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**EVALUATION OF EARLY MATURING PROVITAMIN A MAIZE HYBRIDS FOR
YIELD AND AGRONOMIC PERFORMANCE UNDER DIFFERENT
ENVIRONMENTS IN ZIMBABWE.**

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**A RESEARCH PROJECT SUBMITTED IN PARTIAL FULFILMENT OF THE
REQUIREMENTS OF THE BSC HONOURS DEGREE IN CROP SCIENCE.**

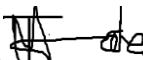
DECLARATION

The work I presented here is my own and has never been previously submitted to this or any other University.

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ABSTRACT

Maize (*Zea mays L*) is the major staple food in sub-Saharan Africa, including Zimbabwe but is nutritionally deficient in provitamin A which has led to high levels of vitamin A deficiency (VAD) in Zimbabwe. Provitamin A (PVA) biofortified maize with high carotenoid content was developed to curb vitamin A deficiency (VAD) but adoption has been constrained by perceptions that biofortified hybrids yield less than conventional maize. This research evaluated grain yield and agronomic performance of twenty-one newly developed early maturing CIMMYT provitamin A maize hybrids alongside four checks (ZS242, ZS244, ZS500 and CZH1815A) to identify superior genotypes for further testing and release. Trials were conducted at three research stations in Zimbabwe (Harare, Gwebi and Rattray Arnold). They comprised of seven environments representing optimum management, low nitrogen stress and combined Grey Leaf Spot (GLS) and *Exserohilum turcicum* (ET) disease inoculated environment. The results showed that genotype, environment and genotype x environment (G X E) interaction effects were highly significant for grain yield and several traits. Under optimum conditions, the top hybrids DSH24135 (7.81 t/ha), DSH24137 (7.79 t/ha) and DSH24139 (7.45 t/ha) were above commercial check, ZS500 (7.28 t/ha). Low-nitrogen stress reduced mean grain yield by approximately 57%, with DSH24147 (4.29 t/ha) and DSH24132 (3.79 t/ha) showing the greatest nitrogen-stress tolerance. Under disease pressure DSH24142 (4.96 t/ha) and DSH24137 (4.86 t/ha) combined high yield with low disease severity. GGE biplot analysis identified DSH24133 and DSH24139 as the most stable, high-yielding genotypes across two distinct mega-environments. DSH24135, DSH24137 and DSH24139 are recommended for advancement to further multi-location trials.

Keywords: provitamin A maize, vitamin A deficiency, grain yield, low nitrogen stress, Grey Leaf Spot, ET (*Exserohilum turcicum*), genotype x environment interaction, GGE biplots.

DEDICATION

I dedicate this work to my family for their unwavering support and encouragement during my academic journey and to all the people who believed in me and supported my studies.

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LIST OF ABBREVIATIONS

AD	Anthesis Date
ANOVA	Analysis of Variance
ASI	Anthesis-Silking Interval
CIMMYT	International Maize and Wheat Improvement Center
EA	Ear Aspect
EPP	Ear Per Plant
ER	Ear Rot
ET	<i>Exserohilum turcicum</i> (Northern Corn Leaf Blight)
GLS	Grey Leaf Spot
GWAS	Genome-Wide Association Studies
G x E	Genotype × Environment interaction
GY	Grain Yield
ha	hectare
HPLC	High Performance Liquid Chromatography
K	Potassium
kg	kilogram
Low N	Low nitrogen
LSD	Least Significant Difference
m	metre
MAS	Marker-Assisted Selection
MOI	Grain Moisture Content
MSV	Maize Streak Virus
N	Nitrogen
P	Phosphorus
PH	Plant Height
PVA	Provitamin A maize
RAE	Retinol Activity Equivalent
RL	Root Lodging
SD	Silking Date
SEN	Senescence
SL	Stem Lodging
SSA	Sub-Saharan Africa

VAD Vitamin A Deficiency

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background

Maize (*Zea mays L.*) is a main staple crop for over 300 million people in sub-Saharan Africa (SSA) and Latin America (Edmeades, 2008). In Zimbabwe, maize is of great importance as it is used as staple food and as a raw material for manufacturing industries (Vasal, 2000, Prasanna *et al.*, 2001). It is also used as feed for livestock as it constitute up to 40-75% of feed rations (Badu-Apraku and Fakorede, 2017). Maize together with wheat (*Triticum aestivum*) and rice (*Oryza sativa*) account for an estimated 42% of the world's total calories and 37% proteins consumed (Erenstein *et al.*, 2022). Maize can be consumed in diversified forms such as roasted, parched, boiled, ground and fermented to make porridge and beverages (Ekpa *et al.*, 2019). It is also a source of nutraceutical compounds such as phenolics, carotenoids, anthocyanins, and phlobaphenes that have a potential of reducing the risk of major chronic diseases such as cancer (Liu, 2004). Per capita consumption of maize in Zimbabwe is up to 180 kg per year compared to only 15 kg in the developed countries such as the United States of America (Altieri and Koohafkan, 2008, Ekpa *et al.*, 2018). On average, maize has nutrition composition of 1.4 to 2% soluble sugars, 10 to 15% water, 4.3 to 4.5% fat, 65 to 70% starch, 8 to 10% protein, 3.5 to 4.5% oil, 1.5 to 2.0% ash, 1.5 to 2.1% crude fibre, 16 kJ 100 g⁻¹ energy. (Ranum *et al.*, 2014, Babu *et al.*, 2013a).

Over-reliance on maize based diets without proper vitamin A supplementation due to poverty in Zimbabwe is associated with high prevalence of hidden hunger and vitamin A deficiency (VAD) (Resnick *et al.*, 2022). In the developing countries including Zimbabwe, vitamin A deficiency (VAD) causes the greatest disease burden (Goredema-Matongera *et al.*, 2021). Vitamin A deficiency affect children especially those below the age of 5 years limiting their growth and increasing their risk of being sick and death. Vitamin A deficiency (VAD) also affect women of reproductive age and it can elevate the risk of maternal morbidity and mortality during pregnancy and shortly after childbirth. Severe maternal VAD can adversely affect neonatal outcomes, contributing to elevated infant mortality within the first few months of life. VAD weakens the immune system, damaging cells crucial for night vision, potentially leading to irreversible blindness known as xerophthalmia (Stevens *et al.*, 2015). About 3

million children under the age of five in SSA live with vitamin A deficiency (Resnick *et al.*, 2022). Globally, the condition is linked to 640 000 child deaths, while up to 500 000 individuals become partially blind or experience total vision loss every year due to vitamin A deficiency related complications (Maqbool *et al.*, 2018). Estimates suggest that around 190 million preschool age children and about 19 million pregnant women in Africa and South Asia are currently affected by vitamin A deficiency (VAD) (Pixley *et al.*, 2013). Approximately, 20 million additional pregnant women in other developing regions also bearing the burden of the deficiency. Within Zimbabwe specifically, surveys indicate that vitamin A deficiency (VAD) affects children under five on a recurring basis approximately every five (Mudadirwa *et al.*, 2023).

Pro vitamin A maize biofortification is an attractive solution to reduce VAD in the developing countries such as Zimbabwe. It is reported to be cheaper, sustainable and a reliable long term alternative to expensive pro vitamin A rich foods especially in remote areas where vitamin A supplementation approaches may not have complete coverage (Babu *et al.*, 2013b, Rosales *et al.*, 2022, Bouis and Saltzman, 2017). Provitamin A biofortification is a genetic improvement process of enhancing provitamin A carotene levels to at least 15 µg/g and its bioavailability in a maize kernel through conventional or molecular breeding methods (Garg *et al.*, 2018). It enhances the vitamin A micronutrient density and its bioavailability in the biofortified crop and it is highly recommended especially for countries like Zimbabwe, Somalia, Madagascar and Mozambique where food choice is limited due to poverty (Saltzman *et al.*, 2013). In an effort to curb VAD in Zimbabwe, the International Maize and Wheat Improvement Centre (CIMMYT) has developed new provitamin A biofortified maize hybrids. These pro vitamin A maize hybrids have high potential to solve VAD in Zimbabwe if they are superior to the old pro vitamin A maize hybrids that are poorly performing under low input and rain-fed smallholder farming systems which produce more than 80 % of the total maize in the country (Menkir *et al.*, 2025). However, the grain yield and agronomic performance of these newly developed hybrids is yet to be known because they have not been tested. This study therefore set out to evaluate the agronomic performance of these newly developed CIMMYT provitamin A maize hybrids to determine the hybrids that performs better than the old pro vitamin A and ordinary maize checks. Superior provitamin A hybrids in terms of grain yield and agronomic traits will be recommended for further testing and release as new pro vitamin A maize varieties.

1.2 Statement of the problem

Vitamin A deficiency (VAD) is a persistent problem which is severely affecting most developing countries including Zimbabwe (Mudadirwa *et al.*, 2023). Children under the age of five, the pregnant and lactating women are the most affected by VAD (Resnick *et al.*, 2022). The lack of sufficient provitamin A in its sufficient quality and quantities for good health is mainly due to limited and infrequent access to vitamin A rich foods. These include fish, organ meats (especially liver, where retinyl esters are stored) dairy products, butter, and eggs, butternuts (*Cucurbita moschata*), green leafy vegetables, and fruits such as papayas (*Carica papaya*) and mangoes (*Mangifera indica*). The scarcity of these foods, largely driven by poverty and their seasonal production result in their intake remaining very low. (Marriott *et al.*, 2020). Due to seasonality of most of the easily available provitamin A rich food and unaffordability of other vitamin A rich food such as eggs, butter and liver, the poor resource people in Zimbabwe heavily depend on ordinary maize with limited access to balanced diets (Akalu *et al.*, 2010). The provitamin A maize hybrids developed by CIMMYT maybe reliable, and cheaper source of vitamin A and have a potential of alleviating the Zimbabwean communities from VAD. However, the main drawback is that the agronomic performance and grain yield of these provitamin A maize hybrids is not known because they are yet to be evaluated.

1.3 Justification

Evaluation of the newly developed provitamin A maize hybrids will help in identifying superior provitamin A hybrids that performs agronomically better than the available provitamin A maize hybrids and ordinary maize checks. These provitamin A hybrids will be recommended for further testing or release as new high yielding provitamin A maize varieties with enhanced provitamin A carotenoid levels. If they are released, these varieties will be cultivated and consumed by humans as a vitamin A supplementation. If successfully adopted, the use of provitamin A maize hybrids will be a cheaper, sustainable and a reliable way of supplementing vitamin A rich diets to communities. This will then alleviate people from vitamin A deficiency and its detrimental effects especially on children under five, the pregnant women and lactating mothers.

1.4 Objectives

1.4.1 Main objective

To identify high yielding and superior provitamin A maize hybrids with desirable agronomic traits, tolerant to low nitrogen and foliar disease stresses (Grey Leaf Spot and *Exserohilum turcicum*) that can be recommended and identified as potential varieties for further testing and release.

1.4.2 Specific objectives

Objective 1

To evaluate the agronomic performance of twenty-one provitamin A maize hybrids under low nitrogen conditions in Zimbabwe.

Objective 2

To assess the performance of twenty-one provitamin A maize hybrids under Grey Leaf Spot and *Exserohilum turcicum* disease stress environments in Zimbabwe.

Objective 3

To evaluate genotype by environment interaction and identify stable provitamin A maize hybrids across diverse environments in Zimbabwe.

1.5 Null Hypothesis

H₀₁. There is no significant difference in grain yield and agronomic performance among the twenty-one CIMMYT provitamin A maize hybrids under low nitrogen environment in Zimbabwe.

H₀₂. There is no significant difference in disease response, grain yield and agronomic performance among the twenty-one CIMMYT provitamin A maize hybrids under Grey Leaf Spot and *Exserohilum turcicum* disease stress conditions in Zimbabwe.

H₀₃. There is no significant genotype x environment interaction among the provitamin A maize hybrids evaluated across test environments.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Importance of maize.

Globally, maize is one of the leading cereal crops, with annual production exceeding 1 billion metric tonnes and harvested from an area of about 200 million hectares worldwide (García-Lara and Serna-Saldivar, 2019). Maize is the most important staple food crop for the majority of Sub-Saharan African countries (Galani *et al.*, 2022). In Zimbabwe, maize (*Zea mays L.*) is the most widely produced cereal crop and serves as a staple food for most households (Admire and Tinashe, 2014). Although maize is not a native crop to this region, it became a staple crop due to its high yield potential, broad adaptation to diverse agro-ecological zones and ease of processing (García-Lara and Serna-Saldivar, 2019, Gwirtz and Garcia-Casal, 2014). Maize is widely preferred in Zimbabwe as a major source of energy and its nutritional composition enhances its value (Goredema-Matongera *et al.*, 2021). It provides essential nutrients and bioactive phytochemical compounds such as carotenoids, phenolic compounds and phytosterols, which are associated with chronic disease prevention (Rouf Shah *et al.*, 2016). In Sub-Saharan Africa, where maize constitutes a major dietary staple, demand is projected to grow rapidly, with consumption expected to rise by about 2.3-fold over the next 30 years (Aramburu-Merlos *et al.*, 2024).

Maize performs multiple roles as a staple crop for human consumption, livestock feed and an industrial raw material, with industrialized countries allocating a larger proportion to animal feed and the manufacture of food and non-food products (Orhun *et al.*, 2013). Maize is consumed as green mealies, roasted, fried, dried, milled or fermented products, forming the basis of many traditional diets across Africa (Ekpa *et al.*, 2019). In Zimbabwe, it is commonly consumed as *sadza/isitshwala*, *mutwiwa* (fermented porridge), *mutakura/inkobe* (a nutritious mixture of maize kernels and legumes), and as maize-based beverages such as *mahewu*, illustrating its daily dietary use and cultural significance (Gadaga *et al.*, 1999, Pswarayi and Gänzle, 2019). However, heavy reliance on maize as a primary staple without sufficient vitamin A supplements or diverse foods such as fruits and vegetables contributes to the persistence of vitamin A deficiency (VAD) in sub-Saharan Africa (Mudadirwa *et al.*, 2023). This is attributed to the fact that conventional white maize contains low concentrations of essential micronutrients, particularly provitamin A carotenoids (Goredema-Matongera *et*

al., 2021). High prevalence of vitamin A deficiency (VAD) is also attributed to insufficient intake of provitamin A, low bioavailability and compromised quality of provitamin A due to post-harvest losses during processing and storage (Tanumihardjo *et al.*, 2010, De Moura *et al.*, 2015, La Frano *et al.*, 2014).

The majority of carotenoids, including provitamin A carotenoids (β -carotene, α -carotene and β -cryptoxanthin) and non-PVA carotenoids (lutein and zeaxanthin) are predominantly deposited in the endosperm and the germ of the maize grain (Nuss and Tanumihardjo, 2010, Trono, 2019). Although the germ contains lipid-associated carotenoids that may enhance bioavailability, the endosperm contributes over 92-96% of the total carotenoid content in maize grain and represents the primary edible portion after milling (Trono, 2019, Sun *et al.*, 2022). Therefore, PVA maize biofortification focuses primarily on enhancing carotenoid accumulation in the endosperm to maximize its nutritional impact (Alamu *et al.*, 2021). β -carotene is the most important PVA carotenoid due to its highest provitamin A activity and its efficient conversion into retinol (vitamin A) in the human body, thereby playing a major role in improving vitamin A status (Maqbool *et al.*, 2018, Wurtzel *et al.*, 2012, Grune *et al.*, 2010). Researchers have identified two loci, *LcyE* (*lycopene epsilon cyclase*) and *CrtRB1* (*β -carotene hydroxylase 1*) which regulate carotenoid flux toward provitamin A compounds in maize endosperm (Babu *et al.*, 2013c, Harjes *et al.*, 2008). This discovery provides a molecular foundation for provitamin A biofortification in maize and is considered a promising strategy to alleviate vitamin A deficiency (VAD) in rural African communities, including Zimbabwe (Zunjare *et al.*, 2018).

2.2 Development of provitamin A maize (PVA).

Following the discovery of functional polymorphisms at the *LcyE* and *CrtRB1* loci, the development of provitamin A (PVA) maize has been fuelled up by a deep understanding of the genetic and biochemical regulation of carotenoid production in maize endosperm (Gebremeskel *et al.*, 2018). These genes are key regulators in the carotenoid biosynthetic pathway, which determines both the quantity and composition of carotenoids accumulated in maize kernels (Messias *et al.*, 2014, Vallabhaneni and Wurtzel, 2009). The *LcyE* (*Lycopene Epsilon Cyclase*) gene controls the metabolic flux at the lycopene branch point, directing carotenoid synthesis either toward the α -branch, which mainly produces lutein, or the β -branch, which leads to the formation of provitamin A carotenoids β -carotene, β -cryptoxanthin and α -carotene (Zunjare *et al.*, 2017). Favourable alleles of *LcyE* reduce the diversion of

metabolic intermediates into the α -branch, thereby increasing flux toward β -carotene accumulation (Lehmann *et al.*, 2021). Similarly, the *CrtRB1* (β -carotene hydroxylase 1) gene regulates the hydroxylation of β -carotene into β -cryptoxanthin and zeaxanthin (Yan *et al.*, 2010, Azmach *et al.*, 2018). Reduced-function alleles of *CrtRB1* slow down this conversion, allowing higher retention of β -carotene in the endosperm, which significantly enhances provitamin A concentration (Yan *et al.*, 2010).

The identification of these favourable alleles revolutionized maize biofortification through the application of marker-assisted selection (MAS) and later genomics-assisted breeding approaches (Liu *et al.*, 2015). Before the discovery of these molecular markers, breeding for high provitamin A content relied largely on phenotypic selection based on kernel colour and direct biochemical analysis, particularly High Performance Liquid Chromatography (HPLC), which was laborious, costly and less efficient (Borrelli and Trono, 2016). The use of DNA markers linked to *LcyE* and *CrtRB1* enabled breeders to select superior genotypes at early stages of plant development with high precision, independent of environmental influence (Babu *et al.*, 2013c, Liu *et al.*, 2015). This significantly accelerated the development of PVA maize hybrids and open-pollinated varieties with enhanced carotenoid content. Studies have shown that introgression of favourable *CrtRB1* alleles through marker-assisted backcrossing can raise provitamin A levels beyond 15-20 $\mu\text{g/g}$, meeting the initial CIMMYT and HarvestPlus target for biofortified maize (Muthusamy *et al.*, 2014). In maize breeding programs in SSA, these advances have been instrumental in developing nutritionally improved cultivars adapted to local agro-ecological conditions (Prasanna *et al.*, 2020).

Beyond the major effects of *LcyE* and *CrtRB1*, recent advances in molecular genetics and genome-wide association studies (GWAS) have revealed that provitamin A accumulation in maize is a quantitatively inherited trait influenced by multiple loci and regulatory genes (Suwarno *et al.*, 2015). Additional genes such as *PSY1*, *ZEP1*, *LUT1* and carotenoid cleavage dioxygenases have been identified as important contributors to total carotenoid biosynthesis, retention and degradation in the endosperm (Harjes *et al.*, 2008). Breeders have moved from single-gene selection to gene pyramiding and genomic selection strategies, combining multiple favourable alleles to maximize provitamin A concentration while maintaining desirable agronomic traits such as grain yield, maturity and disease resistance (Prasanna *et al.*, 2020, Pixley *et al.*, 2013). Consequently, the development of PVA maize now integrates conventional breeding, molecular marker technology and genomic prediction models to

produce superior hybrids with stable carotenoid expression across diverse environments (Crossa *et al.*, 2017). These scientific advancements have strengthened PVA maize as a sustainable food-based strategy for addressing vitamin A deficiency, especially in maize-dependent countries like Zimbabwe and other parts of Southern Africa (Goredema-Matongera *et al.*, 2021).

2.3 Nutritional benefits of PVA maize based diets.

In terms of bioavailability and functional contribution, the nutritional value of vitamin A generated from provitamin A (PVA) maize was shown to be similar to that of well-known plant-based vitamin A sources such as carrots (Siwela *et al.*, 2020). According to recent research, biofortified PVA maize contains approximately 7-15 µg/g of provitamin A carotenoids, which is five-ten times higher than conventional maize (1.5 µg/g) (Mudadirwa *et al.*, 2023). Feeding studies have shown that children who consume 140-200 g of PVA maize per day can obtain approximately 250 µg of retinol activity equivalents (RAE), which accounts for 50-70% of their daily vitamin A needs (Gupta *et al.*, 2019). Although orange-fleshed sweet potatoes and carrots have far greater amounts of β-carotene (around 80-120 µg/g), PVA maize makes a major contribution due to its role as a staple food that is taken in huge quantities (Dai and Row, 2019, Neela and Fanta, 2019). Carotenoid retention levels of 40-90% are reported in processing tests, meaning that the majority of provitamin A is still nutritionally accessible after cooking, increasing its useful dietary value (Taleon *et al.*, 2017). PVA maize-based diets have been shown to increase both biochemical and functional indices of vitamin A status in people plagued by vitamin A deficiency (VAD), especially in sub-Saharan Africa (SSA) (Bouis and Saltzman, 2017). Palmer *et al* (2016) reported that children who consumed PVA maize for six months exhibited a substantial rise in blood β-carotene levels by 0.14 µmol/L ($p < 0.001$) in a randomised controlled experiment conducted in Zambia, whereas serum retinol levels were relatively steady. Significantly, children showed improved pupillary response, a sign of improved visual function, as functional outcomes improved. Baseline assessment indicated vitamin A deficiency (VAD) prevalence of approximately 12.1% among children, highlighting the presence of a measurable burden of deficiency. The intervention reduced the likelihood of clinical symptoms that are directly linked to insufficient vitamin A consumption, such as xerophthalmia and night blindness (Palmer *et al.*, 2016, Nankumbi *et al.*, 2023). These results show that PVA maize intake can

still result in significant health benefits even when biochemical alterations are slight, especially in communities with marginal deficiencies.

Provitamin A (PVA) maize can serve as a useful feed ingredient with quantifiable nutritional and production benefits in animals, especially poultry (Díaz-Gómez *et al.*, 2017b). Feeding experiments have demonstrated the bioavailability and metabolic activity of carotenoids found in PVA maize, such as β -carotene and β -cryptoxanthin. β -carotene is effectively transformed into retinol (vitamin A) in the intestine and stored in the liver, directly influencing the animal's vitamin A status (Moreno *et al.*, 2016). In poultry systems, PVA maize has been linked to increased carotenoids being deposited in tissues, resulting in improved skin and meat pigmentation (higher redness and yellowness values), a crucial quality attribute in consumer markets (Díaz-Gómez *et al.*, 2017a). Several studies reveal improvements in production parameters such as reduced abdomen fat and improved breast muscle yield (Fouad and El-Senousey, 2014). This hence indicate that PVA maize may have a good impact on feed efficiency and carcass characteristics compared to traditional maize based diets. Provitamin A (PVA) maize can promote general health and productivity in domesticated animals. Studies on livestock nutrition reveals that dietary carotenoids contribute to hepatic vitamin A stores and antioxidant capacity (Shastak and Pelletier, 2024). These results show that provitamin A (PVA) maize is not only a source of energy but also a useful feed ingredient that can enhance tissue quality, vitamin A status and possibly production efficiency in agricultural animals, especially in poultry (Odunitan-Wayas *et al.*, 2016).

2.4 Effects of low N and diseases on maize production.

Maize productivity in sub-Saharan Africa remains substantially below its potential, with smallholder yields commonly ranging from 2 t ha⁻¹ to less than 1.5 t ha⁻¹ due to depleted soil nitrogen and foliar diseases, particularly GLS and ET (Shiferaw *et al.*, 2011, Van Ittersum *et al.*, 2013, Prasanna *et al.*, 2021). These stresses frequently co-occur in smallholder systems, where limited fertilizer use and favourable environmental conditions for pathogen development interact to intensify yield losses. Palmer *et al.*, (2021), also stated that low nitrogen in soils and diseases are major factors responsible for very low crop yields and food security currently faced in Eastern and southern African regions. Genetic variability in maize grain was also reported in maize that was grown under low nitrogen conditions and diseased environment (Ertiro *et al.*, 2020). In Zimbabwe and Angola, more than 70% of maize

production is done in areas with a 40 to 60% frequency of a failed season (Kostandini *et al.*, 2013).

Nitrogen is an essential nutrient that is required in large amounts by the maize crop (Asibi *et al.*, 2019). Low nitrogen stress has been documented as one of the most important limitations to maize production in sub-Saharan Africa (SSA) due to low inherent soil fertility and minimal fertilizer application (Gokoma *et al.*, 2025). Maize grown under N-deficient conditions can suffer yield reductions exceeding 50%, with some genotypes experiencing losses of up to 70% depending on the severity of stress (Zhao *et al.*, 2019, Ajala *et al.*, 2018). Similarly, studies demonstrated that low N significantly reduces grain yield through its effects on leaf area development, chlorophyll content, and radiation use efficiency (Su *et al.*, 2020). Reduced nitrogen availability limits photosynthetic capacity and accelerates leaf senescence, thereby shortening the grain-filling period and decreasing kernel weight. Demands for nitrogen in younger maize crop is low but increases as the crop grows to an extent of exhausting all soil nitrogen (Ciampitti and Vyn, 2012). Hence the need for application to maintain crop growth. In Zimbabwe, low fertilizer application rates, often below 20 kg N ha⁻¹ in smallholder systems have been directly linked to poor maize performance and persistent yield gaps (Pasley *et al.*, 2019). Long-term soil fertility studies in Southern Africa further indicate that continuous maize cultivation without adequate nutrient replenishment leads to severe nitrogen mining, exacerbating yield decline over time (Zingore *et al.*, 2007). Grain filling is a stress sensitive stage, therefore is it crucial to apply nitrogen fertilizers because deficiency of nitrogen at this stage result in reduction in grain weight, leaf senescence and chlorosis due to the immobilisation of N from leaves to ears (Ciampitti and Vyn, 2012). Deficiency of nitrogen also increase the chances of kernel abortion, reduced number of kernels and grain yield (Shen *et al.*, 2018).

In parallel, foliar diseases like Grey Leaf Spot (GLS) and *Exserohilum turcicum* (ET) have emerged as major yield-reducing factors across sub-Saharan Africa (Gordon *et al.*, 2006). Grey Leaf Spot has been widely studied since its emergence in eastern and southern Africa in the 1990s. Ward *et al.*, (1999), reported that GLS can cause yield losses ranging from 20% to 60%, depending on disease severity, hybrid susceptibility and environmental conditions. In Zimbabwe, Sibiya *et al.*, (2012), observed significant reductions in grain yield associated with increased GLS severity, particularly in susceptible genotypes grown under high humidity conditions. Similarly, studies confirmed that GLS reduces effective leaf area and

photosynthetic efficiency, leading to premature senescence and poor grain filling (Derera, 2005).

ET (*Exserohilum turcicum*), is another widely spread disease in SSA, particularly in mid- to high-altitude regions with moderate temperatures and high humidity. Research indicates that yield losses due to *E. turcicum* typically range from 15% to 50%, depending on the timing and severity of infection (Gordon *et al.*, 2006). Early infection before silking cause the greatest yield penalties due to its direct effect on photosynthetic capacity during grain development. In southern Africa, studies highlight the increasing importance of *E. turcicum* as a constraint to maize production, particularly under smallholder conditions where resistant varieties and fungicides are rarely used (Jakhar *et al.*, 2017).

The interaction between low nitrogen and foliar diseases often results in greater yield losses than either stress alone. Nitrogen-deficient maize plants exhibit increased susceptibility to foliar pathogens due to reduced vigour, thinner leaves and compromised defence responses (Sun *et al.*, 2020). Conversely, disease infection further limits nitrogen use efficiency by reducing photosynthetic area and assimilate production. Studies demonstrated that maize genotypes grown under low N conditions exhibited higher GLS severity compared to those grown under optimal N, suggesting a strong interaction between nutrient stress and disease development (Worku *et al.*, 2008). This synergistic effect is particularly relevant in Zimbabwe, where both low soil fertility and high disease pressure are prevalent in smallholder farming systems (Mukaro *et al.*, 2024, Kurwakumire *et al.*, 2014). Further evidence from multi-environment trials conducted across SSA supports the significance of combined stress effects (Kamweru *et al.*, 2023). (Ertiro *et al.*, 2017) reported that maize yields under combined low N and disease stress were significantly lower than under individual stress conditions, highlighting the need for simultaneous selection for tolerance to multiple stresses . Additionally, breeding programmes in SSA have emphasized that breeding for resistance to GLS and *E. turcicum* must be integrated with selection for nitrogen use efficiency to achieve stable yields under farmer conditions (Badu-Apraku *et al.*, 2021).

Most high yielding maize varieties bred under optimal conditions often fail to achieve their potential yields under farmer conditions due to lack of tolerance to low N conditions and disease pressure (Cairns *et al.*, 2021). The widespread occurrence of GLS and *E. turcicum*, particularly in high rainfall areas such as the eastern highlands of Zimbabwe, further compounds yield losses (Nsibo *et al.*, 2024). CIMMYT (International Wheat and Maize

Improvement Centre) managed to come up with new varieties that are tolerant to low N and resistant to foliar diseases by breeding and conducting evaluations under managed stress environments (Tarekegne *et al.*, 2024).

2.5 Adoption of provitamin A maize in Zimbabwe.

CIMMYT and HarvestPlus in partnership with several government initiatives, lead the current efforts to develop and promote provitamin A maize across sub-Saharan Africa. Widespread adoption of the newly developed provitamin A maize varieties in smallholder farmers' communities is still a challenge despite that it is highly nutritious than normal maize (Goredema-Matongerera *et al.*, 2021). Provitamin a maize adoption has shown considerable variation across countries and regions, largely influenced by culture, preferences, awareness level and seed access (Zuma *et al.*, 2023). Studies in Zambia, one of the earliest countries to promote orange PVA maize, showed that children easily adapted to orange maize (provitamin A) than the older people due to social pressures and long-standing dietary habits (Lividini and Fiedler, 2015). Although sensory evaluations demonstrated that PVA maize was generally acceptable to consumers, white maize remained the most preferred because of familiarity and established consumption patterns (Mudadirwa *et al.*, 2023). Orange to yellow maize is perceived for animal consumption, resulting in low human consumption and reluctance to adopt biofortified varieties (De Groote *et al.*, 2011).

These perceptions can be changed through awareness campaigns, nutrition education and community demonstrations that emphasize the health benefits of provitamin A maize, particularly its role in reducing vitamin A deficiency (VAD) among vulnerable populations such as children and pregnant women. Feeding provitamin A maize to indigenous and layer chickens can improve carotenoid content in eggs and meat, thereby providing an indirect pathway for enhancing household vitamin A intake (Odunitan-Wayas *et al.*, 2016). The price of PVA maize is often lower compared to of conventional white maize due to consumer's preference and underdeveloped market for orange PVA maize (Meenakshi *et al.*, 2010) . Therefore questions raises regarding whether perceptions and low market prices could have an impact on its consumption. In Zimbabwe, farmers recognise the benefits of provitamin A maize and have been found to be willing to invest in varieties that improve household food security, nutrition and income opportunities (Baudron *et al.*, 2024). HarvestPlus and CIMMYT interventions have reported increasing awareness and growing adoption in several districts, with thousands of smallholder households having accessed vitamin A maize seed by

2020. Nevertheless, access to certified seeds remain a major barrier to sustained adoption despite the knowledge about provitamin A maize among the smallholder farmers in Zimbabwe (Goredema-Matongera *et al.*, 2021). Provitamin A maize seed is often unavailable in local agro-dealer shops or arrives in insufficient quantities. In the 1990s, yellow maize was donated in Zimbabwe as a food aid to the famine, therefore many rural communities came to associate coloured maize with poverty (food for the poor) (Muzhingi *et al.*, 2008). This legacy continues to affect the acceptance of provitamin A maize, even though it is genetically improved and nutritionally superior to ordinary white maize. Similar findings have been reported in other African countries where grain colour strongly influences consumer choices (Mudadirwa *et al.*, 2023). In the Murehwa District Zimbabwe, seed dissemination has often relied on donations, gifts or projects handouts rather than sustainable commercial purchasing systems (Baudron *et al.*, 2024).

2.6 G x E interaction and grain yield stability.

Genotype x Environment (G x E) interactions, describes how differently cultivars respond to changing growing conditions and it influences grain yield performance and stability in maize (Malosetti *et al.*, 2013). A cultivar's overall performance reflects both its genetic makeup and the environment it is grown in. Biotic and abiotic environmental factors have a great influence on quantitative traits like grain yield, hence it is essential to conduct multi-location trials. In Zimbabwe, maize genotypes interact differently with the environment as a result of differences in soil fertility, disease pressure, temperature, season length and season rainfall which affect input application.

The presence of significant values of G x E interactions complicate the selection and recommendation of superior cultivars for different environments because genotype performance may vary from one location to another (Chimonyo *et al.*, 2014). Therefore, varieties evaluated in a single environment may not perform consistently across different testing sites. However, conducting multi-location trials to identify stable cultivars is often expensive. The G x E interaction of crossover-type, where genotype rankings actually reverse across environments necessitates the analysis of genotype stability. There two types of stability, which are dynamic and static. Dynamic stability is more desirable, describing a genotype that delivers high yield in proportion to the productivity level of whatever environment it is grown in. In contrast, static stability refers to genotypes that possess less or

no change in performance regardless of the variation of environments. Crop varieties with static stability fail to capitalise on improved growing conditions.

2.6.1 Principal component analysis (PCA)

Principal Component Analysis (PCA) is a multivariate statistical technique used to summarise and visualise patterns of trait associations among agronomic variables in plant breeding trials. PCA condenses a large set of correlated agronomic variables into a smaller number of uncorrelated components that capture the majority of variation in the dataset, making it easier to interpret complex relationships among traits. Traits that cluster together on a PCA biplot share similar variation patterns and are likely influenced by the same underlying genetic or physiological mechanisms, whilst traits pointing in opposite directions are negatively correlated. The proportion of total variation explained by the first two principal components indicates how well the biplot summarises the overall trait structure, with higher values indicating clearer and more interpretable trait relationships.

2.6.2 Genotype plus Genotype x Environment (GGE) biplots.

GGE biplot analysis was developed to combine and improve the interpretation of G x E interactions. This is through integrating genotype main effects and genotype by environment interaction effects into a single analytical framework while removing environment main effects from the analysis (Neisse *et al.*, 2018). The GGE biplot is a data visualisation tool, which shows a graphical presentation of G x E interaction in a two way data table. The analysis is used for mega-environment identification through the “which-won-where” pattern, that helps identify superior genotypes for specific environments (Khan *et al.*, 2021). GGE biplot is also used in variety evaluation, through ranking genotype performance and assessing the ability of target environments to discriminate among genotypes.

2.6.3 The Analysis of Variance (ANOVA) model.

ANOVA model is used for analysing two way data structure in multi environmental trials. ANOVA is an additive model that explains effectively the main effects of genotype and environment. Its limitation lies in detecting G x E interactions without fully explaining the variation associated with the interaction or how stable individual genotypes are across environments. As a result, GGE biplots are used together with ANOVA for a better understanding of G x E interactions and genotype stability (Hongyu *et al.*, 2014). ANOVA has been widely used in evaluating provitamin A maize grain quality traits under both single

and multi-environments, with most studies reporting significant genotype, environment and G x E interaction effects.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Description of trial/ experimental sites.

The study was conducted across three experimental research stations in Zimbabwe namely Harare (17 °47'S 31 °30'E), Gwebi (17 °40'S 30 °52'E) and Rattray Arnold (17 °19'S 31 °34'E). Harare was used for optimum, low nitrogen and disease stress, while Gwebi and Rattray Arnold were used for optimum and low nitrogen evaluations. Harare station sits at 1 498 m above sea level and averages roughly 820 mm of rainfall annually with a mean temperature of 25 °C. Gwebi lies at an altitude of 1 453 m and receives roughly 800 mm of rainfall annually with an average temperature of 24 °C. Rattray Arnold lies at 1 360 m above sea level, receives approximately 865 mm of rainfall per year and a similar average temperature of 25 °C. A detailed map showing the sites is shown in Figure 3.1 and their characteristics in Table 3.1

Table 3.1: Description of trial sites used in the study

Site	Agro-ecological region	Latitude	Longitude	Altitude	Average annual rainfall (mm)	Average temperature	Management
Harare	2a	17°47'S	31°30'E	1483m	820	25 °C	Optimum Misting Low N
Gwebi	2a	17°40'S	30°52'E	1453m	800	24 °C	Optimum Low N
RARS	2b	17°19'S	31°34'E	1020m	865	25 °C	Optimum Low N



Figure 3.1 Zimbabwe map showing location of the three study sites.

3.2 Maize germplasm

A total of twenty-one newly developed early maturing provitamin A three way hybrids from CIMMYT, three commercial checks which are ZS242, ZS244 and ZS500 and one internal genetic check were used. They were developed and selected for their resilience to various biotic and abiotic stresses targeted by CIMMYT. A detailed list of CIMMYT provitamin A hybrids used in this study is given on Table 3.2.

Table 3.2 Description of germplasm material.

Entry	Genotype	Source	Variety Type
1	DSH24130	CIMMYT	New Hybrid
2	DSH24131	CIMMYT	New Hybrid
3	DSH24132	CIMMYT	New Hybrid
4	DSH24133	CIMMYT	New Hybrid
5	DSH24134	CIMMYT	New Hybrid
6	DSH24135	CIMMYT	New Hybrid
7	DSH24136	CIMMYT	New Hybrid
8	DSH24137	CIMMYT	New Hybrid
9	DSH24138	CIMMYT	New Hybrid
10	DSH24139	CIMMYT	New Hybrid
11	DSH24140	CIMMYT	New Hybrid
12	DSH24141	CIMMYT	New Hybrid
13	DSH24142	CIMMYT	New Hybrid
14	DSH24143	CIMMYT	New Hybrid
15	DSH24144	CIMMYT	New Hybrid
16	DSH24145	CIMMYT	New Hybrid
17	DSH24146	CIMMYT	New Hybrid
18	DSH24147	CIMMYT	New Hybrid
19	DSH24148	CIMMYT	New Hybrid
20	DSH24149	CIMMYT	New Hybrid
21	DSH24150	CIMMYT	New Hybrid
22	ZS244	CIMMYT	Commercial Check
23	ZS500	CIMMYT	Commercial Check
24	CZH1815A	CIMMYT	Internal (PVA) Check
25	ZS242	CIMMYT	Commercial Check

3.3 Experimental design and crop management

Twenty five progenies were established across three different sites in Zimbabwe that is Harare, Gwebi and Rattray Arnold Research Station (RARS). Maize entries were planted in a 5 X 5 α -lattice design with three replications on plots which are 4m long with approximately 17 plants per row. A spacing of 0.90 m inter-row and 0.25 m in-row spacing were used. Sowing of the trials was done in December 2024. Harvesting of maize trials started end of April 2025. Four sites comprised of three different types of environments which are: a) optimum with recommended agronomic management and high rainfall; b) Low Nitrogen stress conditions on fields that had been subjected to prolonged nitrogen depletion for more than 5 years and c) misting block, a diseased environment inoculated with Grey Leaf Spot and ET (*Exserohilum turcicum*). Fertilisation was according to the standard commercial application rates for basal and top dressing for all other trials except in low N conditions. Standard commercial fertiliser rates were applied to all environments except for low nitrogen. Compound D (7%N: 14%P₂O₅: 7%K) was applied as a basal dressing at 300 kg/ha prior to planting. Ammonium nitrate (34% N) was top dressed at a rate of 300 kg/ha in two splits, four weeks and 6 weeks after crop emergence. Weed control combined manual hoeing with the pre-emergence herbicide S-Metolachlor EC Herbicide (82.4% S-metolachlor) and post emergence herbicides Basagran (bentazon based) and stellar star (dicamba and topramezone). The disease stress environment was artificially inoculated with GLS and ET. Inoculation was conducted three times, first at the 6-8 leaf stage then the second and third inoculation were made at 7 day intervals for successful infection and disease build up. The inoculum was introduced into the plant whorl. GLS inoculum consisted of infected leaf material that had been dried and ground into powder form, while ET was applied in liquid suspension form. Mist irrigation was applied throughout to maintain high humidity and leaf wetness. Border rows were included to prevent inoculum escape.

3.3.1 Phenotypic data collection

All data were collected using CIMMYT's standard field protocols using a Fieldbook software. A calibrated digital scale was used to weigh shelled grain harvested from each plot to measure the primary trait, grain yield (GY). Several secondary traits were also recorded: days to 50% silking (SD) and days to 50% anthesis (AD) were recorded as the number of days from planting to the point when half the plants in a plot had reached flowering stage. The anthesis-silking interval (ASI) was calculated by deducting (AD) 50% anthesis from

(SD) 50% silking. Plant height (PH) was determined by measuring the distance from the plant base to the first tassel branch and ear height (EH) was measured as the height from plant base to the internode point where the ear formed or developed. Leaf senescence/stay green (SEN) was assessed in the low N trial on a 0-10 scale where each unit represented 10 % dead leaf area , this raw score was converted to a percentage by dividing it by 10 and multiplied by 100 to obtain total leaf area senesced. Ear aspect (EA) was rated visually by assessing the harvested ears on an appealing 1-5 scale (1= best, 5= worst), while husk cover (HC) was recorded the count of plants per plot with open tipped cobs. Root lodging (RL) was scored as a percentage of lodged plants, leaning more than 45° and stem lodging (SL) as a percentage of plants with stalks fractured below the ear node. Ears per plant (EPP) was calculated by dividing total ears harvested by the total plant count within each plot. Grain yield (GY) was calculated in tonnes per hectare by adjusting raw plot weight to a standard 12.5% grain moisture. Grain moisture (MOI) content was measured with a moisture meter at shelling. Disease severity for Grey Leaf Spot (GLS) and *Exserohilum turcicum* (ET) was scored on a 1-5 scale, where 1 were plants with no disease symptom and 5 were severely diseased plants. Ear rots (ER) were scored at a scale of 1-5 where 1 showed resistance and 5 showed susceptibility.

3.3.2 Data analysis

Each environment was first analysed separately using analysis of variance (ANOVA), allowing an initial assessment of genotype performance within each testing environment. These were followed by a combined analysis of variance (ANOVA) across all seven environments, fitted using the mixed modelling framework recommended by Moore and Dixon (2015), making use of R software version 4.4.3. In this combined model, genotypes was treated as fixed effect while environments, replications (reps) within environments, incomplete blocks with replications, genotype by environment interactions and residual error were all specified as random effects. The statistical model is given as:

$$Y_{ijkb} = \mu + E_j + R(E)_{kj} + IB(Re)_{bkj} + G_i + GE_{ij} + E_{ijkb}$$

Where Y_{ijkb} denotes the measured trait value for the i^{th} genotype evaluated in the j^{th} environment, k^{th} replicate and b^{th} incomplete block. The term μ represents the overall trial mean, E_j captures the effect attribute of the j^{th} environment or location. $R(E)_{kj}$ is the effect of the k^{th} replicate within the j^{th} environment, $IB(Re)_{bkj}$ reflects the influence of the incomplete block nested within the k^{th} replicate in the j^{th} environment. G_i quantifies the effect of the i^{th} genotype (provitamin A hybrid) and GE_{ij} estimates the extent at which the i^{th} genotype

responded differently across the j^{th} environment relative to the overall genotype mean. E_{ijkb} is the associated residual error term. Where significant genotypic differences were detected, means were separated using Fisher's Protected Least Significant Difference (LSD) test at the 5% significance level. Adjusted genotype means were estimated by generating the Best Linear Unbiased Estimates (BLUEs) in META-R software and for genotype comparisons. GGE biplot analysis was applied to examine grain yield stability and performance of hybrids across environment based on the model:

$$\text{GGE model: } Y_{ij} - \mu_i - \beta_j = \sum_{k=1}^t \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

In this model, Y_{ij} denotes the performance of genotype i in environment j , μ is the grand mean of the dataset, j b represents the main effect of environment j , k is the total number of principal components (PC) retained. λ_k is singular value associated with the k th PC, α_{ik} and γ_{jk} are the scores assigned of the i th genotype and j th environment respectively on the k th principal component. ε_{ij} is the residual term for genotype i in environment j . A 'which-won-where' scatterplot was used to delineate mega-environments. A genotype focused comparison biplot was used to rank genotypes based on mean grain yield and stability. A discriminating ability and representativeness biplot was used to identify which environments best distinguished genotype performance while remaining representative of the overall test environment set.

Principal Component Analysis (PCA) was run separately for each environment using a correlation matrix of all measured agronomic traits. The first two principal components (PC1 and PC2) were extracted and used to construct biplots that visualised the relationships among traits and the distribution of genotypes within each environment. Traits with vectors pointing in similar directions on the biplot were interpreted as positively correlated, whilst traits with opposing vectors were negatively correlated. Traits with perpendicular vectors were considered independent of each other. Hierarchical cluster analysis was performed alongside PCA to group genotypes with similar traits profiles across environments.

CHAPTER FOUR

4.0 Results

4.1 Analysis of variance for grain yield and secondary traits of provitamin A maize hybrids across all tested environments.

The combined ANOVA showed that environment had a highly significant effect ($P < 0.001$) on all 15 measured traits, indicating substantial environmental influence on genotype performance. Environment significantly ($P < 0.001$) affected grain yield (GYG), days to anthesis (AD), anthesis-silking interval (ASI), plant height (PH), ear height (EH), root lodging (RL), stalk lodging (SL), ears per plant (EPP), husk cover (HC), ear rot (ER), texture (TEX), moisture content (MOI), number of plants (NP), ear aspect (EA) and ear position (EPO). The magnitude of the environment mean squares, for instance, 596.5 for GYG, 52,022 for PH and 328.99 for MOI far exceeded all other sources of variation, confirming that the testing environments were sufficiently diverse to discriminate among genotypes for the evaluated traits. Genotype effects were highly significant ($P < 0.001$) for grain yield (GYG), plant height (PH), ear height (EH), moisture content (MOI), and number of plants (NP) and significant ($P < 0.01$) for husk cover (HC). Significant differences were also observed for stalk lodging (SL), ears per plant (EPP) and ear rot (ER) at $P < 0.05$. In contrast, genotype effects were non-significant for days to anthesis (AD), anthesis-silking interval (ASI), ear position (EPO), root lodging (RL), texture (TEX) and ear aspect (EA). The genotype $\times$ environment ($G \times E$) interaction was highly significant ($P < 0.001$) for grain yield (GYG), husk cover (HC) and moisture content (MOI) and significant at $P < 0.01$ for root lodging (RL) and ear rot (ER), indicating differential genotypic responses across environments for these traits. Non-significant $G \times E$ interaction effects were observed for days to anthesis (AD), anthesis-silking interval (ASI), plant height (PH), ear height (EH), ear position (EPO), stalk lodging (SL), ears per plant (EPP), texture (TEX), number of plants (NP) and ear aspect (EA), implying relatively stable genotypic expression across environments for these traits. The replicate $\times$ environment interaction was significant ($P < 0.05$) for plant height (PH), ear height (EH), ear position (EPO) and root lodging (RL) and significant at $P < 0.01$ for ear rot (ER), while texture (TEX) and moisture content (MOI) were significant at $P < 0.05$ and $P < 0.001$ respectively, reflecting field heterogeneity among replications across testing sites. The replicate $\times$ block effect within environments was significant ($P < 0.05$) only for anthesis-silking interval (ASI), while the replicate $\times$

environment $\times$ block interaction was highly significant ($P < 0.001$) for grain yield (GYG) and significant ($P < 0.05$) for husk cover (HC).

Table 4.1 Analysis of variance for 15 agronomic traits under optimum, low nitrogen and Grey Leaf Spot and ET *Exserohilum turcicum* inoculated environment.

Source	DF	GYG	AD	ASI	PH	EH	EPO	RL	SL	EPP	HC	ER	TEX	MOI	NP	EA
Genotype	24	5.54***	12.72ns	1.183ns	409***	177.5***	0.001439ns	48.05ns	13.107*	0.1541*	101.1**	105.43*	0.5102ns	2.1***	165.44***	0.3405ns
Replicate	2	2ns	17.17ns	3.799ns	119ns	86.6ns	0.001153ns	18.24ns	19.17ns	0.0602ns	13.1ns	3.67ns	1.8254*	6.5***	19.37ns	0.0187ns
Env	6	596.5***	827.91***	58.686***	52022***	8823.9***	0.030435***	2897.08***	96.711***	5.874***	3411.5***	1809.55***	15.5199***	328.99***	2364.05***	25.7986***
Gen.Env	144	2.88***	8.38ns	1.552ns	171ns	74.3ns	0.001623ns	60.2**	8.433ns	0.0631ns	118.7***	86.52**	0.2959ns	1.24***	38.83ns	0.3947ns
Rep.Env	12	1.29ns	9.87ns	1.16ns	343*	156.4*	0.0029*	81.17*	9.455ns	0.0695ns	110.2*	143.62**	1.837***	1.42*	19.42ns	0.2726ns
Rep.Blk	12	1.09ns	5.48ns	2.505*	133ns	52.5ns	0.00101ns	29.21ns	10.29ns	0.0657ns	58.7ns	62.17ns	0.2463ns	0.62ns	28.01ns	0.418ns
Rep.Env.Blk	72	2.03***	8.04ns	1.375ns	190ns	66.4ns	0.001485ns	30.53ns	8.453ns	0.0467ns	73.8*	78.34ns	0.1822ns	0.72ns	23.02ns	0.2338ns
Residuals	251	1.03	22.03	1.398	177	77.9	0.00156	41.21	8.198	0.0835	54.1	61.33	0.592	0.77	45.73	0.359

Significance codes: ‘***’ $p < 0.001$, ‘**’ $p < 0.01$, ‘*’ $p < 0.05$, ‘ns’ $p > 0.05$. Gen= Genotype, Rep= Replicate, Env= Environment, Gen.Env= Genotype by Environment

interaction, Env.Rep = Environment by Replication interaction, Rep.Block= Replication by Block interaction, Rep.Env.Blk= Replication by Environment by Block

interaction, GYG= Grain Yield, AD= Anthesis Date, ASI= Anthesis-Silking Interval, PH=Plant Height, EPO=Ear Position, RL= Root Lodging, SL=Stem Lodging,

EPP=Ears Per Plant, HC= Husk Cover, ER= Ear Rots, TEX= Ear Texture, MOI= Grain Moisture, NP= Number of Plants and EA= Ear Aspect.

4.2 Mean performance analysis.

The trait Best Linear Unbiased Estimates (BLUEs) for optimum environment were used for means presented in Table 4.2. The mean grain yield (GYG) was 6.51 t/ha with DSH24135 (7.81 t/ha), DSH24137 (7.79 t/ha) and DSH24139 (7.45 t/ha) recording the highest yields, whilst DSH24130 (4.03 t/ha) and DSH24131 (4.94 t/ha) were the lowest-yielding genotypes in the trial. The mean anthesis days and anthesis-silking interval were 69.69 and -0.30 days respectively, with DSH24141 (0.94 days) recording the widest positive ASI and ZS242 (-2.16 days). Mean plant height and ear height were 212.49 cm and 98.10 cm respectively, with ZS242 recording the tallest plants (217.69 cm) and DSH24145 the shortest (205.46 cm). Ears per plant averaged 1.44, being highest in DSH24130 (1.70) and CZH1815A (1.61) and lowest in ZS500 (1.10). Mean husk cover and ear rot were 12.12% and 8.72% respectively, with DSH24140 (20.56%) and DSH24130 (16.27%) recording the highest values for each trait. Grain moisture averaged 14.61% across genotypes, ranging from 13.61% in DSH24143 to 15.50% in DSH24133. Mean senescence score, ear texture and ear aspect were 5.46, 1.67 and 2.36 respectively.

Low N The trait Best Linear Unbiased Estimates (BLUEs) for the low nitrogen environment were used for means presented in Table 4.3. The mean grain yield on a grain basis (GYG) was 2.81 t/ha with DSH24147 (4.29 t/ha), DSH24132 (3.79 t/ha) and ZS244 (3.59 t/ha) recording the highest yields, whilst DSH24143 (1.77 t/ha) and ZS242 (1.72 t/ha) recorded the lowest yields in the trial. Mean anthesis days and anthesis-silking interval were 68.28 and 0.79 days respectively, with DSH24150 (66.35 days) and DSH24149 (1.63 days) recording the earliest anthesis and widest interval respectively. Mean plant height and ear height were 169.03 cm and 84.60 cm respectively, with ZS242 recording the shortest plants (145.67 cm) and DSH24147 the tallest (187.33 cm). Ears per plant averaged 0.85, ranging from 0.71 in DSH24130 to 1.02 in ZS244. Mean husk cover and ear rot were 12.52% and 13.65% respectively, with DSH24148 (27.86%) and ZS242 (37.17%) recording the highest values for each trait respectively. Grain moisture averaged 14.84%, ranging from 13.77% in DSH24146 to 16.67% in DSH24147. Mean senescence score, ear texture and ear aspect were 3.99, 1.43 and 2.32 respectively.

The trait Best Linear Unbiased Estimates (BLUEs) for the disease environment were used for means presented in Table 4.4. The mean grain yield on a grain basis (GYG) was 3.80 t/ha with DSH24142 (4.96 t/ha), DSH24137 (4.86 t/ha) and DSH24139 (4.31 t/ha) recording the highest yields. DSH24149 (2.94 t/ha) and DSH24130 (2.38 t/ha) recorded the lowest yields in the trial. Mean anthesis days and anthesis-silking interval were 71.11 and 0.37 days respectively, with DSH24140 (73.47 days) recording the latest anthesis and DSH24147 (1.67 days) the widest interval. Mean plant height and ear height were 213.17 cm and 102.13 cm respectively, with DSH24142 recording the tallest plants (240.14 cm) and CZH1815A the shortest (205.83 cm). Ears per plant averaged 1.30, ranging from 1.18 in DSH24149 to 1.52 in CZH1815A. Mean husk cover and ear rot were 18.69% and 11.64% respectively, with CZH1815A (35.03%) and DSH24130 (27.66%) recording the highest values for each trait respectively. Grain moisture averaged 12.85%, ranging from 11.77% in DSH24149 to 13.77% in DSH24133. Grey leaf spot (GLS) severity increased progressively across the three assessment periods, with mean scores of 1.48, 1.96 and 3.25 at first, second and third assessment respectively. DSH24130 recorded the lowest GLS scores (0.98, 1.00 and 2.00) whilst CZH1815A (1.64, 2.00 and 4.33) and DSH24149 (2.00, 2.33 and 5.33) recorded among the highest. *Exserohilum turcicum* (ET) severity also increased across assessments, with mean scores of 1.87, 1.97 and 2.25 at first, second and third assessment respectively. DSH24140 (1.02, 0.99 and 2.01) and DSH24143 (1.31, 1.27 and 1.92) recorded the lowest ET scores across assessments, whilst DSH24137 (3.07, 3.05 and 3.02) and DSH24139 (2.46, 2.31 and 2.97) recorded the highest.

Table 4.2: Mean performance for grain yield of the top 10 provitamin A maize hybrids under optimum conditions.

Genotype	GYG	GYF	AD	ASI	PH	EH	EPO	RL	SL	EPP	HC	ER	SEN	TEX	MOI	NP	EA
TOP10																	
DSH24135	7.81	7.64	69.33	0.29	208.54	97.23	0.50	2.07	3.51	1.56	6.11	3.96	5.33	1.83	15.32	24.64	2.25
DSH24137	7.79	7.47	68.38	0.13	210.36	100.22	0.51	2.75	0.00	1.53	8.59	4.79	4.20	1.99	14.37	24.28	2.25
DSH24139	7.45	7.31	69.89	-0.68	212.57	97.47	0.50	4.25	0.00	1.49	2.58	6.72	5.43	1.57	14.66	23.69	2.33
ZS500	7.28	7.64	71.83	-0.02	222.14	103.29	0.50	7.52	1.60	1.10	19.52	15.86	5.10	2.09	15.26	29.79	2.08
DSH24148	7.22	7.31	70.31	-0.66	216.16	102.42	0.52	5.13	0.83	1.28	10.08	7.85	4.87	2.18	15.11	28.71	2.33
DSH24136	7.00	6.87	69.24	-0.34	212.99	97.44	0.50	6.10	1.81	1.38	13.22	6.17	5.33	1.75	14.81	26.36	2.25
DSH24133	6.99	6.90	68.40	-0.82	210.20	96.15	0.49	4.34	0.00	1.57	6.00	4.06	5.77	1.33	15.50	23.35	2.00
CZH1815A	6.84	6.50	69.06	-0.53	206.47	94.45	0.50	6.49	2.50	1.61	18.79	5.74	5.43	1.92	13.73	27.13	2.75
DSH24140	6.83	6.80	71.44	-0.21	214.11	99.47	0.53	4.98	0.00	1.47	20.56	12.15	5.87	1.58	14.06	29.41	2.42
DSH24145	6.79	6.90	68.07	-0.27	205.46	98.12	0.51	6.52	3.39	1.30	11.29	5.46	5.97	1.66	14.75	29.07	2.08
BOTTOM5																	
DSH24138	5.89	6.03	71.04	-0.69	211.29	95.23	0.48	5.75	0.00	1.44	19.35	12.05	4.67	1.41	14.89	23.94	2.17
ZS242	5.81	5.82	70.34	-2.16	217.69	106.88	0.55	8.35	3.37	1.55	15.38	7.25	6.67	1.24	14.17	21.76	2.33
DSH24149	5.62	5.78	70.00	0.04	209.55	94.85	0.48	6.63	1.71	1.32	15.81	11.62	6.33	1.50	13.62	28.25	2.58
DSH24131	4.94	4.81	67.90	-0.13	210.56	92.82	0.49	8.06	0.00	1.59	10.26	9.28	4.20	1.67	14.59	13.77	2.67
DSH24130	4.03	3.99	71.55	-0.47	209.84	97.36	0.51	8.88	6.63	1.70	17.05	16.27	5.97	2.08	14.64	10.89	2.58
Mean of the top 10	7.20	7.13	69.59	-0.31	211.90	98.63	0.51	5.01	1.36	1.43	11.67	7.28	5.33	1.79	14.76	26.64	2.27
Grand mean	6.51	6.53	69.69	-0.30	212.49	98.10	0.50	5.69	1.56	1.44	12.12	8.72	5.46	1.67	14.61	25.44	2.36
LSD	1.16	1.16	1.64	0.60	7.81	6.26	0.02	0.00	0.96	0.16	7.64	3.35	0.92	0.36	0.65	4.48	0.21
CV%	17.11	17.09	2.73	373.00	4.36	7.74	6.74	70.87	223.92	12.08	69.10	86.69	15.71	26.11	4.03	11.47	19.87

GYG=Grain Yield, AD= Anthesis Date, ASI=Anthesis-Silking Interval, PH=Plant Height, EPO=Ear Position, RL=Root Lodging, SL=Stem Lodging,

EPP=Ears Per Plant, HC=Husk Cover, ER=Ear Rots, TEX=Ear Texture, MOI=Grain Moisture, NP=Number of Plants, EA=Ear Aspect.

Table 4.3 Mean performance of grain yield of the top 10 provitamin A maize hybrids under low nitrogen environment.

Genotype	GYG	GYF	AD	ASI	PH	EH	EPO	RL	SL	EPP	HC	ER	SEN	TEX	MOI	NP	EA
TOP10																	
DSH24147	4.29	3.76	67.31	-0.04	187.33	88.29	0.50	6.68	0.00	0.88	3.83	4.89	4.57	1.00	16.67	17.05	1.75
DSH24132	3.79	3.38	68.12	0.88	168.67	86.93	0.51	2.17	7.94	0.92	6.52	19.64	3.97	1.33	14.77	19.97	2.46
ZS244	3.59	3.20	68.33	1.58	187.00	88.09	0.47	1.45	10.42	1.02	12.13	11.63	3.64	1.33	15.53	16.29	1.63
DSH24148	3.37	3.08	68.02	0.89	169.00	84.33	0.50	4.48	1.52	1.01	27.86	14.32	3.60	1.33	14.47	19.01	2.06
DSH24134	3.26	2.81	67.35	0.65	172.33	80.03	0.48	6.87	0.00	0.85	23.71	8.55	3.90	2.00	15.33	17.04	2.99
DSH24140	3.22	2.97	67.56	0.42	173.67	88.91	0.50	4.80	1.52	0.93	11.85	1.68	4.27	1.33	15.53	18.74	2.10
CZH1815A	3.11	2.67	69.46	0.38	162.33	85.43	0.52	2.22	3.53	0.81	6.97	10.81	3.80	1.33	14.33	19.32	2.14
DSH24136	3.07	3.00	67.81	0.58	175.00	82.38	0.49	3.26	0.00	0.88	13.54	4.31	3.90	1.67	14.27	15.26	2.51
DSH24145	3.02	2.80	68.97	0.90	167.33	78.96	0.48	4.87	3.92	0.84	13.35	18.40	3.90	2.00	14.23	18.62	2.99
DSH24130	3.01	2.52	68.75	0.28	170.33	84.33	0.49	4.06	4.17	0.71	12.27	9.55	4.32	1.67	16.20	16.27	2.01
BOTTOM5																	
DSH24146	2.28	2.25	67.75	0.81	165.00	82.79	0.50	5.02	0.00	0.82	18.30	4.35	3.69	1.67	13.77	18.32	2.31
DSH24138	2.09	2.40	68.23	1.24	156.33	87.50	0.52	2.10	0.00	0.96	14.08	19.07	3.83	1.00	15.27	14.68	1.67
DSH24144	2.04	1.88	68.77	1.10	175.33	84.30	0.51	6.60	5.46	0.78	22.55	14.76	3.68	1.67	14.30	17.29	2.74
DSH24143	1.77	1.67	68.17	0.31	165.33	79.97	0.49	7.94	0.00	0.77	22.29	20.78	4.47	1.67	13.77	17.62	2.30
ZS242	1.72	1.69	70.75	0.77	145.67	82.26	0.50	7.38	0.00	0.72	10.92	37.17	4.83	1.33	13.87	20.04	2.81
Mean of the top10	3.37	3.02	68.17	0.65	173.30	84.77	0.49	4.09	3.30	0.89	13.20	10.38	3.99	1.50	15.13	17.76	2.26
Grand Mean	2.81	2.59	68.28	0.79	169.03	84.60	0.50	4.61	1.97	0.85	12.52	13.65	3.99	1.43	14.84	17.37	2.32
LSD	0.84	0.71	0.00	0.00	9.43	0.00	0.00	3.85	0.00	0.00	0.00	0.74	0.49	0.00	0.00	0.00	0.58
CV %	38.40	39.35	3.62	151.25	9.52	11.48	8.22	139.07	271.93	19.41	85.97	102.23	16.54	34.34	8.45	18.66	26.05

GYG=Grain Yield, AD= Anthesis Date, ASI=Anthesis-Silking Interval, PH=Plant Height, EPO=Ear Position, RL=Root Lodging, SL=Stem Lodging,

EPP=Ears Per Plant, HC=Husk Cover, ER=Ear Rots, TEX=Ear Texture, MOI=Grain Moisture, NP=Number of Plants, EA=Ear Aspect.

Table 4.4 Mean performance of grain yield of the top 10 provitamin A maize hybrids under disease inoculated environment.

Genotype	GYG	GYF	AD	ASI	PH	EH	EPO	RL	SL	EPP	HC	ER	TEX	MOI	NP	EA	GLS1	GLS2	GLS3	ET1	ET2	ET3
									TOP10													
DSH24142	4.96	5.06	73.08	0.67	240.14	117.86	0.49	-0.69	0.00	1.35	32.34	4.17	2.81	13.27	17.75	2.33	1.01	1.67	2.00	1.46	2.24	2.30
DSH24137	4.86	4.61	68.53	-0.67	215.81	110.84	0.51	-0.07	0.00	1.30	20.44	7.13	1.89	12.77	18.79	2.67	1.63	2.00	3.00	3.07	3.05	3.02
DSH24139	4.31	4.19	71.56	0.67	215.53	99.44	0.46	2.16	0.00	1.32	2.38	7.69	2.52	13.57	16.74	3.00	2.00	2.00	3.33	2.46	2.31	2.97
DSH24135	4.24	4.07	71.93	-0.33	209.23	103.34	0.49	-0.09	7.02	1.28	12.19	3.04	2.60	13.30	16.62	2.33	1.01	2.00	2.00	2.79	2.66	2.97
DSH24143	4.21	4.15	71.26	0.33	213.65	106.00	0.49	5.44	3.37	1.39	22.39	13.59	2.00	12.50	19.40	3.00	2.00	2.00	2.33	1.31	1.27	1.92
DSH24132	4.09	4.08	70.50	-0.33	220.73	107.92	0.49	1.97	0.00	1.33	25.48	11.47	2.39	12.60	20.34	3.00	1.35	2.00	3.00	2.09	2.34	2.68
DSH24133	4.03	3.88	69.04	0.33	214.63	104.36	0.48	2.37	0.00	1.33	6.25	7.23	2.01	13.77	16.83	2.67	1.35	2.00	3.33	2.40	2.38	2.37
DSH24148	4.03	4.43	71.51	0.67	216.30	105.49	0.48	1.75	1.67	1.28	15.71	10.48	3.17	13.33	17.65	3.00	1.67	2.00	3.33	2.36	2.01	2.35
DSH24140	4.01	3.90	73.47	0.00	207.34	97.19	0.47	0.07	0.00	1.33	26.28	9.79	2.65	12.57	18.28	3.00	1.03	1.33	1.67	1.02	0.99	2.01
CZH1815A	3.96	3.94	70.99	1.00	205.83	97.97	0.47	-0.20	4.99	1.52	35.03	12.04	2.91	12.07	18.79	3.33	1.64	2.00	4.33	1.20	1.72	2.03
									BOTTOM5													
DSH24138	3.40	3.44	73.06	1.00	206.58	98.81	0.48	1.86	0.00	1.41	35.83	19.86	2.28	12.43	15.62	3.00	1.68	2.33	4.33	2.25	1.66	1.99
DSH24150	3.38	3.58	70.59	0.67	208.63	100.32	0.48	6.11	1.96	1.29	3.92	11.02	2.28	12.50	18.56	3.00	1.33	2.00	4.33	1.83	2.03	1.99
DSH24147	3.15	3.08	69.30	1.67	209.21	95.90	0.46	2.99	0.00	1.28	25.08	10.23	2.30	12.57	18.61	3.33	1.69	2.00	3.67	1.42	1.62	2.62
DSH24149	2.94	3.08	72.26	0.00	213.29	95.99	0.45	7.27	3.41	1.18	17.16	18.26	1.94	11.77	18.23	3.67	2.00	2.33	5.33	1.16	1.69	1.66
DSH24130	2.38	2.29	71.51	1.33	214.14	106.50	0.50	3.08	13.26	1.44	29.67	27.66	2.64	12.63	8.38	3.33	0.98	1.00	2.00	1.93	1.98	1.67
Heritability	0.55	0.59	0.69	0.00	0.54	0.46	0.11	0.58	0.30	0.40	0.79	0.73	0.36	0.66	0.72	0.36	0.42	0.74	0.67	0.57	0.43	0.31
Genotype Variance	0.17	0.18	2.22	0.00	27.66	22.46	0.00	9.58	3.28	0.01	87.71	30.64	0.05	0.18	5.22	0.04	0.04	0.10	0.64	0.15	0.09	0.05
Residual Variance	0.41	0.37	2.94	2.00	71.39	78.51	0.00	20.77	23.14	0.03	68.51	33.87	0.29	0.28	6.22	0.23	0.18	0.10	0.95	0.34	0.37	0.35
Grand Mean	3.80	3.80	71.11	0.37	213.17	102.13	0.48	3.34	2.87	1.30	18.69	11.64	2.37	12.85	17.64	3.03	1.48	1.96	3.25	1.87	1.97	2.25
LSD	0.79	0.77	2.41	0.00	10.66	10.26	0.02	5.75	4.35	0.17	12.21	8.24	0.54	0.71	3.61	0.48	0.47	0.46	1.32	0.75	0.67	0.54
CV	16.96	15.95	2.41	378.81	3.96	8.68	7.57	136.62	167.60	12.55	44.28	50.01	22.75	4.11	14.14	15.81	29.00	16.49	29.99	31.20	30.99	26.09
n Replicates	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00
Genotype significance	0.02	0.01	0.00	1.00	0.05	0.09	0.76	0.01	0.31	0.18	0.00	0.00	0.24	0.00	0.00	0.19	0.14	0.00	0.00	0.03	0.11	0.30

4.4 The Principal Component Analysis (PCA) analysis.

The principal component analysis (PCA) and hierarchical cluster analyses revealed distinct patterns of trait associations across the misting (disease inoculated block), optimum and low N environments. Under the optimum environment (Figure 4.1), the first two principal components explained 84.76% of the total variation. Grain yield exhibited strong positive associations with number of plants, ear aspect, plant height, ear height and ear position. In contrast, grain texture, moisture content and husk cover formed separate groups, indicating that yield related and quality related traits contributed independently to phenotypic under optimum growing conditions.

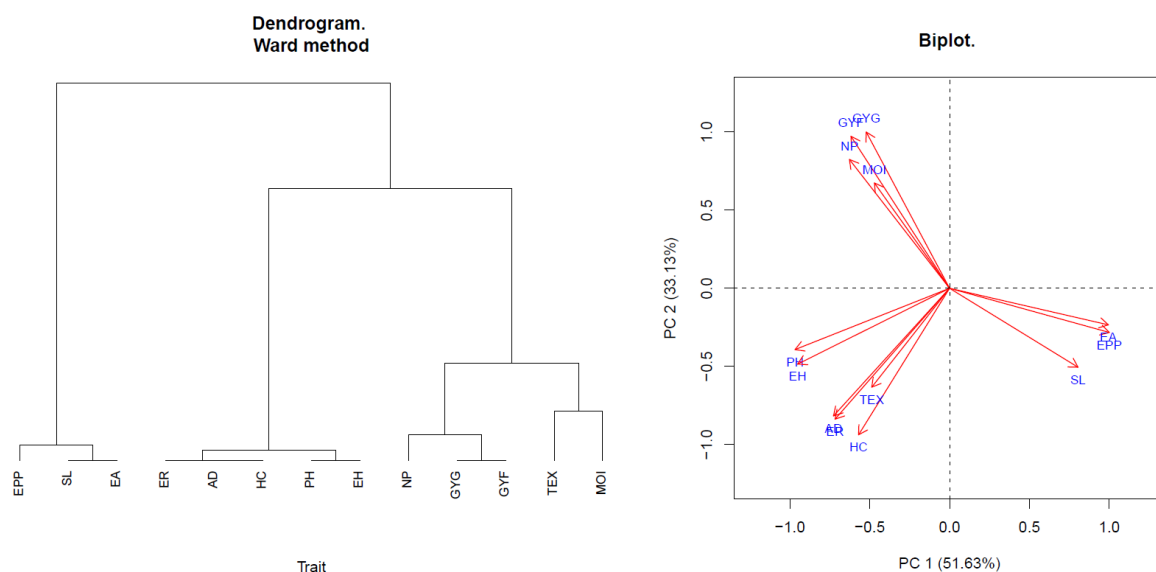


Figure 4.1 Principal Component Analysis for optimum environment.

Under the misting, disease inoculated environment (Figure 4.2), which imposed high disease pressure, the first two principal components explained 65.52% of the total variation, a lower proportion than that observed under optimum environment. Grain yield remained positively associated with plant height, ear height, ear position and ears per plant, indicating that productive genotypes maintained growth and reproduction even under disease pressure. However, grey leaf spot, rust and maize streak virus formed distinct clusters that were clearly separated from yield associated traits. The strong clustering of repeated disease assessments further indicated stable disease expression across growth stages.

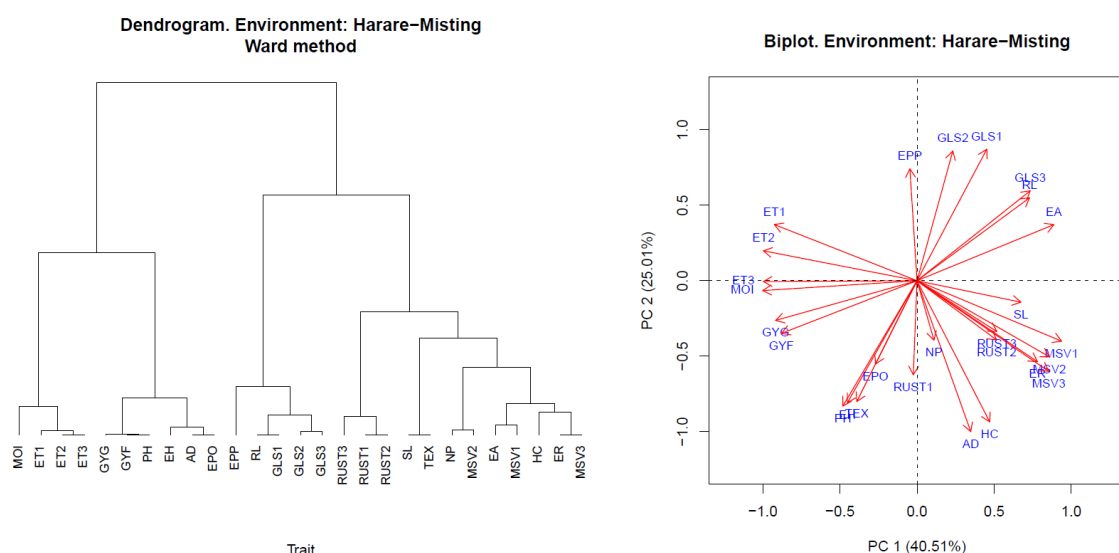


Figure 4.2 Principal Component Analysis for disease stress environment.

The low N environment as shown in figure 4.3, exhibited the highest proportion of explained variation, with the first two principal components accounting for 95.55% of total variation. Unlike both the optimum and misting environments, trait associations under low N were characterised by a clear separation between yield related traits and stress adaptive traits. Grain yield was strongly associated with plant height, ear height, ear position and overall plant vigour. Conversely, anthesis date, ear aspect and leaf senescence were positioned opposite the yield cluster, indicating a negative relationships with grain yield. Leaf senescence emerged as a major contributor to variation under low N environment. The cluster analysis further separated yield and plant architecture traits from senescence and flowering related traits.

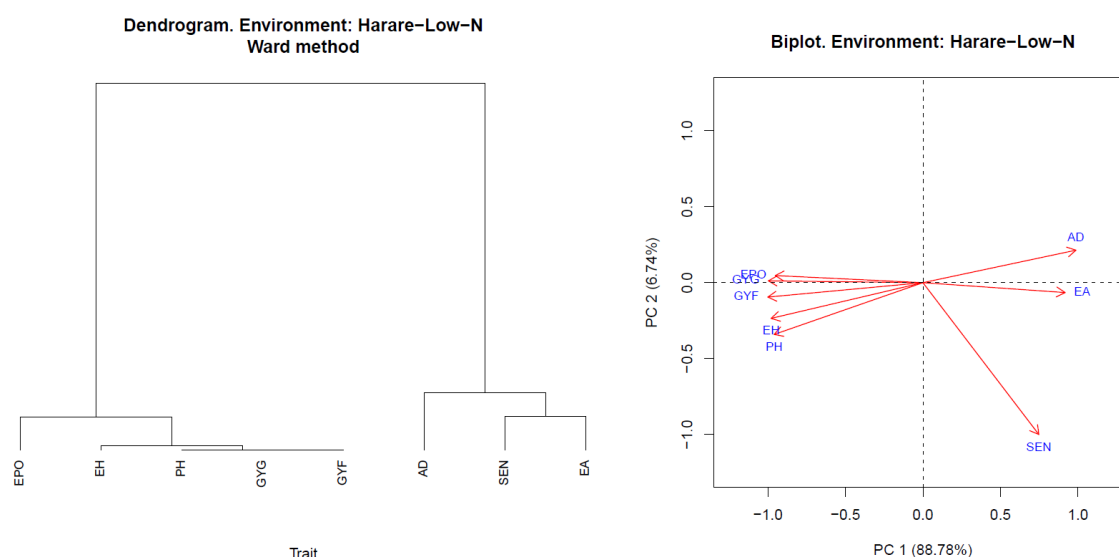


Figure 4.3 Principal Component Analysis for low N environment.

4.5 Genotypes evaluation based on GGE biplots.

The GGE biplot analysis for grain yield of provitamin A maize hybrids evaluated across seven environments is presented in Figures 4.4 to 4.10. The first principal component (PC1) explains 45.59% of the total variance in grain yield data whilst the second principal component (PC2) explains 23.92% and together the biplot accounted for 69.51% of the genotype main effect and genotype by environment interaction for grain yield of the hybrids. The which-won-where biplot revealed two mega-environments and six sectors with three vertex genotypes. Mega-environment 1, which included Harare Optimum (HRE-OPT), Gwebi Optimum (GW-OPT) and Harare Misting (HRE-MIST), was won by DSH24133, whilst mega-environment 2, comprising Rattray Arnold Optimum (R-OPT), Rattray Arnold Low-N (RLN), Harare Low-N (HRE-LN) and Gwebi Low-N (GW-LN), was won by DSH24139; genotypes falling inside the polygon were less responsive compared to the vertex genotypes. The environment vector scatterplot showed that HRE-OPT and GW-OPT had long, closely aligned vectors indicating strong positive correlation and similar discriminating power, while R-OPT projected at a divergent angle reflecting environment-specific genotypic responses and HRE-LN and GW-LN clustered together suggesting redundancy in differentiating genotype performance under low-nitrogen stress conditions. The environment comparison biplot identified HRE-OPT as the most representative and discriminating environment, positioned nearest to the average environment axis with the longest vector, rendering it the most appropriate environment for selecting broadly adapted provitamin A hybrids. Ideal stable and high-yielding genotypes are shown in the ranking biplot and the genotype-focused comparison biplot with the following descending ranking: DSH24133 > DSH24139 > DSH24137 > ZS500 > DSH24148 > DSH24136 > DSH24135 > CZH1815A > DSH24140 > DSH24145, while the ranking of environments based on genotypic performance placed HRE-OPT as the most ideal testing environment, followed by GW-OPT and HRE-MIST, with R-OPT deviating most from the ideal

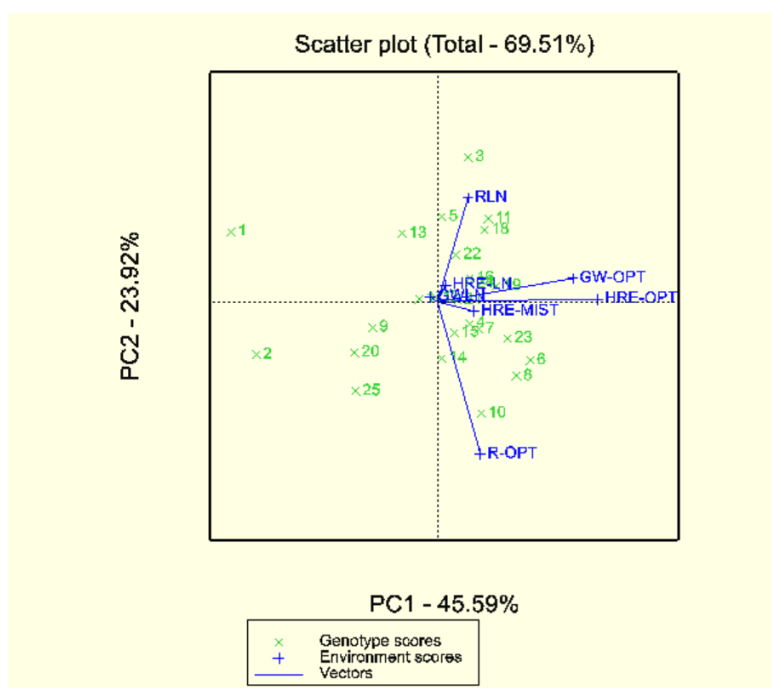


Figure 4.6 Environment vector scatterplot.

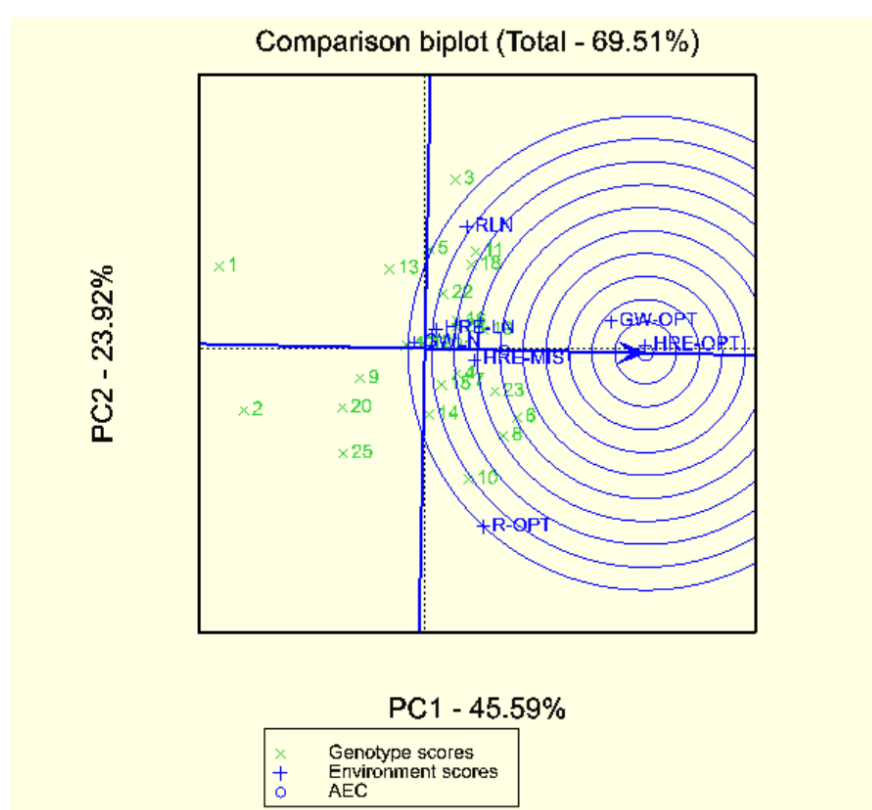


Figure 4.7 Environment comparison biplot.

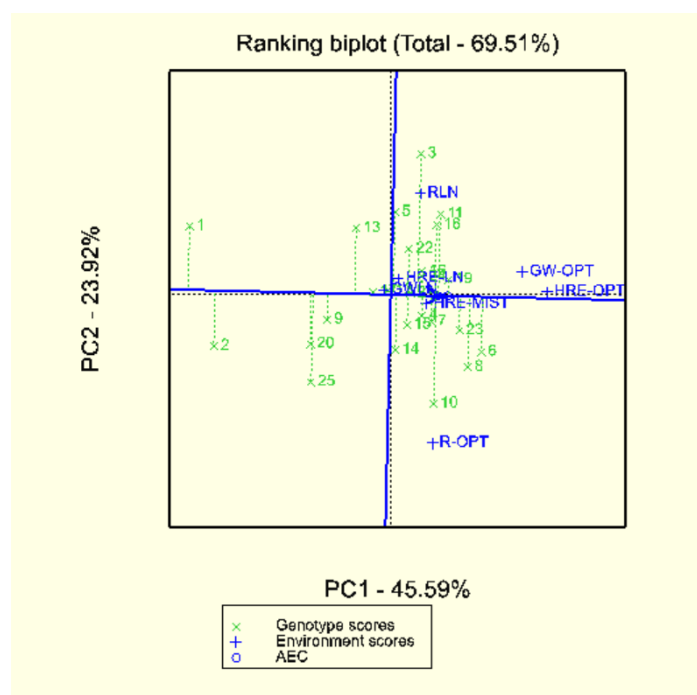


Figure 4.8 Ranking plot for genotypes based on environment.

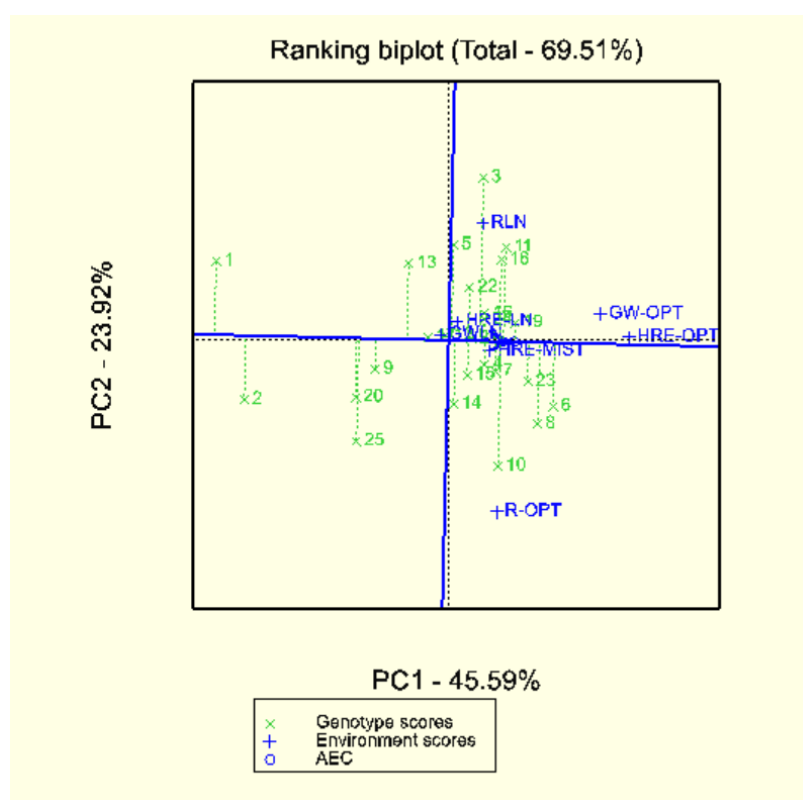


Figure 4.9 Ranking plot for environment based on genotypes.

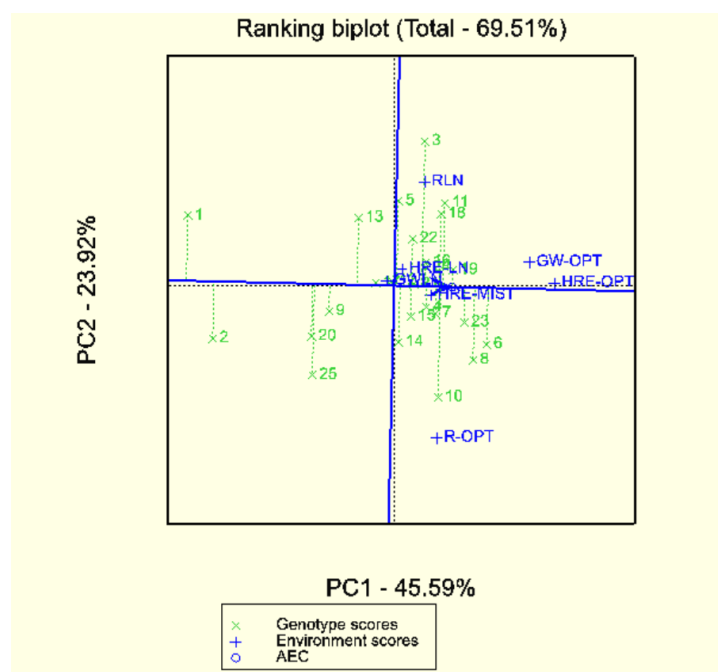


Figure 4.10 Ranking plot based on mean and stability.

CHAPTER FIVE

5.0 DISCUSSION.

5.1 Grain yield across three different management environments.

The strongly significant genotypic differences ($P < 0.001$) observed for grain yield across all environments confirmed genetic variation among the twenty-one newly developed CIMMYT provitamin A maize hybrids and the commercial checks. These findings are consistent with the broader literature on the multi-environment maize trials in sub Saharan Africa (SSA), where significant genotypic differences in grain are widely reported as a prerequisite for effective variety selection (Engida *et al.*, 2024). The yielding abilities of twenty-one newly developed provitamin A maize hybrids differ from the internal PVA check (CZH1815A) and the commercial checks (ZS242, ZS244 and ZS500).

Under optimum conditions, the grand mean grain was 6.51 t/ha, with the top performing hybrids DSH24135 (7.81 t/ha), DSH24137 (7.79 t/ha) and DSH24139 (7.45 t/ha) substantially exceeding the internal provitamin A check CZH1815A (6.84 t/ha) and the commercial check ZS244 (6.49 t/ha). These yields are notably competitive when compared to the commercial check ZS500 (7.28 t/ha), which is one of the most widely grown commercial maize varieties in Zimbabwe. This finding is important because one of the main barriers to provitamin A maize adoption in Zimbabwe and other parts of sub Saharan Africa (SSA) has been the perception that biofortified varieties yield less (Mudadirwa *et al.*, 2023). The range in yield performance under optimum environment, from a high of 7.81 t/ha (DSH24135) to a low of 4.03 t/ha (DSH24130), highlights that not all the newly developed hybrids are equally competitive. The bottom performing hybrids DSH24131 (4.94 t/ha) and DSH24130 (4.03 t/ha) fell well below the grand mean and the commercial check. These results emphasise the importance of multi-environment evaluation prior to variety recommendation, a principle consistently advocated in the provitamin A maize literature (Goredema-Matongera *et al.*, 2021).

5.2 Agronomic performance under low nitrogen.

The low nitrogen environment produced the most drastic reduction in grain yield, with the grand mean dropping to 2.81 t/ha compared to 6.51 t/ha under optimum condition, representing a yield reduction of approximately 57%. This magnitude of yield reduction

under low N stress aligns well with the documented reports in the literature. Zhao *et al.* (2019), reported yield reductions of 50% to 70% under severe nitrogen deficiency in maize genotypes in sub Saharan Africa (SSA). Gokoma *et al.* (2025), similarly noted that low nitrogen stress consistently suppresses grain yield in maize germplasm across trials in sub Saharan Africa while Pasley *et al.* (2019) linked low fertilizer application rates common in Zimbabwean smallholder systems to persistent yield gaps.

Despite the overall yield suppression under low N, there was notable variation among genotypes, which confirms the existence of differential nitrogen use efficiency among the tested hybrids. DSH24147 (4.29 t/ha), DSH24132 (3.79 t/ha) and ZS244 (3.59 t/ha) were the highest yielding genotypes under low N, while DSH24143 (1.77 t/ha) and ZS242 (1.72 t/ha) recorded the lowest yields. The comparatively strong performance of DSH24147 under low N stress is particularly notable because this hybrid did not rank among the top performers under optimum conditions (6.76 t/ha, ranking twelfth under optimum). This crossover in ranking between optimum and low N environments is evidence of significant genotype by environment interaction, which the ANOVA results confirmed to be highly significant ($P < 0.001$) for grain yield.

The strong performance of ZS244 under low N conditions (3.59 t/ha, third highest) is noteworthy given its commercial status as an established check variety in Zimbabwe. It suggests that ZS244 has inherent N-use efficiency traits that newer hybrid developers could aim to combine with high provitamin A content. Conversely, the very poor performance of ZS242 under low N (1.72 t/ha, lowest in the trial) highlights its sensitivity to nitrogen stress. This is particularly relevant to Zimbabwe where ZS242 is used by some smallholder farmers but is being grown under nutrient-depleted conditions, a combination that this study confirms to be agronomically problematic.

Plant height also decreased markedly under low N, averaging 169.03 cm compared to 212.49 cm under optimum, with a grand mean reduction of over 43 cm. Reduced plant height under nitrogen deficiency is a well-established physiological response to nutrient stress, as nitrogen limitation curtails cell division, reduces leaf area index and suppresses vegetative growth (Ciampitti and Vyn, 2012). The reduction in ears per plant from a mean of 1.44 under optimum to 0.85 under low N is consistent with reports that nitrogen deficiency increases kernel abortion and reduces the number of productive ears per plant (Shen *et al.*, 2018).

The senescence scores observed under low N (grand mean 3.99 on a scale of 1 to 10) confirmed that nitrogen-deficient plants underwent accelerated leaf senescence, which reduces the photosynthetic period available for grain filling. Genotypes with lower

senescence scores under low N, such as ZS244 (3.64), DSH24148 (3.60) and CZH1815A (3.80), are likely candidates with stay-green characteristics that contribute to tolerance under nitrogen-deficient conditions. Stay green is recognised as a valuable adaptive trait for low input environments in Zimbabwe.

5.3 Disease response under the misting (disease inoculated) environment.

The PCA analysis revealed that under the misting environment the first two principal components explained 65.52% of total variation, a markedly lower proportion than the 84.76% explained under optimum and 95.55% explained under low N. This indicates that that stress introduces more complex and less predictable patterns of phenotypic expression, which is consistent with the interactive effects of multiple pathogens and the differential host resistance mechanisms present in diverse hybrid germplasm. Disease scoring revealed that Grey Leaf Spot (GLS), ET (*Exserohilum turcicum*), rust and maize streak virus formed distinct clusters clearly separated from yield related traits. This separation indicates that the disease resistance mechanisms expressed by the top performer provitamin A hybrids did not significantly compromise their yielding capacity. Hybrids that maintained high grain yield under the disease environment while recording low disease severity scores represent candidates with effective field resistance to the foliar diseases evaluated.

The findings are consistent with the literature on Grey leaf (GLS) and *Exserohilum turcicum* (ET) in Zimbabwe and parts of sub Saharan Africa (SSA). Ward *et al.* (1999), documented that GLS can reduce yields by 20-60% depending on genotype susceptibility and environmental conditions. Likewise, *Exserohilum turcicum* (ET) may result in significant yield reductions under severe disease pressure depending on genotype susceptibility and timing of infection. The range in disease scores observed among the tested genotypes demonstrates that the new CIMMYT provitamin A hybrids vary in their resistance and that several hybrids maintained acceptable agronomic performance even under stress.

5.4 Genotype by Environment Interaction.

The GGE biplot analysis provided a valuable visual representation of how genotypes and environments interacted. The which-won-where biplot showed that no single hybrid consistently dominated all environments, confirming the presence of crossover G x E interactions where genotype rankings changed substantially across environments. This is a common finding in African maize breeding trials where environmental diversity, including

differences in altitude, rainfall distribution, soil nitrogen status and disease pressure, creates highly heterogeneous selection environments (Eze *et al.*, 2020).

Despite the complex G x E interactions, the discriminating ability and representativeness analysis from the GGE biplot identified that certain environments were more informative and representative of the overall target environment set. The optimum environment at Harare provided high discrimination among genotypes and was largely representative of the broader test set, making it the most informative single environment for initial variety screening. This finding aligns with recommendations by CIMMYT that high-quality optimum managed stress trials at well-established research stations should anchor multi-environment evaluation programmes in Southern Africa (Tarekegne *et al.*, 2024).

Several hybrids demonstrated relatively broad adaptation across both optimum and stress environments. DSH24148 ranked among the top performers under both optimum (7.22 t/ha) and low N (3.37 t/ha) conditions, and DSH24140 also showed competitive performance across multiple environments. Such broadly adapted genotypes are particularly valuable for smallholder farmers in Zimbabwe, who often grow maize under mixed management conditions that may combine some degree of fertiliser input with unpredictable nitrogen availability and periodic disease pressure.

5.5 Secondary traits and their implications.

Anthesis date and anthesis-silking interval (ASI) showed non-significant genotypic differences, suggesting that the twenty-five entries evaluated are phenologically similar in terms of flowering timing. The near-zero grand mean ASI under optimum conditions (-0.30 days) indicates good synchronisation between pollen shedding and silk emergence, which is associated with effective pollination and grain set. Under low N stress, the mean ASI shifted to 0.79 days, indicating a slight delay in silk emergence relative to anthesis, a physiological response to nitrogen stress that has been linked to kernel abortion in susceptible genotypes (Shen *et al.*, 2018).

Ear aspect scores averaged 2.36 under optimum conditions, indicating generally good ear quality across the trial. The best ear aspect scores were recorded by DSH24133 (2.00) and DSH24147 (2.75 under optimum, 1.75 under low N), reflecting that these hybrids produced visually appealing ears even under stress. Ear aspect is an important criterion in variety acceptance in farmer communities and influences the commercial viability of hybrid promotion in Zimbabwe (Mushayi *et al.*, 2025).

Husk cover and ear rot were important quality traits where significant G x E interaction was detected. High husk cover (percentage of ears with open tips) indicates susceptibility to mycotoxin contamination and post-harvest losses. Under optimum conditions, DSH24140 (20.56%) and ZS500 (19.52%) recorded the highest husk cover percentages. The positive correlations between husk cover and ear rot observed in the PCA analysis is consistent with the biological mechanism whereby inadequate tip coverage allows pathogen entry and promotes ear rot development. Selecting for tight husk cover, particularly in the context of PVA maize that is intended for household food consumption and child nutrition, is therefore an important breeding criterion to prevent aflatoxin and fumonisin contamination.

Grain moisture content at harvest averaged 14.61% under optimum conditions and 14.84% under low N, both of which are close to the 12.5% target moisture content used for yield adjustment. Significant genotypic differences in moisture content ($P < 0.001$) and significant G x E interaction for this trait suggest that some genotypes are better suited to early moisture dry-down.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS.

6.1 Conclusions

The significant genotype, environment and genotype x environment interaction effects for grain yield confirmed the importance of multi-environment testing when selecting superior provitamin A maize hybrids. DSH24135, DSH24137 and DSH24139 consistently exhibited superior grain yield and desirable agronomic traits across environments and outperformed several commercial checks. Traits such as plant height, ears per plant, anthesis-silking interval, ear aspect and senescence demonstrated importance as secondary traits in selecting superior genotypes under low nitrogen and disease stress environment. DSH24147 demonstrated outstanding adaptation under low nitrogen conditions and may serve as a valuable source of low N tolerance in future breeding programmes. The study demonstrated that competitive grain yield and stress tolerance can be combined in provitamin A maize germplasm, supporting efforts to improve both nutritional security and maize productivity in Zimbabwe.

6.2 Recommendations

DSH24135, DSH24137 and DSH24139 respectively, are recommended for advancement to further trial stages, given their combined yield and stability performance. It is recommended that future studies test these hybrids across more locations and seasons to further confirm their stability and broad adaptation.

APPENDICES

Appendix 1: Grain yield combined ANOVA table.

Response:	GYG					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	132.9	5.54	5.3627	1.14E-12	***
Replicate	2	4	2	1.9405	0.1458	ns
Environment	6	3579	596.5	577.4875	2.20E-16	***
Genotype.Environment	144	414.4	2.88	2.7861	5.70E-13	***
Replicate.Environment	12	15.5	1.29	1.2477	0.2509	ns
Replicate.Block	12	13.1	1.09	1.0593	0.3954	ns
Replicate.Environment.Block	72	145.9	2.03	1.9614	7.30E-05	***
Residuals	251	259.3	1.03			

Appendix 2: Anthesis Date combined ANOVA table.

Response:	AD					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	305.3	12.72	0.5774	0.9461	
Replicate	2	34.3	17.17	0.7793	0.4596	
Environment	6	4967.4	827.91	37.5828	<2e-16	***
Genotype:Environment	144	1207	8.38	0.3805	1	
Replicate:Environment	12	118.4	9.87	0.4478	0.9428	
Replicate:Block	12	65.7	5.48	0.2486	0.9954	
Replicate:Environment:Block	72	578.9	8.04	0.365	1	
Residuals	322	7093.3	22.03			

Appendix 3: Anthesis Silking Interval combined ANOVA table.

Response:	ASI					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	28.38	1.183	0.846	0.67651	
Replicate	2	7.6	3.799	2.7177	0.06753	.
Environment	6	352.12	58.686	41.981	2.00E-16	***
Genotype:Environment	144	223.46	1.552	1.1101	0.22365	
Replicate:Environment	12	13.92	1.16	0.8295	0.61992	
Replicate:Block	12	30.06	2.505	1.792	0.04837	*
Replicate:Environment:Block	72	99	1.375	0.9836	0.52008	

Appendix 4: Plant height combined ANOVA table.

Response:	PH					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	9828	409	2.3148	0.000579	***
Replicate	2	238	119	0.6719	0.511422	
Environment	6	312133	52022	294.0696	2.20E-16	***
Genotype:Environment	144	24569	171	0.9645	0.593525	
Replicate:Environment	12	4120	343	1.9409	0.029132	*
Replicate:Block	12	1591	133	0.7494	0.702402	
Replicate:Environment:Block	72	13664	190	1.0727	0.336237	
Residuals	326	57671	177			

Appendix 5: Ear height combined ANOVA table.

Response:	EH					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	4259	177.5	2.2781	0.000733	***
Replicate	2	173	86.6	1.1114	0.330328	
Environment	6	52944	8823.9	113.2649	2.20E-16	***
Genotype:Environment	144	10695	74.3	0.9534	0.624703	
Replicate:Environment	12	1877	156.4	2.0076	0.023071	*
Replicate:Block	12	630	52.5	0.674	0.776349	
Replicate:Environment:Block	72	4782	66.4	0.8526	0.791223	
Residuals	326	25397	77.9			

Appendix 6: Ear position combined ANOVA table.

Response:	EPO					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	0.03454	0.001439	0.9229	0.57065	
Replicate	2	0.00231	0.001153	0.7394	0.4782	
Environment	6	0.18261	0.030435	19.5159	2.00E-16	***
Genotype:Environment	144	0.23369	0.001623	1.0406	0.38216	
Replicate:Environment	12	0.0348	0.0029	1.8594	0.03853	*
Replicate:Block	12	0.01212	0.00101	0.6475	0.80085	
Replicate:Environment:Block	72	0.10688	0.001485	0.9519	0.58964	
Residuals	326	0.5084	0.00156			

Appendix 7: Root lodging combined ANOVA table.

Response:	RL					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	1153.2	48.05	1.1659	0.271173	
Replicate	2	36.5	18.24	0.4426	0.642761	
Environment	6	17382.5	2897.08	70.2982	2.20E-16	***
Genotype:Environment	144	8669.1	60.2	1.4608	0.002951	**
Replicate:Environment	12	974	81.17	1.9696	0.026363	*
Replicate:Block	12	350.5	29.21	0.7088	0.742928	
Replicate:Environment:Block	72	2198.3	30.53	0.7409	0.937598	
Residuals	326	13434.9	41.21			

Appendix 8: Stem lodging combined ANOVA table.

Response:	SL					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	314.57	13.107	1.5988	0.03915	*
Replicate	2	38.34	19.17	2.3383	0.09811	.
Environment	6	580.27	96.711	11.7968	5.61E-12	***
Genotype:Environment	144	1214.37	8.433	1.0287	0.41365	
Replicate:Environment	12	113.45	9.455	1.1533	0.31631	
Replicate:Block	12	123.47	10.29	1.2551	0.24429	
Replicate:Environment:Block	72	608.64	8.453	1.0311	0.4184	
Residuals	326	2672.58	8.198			

Appendix 9: Ears per plant combined ANOVA table.

Response:	EPP					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	3.698	0.1541	1.8444	0.01025	*
Replicate	2	0.12	0.0602	0.7212	0.48694	
Environment	6	35.244	5.874	70.3175	2.00E-16	***
Genotype:Environment	144	9.091	0.0631	0.7558	0.97261	
Replicate:Environment	12	0.833	0.0695	0.8314	0.61793	
Replicate:Block	12	0.789	0.0657	0.7866	0.66431	
Replicate:Environment:Block	72	3.36	0.0467	0.5586	0.99827	
Residuals	326	27.232	0.0835			

Appendix 10: Husk cover combined ANOVA table.

Response:	HC					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	2426.2	101.1	1.8687	0.008916	**
Replicate	2	26.1	13.1	0.2416	0.78552	
Environment	6	20469.1	3411.5	63.0639	2.20E-16	***
Genotype:Environment	144	17094.1	118.7	2.1944	3.51E-09	***
Replicate:Environment	12	1321.8	110.2	2.0362	0.020857	*
Replicate:Block	12	703.8	58.7	1.0842	0.372544	
Replicate:Environment:Block	72	5310.5	73.8	1.3634	0.037955	*
Residuals	326	17635.3	54.1			

Appendix 11: Ear rot combined ANOVA table.

Response:	ER					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	2530.2	105.43	1.719	0.020678	*
Replicate	2	7.3	3.67	0.0599	0.94186	
Environment	6	10857.3	1809.55	29.5051	2.20E-16	***
Genotype:Environment	144	12459.4	86.52	1.4108	0.006259	**
Replicate:Environment	12	1723.5	143.62	2.3418	0.006844	**
Replicate:Block	12	746	62.17	1.0137	0.43573	
Replicate:Environment:Block	72	5640.2	78.34	1.2773	0.080701	.
Residuals	326	19993.6	61.33			

Appendix 12: Ear texture combined ANOVA table.

Response:	TEX					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	12.246	0.5102	0.8619	0.654928	
Replicate	2	3.651	1.8254	3.0834	0.047141	*
Environment	6	93.12	15.5199	26.216	2.20E-16	***
Genotype:Environment	144	42.606	0.2959	0.4998	0.999998	
Replicate:Environment	12	22.044	1.837	3.1031	0.00035	***
Replicate:Block	12	2.956	0.2463	0.4161	0.956933	
Replicate:Environment:Block	72	13.116	0.1822	0.3077	1	
Residuals	326	192.993	0.592			

Appendix 13: Moisture content combined ANOVA table.

Response:	MOI					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	50.41	2.1	2.7264	3.78E-05	***
Replicate	2	12.99	6.5	8.4315	0.000269	***
Environment	6	1973.95	328.99	427.0059	2.20E-16	***
Genotype:Environment	144	177.86	1.24	1.6031	0.000291	***
Replicate:Environment	12	17.01	1.42	1.8401	0.041143	*
Replicate:Block	12	7.42	0.62	0.8027	0.647678	
Replicate:Environment:Block	72	51.54	0.72	0.9292	0.639022	
Residuals	326	251.17	0.77			

Appendix 14: Number of plants combined ANOVA table.

Response:	NP					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	3970.6	165.44	3.6176	7.30E-08	***
Replicate	2	38.7	19.37	0.4236	0.655	
Environment	6	14184.3	2364.05	51.693	2.20E-16	***
Genotype:Environment	144	5591.9	38.83	0.8491	0.8694	
Replicate:Environment	12	233	19.42	0.4246	0.9534	
Replicate:Block	12	336.1	28.01	0.6125	0.8316	
Replicate:Environment:Block	72	1657.7	23.02	0.5034	0.9997	
Residuals	326	14908.8	45.73			

Appendix 15: Ear aspect combined ANOVA table.

Response:	EA					
	Df	Sum	Sq	Mean	Sq	F
Genotype	24	8.172	0.3405	0.9485	0.5353	
Replicate	2	0.037	0.0187	0.0521	0.9493	
Environment	6	154.792	25.7986	71.8665	<2e-16	***
Genotype.Environment	144	56.833	0.3947	1.0994	0.2447	
Replicate.Environment	12	3.271	0.2726	0.7594	0.6922	
Replicate.Block	12	5.016	0.418	1.1644	0.3078	
Replicate.Environment:Block	72	16.835	0.2338	0.6513	0.9854	
Residuals	326	117.027	0.359			

Appendix 16: Genotype mean performance under optimum, Grain yield, field weight, Anthesis Date Anthesis silking interval, Plant height Ear height, Ear position, Root lodging.

Environment	Genotype	GYG	GYF	AD	ASI	PH	EH	EPO	RL
OVERALL	DSH24135	7.81	7.64	69.33	0.29	208.54	97.23	0.50	2.07
OVERALL	DSH24137	7.79	7.47	68.38	0.13	210.36	100.22	0.51	2.75
OVERALL	DSH24139	7.45	7.31	69.89	-0.68	212.57	97.47	0.50	4.25
OVERALL	ZS500	7.28	7.64	71.83	-0.02	222.14	103.29	0.50	7.52
OVERALL	DSH24148	7.22	7.31	70.31	-0.66	216.16	102.42	0.52	5.13
OVERALL	DSH24136	7.00	6.87	69.24	-0.34	212.99	97.44	0.50	6.10
OVERALL	DSH24133	6.99	6.90	68.40	-0.82	210.20	96.15	0.49	4.34
OVERALL	CZH1815A	6.84	6.50	69.06	-0.53	206.47	94.45	0.50	6.49
OVERALL	DSH24140	6.83	6.80	71.44	-0.21	214.11	99.47	0.53	4.98
OVERALL	DSH24145	6.79	6.90	68.07	-0.27	205.46	98.12	0.51	6.52
OVERALL	DSH24144	6.78	6.79	68.15	0.29	211.56	99.43	0.51	2.23
OVERALL	DSH24147	6.76	6.87	68.73	-0.52	206.92	92.84	0.51	6.97
OVERALL	DSH24143	6.75	6.67	69.13	-0.68	214.50	100.37	0.51	5.22
OVERALL	DSH24150	6.56	6.77	69.87	-0.61	208.95	96.44	0.51	3.67
OVERALL	ZS244	6.49	7.10	70.80	0.23	223.44	102.84	0.51	5.87
OVERALL	DSH24141	6.37	6.50	67.76	0.94	205.93	87.92	0.47	4.41
OVERALL	DSH24134	6.28	6.23	69.85	-0.26	210.18	96.59	0.51	5.68
OVERALL	DSH24132	6.25	6.21	69.54	0.31	218.94	103.76	0.51	6.69
OVERALL	DSH24146	6.21	6.22	70.39	-0.74	207.67	93.46	0.49	6.10
OVERALL	DSH24142	6.08	6.15	71.25	0.07	226.20	105.37	0.50	7.73
OVERALL	DSH24138	5.89	6.03	71.04	-0.69	211.29	95.23	0.48	5.75
OVERALL	ZS242	5.81	5.82	70.34	-2.16	217.69	106.88	0.55	8.35
OVERALL	DSH24149	5.62	5.78	70.00	0.04	209.55	94.85	0.48	6.63
OVERALL	DSH24131	4.94	4.81	67.90	-0.13	210.56	92.82	0.49	8.06
OVERALL	DSH24130	4.03	3.99	71.55	-0.47	209.84	97.36	0.51	8.88
OVERALL	Heritability	0.61	0.61	0.66	0.15	0.64	0.61	0.19	0.00
OVERALL	Genotype Variance	0.42	0.41	0.96	0.05	19.35	11.59	0.00	0.00
OVERALL	GenxLoc Variance	0.67	0.66	0.75	0.15	3.53	2.80	0.00	14.56
OVERALL	Residual Variance	1.24	1.25	3.61	1.25	85.74	57.68	0.00	16.28
OVERALL	Grand Mean	6.51	6.53	69.69	-0.30	212.49	98.10	0.50	5.69
OVERALL	LSD	1.16	1.16	1.64	0.60	7.81	6.26	0.02	0.00
OVERALL	CV	17.11	17.09	2.73	373.00	4.36	7.74	6.74	70.87
OVERALL	n Replicates	3	3	3	3	3	3	3	3
OVERALL	n Environments	4	4	4	2	3	3	3	4
OVERALL	Genotype significance	0.00	0.00	0.00	0.70	0.00	0.01	0.56	1.00
OVERALL	GenxEnv significance	0.00	0.00	0.02	0.34	0.65	0.58	0.10	0.00
OVERALL	GenxEnv significance	0.00	0.00	0.02	0.34	0.65	0.58	0.10	0.00

Appendix 17: Genotype mean performance under optimum, Stem lodging, Ears per plant, Husk cover, Ear rots, Senescence, Texture, Moisture content, Number of plants, Ear aspect.

Environment	Genotype	SL	EPP	HC	ER	SEN	TEX	MOI	NP	EA
OVERALL	DSH24135	3.51	1.56	6.11	3.96	5.33	1.83	15.32	24.64	2.25
OVERALL	DSH24137	0.00	1.53	8.59	4.79	4.20	1.99	14.37	24.28	2.25
OVERALL	DSH24139	0.00	1.49	2.58	6.72	5.43	1.57	14.66	23.69	2.33
OVERALL	ZS500	1.60	1.10	19.52	15.86	5.10	2.09	15.26	29.79	2.08
OVERALL	DSH24148	0.83	1.28	10.08	7.85	4.87	2.18	15.11	28.71	2.33
OVERALL	DSH24136	1.81	1.38	13.22	6.17	5.33	1.75	14.81	26.36	2.25
OVERALL	DSH24133	0.00	1.57	6.00	4.06	5.77	1.33	15.50	23.35	2.00
OVERALL	CZH1815A	2.50	1.61	18.79	5.74	5.43	1.92	13.73	27.13	2.75
OVERALL	DSH24140	0.00	1.47	20.56	12.15	5.87	1.58	14.06	29.41	2.42
OVERALL	DSH24145	3.39	1.30	11.29	5.46	5.97	1.66	14.75	29.07	2.08
OVERALL	DSH24144	1.33	1.49	6.06	6.10	4.87	1.58	14.75	28.86	2.33
OVERALL	DSH24147	0.00	1.52	15.11	6.41	6.30	1.33	14.32	29.14	2.75
OVERALL	DSH24143	1.69	1.55	14.93	10.77	6.10	1.50	13.61	28.16	2.50
OVERALL	DSH24150	1.50	1.29	4.25	7.79	6.43	1.67	14.82	27.40	2.42
OVERALL	ZS244	2.86	1.23	15.81	10.43	5.10	2.01	14.72	28.80	2.25
OVERALL	DSH24141	2.22	1.51	7.44	7.63	5.30	1.42	14.03	25.85	2.42
OVERALL	DSH24134	0.00	1.42	5.85	5.97	5.30	1.75	15.30	22.09	2.33
OVERALL	DSH24132	0.00	1.47	14.43	11.25	5.10	1.59	14.39	27.00	2.33
OVERALL	DSH24146	4.17	1.33	6.34	6.71	5.20	1.49	15.10	29.36	2.42
OVERALL	DSH24142	0.00	1.29	18.14	15.72	5.67	1.58	14.83	24.20	2.17
OVERALL	DSH24138	0.00	1.44	19.35	12.05	4.67	1.41	14.89	23.94	2.17
OVERALL	ZS242	3.37	1.55	15.38	7.25	6.67	1.24	14.17	21.76	2.33
OVERALL	DSH24149	1.71	1.32	15.81	11.62	6.33	1.50	13.62	28.25	2.58
OVERALL	DSH24131	0.00	1.59	10.26	9.28	4.20	1.67	14.59	13.77	2.67
OVERALL	DSH24130	6.63	1.70	17.05	16.27	5.97	2.08	14.64	10.89	2.58
OVERALL	Heritability	0.04	0.81	0.39	0.12	0.42	0.61	0.75	0.87	0.17
OVERALL	Genotype Variance	0.11	0.02	11.67	1.57	0.18	0.04	0.21	18.91	0.01
OVERALL	GenxLoc Variance	1.60	0.00	30.94	14.95	.	0.04	0.16	5.48	0.06
OVERALL	Residual Variance	12.27	0.03	70.12	57.16	0.74	0.19	0.35	8.51	0.22
OVERALL	Grand Mean	1.56	1.44	12.12	8.72	5.46	1.67	14.61	25.44	2.36
OVERALL	LSD	0.96	0.16	7.64	3.35	0.92	0.36	0.65	4.48	0.21
OVERALL	CV	223.92	12.08	69.10	86.69	15.71	26.11	4.03	11.47	19.87
OVERALL	n Replicates	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00
OVERALL	n Environments	2.00	3.00	3.00	3.00	1.00	4.00	4.00	3.00	4.00
OVERALL	Genotype significance	0.92	0.00	0.16	0.72	0.11	0.00	0.00	0.00	0.57
OVERALL	GenxEnv significance	0.29	0.53	0.00	0.01	.	0.01	0.00	0.00	0.00
OVERALL	GenxEnv significance	0.29	0.53	0.00	0.01	.	0.01	0.00	0.00	0.00

Appendix 18: Genotype mean performance under low N, Grain yield, field weight, Anthesis Date Anthesis silking interval, Plant height Ear height, Ear position, Root lodging.

Environment	Genotype	GYG	GYF	AD	ASI	PH	EH	EPO	RL
OVERALL	DSH24147	4.29	3.76	67.31	-0.04	187.33	88.29	0.50	6.68
OVERALL	DSH24132	3.79	3.38	68.12	0.88	168.67	86.93	0.51	2.17
OVERALL	ZS244	3.59	3.20	68.33	1.58	187.00	88.09	0.47	1.45
OVERALL	DSH24148	3.37	3.08	68.02	0.89	169.00	84.33	0.50	4.48
OVERALL	DSH24134	3.26	2.81	67.35	0.65	172.33	80.03	0.48	6.87
OVERALL	DSH24140	3.22	2.97	67.56	0.42	173.67	88.91	0.50	4.80
OVERALL	CZH1815A	3.11	2.67	69.46	0.38	162.33	85.43	0.52	2.22
OVERALL	DSH24136	3.07	3.00	67.81	0.58	175.00	82.38	0.49	3.26
OVERALL	DSH24145	3.02	2.80	68.97	0.90	167.33	78.96	0.48	4.87
OVERALL	DSH24130	3.01	2.52	68.75	0.28	170.33	84.33	0.49	4.06
OVERALL	DSH24142	2.83	2.70	69.02	1.11	174.00	91.46	0.51	2.93
OVERALL	DSH24150	2.80	2.43	66.35	0.96	167.67	83.42	0.48	5.88
OVERALL	DSH24131	2.72	2.22	66.84	0.52	161.67	82.80	0.50	3.80
OVERALL	DSH24135	2.72	2.63	68.60	0.98	163.67	83.72	0.51	6.63
OVERALL	DSH24137	2.67	2.65	66.97	0.98	155.67	82.32	0.50	3.43
OVERALL	DSH24139	2.66	2.53	69.71	0.27	171.33	81.31	0.48	2.65
OVERALL	DSH24133	2.64	2.54	67.80	0.96	176.33	88.14	0.50	0.50
OVERALL	DSH24149	2.56	2.31	67.91	1.63	184.33	83.72	0.51	1.96
OVERALL	ZS500	2.48	2.32	69.44	1.19	175.33	90.74	0.53	13.41
OVERALL	DSH24141	2.42	2.42	69.00	0.31	155.00	82.96	0.51	4.18
OVERALL	DSH24146	2.28	2.25	67.75	0.81	165.00	82.79	0.50	5.02
OVERALL	DSH24138	2.09	2.40	68.23	1.24	156.33	87.50	0.52	2.10
OVERALL	DSH24144	2.04	1.88	68.77	1.10	175.33	84.30	0.51	6.60
OVERALL	DSH24143	1.77	1.67	68.17	0.31	165.33	79.97	0.49	7.94
OVERALL	ZS242	1.72	1.69	70.75	0.77	145.67	82.26	0.50	7.38
OVERALL	Heritability	0.34	0.40	0.00	0.00	0.13	0.00	0.00	0.29
OVERALL	Genotype Variance	0.12	0.12	0.00	0.00	12.37	0.00	0.00	2.76
OVERALL	GenxLoc Variance	0.09	0.01	0.98	0.10		2.91	0.00	0.00
OVERALL	Residual Variance	1.16	1.04	6.09	1.41	259.11	94.37	0.00	41.10
OVERALL	Grand Mean	2.81	2.59	68.28	0.79	169.03	84.60	0.50	4.61
OVERALL	LSD	0.84	0.71	0.00	0.00	9.43	0.00	0.00	3.85
OVERALL	CV	38.40	39.35	3.62	151.25	9.52	11.48	8.22	139.07
OVERALL	n Replicates	3	3	3	3	3	3	3	3
OVERALL	n Environments	2	2	2	2	2	2	2	2
OVERALL	Genotype significance	0.33	0.17	1.00	1.00	0.70	1.00	1.00	0.27
OVERALL	GenxEnv significance	0.54	0.94	0.13	0.19	.	0.55	0.45	1.00

Appendix 19: Genotype mean performance under low N, Stem lodging, Ears per plant, Husk cover, Ear rots, Senescence, Texture, Moisture content, Number of plants, Ear aspect.

Environment	Genotype	SL	EPP	HC	ER	SEN	TEX	MOI	NP	EA
OVERALL	DSH24147	0.00	0.88	3.83	4.89	4.57	1.00	16.67	17.05	1.75
OVERALL	DSH24132	7.94	0.92	6.52	19.64	3.97	1.33	14.77	19.97	2.46
OVERALL	ZS244	10.42	1.02	12.13	11.63	3.64	1.33	15.53	16.29	1.63
OVERALL	DSH24148	1.52	1.01	27.86	14.32	3.60	1.33	14.47	19.01	2.06
OVERALL	DSH24134	0.00	0.85	23.71	8.55	3.90	2.00	15.33	17.04	2.99
OVERALL	DSH24140	1.52	0.93	11.85	1.68	4.27	1.33	15.53	18.74	2.10
OVERALL	CZH1815A	3.53	0.81	6.97	10.81	3.80	1.33	14.33	19.32	2.14
OVERALL	DSH24136	0.00	0.88	13.54	4.31	3.90	1.67	14.27	15.26	2.51
OVERALL	DSH24145	3.92	0.84	13.35	18.40	3.90	2.00	14.23	18.62	2.99
OVERALL	DSH24130	4.17	0.71	12.27	9.55	4.32	1.67	16.20	16.27	2.01
OVERALL	DSH24142	2.08	0.90	13.70	14.67	4.42	1.33	15.10	17.34	2.40
OVERALL	DSH24150	0.00	0.74	8.08	11.35	4.47	1.33	15.03	18.97	2.04
OVERALL	DSH24131	3.70	0.92	10.49	7.28	3.19	1.00	15.10	16.02	1.89
OVERALL	DSH24135	2.08	0.79	12.21	11.98	3.90	1.00	15.20	14.97	2.43
OVERALL	DSH24137	0.00	0.90	3.78	11.46	3.35	1.33	14.63	17.40	2.40
OVERALL	DSH24139	0.00	0.88	7.31	9.86	4.13	1.33	14.40	16.69	2.40
OVERALL	DSH24133	0.00	0.78	12.98	26.25	3.96	1.67	14.27	18.33	3.16
OVERALL	DSH24149	3.03	0.85	10.60	5.16	4.25	1.67	14.93	15.72	1.95
OVERALL	ZS500	0.00	0.89	6.31	17.90	3.72	1.33	15.20	16.64	1.89
OVERALL	DSH24141	0.00	0.80	7.45	25.31	3.98	1.33	14.87	16.72	2.95
OVERALL	DSH24146	0.00	0.82	18.30	4.35	3.69	1.67	13.77	18.32	2.31
OVERALL	DSH24138	0.00	0.96	14.08	19.07	3.83	1.00	15.27	14.68	1.67
OVERALL	DSH24144	5.46	0.78	22.55	14.76	3.68	1.67	14.30	17.29	2.74
OVERALL	DSH24143	0.00	0.77	22.29	20.78	4.47	1.67	13.77	17.62	2.30
OVERALL	ZS242	0.00	0.72	10.92	37.17	4.83	1.33	13.87	20.04	2.81
OVERALL	Heritability	0.00	0.00	0.00	0.00	0.24	0.00	0.00	0.00	0.32
OVERALL	Genotype									
OVERALL	Variance	0.00	0.00	0.00	0.07	0.04	0.00	0.00	0.00	0.06
OVERALL	GenxLoc Variance	.	.	.	.	0.08	.	.	.	.
OVERALL	Residual Variance	28.83	0.03	115.91	194.61	0.44	0.24	1.57	10.51	0.37
OVERALL	Grand Mean	1.97	0.85	12.52	13.65	3.99	1.43	14.84	17.37	2.32
OVERALL	LSD	0.00	0.00	0.00	0.74	0.49	0.00	0.00	0.00	0.58
OVERALL	CV	271.93	19.41	85.97	102.23	16.54	34.34	8.45	18.66	26.05
OVERALL	n Replicates	3	3	3	3	3	3	3	3	3
OVERALL	n Environments	2	2	2	2	2	2	2	2	2
OVERALL	Genotype									
OVERALL	significance	1.00	1.00	1.00	1.00	0.50	1.00	1.00	1.00	0.29
OVERALL	GenxEnv									
OVERALL	significance	.	.	.	.	0.15	.	.	.	.

Appendix 20: Genotype mean performance disease inoculated area, Grain yield, field weight, Anthesis Date, Anthesis silking interval, Plant height Ear height, Ear position, Root lodging, Stem lodging, Ears per plant, Husk cover.

Genotype	GYG	GYF	AD	ASI	PH	EH	EPO	RL	SL	EPP	HC
CZH1815A	3.96	3.94	70.99	1.00	205.83	97.97	0.47	-0.20	4.99	1.52	35.03
DSH24130	2.38	2.29	71.51	1.33	214.14	106.50	0.50	3.08	13.26	1.44	29.67
DSH24131	3.58	3.47	67.14	0.33	210.30	90.70	0.43	4.09	0.00	1.58	9.71
DSH24132	4.09	4.08	70.50	-0.33	220.73	107.92	0.49	1.97	0.00	1.33	25.48
DSH24133	4.03	3.88	69.04	0.33	214.63	104.36	0.48	2.37	0.00	1.33	6.25
DSH24134	3.89	3.77	69.45	0.00	212.98	100.99	0.47	2.47	0.00	1.23	7.68
DSH24135	4.24	4.07	71.93	-0.33	209.23	103.34	0.49	-0.09	7.02	1.28	12.19
DSH24136	3.93	3.82	72.58	0.67	212.29	98.27	0.46	3.36	3.63	1.17	17.31
DSH24137	4.86	4.61	68.53	-0.67	215.81	110.84	0.51	-0.07	0.00	1.30	20.44
DSH24138	3.40	3.44	73.06	1.00	206.58	98.81	0.48	1.86	0.00	1.41	35.83
DSH24139	4.31	4.19	71.56	0.67	215.53	99.44	0.46	2.16	0.00	1.32	2.38
DSH24140	4.01	3.90	73.47	0.00	207.34	97.19	0.47	0.07	0.00	1.33	26.28
DSH24141	3.48	3.85	68.02	1.00	203.53	88.83	0.44	4.22	4.44	1.31	12.12
DSH24142	4.96	5.06	73.08	0.67	240.14	117.86	0.49	-0.69	0.00	1.35	32.34
DSH24143	4.21	4.15	71.26	0.33	213.65	106.00	0.49	5.44	3.37	1.39	22.39
DSH24144	3.90	3.82	71.51	0.00	208.27	105.19	0.50	-0.38	2.67	1.33	8.67
DSH24145	3.64	3.71	69.90	1.00	208.24	93.55	0.45	13.90	6.77	1.15	19.02
DSH24146	3.44	3.32	70.92	-0.33	200.51	96.45	0.48	1.80	8.33	1.19	5.95
DSH24147	3.15	3.08	69.30	1.67	209.21	95.90	0.46	2.99	0.00	1.28	25.08
DSH24148	4.03	4.43	71.51	0.67	216.30	105.49	0.48	1.75	1.67	1.28	15.71
DSH24149	2.94	3.08	72.26	0.00	213.29	95.99	0.45	7.27	3.41	1.18	17.16
DSH24150	3.38	3.58	70.59	0.67	208.63	100.32	0.48	6.11	1.96	1.29	3.92
ZS242	3.64	3.55	72.48	-0.33	217.72	114.50	0.52	16.95	3.70	1.43	12.96
ZS244	3.93	4.18	72.84	1.00	219.64	108.16	0.49	-0.33	3.33	1.08	27.25
ZS500	3.56	3.74	74.25	-1.00	224.76	108.79	0.49	3.28	3.20	0.94	36.46
Statistic											
Heritability	0.55	0.59	0.69	0.00	0.54	0.46	0.11	0.58	0.30	0.40	0.79
Genotype Variance	0.17	0.18	2.22	0.00	27.66	22.46	0.00	9.58	3.28	0.01	87.71
Residual Variance	0.41	0.37	2.94	2.00	71.39	78.51	0.00	20.77	23.14	0.03	68.51
Grand Mean	3.80	3.80	71.11	0.37	213.17	102.13	0.48	3.34	2.87	1.30	18.69
LSD	0.79	0.77	2.41	0.00	10.66	10.26	0.02	5.75	4.35	0.17	12.21
CV	16.96	15.95	2.41	378.81	3.96	8.68	7.57	136.62	167.60	12.55	44.28
n Replicates	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00
Genotype significance	0.02	0.01	0.00	1.00	0.05	0.09	0.76	0.01	0.31	0.18	0.00

Appendix 21: Genotype mean performance under disease inoculated environment, Ear rots, Senescence, Texture, Moisture content, Number of plants, Ear aspect GLS and ET assessments.

Genotype	ER	TEX	MOI	NP	EA	GLS1	GLS2	GLS3	ET1	ET2	ET3
CZH1815A	12.04	2.91	12.07	18.79	3.33	1.64	2.00	4.33	1.20	1.72	2.03

DSH24130	27.66	2.64	12.63	8.38	3.33	0.98	1.00	2.00	1.93	1.98	1.67
DSH24131	9.78	1.96	12.53	11.76	3.67	1.65	2.00	2.33	2.09	2.25	2.28
DSH24132	11.47	2.39	12.60	20.34	3.00	1.35	2.00	3.00	2.09	2.34	2.68
DSH24133	7.23	2.01	13.77	16.83	2.67	1.35	2.00	3.33	2.40	2.38	2.37
DSH24134	5.83	2.82	13.93	15.36	3.00	1.34	1.67	2.00	2.30	2.64	2.70
DSH24135	3.04	2.60	13.30	16.62	2.33	1.01	2.00	2.00	2.79	2.66	2.97
DSH24136	11.92	2.46	12.87	19.26	2.67	1.31	2.00	3.67	1.63	2.00	1.99
DSH24137	7.13	1.89	12.77	18.79	2.67	1.63	2.00	3.00	3.07	3.05	3.02
DSH24138	19.86	2.28	12.43	15.62	3.00	1.68	2.33	4.33	2.25	1.66	1.99
DSH24139	7.69	2.52	13.57	16.74	3.00	2.00	2.00	3.33	2.46	2.31	2.97
DSH24140	9.79	2.65	12.57	18.28	3.00	1.03	1.33	1.67	1.02	0.99	2.01
DSH24141	5.04	2.28	12.37	16.69	3.00	1.68	2.00	3.00	2.22	2.36	2.71
DSH24142	4.17	2.81	13.27	17.75	2.33	1.01	1.67	2.00	1.46	2.24	2.30
DSH24143	13.59	2.00	12.50	19.40	3.00	2.00	2.00	2.33	1.31	1.27	1.92
DSH24144	8.36	1.83	13.50	19.37	2.67	1.32	2.00	4.33	2.19	1.71	2.01
DSH24145	11.89	2.30	13.17	19.62	3.00	1.64	2.00	4.33	1.70	1.72	2.00
DSH24146	9.46	2.31	13.10	21.03	3.00	1.36	2.33	4.33	1.41	1.71	2.04
DSH24147	10.23	2.30	12.57	18.61	3.33	1.69	2.00	3.67	1.42	1.62	2.62
DSH24148	10.48	3.17	13.33	17.65	3.00	1.67	2.00	3.33	2.36	2.01	2.35
DSH24149	18.26	1.94	11.77	18.23	3.67	2.00	2.33	5.33	1.16	1.69	1.66
DSH24150	11.02	2.28	12.50	18.56	3.00	1.33	2.00	4.33	1.83	2.03	1.99
ZS242	9.01	1.47	12.53	16.04	3.33	2.00	3.00	3.67	0.89	1.32	1.66
ZS244	16.65	2.50	12.90	20.98	3.33	1.00	1.67	3.00	1.70	1.68	2.02
ZS500	29.34	3.02	12.80	20.31	3.33	1.32	1.67	2.67	1.78	2.01	2.37
Statistic											
Heritability	0.73	0.36	0.66	0.72	0.36	0.42	0.74	0.67	0.57	0.43	0.31
Genotype Variance	30.64	0.05	0.18	5.22	0.04	0.04	0.10	0.64	0.15	0.09	0.05
Residual Variance	33.87	0.29	0.28	6.22	0.23	0.18	0.10	0.95	0.34	0.37	0.35
Grand Mean	11.64	2.37	12.85	17.64	3.03	1.48	1.96	3.25	1.87	1.97	2.25
LSD	8.24	0.54	0.71	3.61	0.48	0.47	0.46	1.32	0.75	0.67	0.54
CV	50.01	22.75	4.11	14.14	15.81	29.00	16.49	29.99	31.20	30.99	26.09
n Replicates	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00	3.00
Genotype significance	0.00	0.24	0.00	0.00	0.19	0.14	0.00	0.00	0.03	0.11	0.30

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