT S1-85	53.5	52	1.5	145.5	63	3	4	1777.78
TZE COMP 3 DT S1-191	54	52	2	159.5	61.5	3	4	1866.67
TZE COMP 3 DT S1-89	55	53	2	179.5	75	2.5	4	2311.11
TZE COMP 3 DT S1-162	55	53	2	173.5	87	2.5	4.5	2222.22
TZE COMP 3 DT S1-212	53	51	2	177.5	82.5	2.5	4.5	1777.78
TZE COMP 3 DT S1-182	55	52.5	2.5	160.5	61.5	2.5	3.5	1777.78
TZE COMP 3 DT S1-187	54	55	-1	185	91	2	3.5	1511.11
TZE COMP 3 DT S1-95	54.5	52.5	2	165	60	3	4	2133.33
TZE COMP 3 DT S1-64	53	51	2	171	72.5	3	3.5	2666.67
TZE COMP 3 DT S1-194	53.5	53.5	0	187.5	106.5	2	4	1600
TZE COMP 3 DT S1-81	54	52.5	1.5	143	84	3	3.5	2577.78
TZE COMP 3 DT S1-91	54	52	2	167.5	64.5	3.5	3.5	2222.22
TZE COMP 3 DT S1-149	55	52.5	2.5	180	87.5	1.5	4	2222.22
TZE COMP 3 DT S1-142	54.5	53.5	1	159	71.5	3.5	4	2044.44
TZE COMP 3 DT S1-96	56	54	2	177	88	2.5	4	1511.11
TZE COMP 3 DT S1-23	55	53.5	1.5	135	80.5	2.5	4	3288.89
TZE COMP 3 DT S1-140	52	52.5	-0.5	177.5	98	2.5	4	1511.11
TZE COMP 3 DT S1-174	54.5	53	1.5	146.5	67.5	3	4.5	1422.22
TZE COMP 3 DT S1-128	54	52	2	150	40	2.5	4	2577.78
TZE COMP 3 DT S1-13	55.5	53.5	2	175	80	3	4	3288.89
TZE COMP 3 DT S1-183	55.5	53.5	2	182.5	71	3	4	1333.33
TZE COMP 3 DT S1-145	55	53.5	1.5	173	89.5	2	3	1688.89
TZE COMP 3 DT S1-58	53.5	52.5	1	157	73	1.5	4	1955.56
TZE COMP 3 DT S1-172	54	52.5	1.5	177.5	75	3	4.5	1955.56
TZE COMP 3 DT S1-206	55	52.5	2.5	197.5	88	3	4.5	2133.33
TZE COMP 3 DT S1-51	55	53	2	194.5	83.5	2.5	3.5	3377.78
TZE COMP 3 DT S1-173	54	52	2	172.5	92.5	3	3.5	2311.11
TZE COMP 3 DT S1-87	54.5	52.5	2	169.5	87.5	2.5	4	1866.67
TZE COMP 3 DT S1-152	55	53	2	156.5	69	2	5	1422.22
TZE COMP 3 DT S1-90	54	51.5	2.5	135.5	64	2.5	4	2577.78
TZE COMP 3 DT S1-204	53	50.5	2.5	183	63	3	4	3555.56
TZE COMP 3 DT S1-137	54.5	52.5	2	166	63.5	3	4	533.33

TZE COMP 3 DT S1-211	54.5	52.5	2	166	63.5	3	4	266.67
TZE COMP 3 DT S1-77	53.5	51.5	2	156.5	63.5	2.5	4	2311.11
TZE COMP 3 DT S1-166	55	52	3	171.5	77.5	2	4.5	2133.33
TZE COMP 3 DT S1-184	54.5	70.5	-16	162	56.5	2.5	4	2311.11
TZE COMP 3 DT S1-122	58	55.5	2.5	166	60	3	3.5	1422.22
TZE COMP 3 DT S1-15	54	53.5	0.5	148.5	74.5	3	4.5	1777.78
TZE COMP 3 DT S1-41	53.5	54.5	-1	142.5	55	3	4	1866.67
TZE COMP 3 DT S1-115	55	53.5	1.5	138	65	3.5	3.5	2133.33
TZE COMP 3 DT S1-100	54	55	-1	177.5	90	2.5	5	1688.89
TZE COMP 3 DT S1-198	53	51.5	1.5	160.5	72	2.5	3	2844.44
TZE COMP 3 DT S1-216	54	52	2	147.5	73	2	4	1955.56
TZE COMP 3 DT S1-197	54	52.5	1.5	152	66.5	2.5	4	800
TZE COMP 3 DT S1-175	54.5	52	2.5	160	79.5	1.5	4.5	1511.11
TZE COMP 3 DT S1-201	54.5	53	1.5	166.5	85.5	3	4.5	2400
TZE COMP 3 DT S1-210	53.5	51.5	2	169.5	76	3	3.5	3288.89
TZE COMP 3 DT S1-132	54	53.5	0.5	179	80.5	2	4.5	1777.78
TZE COMP 3 DT S1-171	55.5	53.5	2	154.5	57	2.5	4.5	2044.44
TZE COMP 3 DT S1-101	55.5	54.5	1	179	91	2.5	4.5	1155.56
TZE COMP 3 DT S1-79	54.5	53	1.5	163.5	72.5	2.5	4	1155.56
TZE COMP 3 DT S1-164	49	53	-4	132.5	57.5	3	4	1155.56
TZE COMP 3 DT S1-193	55	53.5	1.5	148.5	66	3	4	2222.22
TZE COMP 3 DT S1-75	56	54	2	155.5	67	3	5	1422.22
TZE COMP 3 DT S1-5	54.5	52.5	2	175	77.5	3	4	1600
TZE COMP 3 DT S1-190	53	51.5	1.5	180	86.5	3	5	1422.22
TZE COMP 3 DT S1-16	54.5	52	2.5	166	69.5	3.5	4	2400
TZE COMP 3 DT S1-18	52.5	53	-0.5	178	66	2.5	4.5	2933.33
TZE COMP 3 DT S1-7	53	51	2	155	67	2.5	4.5	2311.11
TZE COMP 3 DT S1-97	55	53	2	164	62	2.5	4	1688.89
TZE COMP 3 DT S1-60	55	54	1	153.5	66.5	3	4	1866.67
TZE COMP 3 DT S1-222	55.5	53.5	2	153	66.5	2.5	5	800
TZE COMP 3 DT S1-48	54.5	52.5	2	163.5	75	2.5	4	3200
TZE COMP 3 DT S1-125	53.5	52	1.5	178.5	106.5	2	4	2488.89
TZE COMP 3 DT S1-167	54.5	52.5	2	171.5	77.5	3	4.5	3200
TZE COMP 3 DT S1-1	54.5	52.5	2	177.5	90	3	3	3377.78
TZE COMP 3 DT S1-106	53.5	53	0.5	135.5	79.5	2.5	4	2044.44
TZE COMP 3 DT S1-92	54	53	1	198	87	2.5	4	2488.89
TZE COMP 3 DT S1-35	54.5	53.5	1	157	56	3	4	2755.56
TZE COMP 3 DT S1-29	53.5	53	0.5	167	78	3	4	2755.56

TZE COMP 3 DT S1-71	55.5	53.5	2	149	60	2.5	4	2666.67
TZE COMP 3 DT S1-72	56	54	2	159.5	62	3	4	1688.89
TZE COMP 3 DT S1-138	56.5	52.5	4	162	69	2	4	2133.33
TZE COMP 3 DT S1-124	54	52.5	1.5	176	75	2.5	4	2400
TZE COMP 3 DT S1-195	54	53	1	160.5	75.5	3	5.5	1333.33
TZE COMP 3 DT S1-189	54	55	-1	152.5	75.5	1.5	3.5	1244.44
TZE COMP 3 DT S1-214	55	53.5	1.5	165.5	78.5	2.5	4	2133.33
TZE COMP 3 DT S1-104	54.5	53	1.5	200	79	1.5	3.5	1866.67
TZE COMP 3 DT S1-153	54.5	53	1.5	170.5	77	2.5	4.5	1066.67
TZE COMP 3 DT S1-20	53.5	51.5	2	153.5	53	3	5	800
TZE COMP 3 DT S1-53	54	53.5	0.5	135.5	64	2.5	3.5	2311.11
TZE COMP 3 DT S1-159	54.5	53	1.5	160	79.5	2.5	4.5	2488.89
TZE COMP 3 DT S1-2	53	52.5	0.5	162	76	3	4	2844.44
TZE COMP 3 DT S1-52	55.5	53.5	2	148.5	70	3	5	1422.22
TZE COMP 3 DT S1-155	55	53.5	1.5	174	86	3	4.5	1866.67
TZE COMP 3 DT S1-213	56	53.5	2.5	172	87	3	4.5	2933.33
TZE COMP 3 DT S1-160	54	54	0	175.5	84	3	4	2488.89
TZE COMP 3 DT S1-34	55.5	53	2.5	165	77.5	2.5	4	2044.44
TZE COMP 3 DT S1-49	55.5	53.5	2	177.5	80.5	3.5	4.5	2400
TZE COMP 3 DT S1-59	55	53.5	1.5	180	94	3	4	3200
TZE COMP 3 DT S1-192	53	51.5	1.5	171.5	75	3	4	2222.22
TZE COMP 3 DT S1-209	55	53	2	167.5	80	3	3.5	1777.78
TZE COMP 3 DT S1-14	54	51.5	2.5	168	76	2	3.5	3822.22
TZE COMP 3 DT S1-151	53.5	52	1.5	172.5	80	3	4	2933.33
TZE COMP 3 DT S1-154	55	53	2	154.5	81.5	3	4	2044.44
TZE COMP 3 DT S1-12	55.5	53	2.5	172.5	84.5	3	4.5	1600
TZE COMP 3 DT S1-19	56	55	1	170	74	3.5	4.5	2400
TZE COMP 3 DT S1-141	55	53.5	1.5	168	74.5	3	4.5	266.67
TZE COMP 3 DT S1-186	55	52.5	2.5	162	77	3.5	4.5	1600
TZE COMP 3 DT S1-105	54.5	53	1.5	175	85.5	2	4.5	3111.11
TZE COMP 3 DT S1-179	54	52	2	168	70	4	4	977.78
TZE COMP 3 DT S1-6	54	52	2	181	99	1.5	4	2400
TZE COMP 3 DT S1-24	54.5	53	1.5	163	67.5	2.5	5	1777.78
TZE COMP 3 DT S1-9	53.5	54	-0.5	179.5	76.5	3	3.5	4711.11
TZE COMP 3 DT S1-196	53	52	1	178	66.5	3	4.5	1688.89
TZE COMP 3 DT S1-38	54.5	53	1.5	147.5	62.5	2.5	4.5	1600
TZE COMP 3 DT S1-165	55	53	2	184	89	2.5	3.5	4533.33
TZE COMP 3 DT S1-143	53.5	52.5	1	175	91.5	3	4.5	977.78

TZE COMP 3 DT S1-50	54	52.5	1.5	167	76.5	2.5	4.5	888.89
TZE COMP 3 DT S1-139	54.5	52.5	2	163	77.5	3	4	2311.11
TZE COMP 3 DT S1-69	54.5	53	1.5	130	76.5	2	4	2666.67
TZE COMP 3 DT S1-80	55.5	53	2.5	175	85	2.5	4.5	1688.89
TZE COMP 3 DT S1-82	53.5	55	-1.5	166	67.5	2.5	4	1866.67
TZE COMP 3 DT S1-161	55	53	2	174	74	2	4.5	2222.22
TZE COMP 3 DT S1-43	55	53.5	1.5	210	100	2	4	2488.89
TZE COMP 3 DT S1-30	55	52.5	2.5	195.5	81.5	3	3	2311.11
TZE COMP 3 DT S1-112	54.5	52.5	2	178	72	3	4.5	977.78
TZE COMP 3 DT S1-65	54	52	2	210	102	3	4	2577.78
TZE COMP 3 DT S1-170	53.5	51.5	2	177.5	78.5	2	3.5	1600
TZE COMP 3 DT S1-156	55.5	53.5	2	181	80	3	4	2844.44
TZE COMP 3 DT S1-62	53	51	2	146	86	3	4.5	2133.33
TZE COMP 3 DT S1-99	55.5	53.5	2	168	72	2.5	4.5	1866.67
TZE COMP 3 DT S1-93	54.5	52.5	2	148.5	53.5	2.5	4.5	1688.89
TZE COMP 3 DT S1-135	54	55	-1	173	66	2	5	977.78
TZE COMP 3 DT S1-136	54.5	53.5	1	150	65	2	5	888.89
TZE COMP 3 DT S1-202	55.5	54	1.5	152	60	2.5	4	2577.78
TZE COMP 3 DT S1-188	54	52.5	1.5	179.5	81.5	3	4	3377.78
TZE COMP 3 DT S1-57	55	53.5	1.5	187.5	80.5	3.5	4.5	2844.44
TZE COMP 3 DT S1-3	52.5	54	-1.5	158	70.5	3	4.5	1866.67
TZE COMP 3 DT S1-22	55	53	2	169.5	93.5	2.5	4	2044.44
TZE COMP 3 DT S1-168	55	53	2	181	96	3.5	4	2400
TZE COMP 3 DT S1-63	55	53	2	189	97.5	3	5	2666.67
TZE COMP 3 DT S1-217	54.5	56	-1.5	149	84.5	2	4.5	1333.33
TZE COMP 3 DT S1-163	54	52.5	1.5	169.5	85	2.5	3.5	2488.89
TZE COMP 3 DT S1-84	55	52.5	2.5	190	91	3	4	1777.78
TZE COMP 3 DT S1-54	55.5	54	1.5	171.5	71.5	3	4.5	1688.89
TZE COMP 3 DT S1-200	55	53.5	1.5	169.5	84.5	2.5	4	2400
TZE COMP 3 DT S1-117	54	52.5	1.5	170.5	76.5	2.5	4	977.78
TZE COMP 3 DT S1-223	53	52.5	0.5	165.5	73.5	3	4	3111.11
TZE COMP 3 DT S1-121	53.5	52	1.5	150	78	3	4.5	1688.89
TZE COMP 3 DT S1-66	54	51	3	179	72.5	3.5	4	1244.44
TZE COMP 3 DT S1-116	54.5	52.5	2	172.5	64	3	4.5	2488.89
TZE COMP 3 DT S1-86	52.5	53	-0.5	156.5	62.5	3	4	1600
TZE COMP 3 DT S1-219	54	52	2	164	68.5	3	4	2133.33
TZE COMP 3 DT S1-21	55	54	1	165.5	79	2.5	5	1333.33
TZE COMP 3 DT S1-224	55.5	53.5	2	156	77.5	3	5	2488.89

TZE COMP 3 DT S1-127	56	54.5	1.5	156.5	82.5	3	5.5	3466.67
TZE COMP 3 DT S1-98	54	52.5	1.5	162	70	3	5	888.89
TZE COMP 3 DT S1-148	55.5	53.5	2	150.5	79	2.5	4.5	711.11
TZE COMP 3 DT S1-113	55.5	53.5	2	169	71	2.5	4.5	2488.89
TZE COMP 3 DT S1-123	56	53.5	2.5	159.5	65	3	4.5	1422.22
TZE COMP 3 DT S1-181	54	52.5	1.5	163.5	68	3	4.5	977.78
TZE COMP 3 DT S1-46	54.5	53	1.5	158.5	69.5	3	4	2488.89
TZE COMP 3 DT S1-130	54.5	53.5	1	157.5	81	3	4.5	711.11
TZE COMP 3 DT S1-55	55	53.5	1.5	137.5	50.5	3	4.5	1333.33
TZE COMP 3 DT S1-17	55	53	2	160	80.5	2.5	4	622.22
TZE COMP 3 DT S1-27	54	52.5	1.5	143.5	72	2.5	4	1866.67
TZE COMP 3 DT S1-44	53.5	52	1.5	160	75	2.5	4	2400
TZE COMP 3 DT S1-78	56	54	2	157	86	3	5	2933.33
TZE COMP 3 DT S1-32	54	53	1	155	70	3	4	1866.67
TZE COMP 3 DT S1-45	54.5	53	1.5	157.5	85	3	5	1333.33
TZE COMP 3 DT S1-215	43.5	52	-8.5	181	72.5	3	4	2666.67
TZE COMP 3 DT S1-177	55	53.5	1.5	184	77.5	2.5	4	1955.56
TZE COMP 3 DT S1-218	56	54	2	184.5	83	3	4	1600
TZE COMP 3 DT S1-76	55.5	54	1.5	170	65.5	2.5	4	1688.89
TZE COMP 3 DT S1-110	55.5	54	1.5	199	96.5	3	4	2400
TZE COMP 3 DT S1-83	55.5	53.5	2	184.5	85.5	2	4	1866.67
TZE COMP 3 DT S1-205	54	51.5	2.5	174	100.5	2.5	4	1688.89
TZE COMP 3 DT S1-119	55	53.5	1.5	165.5	84.5	2.5	4	3555.56
TZE COMP 3 DT S1-56	54	55	-1	164	77.5	3	4	2311.11
TZE COMP 3 DT S1-108	55	53.5	1.5	172.5	84.5	2.5	3	1422.22
TZE COMP 3 DT S1-169	56.5	53	3.5	171	63	3	4.5	2133.33
TZE COMP 3 DT S1-109	55	53.5	1.5	189.5	83.5	3	4	2311.11
TZE COMP 3 DT S1-70	54	51.5	2.5	186.5	82	2.5	3	3911.11
TZE COMP 3 DT S1-88	54	52	2	145	89.5	2.5	4	1600
TZE COMP 3 DT S1-26	54	53	1	160	79	2.5	3.5	3200
TZE COMP 3 DT S1-47	53.5	51.5	2	179.5	69	2.5	4	2400
TZE COMP 3 DT S1-73	54.5	54	0.5	180	87.5	3	4	977.78
TZE COMP 3 DT S1-147	55.5	54	1.5	180	65.5	3	4	1333.33
TZE COMP 3 DT S1-4	53.5	51.5	2	174	69	3	4	2400
TZE COMP 3 DT S1-102	55.5	53.5	2	181.5	78	2	4.5	1511.11
TZE COMP 3 DT S1-120	56	53	3	172.5	82	3	4.5	1511.11
TZE COMP 3 DT S1-207	54.5	52.5	2	187.5	88.5	3	4.5	2488.89
TZE COMP 3 DT S1-114	53.5	52	1.5	182	71	3	3.5	1688.89

Appendix v: Mean Values for the 10 traits of the 227 S_1 lines of ACR 9331 DMR SR evaluated under Low-N in Zaria and Mokwa

PEDIGREE	DYSK	P0LLEN	ASI	PLHT	EHT	HUSK	STAY GREEN	EARS/P	EASP	GY
Acr 9931 DMRSR S1-173	65.5	64.5	1	111	42.5	4	6.5	0.68	6	244.44
Acr 9931 DMRSR S1-151	67	64.5	2.5	121.5	49.5	3.5	5	0.64	4.5	888.89
Acr 9931 DMRSR S1-58	66	65	1	108	53.5	4	7	0.43	5.5	444.44
Acr 9931 DMRSR S1-236	71	69.5	1.5	118	41	3.5	5.5	1.25	6	222.22
Acr 9931 DMRSR S1-147	66.5	65.5	1	116	45	3.5	6	0.63	5	677.78
Acr 9931 DMRSR S1-77	67	66	1	87	30	5	6	0.51	6	311.11
Acr 9931 DMRSR S1-88	65.5	63.5	2	107.5	56.5	3.5	6.5	0.43	6.5	266.67
Acr 9931 DMRSR S1-90	67.5	64.5	3	98	45.5	3.5	6	0.57	5	500
Acr 9931 DMRSR S1-169	65	65	0	88.5	25	3.5	7	1.83	6	333.33
Acr 9931 DMRSR S1-51	62	61	1	107	52	4	5.5	0.55	4.5	800
Acr 9931 DMRSR S1-38	65	64.5	0.5	112.5	47	3.5	6.5	0.55	6	455.56
Acr 9931 DMRSR S1-120	66	66	0	109.5	40	4	7	0.75	5.5	288.89
Acr 9931 DMRSR S1-239	64.5	63.5	1	100	39.5	3	6.5	0.48	6	477.78
Acr 9931 DMRSR S1-73	67.5	67	0.5	109.5	37	3	5	0.68	5	666.67
Acr 9931 DMRSR S1-178	66	64.5	1.5	87.5	26.5	4.5	6	0.71	6.5	344.44
Acr 9931 DMRSR S1-164	66	66	0	129	49	4	6	0.48	6	622.22
Acr 9931 DMRSR S1-70	70	67.5	2.5	111	32	4	6	0.39	6	377.78
Acr 9931 DMRSR S1-107	66.5	64	2.5	111	39	3.5	6	0.5	6.5	266.67
Acr 9931 DMRSR S1-101	67	65.5	1.5	98.5	34.5	3.5	6	0.58	7	211.11
Acr 9931 DMRSR S1-143	66.5	65.5	1	117.5	41	4	5.5	0.71	5.5	600
Acr 9931 DMRSR S1-144	70.5	67.5	3	108.5	35	3.5	6	0.55	7.5	311.11
Acr 9931 DMRSR S1-210	61	60	1	128	43	3	6	0.67	7	266.67
Acr 9931 DMRSR S1-196	72.5	69.5	3	124	44.5	3.5	6	0.4	6.5	400
Acr 9931 DMRSR S1-65	64	63	1	90	35	3	6	0.42	7	411.11
Acr 9931 DMRSR S1-11	59.5	59.5	0	117.5	42	4.5	5.5	0.96	4	1411.11
Acr 9931 DMRSR S1-5	69	68	1	101	35	4.5	5.5	0.67	6	366.67
Acr 9931 DMRSR S1-30	65	63.5	1.5	105	37.5	4	6	0.61	6	633.33
Acr 9931 DMRSR S1-176	59	59	0	96	38	5	7	0.55	6.5	322.22
Acr 9931 DMRSR S1-242	62.5	61	1.5	116.5	41	4	5.5	0.67	6	577.78
Acr 9931 DMRSR S1-71	66.5	64	2.5	105	36	4	6	0.63	5	533.33
Acr 9931 DMRSR S1-225	68.5	66	2.5	116	45.5	4	7	0.48	7.5	155.56
Acr 9931 DMRSR S1-171	66	63.5	2.5	129	43.5	5	6.5	0.62	7	333.33
Acr 9931 DMRSR S1-92	62	62	0	95	31.5	4.5	6.5	0.47	6.5	388.89
Acr 9931 DMRSR S1-62	62	62	0	107	44	3.5	7	0.88	6.5	444.44
Acr 9931 DMRSR S1-208	62	61.5	0.5	96	40	4	6.5	0.56	6	444.44

Acr 9931 DMRSR S1-125	66	64.5	1.5	107.5	36.5	3	7	1.3	7	377.78
Acr 9931 DMRSR S1-231	71	70	1	109.5	37.5	4	6.5	1.14	6	211.11
Acr 9931 DMRSR S1-129	64.5	64.5	0	104	33	3.5	6	0.74	5.5	555.56
Acr 9931 DMRSR S1-74	64.5	64.5	0	124	48	4	6.5	0.95	5	800
Acr 9931 DMRSR S1-124	68.5	66.5	2	100.5	42.5	4	7	0.31	7	188.89
Acr 9931 DMRSR S1-94	66.5	66	0.5	113	34	5.5	6	0.58	6	422.22
Acr 9931 DMRSR S1-227	64.5	63.5	1	101	36.5	4	6	0.69	5.5	433.33
Acr 9931 DMRSR S1-29	65.5	63.5	2	107	47.5	4	6	0.79	6.5	600
Acr 9931 DMRSR S1-135	71.5	70	1.5	90	29	4.5	6.5	0.34	7	211.11
Acr 9931 DMRSR S1-232	68	66	2	128	37.5	3.5	6	0.66	6.5	211.11
Acr 9931 DMRSR S1-106	67	66	1	120.5	39	3.5	6.5	0.56	7	400
Acr 9931 DMRSR S1-156	67	65	2	90	28	5	7	0.38	6.5	266.67
Acr 9931 DMRSR S1-121	72	70.5	1.5	91.5	27	5	6.5	0.27	6.5	133.33
Acr 9931 DMRSR S1-131	73	71.5	1.5	85	28	4	5.5	0.47	7	355.56
Acr 9931 DMRSR S1-189	65.5	64.5	1	91	38.5	3	5.5	0.74	6	644.44
Acr 9931 DMRSR S1-54	70	67.5	2.5	99	39	4	6	0.56	6	500
Acr 9931 DMRSR S1-8	70	70	0	80	33	3	7	1	7	133.33
Acr 9931 DMRSR S1-138	72.5	70.5	2	113	41.5	3	6	0.71	5.5	511.11
Acr 9931 DMRSR S1-63	66	66	0	95	37.5	3.5	7.5	0.34	7	177.78
Acr 9931 DMRSR S1-25	72.5	71	1.5	121.5	64	4	6.5	0.45	5.5	188.89
Acr 9931 DMRSR S1-35	64	64	0	102.5	37.5	4.5	6.5	0.32	6.5	133.33
Acr 9931 DMRSR S1-52	67	65.5	1.5	115	40.5	3.5	5.5	0.39	6	322.22
Acr 9931 DMRSR S1-86	66	64.5	1.5	96	39	3.5	6.5	0.78	5.5	388.89
Acr 9931 DMRSR S1-40	65.5	64.5	1	110	42	3.5	6.5	0.54	5.5	611.11
Acr 9931 DMRSR S1-53	61	60.5	0.5	98.5	41	4	6.5	1.13	5	466.67
Acr 9931 DMRSR S1-223	59.5	59.5	0	89	32	4.5	6	0.35	6	344.44
Acr 9931 DMRSR S1-185	67	66	1	116	43.5	3.5	5.5	0.59	4.5	811.11
Acr 9931 DMRSR S1-226	68.5	67	1.5	134	56.5	5.5	5.5	0.48	6	444.44
Acr 9931 DMRSR S1-84	65	64	1	117	39	3.5	5	0.83	4.5	777.78
Acr 9931 DMRSR S1-118	65.5	64.5	1	90	47	5	6.5	0.39	6.5	222.22
Acr 9931 DMRSR S1-91	68	65	3	122	41.5	3.5	6.5	0.3	5	344.44
Acr 9931 DMRSR S1-213	66	66	0	95	28	0	6	0.6	6	222.22
Acr 9931 DMRSR S1-127	63	63	0	107.5	46	3.5	6.5	0.37	6	533.33
Acr 9931 DMRSR S1-64	70	68	2	111.5	36.5	4.5	5.5	0.84	5	522.22
Acr 9931 DMRSR S1-2	64.5	63	1.5	119	61	4.5	5	0.73	5.5	955.56
Acr 9931 DMRSR S1-116	63.5	63	0.5	117.5	45	3.5	5	0.96	5	744.44
Acr 9931 DMRSR S1-177	62.5	61.5	1	120.5	39	3.5	5.5	0.53	5.5	777.78
Acr 9931 DMRSR S1-251	67.5	66	1.5	90.5	32.5	5	6	0.44	6	244.44

Acr 9931 DMRSR S1-117	69	67	2	92	37.5	3.5	6	0.56	5	555.56
Acr 9931 DMRSR S1-78	66	64	2	101	36.5	3.5	6.5	0.61	5.5	577.78
Acr 9931 DMRSR S1-96	63.5	63.5	0	106.5	41	3.5	6	0.73	5	322.22
Acr 9931 DMRSR S1-34	65.5	64	1.5	102	28	4	5	0.53	5.5	211.11
Acr 9931 DMRSR S1-55	61.5	61	0.5	114.5	34	4	5.5	0.68	5.5	966.67
Acr 9931 DMRSR S1-81	63.5	63	0.5	104	44	5	7.5	0.55	6.5	244.44
Acr 9931 DMRSR S1-155	66.5	65.5	1	110	48	4	6	0.45	5.5	355.56
Acr 9931 DMRSR S1-12	72.5	70	2.5	105.5	48.5	4	6	0.44	6	255.56
Acr 9931 DMRSR S1-110	73	70	3	108	45	3	6	0.67	6	377.78
Acr 9931 DMRSR S1-128	64.5	64	0.5	101.5	41.5	4.5	5	0.72	5	688.89
Acr 9931 DMRSR S1-237	70	69.5	0.5	100	35	5	5.5	0.4	6.5	411.11
Acr 9931 DMRSR S1-215	68	67.5	0.5	86.5	30	5	6.5	0.47	7	155.56
Acr 9931 DMRSR S1-241	65.5	64	1.5	107.5	30	4.5	6	0.53	6	422.22
Acr 9931 DMRSR S1-122	68.5	65.5	3	120	47	5	5	0.26	7.5	311.11
Acr 9931 DMRSR S1-44	67	66.5	0.5	100	32	3	6	0.65	6.5	344.44
Acr 9931 DMRSR S1-142	70.5	69	1.5	107.5	45	3.5	5	0.66	6	588.89
Acr 9931 DMRSR S1-211	70	68.5	1.5	126	52.5	3	5.5	0.47	7	288.89
Acr 9931 DMRSR S1-141	69.5	67.5	2	111	35.5	3.5	5	0.35	6	377.78
Acr 9931 DMRSR S1-119	64.5	64	0.5	97.5	34.5	3	5.5	0.72	5.5	466.67
Acr 9931 DMRSR S1-152	69	68	1	116	49	4.5	6.5	0.79	7	266.67
Acr 9931 DMRSR S1-154	65.5	64.5	1	134	55	3	5	0.86	5	944.44
Acr 9931 DMRSR S1-76	67	65	2	106	43.5	3.5	5.5	0.61	5.5	444.44
Acr 9931 DMRSR S1-233	69.5	68	1.5	102.5	38.5	3	5.5	0.48	6	355.56
Acr 9931 DMRSR S1-115	67.5	66	1.5	94	35	4.5	7	0.67	7	177.78
Acr 9931 DMRSR S1-45	64	63.5	0.5	102	31	3.5	6	0.46	6.5	211.11
Acr 9931 DMRSR S1-102	66	66	0	96	30	3.5	6	0.66	5	577.78
Acr 9931 DMRSR S1-184	68	66	2	87	25	3	6.5	2.08	5	355.56
Acr 9931 DMRSR S1-186	65.5	65	0.5	97	35	4	6	0.53	6	555.56
Acr 9931 DMRSR S1-47	66.5	65	1.5	102.5	31.5	4.5	5.5	0.34	5.5	300
Acr 9931 DMRSR S1-137	65	65	0	106.5	39.5	3.5	5.5	0.63	5.5	600
Acr 9931 DMRSR S1-19	63	63	0	102.5	43.5	4.5	6.5	0.36	6.5	266.67
Acr 9931 DMRSR S1-228	65	64.5	0.5	95.5	44	4.5	7.5	0.65	6	366.67
Acr 9931 DMRSR S1-134	69.5	67.5	2	101.5	42	4.5	5.5	0.33	6.5	311.11
Acr 9931 DMRSR S1-216	68.5	66	2.5	113	42	4	4.5	0.5	6	666.67
Acr 9931 DMRSR S1-165	65	64	1	101.5	40	4	6	0.54	5.5	466.67
Acr 9931 DMRSR S1-207	64	62.5	1.5	113	36	3.5	6.5	0.44	6	222.22
Acr 9931 DMRSR S1-41	61	61	0	118	41.5	4.5	5.5	0.53	5.5	644.44
Acr 9931 DMRSR S1-18	61	61	0	106	33	5	7.5	0.37	6	300

Acr 9931 DMRSR S1-4	61	61	0	112	49	3.5	6	0.58	5.5	488.89
Acr 9931 DMRSR S1-166	67	65	2	128.5	47	3	6	0.61	6	522.22
Acr 9931 DMRSR S1-75	66.5	64.5	2	106	45	3.5	6	0.57	5.5	422.22
Acr 9931 DMRSR S1-69	64	63	1	93.5	33	4.5	6	0.35	6	166.67
Acr 9931 DMRSR S1-111	70	68	2	95	35	4	5.5	0.36	6	266.67
Acr 9931 DMRSR S1-240	64.5	63.5	1	125	43	5	6	0.44	5.5	466.67
Acr 9931 DMRSR S1-50	66.5	66	0.5	78	31.5	4.5	6	1	8	44.44
Acr 9931 DMRSR S1-36	69	66	3	103.5	43.5	4.5	6	0.22	6	255.56
Acr 9931 DMRSR S1-33	65.5	64	1.5	109.5	46	5.5	5.5	0.48	6	466.67
Acr 9931 DMRSR S1-235	61.5	61.5	0	91.5	39	5	6	0.53	6	400
Acr 9931 DMRSR S1-229	60	60	0	99	34	5.5	6.5	0.72	5.5	533.33
Acr 9931 DMRSR S1-126	65.5	64.5	1	111.5	37.5	4	5	0.56	5.5	622.22
Acr 9931 DMRSR S1-16	67.5	65.5	2	86	30.5	3.5	6.5	0.98	6	222.22
Acr 9931 DMRSR S1-82	67	65.5	1.5	113	46.5	4.5	6	0.57	6	466.67
Acr 9931 DMRSR S1-39	70.5	68	2.5	104	37.5	3.5	5.5	0.44	6	277.78
Acr 9931 DMRSR S1-193	65.5	64	1.5	106	45	4.5	6	0.48	6.5	511.11
Acr 9931 DMRSR S1-139	66.5	64.5	2	86	33	3.5	6.5	0.39	7	122.22
Acr 9931 DMRSR S1-188	65.5	64	1.5	106	45	4.5	6	0.48	6.5	511.11
Acr 9931 DMRSR S1-158	66	64.5	1.5	75.5	28	5	6.5	0.36	7.5	111.11
Acr 9931 DMRSR S1-48	63	62	1	124	52.5	4	5.5	0.77	5.5	877.78
Acr 9931 DMRSR S1-93	67	64.5	2.5	102.5	44	3.5	5.5	0.85	6	622.22
Acr 9931 DMRSR S1-199	63	61.5	1.5	95	38.5	4.5	6.5	0.34	6.5	277.78
Acr 9931 DMRSR S1-97	64	62	2	126.5	52.5	3	5	0.49	6	822.22
Acr 9931 DMRSR S1-170	65.5	64	1.5	106	45	4.5	6	0.48	6.5	511.11
Acr 9931 DMRSR S1-220	63.5	63	0.5	104	40	5	5.5	0.67	4.5	466.67
Acr 9931 DMRSR S1-190	62	61.5	0.5	131.5	39	3.5	6	0.55	5	555.56
Acr 9931 DMRSR S1-195	62	61.5	0.5	111.5	33.5	4.5	5.5	0.48	5.5	288.89
Acr 9931 DMRSR S1-253	68	66	2	104	40	4.5	5.5	0.51	5.5	544.44
Acr 9931 DMRSR S1-103	63.5	62	1.5	91.5	40	3	6	0.64	5.5	477.78
Acr 9931 DMRSR S1-72	71	69	2	81.5	28	4.5	7	0.15	7	311.11
Acr 9931 DMRSR S1-202	64	62	2	76.5	32	5.5	6	0.53	6.5	311.11
Acr 9931 DMRSR S1-252	63	62	1	84.5	37.5	4	6	0.47	6	366.67
Acr 9931 DMRSR S1-89	66.5	66	0.5	95.5	30.5	3.5	5.5	0.61	6.5	300
Acr 9931 DMRSR S1-99	64	63.5	0.5	111.5	37.5	4.5	6	0.39	6.5	233.33
Acr 9931 DMRSR S1-157	64	64	0	105	40	4	6.5	1.38	6	255.56
Acr 9931 DMRSR S1-150	75	72	3	115	40	4	5	0.38	5.5	322.22
Acr 9931 DMRSR S1-104	64.5	63	1.5	108.5	36.5	4	6.5	0.58	6	400
Acr 9931 DMRSR S1-234	71	69	2	100.5	28.5	4	5.5	0.16	6.5	266.67

Acr 9931 DMRSR S1-31	68	66	2	144	52.5	3	5	0.69	4	988.89
Acr 9931 DMRSR S1-249	70.5	67.5	3	107.5	44	3.5	3	0.38	5.5	311.11
Acr 9931 DMRSR S1-3	69	67	2	102	42.5	4	5.5	0.5	6	344.44
Acr 9931 DMRSR S1-148	69	66.5	2.5	133	41	3.5	5.5	0.5	5.5	400
Acr 9931 DMRSR S1-182	70.5	67.5	3	114	44	4.5	6.5	0.45	6.5	377.78
Acr 9931 DMRSR S1-136	64	64	0	110.5	55.5	4	6	0.56	5	522.22
Acr 9931 DMRSR S1-21	68	66	2	110	46	4.5	6.5	0.34	6.5	366.67
Acr 9931 DMRSR S1-191	68	66	2	123.5	47.5	3	5	0.65	5.5	588.89
Acr 9931 DMRSR S1-153	68.5	68	0.5	107.5	35	3.5	6.5	0.42	7	444.44
Acr 9931 DMRSR S1-66	64	63.5	0.5	113.5	42	3	5.5	0.73	5	611.11
Acr 9931 DMRSR S1-180	67.5	67	0.5	109.5	37.5	4.5	7	0.4	7	277.78
Acr 9931 DMRSR S1-214	63.5	63.5	0	119.5	49	4	6	0.71	4.5	755.56
Acr 9931 DMRSR S1-59	65.5	64.5	1	104	45	4	7	0.83	6	133.33
Acr 9931 DMRSR S1-181	68	66	2	84	28	4.5	6	0.33	7.5	66.67
Acr 9931 DMRSR S1-95	68.5	66.5	2	92.5	28	3.5	6.5	0.22	7	222.22
Acr 9931 DMRSR S1-160	68.5	68	0.5	75	27.5	4.5	6	0.5	8	244.44
Acr 9931 DMRSR S1-98	67.5	66	1.5	107	41	3.5	6	0.44	6.5	244.44
Acr 9931 DMRSR S1-212	67.5	65	2.5	89	28	4	6	0.23	7	311.11
Acr 9931 DMRSR S1-145	62.5	62.5	0	87.5	31	4	6.5	0.49	7	333.33
Acr 9931 DMRSR S1-219	67	65	2	104.5	26.5	3	6	0.7	7	222.22
Acr 9931 DMRSR S1-85	70	67	3	120.5	34	4	7	0.17	6.5	233.33
Acr 9931 DMRSR S1-174	64.5	63	1.5	89.5	25	4	6.5	0.5	6	377.78
Acr 9931 DMRSR S1-192	69.5	69	0.5	94.5	31.5	4.5	5	0.41	7	288.89
Acr 9931 DMRSR S1-130	71.5	69.5	2	88	34	3.5	5.5	0.34	6	255.56
Acr 9931 DMRSR S1-23	67	67	0	84	27	4	5.5	0.46	7	222.22
Acr 9931 DMRSR S1-49	66	64.5	1.5	98.5	31	4	6.5	0.62	7	455.56
Acr 9931 DMRSR S1-123	65.5	65	0.5	105.5	42	3.5	6.5	0.6	5.5	366.67
Acr 9931 DMRSR S1-108	72.5	70.5	2	128.5	42.5	3.5	5.5	0.3	6	344.44
Acr 9931 DMRSR S1-206	67	67	0	80	25	4	6.5	0.7	8	222.22
Acr 9931 DMRSR S1-224	70	69	1	92.5	31.5	3.5	7	0.35	6.5	222.22
Acr 9931 DMRSR S1-205	64.5	64	0.5	91.5	39.5	4.5	5.5	0.51	5	422.22
Acr 9931 DMRSR S1-183	72.5	70	2.5	84.5	41.5	3.5	6	0.45	6.5	222.22
Acr 9931 DMRSR S1-209	65.5	64.5	1	117	36	4	6	0.36	6.5	388.89
Acr 9931 DMRSR S1-218	65	64	1	116.5	44	3.5	5.5	0.41	6	500
Acr 9931 DMRSR S1-140	63.5	63.5	0	102.5	37.5	3	5	0.67	6	555.56
Acr 9931 DMRSR S1-238	68.5	67.5	1	98	43.5	4	6	0.41	7.5	266.67
Acr 9931 DMRSR S1-179	70	67.5	2.5	111	33.5	4	6	0.3	6.5	366.67
Acr 9931 DMRSR S1-109	63.5	63.5	0	97.5	25.5	3	5.5	0.7	6	388.89

Acr 9931 DMRSR S1-87	66.5	66.5	0	104.5	45.5	4.5	5.5	0.59	5.5	600
Acr 9931 DMRSR S1-248	62	61.5	0.5	122	41	4	5	0.78	5	1211.11
Acr 9931 DMRSR S1-250	65.5	65.5	0	100.5	50	4	6.5	0.68	6	222.22
Acr 9931 DMRSR S1-172	67	65.5	1.5	121	45	2.5	6	0.43	4.5	466.67
Acr 9931 DMRSR S1-201	65.5	63.5	2	93	32.5	4.5	6.5	0.3	6.5	222.22
Acr 9931 DMRSR S1-83	69	68	1	110	39	3.5	6	0.46	6.5	288.89
Acr 9931 DMRSR S1-13	60.5	60.5	0	118.5	39	3.5	6.5	0.66	4.5	677.78
Acr 9931 DMRSR S1-198	64	63.5	0.5	91	32	3.5	6.5	0.29	7	400
Acr 9931 DMRSR S1-24	67.5	66	1.5	108.5	36.5	4	6.5	0.52	6	377.78
Acr 9931 DMRSR S1-26	70.5	68	2.5	88	30	4	6	0.46	6	444.44
Acr 9931 DMRSR S1-15	70	67.5	2.5	104.5	38.5	4.5	6.5	1.03	6	288.89
Acr 9931 DMRSR S1-105	70	68	2	82	32	4	6	1.5	7	444.44
Acr 9931 DMRSR S1-243	69	67	2	102.5	37.5	4.5	6	0.55	6	244.44
Acr 9931 DMRSR S1-68	73	71	2	105.5	46.5	5	6.5	0.29	8	533.33
Acr 9931 DMRSR S1-230	65.5	65	0.5	110	41.5	3.5	5.5	0.73	5	722.22
Acr 9931 DMRSR S1-56	63.5	63.5	0	121.5	35.5	4	6	0.5	6	411.11
Acr 9931 DMRSR S1-133	74	71	3	110	45	3	6	0.67	6	244.44
Acr 9931 DMRSR S1-175	72.5	69.5	3	103	36.5	3	6.5	0.83	6	244.44
Acr 9931 DMRSR S1-9	66.5	65.5	1	101	41.5	4	6.5	0.51	6	400
Acr 9931 DMRSR S1-114	61	60	1	104.5	38.5	4	7	0.48	7	300
Acr 9931 DMRSR S1-100	68	66.5	1.5	84	37.5	4	6.5	0.25	7	411.11
Acr 9931 DMRSR S1-6	66.5	66	0.5	110	41	3.5	6.5	1.3	5	322.22
Acr 9931 DMRSR S1-43	67.5	66	1.5	123.5	45.5	3.5	6	0.52	6	422.22
Acr 9931 DMRSR S1-37	67.5	65.5	2	121.5	31.5	3.5	6.5	0.44	7	300
Acr 9931 DMRSR S1-79	59	59	0	116	36.5	3	6	0.62	4.5	733.33
Acr 9931 DMRSR S1-80	61.5	60.5	1	140.5	53	4	6	0.69	4	922.22
Acr 9931 DMRSR S1-146	67	65	2	104	30	4	6	0.4	6	411.11
Acr 9931 DMRSR S1-132	60	60	0	128	57	5	6	1	5	400
Acr 9931 DMRSR S1-1	64.5	63.5	1	109	31	4.5	6	0.53	5.5	333.33
Acr 9931 DMRSR S1-257	63	61.5	1.5	124	48.5	3.5	5	0.68	4	1355.56
Acr 9931 DMRSR S1-203	62.5	61	1.5	97.5	34	4	6.5	0.48	6.5	444.44
Acr 9931 DMRSR S1-197	60.5	60.5	0	125.5	42	3.5	6.5	0.38	5.5	266.67
Acr 9931 DMRSR S1-222	61	61	0	113	40	4.5	6.5	0.59	5.5	544.44
Acr 9931 DMRSR S1-112	66.5	64.5	2	111.5	46	3	5	0.59	4	788.89
Acr 9931 DMRSR S1-7	66	64	2	92	28.5	4	6	0.28	7	533.33
Acr 9931 DMRSR S1-161	68	68	0	92	39	3.5	6	0.61	7	400
Acr 9931 DMRSR S1-28	71	69.5	1.5	100	35	4	6	0.28	6.5	377.78
Acr 9931 DMRSR S1-254	68	66.5	1.5	114.5	42	3.5	7	0.29	7	377.78

Acr 9931 DMRSR S1-61	69	66.5	2.5	106	30	4.5	6	0.3	6	333.33
Acr 9931 DMRSR S1-167	67	65.5	1.5	87.5	30	5	7	0.44	7	344.44
Acr 9931 DMRSR S1-10	71.5	68.5	3	94	40	3	6	0.49	6.5	388.89
Acr 9931 DMRSR S1-60	66	65	1	82	30	3	7	7	6	622.22
Acr 9931 DMRSR S1-163	69	67.5	1.5	123.5	39.5	3.5	5	0.63	5	755.56
Acr 9931 DMRSR S1-221	68	66	2	90	41	4	6	0.56	7	398.89
Acr 9931 DMRSR S1-168	67.5	66	1.5	109.5	36.5	5	5.5	0.51	6.5	355.56
Acr 9931 DMRSR S1-42	65.5	65.5	0	107.5	44	4.5	6.5	0.73	6	300
Acr 9931 DMRSR S1-57	71.5	69.5	2	109	45	4	5	0.56	5.5	577.78
Acr 9931 DMRSR S1-67	67	66	1	100.5	30.5	5	6	0.25	8	266.67
Acr 9931 DMRSR S1-246	68	66.5	1.5	102.5	28.5	4.5	5.5	0.83	6	355.56
Acr 9931 DMRSR S1-200	69	66.5	2.5	107.5	27.5	3.5	6.5	0.41	6	355.56
Acr 9931 DMRSR S1-255	72	69	3	113	30.5	4.5	6	0.2	6.5	200
Acr 9931 DMRSR S1-217	67.5	65.5	2	110	41.5	5	6.5	0.48	6	311.11
Acr 9931 DMRSR S1-244	70	68	2	126	39	3	5	0.61	6	400
Acr 9931 DMRSR S1-22	68.5	66	2.5	97.5	27.5	3.5	5.5	0.33	6.5	244.44
Acr 9931 DMRSR S1-245	67.5	66.5	1	114	45	2.5	6	0.53	6.5	466.67
Acr 9931 DMRSR S1-159	67	66	1	109.5	43	4.5	6	0.46	6	555.56
Acr 9931 DMRSR S1-162	69.5	68	1.5	101	35.5	4	6	0.35	7	322.22
Acr 9931 DMRSR S1-20	70.5	68	2.5	98.5	30	4.5	5.5	0.55	6.5	455.56
Acr 9931 DMRSR S1-27	71	69	2	106.5	41	4	5.5	0.56	7.5	377.78
Acr 9931 DMRSR S1-149	67	65	2	86	37.5	4	6	0.32	6	300
Acr 9931 DMRSR S1-256	68.5	66.5	2	84.5	26	4.5	7	0.26	6	488.89
Acr 9931 DMRSR S1-194	68	67	1	98	30	4.5	5.5	0.53	5.5	844.44
Acr 9931 DMRSR S1-113	67	66	1	97.5	32.5	4	6.5	0.42	6	277.78
Acr 9931 DMRSR S1-187	73	70	3	90	25	3	6	0.4	6	311.11
Acr 9931 DMRSR S1-14	69	67	2	93.5	32.5	3.5	6.5	0.36	6	300
Acr 9931 DMRSR S1-32	63	62.5	0.5	117.5	42.5	4	5.5	0.5	5	555.56
Acr 9931 DMRSR S1-247	67.5	66	1.5	104	42.5	4	5.5	0.38	6	288.89
Acr 9931 DMRSR S1-17	72	69.5	2.5	94	32.5	4.5	6	0.38	6.5	277.78
Acr 9931 DMRSR S1-204	70.5	69	1.5	107.5	33	3.5	5.5	1.17	8	577.78
Acr 9931 DMRSR S1-46	65.5	63.5	2	105	57.5	4.5	6.5	0.72	6	388.89

Appendix vi: Mean Values for the 9 traits of the 257 S_1 lines of ACR 9331 DMR SR evaluated under High-N in Zaria and Mokwa

Pedigree	D.Silk	D.Pollen	ASI	PLHT	EHT	HUSK	EAR/Plant	EASP	GY
Acr 9931 DMRSR S1-173	53	51	2	180	88	3	0.73	4	1244.44
Acr 9931 DMRSR S1-151	52	50	2	160	90	3	1.5	5	2666.67
Acr 9931 DMRSR S1-58	52	50	2	157	68	3	1.73	11	2488.89
Acr 9931 DMRSR S1-236	53	51	2	156.5	63	2	1.08	4.5	1955.56
Acr 9931 DMRSR S1-147	52.5	50	2.5	149.5	66.5	3	1.39	4	2666.67
Acr 9931 DMRSR S1-77	49	47	2	151	70	3	1.25	4	2133.33
Acr 9931 DMRSR S1-88	55	53	2	155	74	2	2.03	8	2400
Acr 9931 DMRSR S1-90	51	49	2	143.5	67.5	2.5	1.11	4	2666.67
Acr 9931 DMRSR S1-169	52.5	50	2.5	153	56	3.5	1.4	5	2488.89
Acr 9931 DMRSR S1-51	52	50	2	155	81	3	1.58	5	3555.56
Acr 9931 DMRSR S1-38	52.5	51	1.5	153.5	63	2.5	1.22	4	2844.44
Acr 9931 DMRSR S1-120	53	50	3	137	67	2	0.78	4	1955.56
Acr 9931 DMRSR S1-239	52	50	2	132.5	65.5	2.5	1.25	3.5	2044.44
Acr 9931 DMRSR S1-73	53	52	1	145.5	77	3	1.02	4	2400
Acr 9931 DMRSR S1-178	53	51.5	1.5	167	85	3	1.39	4.5	3022.22
Acr 9931 DMRSR S1-164	53.5	51.5	2	187.5	79	3.5	1.05	4	3644.44
Acr 9931 DMRSR S1-70	53	51	2	156.5	72	3	2.4	12.5	2844.44
Acr 9931 DMRSR S1-190	53.5	51.5	2	187.5	79	3.5	1.05	4	3611.11
Acr 9931 DMRSR S1-101	56	55	1	139.5	60.5	2.5	1.52	4.5	1866.67
Acr 9931 DMRSR S1-143	53	50	3	152	67.5	3	1.45	3.5	3022.22
Acr 9931 DMRSR S1-144	53	51	2	175	85.5	2	2.35	5	1377.78
Acr 9931 DMRSR S1-210	54	52	2	160.5	66.5	3	0.75	6.5	622.22
Acr 9931 DMRSR S1-196	53.5	51.5	2	154.5	65.5	2.5	1.07	4	2933.33
Acr 9931 DMRSR S1-65	54	51.5	2.5	149.5	61	3	1.5	4	2844.44
Acr 9931 DMRSR S1-11	52.5	50.5	2	149.5	77	3.5	0.95	3	3022.22
Acr 9931 DMRSR S1-5	53	51.5	1.5	160.5	80.5	2.5	1.05	4.5	1688.89
Acr 9931 DMRSR S1-30	51	49	2	153	67	3	1.69	4	3733.33
Acr 9931 DMRSR S1-176	52.5	52.5	0	142.5	68.5	3.5	1.01	4.5	2844.44
Acr 9931 DMRSR S1-242	54	52	2	153	69	3	1.01	4	2488.89
Acr 9931 DMRSR S1-71	54.5	52.5	2	152	58	2.5	1.17	3.5	2400
Acr 9931 DMRSR S1-225	55.5	52	3.5	143	50.5	2.5	0.54	4	533.33
Acr 9931 DMRSR S1-171	55.5	53.5	2	157	73	3	0.63	4	1155.56
Acr 9931 DMRSR S1-92	56	53	3	190	95	2	0.88	4	2666.67
Acr 9931 DMRSR S1-62	54.5	52.5	2	158.5	72	2.5	0.81	5	1955.56
Acr 9931 DMRSR S1-208	54	52.5	1.5	101.5	73.5	2.5	1.14	4.5	2222.22

Acr 9931 DMRSR S1-125	53	52.5	0.5	148	54	3	1.81	8.5	2311.11
Acr 9931 DMRSR S1-231	53	51.5	1.5	145.5	57	2.5	0.85	4.5	1066.67
Acr 9931 DMRSR S1-129	52.5	51	1.5	162	76.5	2.5	1.07	4	1777.78
Acr 9931 DMRSR S1-74	57	56	1	217	90	3	1.56	5	3022.22
Acr 9931 DMRSR S1-124	53	52	1	145.5	56.5	3	1.08	4.5	2311.11
Acr 9931 DMRSR S1-94	54.5	52	2.5	181.5	79.5	3.5	0.93	5.5	2222.22
Acr 9931 DMRSR S1-227	52	50.5	1.5	151	64.5	3	1	4.5	1600
Acr 9931 DMRSR S1-29	52.5	51	1.5	150	78	3	0.59	4	1600
Acr 9931 DMRSR S1-135	52	50.5	1.5	154	75.5	3.5	0.53	5.5	1222.22
Acr 9931 DMRSR S1-232	53.5	51.5	2	163.5	78	3	0.99	4	1777.78
Acr 9931 DMRSR S1-106	54	52.5	1.5	175	80	3	1.17	3	2311.11
Acr 9931 DMRSR S1-156	50	48	2	181	92	3	1	4	888.89
Acr 9931 DMRSR S1-121	53	52	1	165.5	68.5	3	2.16	7	1511.11
Acr 9931 DMRSR S1-131	52.5	51.5	1	167.5	75	2.5	1.23	4	1955.56
Acr 9931 DMRSR S1-189	50.5	48.5	2	152.5	68.5	2.5	0.91	4	2311.11
Acr 9931 DMRSR S1-54	53	52	1	153.5	67	3	0.93	3.5	2488.89
Acr 9931 DMRSR S1-8	53	52	1	150	90	3	1.33	4	533.33
Acr 9931 DMRSR S1-138	54	51.5	2.5	152	73.5	3.5	1.03	4	2577.78
Acr 9931 DMRSR S1-63	53.5	52.5	1	167.5	82	2.5	1.14	4	1955.56
Acr 9931 DMRSR S1-25	52.5	51.5	1	193.5	91	3	1.03	4	2844.44
Acr 9931 DMRSR S1-35	54	52	2	160	90	2	1.47	4	3733.33
Acr 9931 DMRSR S1-52	52	50	2	155.5	59.5	2.5	1.46	3.5	3022.22
Acr 9931 DMRSR S1-86	50.5	50	0.5	160	75	2.5	0.97	4	1244.44
Acr 9931 DMRSR S1-40	53	51	2	153	71.5	3.5	0.83	4	2488.89
Acr 9931 DMRSR S1-53	53	51.5	1.5	154	64.5	3.5	1.08	4	2400
Acr 9931 DMRSR S1-223	53	51.5	1.5	154	64.5	3.5	1.08	4	2400
Acr 9931 DMRSR S1-185	52	51	1	166	62.5	3.5	1.1	4.5	1066.67
Acr 9931 DMRSR S1-226	52.5	51.5	1	149.5	62	3	0.33	4.5	2133.33
Acr 9931 DMRSR S1-84	52.5	51.5	1	151.5	75.5	4	1.1	4.5	2755.56
Acr 9931 DMRSR S1-118	51.5	49.5	2	151.5	70	3	0.98	4	2222.22
Acr 9931 DMRSR S1-91	52.5	51	1.5	148	65	3	1.42	4	1244.44
Acr 9931 DMRSR S1-213	52.5	51	1.5	145.5	60	3.5	0.69	4.5	1955.56
Acr 9931 DMRSR S1-127	51.5	50.5	1	163	67.5	2	1.18	3.5	2133.33
Acr 9931 DMRSR S1-64	52	51	1	162.5	63	3.5	1.16	3.5	2488.89
Acr 9931 DMRSR S1-2	53	52	1	152.5	76.5	3.5	1.04	4.5	2844.44
Acr 9931 DMRSR S1-116	53	51	2	154.5	75.5	2.5	1.08	4	1955.56
Acr 9931 DMRSR S1-177	53.5	52	1.5	151.5	66	3	2.07	3.5	2577.78
Acr 9931 DMRSR S1-251	55	52.5	2.5	150.5	55.5	2.5	0.92	5	2755.56

Acr 9931 DMRSR S1-117	53	51.5	1.5	156.5	60	2.5	1.09	4.5	2400
Acr 9931 DMRSR S1-78	53	51	2	161	83	3	1.15	4	2311.11
Acr 9931 DMRSR S1-96	52	51	1	158	71.5	3.5	1.05	4.5	1777.78
Acr 9931 DMRSR S1-34	53	52	1	149.5	52	3	0.74	5	2488.89
Acr 9931 DMRSR S1-55	59	57	2	141	81.5	3.5	1.29	4	1688.89
Acr 9931 DMRSR S1-81	54	51.5	2.5	143	67	3	0.77	4.5	1866.67
Acr 9931 DMRSR S1-155	53.5	52	1.5	145	59	2.5	0.87	4	2222.22
Acr 9931 DMRSR S1-12	54	53	1	189	95	3	0.9	4	2666.67
Acr 9931 DMRSR S1-110	68.5	65	3.5	123	52.5	3.5	0.63	5.5	684.44
Acr 9931 DMRSR S1-126	54	52	2	150	70	4	1.15	5	2844.44
Acr 9931 DMRSR S1-237	54	52	2	170	76	3	1.11	4.5	1688.89
Acr 9931 DMRSR S1-215	53	50.5	2.5	154	72	3	1.8	4.5	1511.11
Acr 9931 DMRSR S1-241	53	51	2	152	66	3.5	1.04	4.5	2222.22
Acr 9931 DMRSR S1-122	51	50	1	155	83	3	0.81	5	2311.11
Acr 9931 DMRSR S1-44	52.5	51	1.5	152.5	64.5	3	0.75	4.5	1422.22
Acr 9931 DMRSR S1-142	53.5	51.5	2	167	84	3	1.22	4	2133.33
Acr 9931 DMRSR S1-211	52	50	2	199	77	3	0.76	4	1777.78
Acr 9931 DMRSR S1-141	53.5	52	1.5	158.5	71.5	2.5	0.93	4	2311.11
Acr 9931 DMRSR S1-119	53	51	2	147	63	2.5	1.02	4	2311.11
Acr 9931 DMRSR S1-152	53	52	1	154	64	3	1.47	4.5	1511.11
Acr 9931 DMRSR S1-154	53.5	51.5	2	166.5	67	3	1.43	4	2577.78
Acr 9931 DMRSR S1-76	54	50.5	3.5	165.5	85.5	3.5	1	4	2755.56
Acr 9931 DMRSR S1-233	53	51.5	1.5	146.5	64	2.5	1.42	4	2577.78
Acr 9931 DMRSR S1-115	53	51	2	154	41	3	1	5	177.78
Acr 9931 DMRSR S1-45	54.5	52	2.5	151	65	2.5	1	4	1155.56
Acr 9931 DMRSR S1-102	53	51.5	1.5	150.5	60	2.5	1.44	4	2400
Acr 9931 DMRSR S1-184	52.5	51	1.5	163.5	71.5	2.5	0.88	4.5	1333.33
Acr 9931 DMRSR S1-186	53	51	2	162.5	80.5	3	1.07	3.5	2933.33
Acr 9931 DMRSR S1-47	53	51	2	174.5	80.5	2	1.14	4	3022.22
Acr 9931 DMRSR S1-137	52.5	50.5	2	147	68.5	1.5	1.75	4	2844.44
Acr 9931 DMRSR S1-19	51	49	2	149	80	3	1.63	4	1955.56
Acr 9931 DMRSR S1-228	51.5	50	1.5	157.5	61	3	1.07	4.5	2400
Acr 9931 DMRSR S1-134	52.5	51.5	1	155.5	65	2.5	1.25	4	2133.33
Acr 9931 DMRSR S1-216	54	52	2	162	64.5	3	1.04	4	2755.56
Acr 9931 DMRSR S1-165	53.5	51.5	2	154	65.5	2.5	1.46	3.5	2311.11
Acr 9931 DMRSR S1-207	52.5	51	1.5	149	58.5	3	0.84	4.5	2400
Acr 9931 DMRSR S1-41	54.5	52.5	2	150.5	63	3	0.97	4	2577.78
Acr 9931 DMRSR S1-18	53	52	1	151	44	3	0.75	4	1955.56

Acr 9931 DMRSR S1-4	53	52	1	155	58.5	3	1.24	4	2133.33
Acr 9931 DMRSR S1-166	53	51.5	1.5	184	78	3	1.07	4	2666.67
Acr 9931 DMRSR S1-75	53.5	52	1.5	159	65.5	3.5	0.93	5	1600
Acr 9931 DMRSR S1-69	53.5	51.5	2	155	57	3	0.86	4	1866.67
Acr 9931 DMRSR S1-111	53	52	1	166	73	3	1.18	4	1955.56
Acr 9931 DMRSR S1-240	52.5	51	1.5	146	66	3.5	1.12	3	3022.22
Acr 9931 DMRSR S1-50	54	53	1	155	55	3	1.33	5	533.33
Acr 9931 DMRSR S1-36	51	49	2	154	66	4	1	4	2844.44
Acr 9931 DMRSR S1-33	52	50.5	1.5	165	67.5	3.5	1	4	1955.56
Acr 9931 DMRSR S1-235	53	52	1	149	57	3	1	4.5	2133.33
Acr 9931 DMRSR S1-229	54	53	1	150	67.5	3	1.07	4.5	2488.89
Acr 9931 DMRSR S1-126	52.5	50.5	2	150	56.5	3	1	4	1955.56
Acr 9931 DMRSR S1-16	54	51.5	2.5	145	63	3	0.95	4	2400
Acr 9931 DMRSR S1-82	52.5	51.5	1	148	57	3	1.25	4	2844.44
Acr 9931 DMRSR S1-39	53	51	2	177.5	100	3	0.9	4	3822.22
Acr 9931 DMRSR S1-193	54.5	53	1.5	152.5	64.5	3	1.1	4	2044.44
Acr 9931 DMRSR S1-139	54	52	2	148	63	3	1.21	5	2488.89
Acr 9931 DMRSR S1-188	54	52	2	148	63	3	1.21	5	2488.89
Acr 9931 DMRSR S1-158	52.5	51.5	1	145.5	58	3	1.07	4	2400
Acr 9931 DMRSR S1-48	53.5	52.5	1	163	57.5	3	1.14	4	2400
Acr 9931 DMRSR S1-93	53	51.5	1.5	173	73.5	4	1.21	4	2933.33
Acr 9931 DMRSR S1-199	54.5	53	1.5	148	63.5	3	1.34	4.5	1688.89
Acr 9931 DMRSR S1-97	52	51	1	151	68	3	0.9	3	4266.67
Acr 9931 DMRSR S1-170	54.5	54	0.5	146.5	49	3	0.8	4.5	266.67
Acr 9931 DMRSR S1-220	52.5	51	1.5	164.5	74.5	3	1.05	4	2755.56
Acr 9931 DMRSR S1-190	53.5	52.5	1	156	67.5	3	0.97	4	3111.11
Acr 9931 DMRSR S1-195	54	51	3	148.5	61.5	3	1.07	4.5	2133.33
Acr 9931 DMRSR S1-253	54.5	53.5	1	153	65.5	2.5	1.08	4	2133.33
Acr 9931 DMRSR S1-103	53	52	1	150	60	4	1	4	2133.33
Acr 9931 DMRSR S1-72	54.5	52.5	2	148	62	4	0.9	4.5	1422.22
Acr 9931 DMRSR S1-202	54	52	2	149	68	3	1.25	3.5	3111.11
Acr 9931 DMRSR S1-252	53.5	51.5	2	144	67	2.5	0.96	3.5	1955.56
Acr 9931 DMRSR S1-89	53	53	0	155	74	3	0.89	4	1066.67
Acr 9931 DMRSR S1-99	65	64	1	115	35	5	0.6	6	4444.44
Acr 9931 DMRSR S1-157	55.5	54	1.5	155.5	60.5	3	0.83	5.5	1066.67
Acr 9931 DMRSR S1-150	54.5	53.5	1	150	63	3.5	1	4	3288.89
Acr 9931 DMRSR S1-104	53.5	52	1.5	148	57	3	1	4.5	1777.78
Acr 9931 DMRSR S1-234	54.5	52.5	2	158.5	66	3	0.9	4.5	1955.56

Acr 9931 DMRSR S1-31	54.5	53	1.5	176.5	82	2.5	1.25	4	3111.11
Acr 9931 DMRSR S1-249	53.5	52	1.5	157.5	67	3	0.79	4	2400
Acr 9931 DMRSR S1-3	55.5	53.5	2	147	58.5	2.5	1.03	4	2133.33
Acr 9931 DMRSR S1-148	55	53	2	146.5	46.5	3	0.89	4	2222.22
Acr 9931 DMRSR S1-182	54	53	1	169	42	2	1.07	3	2488.89
Acr 9931 DMRSR S1-136	55	53	2	151	50	2	0.88	3	2133.33
Acr 9931 DMRSR S1-21	53.5	51	2.5	162	68.5	2.5	1.38	4	2133.33
Acr 9931 DMRSR S1-191	53	52	1	166.5	74.5	3	1.04	4	2044.44
Acr 9931 DMRSR S1-153	53.5	52.5	1	137	59.5	3	2.5	4.5	2488.89
Acr 9931 DMRSR S1-66	53.5	51.5	2	157.5	57	3	1.39	4.5	2133.33
Acr 9931 DMRSR S1-180	52	51	1	151	57.5	3	0.94	3.5	1955.56
Acr 9931 DMRSR S1-214	53.5	51.5	2	164.5	71.5	3	0.63	4	2222.22
Acr 9931 DMRSR S1-59	52.5	50.5	2	150.5	67.5	3	0.79	4	1422.22
Acr 9931 DMRSR S1-181	53	55	-2	150	63	3	0.6	4	888.89
Acr 9931 DMRSR S1-95	53.5	51.5	2	148	64.5	3	0.31	4	2044.44
Acr 9931 DMRSR S1-89	55	53	2	177	71	3	0.67	5	533.33
Acr 9931 DMRSR S1-98	55.5	54.5	1	152	60	3.5	0.84	3.5	1511.11
Acr 9931 DMRSR S1-212	54.5	53	1.5	151.5	53	3	0.9	4	1777.78
Acr 9931 DMRSR S1-145	54	52	2	145	58	4	0.89	3	2488.89
Acr 9931 DMRSR S1-219	54	52	2	156	53	3	0.83	4	1422.22
Acr 9931 DMRSR S1-85	53	50.5	2.5	160.5	68.5	3	0.54	4	1511.11
Acr 9931 DMRSR S1-174	52.5	50	2.5	153	62.5	3	1.14	4.5	3200
Acr 9931 DMRSR S1-192	53	52	1	151	52.5	3	0.77	8.5	2666.67
Acr 9931 DMRSR S1-130	55	53.5	1.5	155	70	3	1.18	9	2044.44
Acr 9931 DMRSR S1-23	54.5	52.5	2	146.5	64	2.5	1.3	3.5	2222.22
Acr 9931 DMRSR S1-49	54	53	1	149	62	3	0.53	3	1777.78
Acr 9931 DMRSR S1-123	54	53	1	156	70	3	0.61	4	1777.78
Acr 9931 DMRSR S1-103	54	52.5	1.5	149.5	71.5	3	1.1	4	1866.67
Acr 9931 DMRSR S1-206	53	52	1	142.5	55	2.5	0.41	4.5	355.56
Acr 9931 DMRSR S1-224	54.5	52.5	2	129	59	3	0.58	4	1066.67
Acr 9931 DMRSR S1-205	53.5	52	1.5	149	54.5	3	0.97	3.5	2400
Acr 9931 DMRSR S1-183	54	52	2	150.5	72.5	3	1.11	4	1600
Acr 9931 DMRSR S1-209	52	51	1	158	73	2	0.64	3	1422.22
Acr 9931 DMRSR S1-218	52	50	2	160.5	64	2	0.98	4	1688.89
Acr 9931 DMRSR S1-140	51.5	50.5	1	162.5	71.5	1.5	0.7	7	2844.44
Acr 9931 DMRSR S1-238	68	65.5	2.5	94	33.5	3.5	0.46	6	3288.89
Acr 9931 DMRSR S1-179	67.5	65	2.5	107.5	35.5	4	0.23	7	3466.67
Acr 9931 DMRSR S1-109	55	53	2	156	75	3	0.99	4.5	800

Acr 9931 DMRSR S1-87	58	56	2	173	89	4	0.94	4	2666.67
Acr 9931 DMRSR S1-248	53	51.5	1.5	166	71.5	3	0.81	3	3288.89
Acr 9931 DMRSR S1-250	52.5	51	1.5	153	73	3	0.92	4	444.44
Acr 9931 DMRSR S1-172	54.5	52.5	2	159	75	2.5	2.21	10	2666.67
Acr 9931 DMRSR S1-201	54	52	2	158	78.5	3	1.26	4	1244.44
Acr 9931 DMRSR S1-83	53	51.5	1.5	157.5	70	2.5	1.2	3.5	2933.33
Acr 9931 DMRSR S1-13	53	52	1	155.5	68.5	3.5	1.28	3.5	3822.22
Acr 9931 DMRSR S1-198	53.5	51.5	2	161	62.5	4	0.63	4	888.89
Acr 9931 DMRSR S1-24	54	51.5	2.5	153	57	2.5	1.1	3.5	2222.22
Acr 9931 DMRSR S1-26	55	54	1	156	61	3	1.17	4	3022.22
Acr 9931 DMRSR S1-15	54.5	53.5	1	149.5	66	3	0.64	5	1600
Acr 9931 DMRSR S1-105	53.5	51.5	2	152.5	61.5	3	2.25	4	355.56
Acr 9931 DMRSR S1-243	53.5	52	1.5	133	61.5	3	1.05	4	1333.33
Acr 9931 DMRSR S1-68	54	51.5	2.5	153	67	3.5	0.83	4	1511.11
Acr 9931 DMRSR S1-230	53	50.5	2.5	164.5	71	3	1.46	4	2755.56
Acr 9931 DMRSR S1-56	54.5	52.5	2	143.5	45.5	2.5	0.87	3.5	2400
Acr 9931 DMRSR S1-133	55	53	2	156.5	68	2.5	1.24	3.5	1866.67
Acr 9931 DMRSR S1-175	54	53	1	105.5	77	3	0.92	3.5	1244.44
Acr 9931 DMRSR S1-9	54	52.5	1.5	147.5	61.5	3.5	0.89	5	1600
Acr 9931 DMRSR S1-111	55	52	3	150	60	3	1	4	1600
Acr 9931 DMRSR S1-211	52.5	52.5	0	151	66.5	3	1.64	4.5	2755.56
Acr 9931 DMRSR S1-6	54	52.5	1.5	152.5	55	1.5	0.85	4	1244.44
Acr 9931 DMRSR S1-43	54	52	2	200	75	2	1.4	4	2666.67
Acr 9931 DMRSR S1-37	55	53	2	179	69	2.5	1.35	4.5	2222.22
Acr 9931 DMRSR S1-79	54	52	2	158.5	71.5	3	1.24	4	2346.67
Acr 9931 DMRSR S1-80	54	52	2	190	80	3	2.25	4	1244.44
Acr 9931 DMRSR S1-146	54.5	52.5	2	163.5	80	3	2.41	4	3377.78
Acr 9931 DMRSR S1-132	53	51.5	1.5	156.5	80	3	1.05	4.5	1244.44
Acr 9931 DMRSR S1-1	54	52.5	1.5	154	64	3	1.69	7	2133.33
Acr 9931 DMRSR S1-257	53.5	52.5	1	160	68	4	2.42	12	4522.22
Acr 9931 DMRSR S1-203	54	52	2	150	68.5	3	1.09	4.5	2044.44
Acr 9931 DMRSR S1-197	53.5	51.5	2	182	81.5	3	1.1	4	2133.33
Acr 9931 DMRSR S1-222	55	52	3	160	64	4	1.13	4	2844.44
Acr 9931 DMRSR S1-112	53	52	1	151	60	3	1	4	2311.11
Acr 9931 DMRSR S1-7	53	51.5	1.5	135.5	65.5	2.5	2.21	9	2488.89
Acr 9931 DMRSR S1-161	54	52	2	158.5	72.5	3	2.5	4	1688.89
Acr 9931 DMRSR S1-28	54.5	53	1.5	160.5	60	3.5	1.14	4	800
Acr 9931 DMRSR S1-258	53	50	3	150	71	3	0.81	4	2488.89

Acr 9931 DMRSR S1-61	53	52	1	144.5	61.5	3	1.46	5	1511.11
Acr 9931 DMRSR S1-167	54	52.5	1.5	144.5	58.5	3.5	1.71	13.5	2400
Acr 9931 DMRSR S1-110	53	53	0	149	38	2	1.2	4	2844.44
Acr 9931 DMRSR S1-60	53	52	1	153	59	3	1	5	888.89
Acr 9931 DMRSR S1-163	53.5	52	1.5	147	65.5	3	1.13	4	888.89
Acr 9931 DMRSR S1-221	54	52.5	1.5	151.5	65	3	1.21	6.5	1600
Acr 9931 DMRSR S1-168	54	52	2	179.5	76.5	4	1.09	4.5	2133.33
Acr 9931 DMRSR S1-42	54	52	2	170.5	71.5	3.5	1.06	4	1600
Acr 9931 DMRSR S1-57	54	52	2	159.5	62	3	1.21	3.5	2311.11
Acr 9931 DMRSR S1-67	51.5	50.5	1	150	75	4	1.47	7.5	2577.78
Acr 9931 DMRSR S1-246	53	51.5	1.5	159	75.5	3.5	1.02	4	1688.89
Acr 9931 DMRSR S1-200	53.5	52	1.5	163	69	2.5	1.22	3.5	3377.78
Acr 9931 DMRSR S1-255	52.5	50.5	2	185	100	3.5	0.95	5	2044.44
Acr 9931 DMRSR S1-217	53	51	2	167	53	4	1.19	5	3555.56
Acr 9931 DMRSR S1-244	54.5	52.5	2	198	80.5	3	0.94	4	1600
Acr 9931 DMRSR S1-22	54	52.5	1.5	171	79.5	3	0.96	4	2488.89
Acr 9931 DMRSR S1-245	54	51.5	2.5	179.5	76	2.5	0.96	4	2488.89
Acr 9931 DMRSR S1-159	54.5	53.5	1	151.5	73.5	3	1.63	4	3377.78
Acr 9931 DMRSR S1-162	53	51.5	1.5	154	58.5	2.5	1.54	4	3111.11
Acr 9931 DMRSR S1-20	54.5	53	1.5	177.5	66	3	1.41	4	1422.22
Acr 9931 DMRSR S1-27	55	54	1	192	100	3	1.3	4	1333.33
Acr 9931 DMRSR S1-149	53.5	51	2.5	189.5	87	2.5	0.94	4	1777.78
Acr 9931 DMRSR S1-256	53	51.5	1.5	160.5	74	2.5	1.1	4.5	2400
Acr 9931 DMRSR S1-194	64	63	1	101	34	4.5	1	6	524.44
Acr 9931 DMRSR S1-113	53	52	1	146	53	3	1.1	4	1777.78
Acr 9931 DMRSR S1-187	54.5	52	2.5	154	75.5	2.5	0.95	4	1777.78
Acr 9931 DMRSR S1-14	53	51.5	1.5	151	55.5	3.5	1.97	4	2488.89
Acr 9931 DMRSR S1-32	53.5	51.5	2	151.5	58.5	3.5	1.11	5	1155.56
Acr 9931 DMRSR S1-247	53	52	1	149	70	5	1.7	5	2844.44
Acr 9931 DMRSR S1-17	53.5	52	1.5	165	79.5	3	2.08	4.5	1244.44
Acr 9931 DMRSR S1-204	54	51	3	160	80	2	0.5	3	1066.67
Acr 9931 DMRSR S1-46	53.5	51.5	2	159	77.5	3	2.68	5	1600

Appendix vii: 2011 WEATHER DATA (ZARIA)

MONTH	% RELATIVE HUMIDITY (10am)	% RELATIVE HUMIDITY (4pm)	AIR TEMPERATURE (0C) Min	AIR TEMPERATURE (0C) Min	EARTH TEMPERATURE (30cm)	EARTH TEMPERATURE (30cm)	SUNSHINE (HOURS)	AVERAGE WIND SPEED (KM/DAY)	TOTAL RAINFALL (mm)	OPEN PAN EVAPORATION (mm/DAY)
1	17.7097	14.2581	30.1613	13.0645	22.4968	23.3742	7.4516	183.2552		10.8871
2	20.3929	16.1071	36.3929	18.3214	26.8893	27.9036	7.4214	131.9350		12.5357
3	13.0000	9.1290	38.6129	19.6452	28.9645	30.2839	7.1194	161.0935		14.8903
4	31.5556	20.7037	38.1111	22.2593	30.7808	31.6360	6.7115	187.5496	13.9000	14.3115
5	64.4839	47.2258	35.3226	22.0323	29.1387	30.6226	6.9645	212.1455	123.3000	10.4968
6	76.4667	61.1000	32.3333	20.8667	26.5800	27.0700	6.2100	193.2383	162.5000	7.0667
7	85.1935	70.8710	30.8710	20.0323	25.9645	26.4065	6.1581	148.4581	223.9000	5.8516
8	80.1290	72.2258	30.2903	19.6129	25.7742	26.2806	4.6581	136.1942	239.9000	5.8567
9	76.7143	68.6296	31.9643	18.9286	26.5286	27.1679	6.4429	127.7963	113.8000	5.4852
10	64.4516	50.1290	44.0968	18.0968	26.2065	26.8839	6.6258	71.8471	54.0000	5.5692
11	18.0333	16.1000	34.2000	11.9667	23.9533	25.2200	8.9400	104.1480		
12	16.9032	12.8065	31.3548	12.4839	22.6355	23.7452	7.5613	157.0300		

IAR, ABU, Meterological centre.