COMBINING ABILITY AND HETEROTIC GROUPING OF SELECTED YELLOW MAIZE (*Zea mays* L.) INBRED LINES FOR RESISTANCE TO MAIZE STREAK VIRUS DISEASE

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DEPARTMENT OF CROP SCIENCE

UNIVERSITY OF GHANA

LEGON

JANUARY, 2023

DECLARATION

I hereby declare that save the works of other researchers which have been duly cited, this work is the result of my own and original research and has not been submitted anywhere in Ghana or in the world for the award of any degree.

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DATE: 20/09/2023

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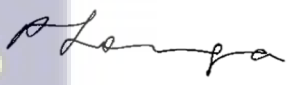
DATE: 20/09/2023



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ABSTRACT

Maize streak virus disease (MSVD) is a major constraint to maize production in sub-Saharan Africa. Developing nutritious and high-yielding yellow maize hybrids to complement white maize is an important step in achieving food and nutrition security in the face of MSVD for sustainable food systems in Ghana. The objectives of this study were to (i) determine the combining ability effects of yellow maize inbred lines for grain yield and other yield-related components, (ii) classify the inbred lines into heterotic groups, and (iii) assess the performance of the resultant single cross hybrids and inbred lines across maize streak infested environments. Eight yellow maize inbred lines were used to develop 28 F1 hybrids in a half diallel mating design. The hybrids, plus four standard checks were evaluated using a 8 × 4 alpha lattice design with two replications in the field. The inbred lines were evaluated adjacent to the hybrids using a randomized complete block design whilst in the greenhouse, evaluation was done using a completely randomized design with two replications. Both hybrids and inbred lines were screened under artificial MSV inoculation, natural MSV inoculation, and controlled environments. General combining ability (GCA) effects were not significant for most traits including grain yield whereas specific combining ability effects were significant for most traits. This suggested that the inheritance of these traits was conditioned by non-additive gene action. Inbred lines were grouped into two distinct heterotic groups based on significant SCA values. WYML 6 × WYML 8, 9450 × WYML 10, PIONEER, and WYML 12 × WYML 9 were the best-performing hybrids for grain yield across environments, indicating tolerance of resistance to MSV. However, grain yield in the naturally-infested environment was lower than in the artificially-infested environment. This suggested that there could be mixed infections or that the strain of MSV present in the natural environment could differ from that used for artificial inoculation. The area under the disease progress curve showed that MSV infested less than 50% of all fields in the study.

Keywords: *Zea mays*, combining ability, heterosis, heterotic groupings, maize streak virus.

DEDICATION

I dedicate this work first to my late father E.T. Narh-Madey who sparked a yearning for knowledge in me, and with whom I studied through many cold nights under the illumination of kerosene-fueled lamps. He taught me that the value of a good book is beyond gold, I miss your guidance but your legacy lives on. To my family, friends, colleagues, mentors, and all who made this journey interesting with lots of lessons. To my mother whose love knows no boundaries.

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LIST OF ABBREVIATIONS

FAOSTAT	Food and Agriculture Organization Corporate Statistical Database
SRID-MoFA	Statistics and Information Directorate of the Ministry of Food and Agriculture
USDA	United States Department of Agriculture
DOC's	Day Old Chicks
FAO	Food and Agriculture Organization
MSV	Maize Streak Virus
MSVD	Maize Streak Virus Disease
NCLB	Northern Corn Leaf Blight
GLS	Gray Leaf Spot
MSV- A	Maize Streak Virus Subtype A
MSV-B	Maize Streak Virus Subtype B
MSV-D	Maize Streak Virus Subtype C
MSV-E	Maize Streak Virus Subtype C
MSV-Nm	Maize Streak Virus Nigerian Mild Isolate
MSV-Ns	Maize Streak Virus Nigerian Severe Isolate
IITA	International Institute of Tropical Agriculture

OPV's	Open-Pollinated Varieties
GCA	General Combining Ability
SCA	Specific Combining Ability
HSGCA	Heterotic Group's Specific and General Combining Ability
HGCAMT	Heterotic General Combining Ability of Multiple Traits
WACCI	West Africa Center for Crop Improvement
RSA	Root system Architecture
SAM	Shoot Apical Meristem
HU	Heat Units
GDU	Growing Degree Units
C4 plants	Carbon Fixation Pathway
RMS	Radial Microtubule System
COVID-19	Coronavirus Disease of 2019
RS	Resistant Starch
WCA	West and Central Africa
GMO	Genetically Modified Organisms
CSIR-CRI	Center for Scientific and Industrial Research – Crop Research Institute
SSA	Sub-Saharan Africa

ECB	European Corn Borer
Bt	*Bacillus thuringiensis*
IRAC	Insecticide Resistance Action Committee
DDT	Dichloro-diphenyl-trichloroethane
HPR	Host Plant Resistance
DMIBOA	2,4-dihydroxy-7-methoxy-1,4-benzoxazin-3-one
MBOA	6-methoxybenzoxalinone
PIs	Proteinase Inhibitors
BPH	Brown Planthopper
NLRs	Nucleotide Binding/Leucine Rich Repeats
TF	Transcription Factors
QTL	Quantitative Trait Loci
QDR	Quantitative Disease Resistance
PAMPs	Pathogen Associated Molecular Patterns
MAMPs	Microbe Associated Molecular Patterns
PRRs	Pattern Recognition on Receptors
PTI	PAMP-Triggered Immunity
ETI	Effector-Triggered Immunity

TZY	Tropical Zea Yellow
CIMMYT	International Maize and Wheat Improvement Center
E-QTLs	Epistatic QTLs
GEI	Genotype by Environment Interaction
DNA	Deooxyribonucleic Acid
IPC	Interaction Principal Component Analysis
EP	Ear Photometry
PVP	Plant Variety Protection
GGE	Genotype Main Effects plus Genotype by Environment Interaction
ASL	Above Sea Level
RCBD	Randomized Complete Block Design
CRD	Completely Randomized Design
CSIR-SRI	Center for Scientific and Industrial Research – Soil Research Institute
WAP	Weeks after Planting

CHAPTER ONE

INTRODUCTION

Maize (*Zea mays* L.) is a staple food ranked as the third most important cereal after rice (*Oryza sativa*) and wheat (*Triticum aestivum* L*)* in the world (Liu *et al.,* 2020; McCann & McCann, 2009). Maize has many uses; it is used in the biofuel and bioenergy industries, as a model for research, and directly serves as food for humans and as feed for animals (Lui *et al.,* 2020). It provides vitamins, minerals, proteins, and carbohydrates found in maize products like corn syrup and corn starch (Bennetzen & Hake, 2009). Global maize production has increased at an annual average rate of 3.41% from 1970 to 2019 (FAOSTAT, 2022). However, in West Africa, maize production has been declining over the years compared to Northern and Southern Africa. In Ghana, although maize accounts for over 50% of cereal production and has reportedly replaced pearl millet and sorghum as traditional staple crops in Northern Ghana, average yields are reported to be 1700 kg/ha against an achievable 6000 kg/ha (MoFA, 2012). Abiotic and biotic stresses have been cited for the consistent reduction in yield. Abiotic stresses such as high and low soil temperatures, drought, salinity, and intense waterlogging are the major environmental effects that adversely affect yield. Biotic stresses such as weed competition, pests, and diseases have reduced the yield of maize (Kaul *et al.,* 2019).

Yellow maize is preferred for feed production in the poultry industry; it provides a rich source of α-carotene, β-carotene, and β-cryptoxanthin responsible for yellow coloration in egg yolk, poultry skin or fat when added at 30% upwards in the diet (Díaz-Gómez *et al.,* 2017). Whereas low-cost and high-quality yellow maize is available for poultry feed production in India, Brazil, and the USA, Ghana is on the opposite trajectory (Sumberg & Okali, 2013; FAO, 2014; Hellin *et al.,* 2015).

The concepts of general combining ability (GCA) and specific combining abilities (SCA) have key influences on population development and inbred line evaluation for crop breeding. Combining ability has been defined as the use of a specific mating design to estimate the value of genotypes based on the performance of their offspring or the mean performance of genotypes in a series of hybrid combinations (Sprague & Tatum, 1942; Fasahat *et al.,* 2016). GCA is due to the additive genetic effect of the mean performance of combinations of a hybrid relative to a specific mating design (Nduwumuremyi *et al.,* 2013; Acquaah, 2012; Awata *et al.,* 2022). SCA is due to non-additive gene action and reflects the better or worse performance of combinations of crosses compared to the average performance of the lines involved (Acquaah, 2012; Falconer & Mackey, 1983). High GCA values are indicative of the flow of desirable additive genes from parents to offspring as well as indicate high heritability, lower environmental effects, large adaptability, and high response to selection (Fasahat *et al.,* 2016; Awata *et al.,* 2022). GCA/SCA ratios determine the gene action involved in regulating a trait: a relatively lower ratio (<1) indicates that genes are under the control of non-additive (dominance or epistasis effects) whereas relatively larger ratios (closer to 1) are indicative of the preponderance of additive genetic effects (Acquaah, 2012; Falconer & Mackey, 1983). Combining abilities have been used in many studies of maize (Elmyhun *et al.,* 2020; Obeng-Bio *et al.,* 2019; Makumbi *et al.,* 2011), rice (Qu *et al.,* 2012), sorghum (Kumar & Jhariya, 2013), among others. GCA is applied in the selection of parental lines based on the performance of the progeny usually in the F_1 generation. Low GCA indicates the parental mean does not vary largely from the general population mean. In contrast, a high GCA value reflects parental lines as superior to the population mean, due to the high potency of desirable gene flow from parents to offspring thus lower environmental effects (Fasahat *et al.,* 2016).

A heterotic group is a collection of germplasm that exhibits a lower degree of heterosis when crossed to a member of its group as opposed to when crossed from members of an external group (Lee, 1995). Several methods have been used in the heterotic grouping of inbred lines. These include the conventional method using SCA effects of hybrids. Hybrids with significant positive SCAs are

classified into different groups whereas those with significant negative SCAs are grouped into the same group (Akinwale *et al.,* 2014; Diatta *et al.,* 2022).

Over time, the cultivation of maize had an impact on the dynamics of maize diseases, leading to fluctuations in the significance of maize disease epidemics (Zhu *et al.,* 2021). The prevalence of disease outbreaks in farmers' fields, for example, has a close relationship with the pathogen, ecology, varieties, agronomic practices, and environmental conditions (Savary *et al.,* 2019). Viruses have innumerable negative impacts on the growth, development, and yield of maize (Boddupalli *et al.,* 2020; Wright *et al.,* 2014). Their interaction with maize plants results in serious constraints on production (Varsani *et al.,* 2009). Maize Streak Virus (MSV, genus: *Mastrevirus*, family: *Geminiviridae*), a prominent member of the maize viral diseases family has been cited for yield reduction or loss in maize-producing regions in sub-Saharan Africa (SSA) by many authors (Maphumulo *et al.,* 2021; Garcia-Oliveira *et al.,* 2020; Oppong *et al.,* 2019; Shepherd *et al.,* 2010). Additionally, consistent yield reduction between 6 -10% due to maize streak virus disease (MSVD) infestation has been reported to result in losses between $120 – $420 million (Martin & Shepherd, 2009). MSV infestation was reported to reduce the yield of maize to as high as 71% and up to 100% in susceptible genotypes (Alegbejo *et al.,* 2002; Bosque-Perez *et al.,* 1998). This makes MSV, the causal agent of MSVD the most important maize disease on the African continent (Awata, 2012; Varsani *et al.,* 2009; Bosque-Pérez, 2000), and the third most important worldwide after northern corn leaf blight (NCLB) and grey leaf spot (GLS) (Pingali & Pandey, 2000). MSV, prevalent in Ghanaian maize farms and primarily confined to the African continent is transmitted by leafhoppers (*Cicadulina mbila* Naude) of the genus: *Cicadulina* and family: *Cicadellidae* (Nkurunziza *et al.,* 2019; Oppong *et al.,* 2015; Martin & Shepherd, 2009). Different levels of virulence and inter and intra-molecular diversity exist between the eleven identified MSV strains (MSV-A to MSV-K) (Oppong *et al.,* 2015; Martin & Rybicki, 2002; Isnard *et al.,* 1998). MSV-A isolates are known to produce the most severe symptoms (Martin *et al.,* 2002). Subtypes A_1, A_2, and A_5 were the most pathogenic among all of the five

genetically distinct MSV isolates (Oppong *et al.,* 2015; Martin & Shepherd, 2009). However close the phylogenetic relationship existing between MSV-A and MSV-B, there have not been any reports of MSV-B isolates identified in West Africa (Varsani *et al.,* 2009). Studies in Ghana, have found a predominance of MSV-A_1 isolate and concluded that developing a resistant variety to the isolate may be a solution to the problem, however, its high pathogenicity could as well result in an epidemic (Oppong *et al.,* 2015; Oppong, 2013).

Typical of vector-borne diseases, MSV has a highly unpredictable epidemiology, making its control difficult (Oppong, 2013; Martin & Shepherd, 2009). MSVD may not have any significant influence on productivity in the current year but it may wreak havoc on to yield of maize planted in the same field in subsequent years (Martin & Shepherd, 2009; Efron *et al.,* 1989). The unpredictable nature of the epidemiology of MSV has been explained as a function of ecological factors and multiple environmental interactions (Martin & Shepherd, 2009; Alegbejo *et al.,* 2002). Reynaud *et al.* (2009) made a strong case for the impact of recurrent climatic variables on leafhopper populations and MSD epidemics and asserts that this can be harnessed in prognosticating epidemics. Further, Yang *et al.* (2017) underscored the substance of pathogen and climatic variables' interaction on the severity of disease development and impact on maize. For instance, successive maize cultivation on the same piece of land coupled with drought and uneven rainfall patterns were noted to trigger acute outbreaks of MSD (Dabrowski *et al.,* 1991; Efron *et al.,* 1989). The search for resistance to MSD is key to most African maize breeding programs, regarding it as a key trait in any maize improvement program (Badu-Apraku *et al.,* 2021; Pingali & Pandey, 2000).

The development of MSV-resistant varieties has been marred by the breakdown of resistance in many instances. Some maize varieties known to be resistant suffer resistance breakdown when exposed to potent strains/isolates (Rodier *et al.,* 1995). Resistance breakdown is common with maize varieties in sub-Saharan Africa where MSD is prominent. However, Buddenhagen & Bosque-Perez (1999) reported that resistance breakdown in Nigeria is not a common phenomenon, where resistant varieties

have long been deployed over large areas. Resistance may exhibit reduced symptom severity with lower incidence of the virus in fields whereas highly resistant varieties may show lower levels of virus titer, for example, in IITA open-pollinated varieties (OPV's) and hybrids (Soto *et al.,* 1982; Mbey-yame, 1991). Several studies reported variations in MSV symptom severity caused by MSV strains or isolates. Nigeria-mild (MSV-Nm) and Nigeria-severe (MSV-Ns) strains of MSV were differentiated based on five characteristics such as streak width, streak length, chlorosis severity, latency, and host range (Boulton *et al.,* 1991). Variations in maize streak development were reported in some studies as well as previously resistant germplasm becoming susceptible upon exposure to different MSV strains (Njuguna, 1996; Rodier *et al.,* 1995). Measuring symptom variation in maize streak development could expose the variability of MSV resistance in inbred lines (Mawere *et al.,* 2006). MSV control through the development of resistant lines requires a deeper understanding of the pathogen-host-environment interaction (Gichuru *et al.,* 2011; Revilla *et al.,* 2021).

While combining abilities have been studied, the reactions of the West Africa Center for Crop Improvement (WACCI) newly developed yellow inbred lines to MSV and their combining abilities for grain yield and other agronomic traits have are not known. Furthermore, there is a need to classify these inbred lines into heterotic groups to aid the development of locally adapted yellow hybrid varieties with MSV resistance. This would increase production to meet the demand for yellow maize in Ghana. Therefore, the overall goal of the study was to develop yellow maize hybrids and select the best-performing hybrids that are resistant to MSV.

The specific objectives of this study were to:

i. determine the combining ability of inbred lines for grain yield and other yield-related components

ii. classify inbred lines into heterotic groups, and

iii. assess the performance of single cross hybrids and inbred lines across maize streak-infested environments.

CHAPTER TWO

LITERATURE REVIEW

2.1 Maize Biology and Importance

Maize is a preferred staple food in Africa, occupying roughly 27 million ha, contributing more than 50% of daily calorie requirements, and serving as a food security crop for most people in SSA (Abate *et al.,* 2017; Kamara *et al.,* 2020). Maize is a member of the monocot (Monocot or Poaceae) family together with grasses. The genus includes four species; *Zea luxurians*, *Zea perennis*, *Zea diploperennis,* and *Zea mays*. Commercially, only *Zea mays* is cultivated on a worldwide scale (Acquaah, 2012; Kamara *et al.,* 2020). The monoecious diploid organism (2n = 20) has distinct root formations occurring at the embryonic and postembryonic stages of plant development and culminating in its definite root system architecture (RSA) (Hake, 2009). The uniqueness of maize rootstock is seen in anchorage, water, and nutrient uptake, controlled by an amalgamation of environmental interactions, root-rhizosphere interaction, and inherent genetic programming (Durieux *et al.,* 1994; Watt *et al.,* 2006; Hake, 2009).

A primary root emerging from the basal pole of the embryo together with other seminal roots around the scutella node form the embryonic root system (Hund *et al.,* 2011). The postembryonic root system on the other hand is separated into consecutive shoot nodes where roots emerge from the shoots and roots initiated from the pericycle which form lateral roots (Figure 2.1: a,b) (Muthreich *et al.,* 2010). At the initiation of germination, the distal end of the root, around the area of active cell division and covered by the root cap must penetrate the coleorhiza of freshly developed primary roots; this endogenous root formation is only common to the *Poaceae* family opposed to exogenous root formation in other angiosperms (Feldman, 1994; Hochholdinger, 2009). Seminal roots formed at the

scutella are completed between 22 to 40 days post-pollination but there is the absence of coleorhiza formation due to differentiation of the node tissue at the scutella (Hochholdinger *et al.,* 2004; Hund *et al.,* 2011).

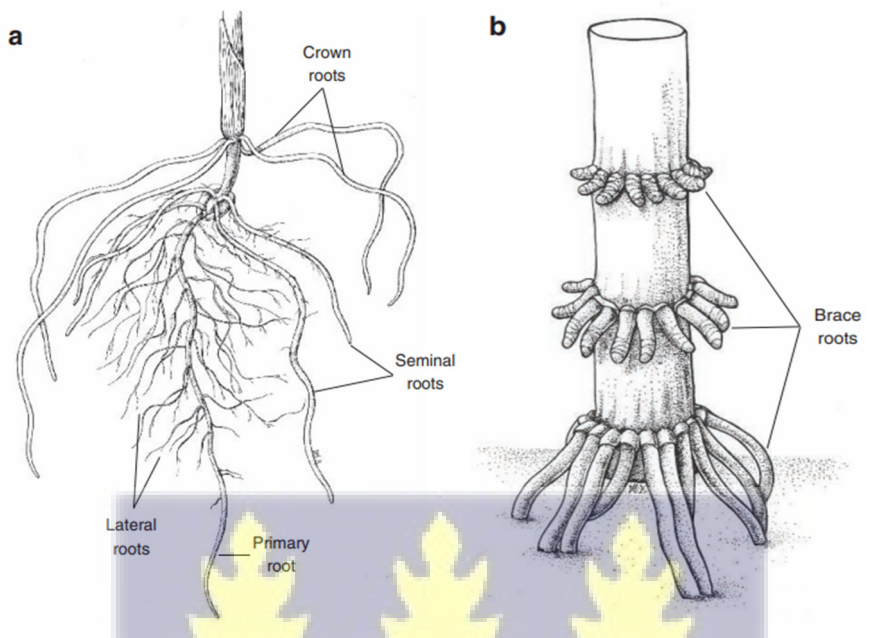


Figure 2.1 **a** Seminal and primary roots formed at the embryonic stage and crown and lateral roots formed at the pre-embryonic stage. **b** Brace roots found on the aboveground of a maize plant (Kynast, 2012).

The genetic conformation of the seed influences the embryonic root system as does the seminal roots; the latter can vary between 0 and 13 per seedling (Kiesselbach, 1999). The functionality of the primary and seminal roots fluctuates for different inbred lines (Kozinka & Luxová, 1971). The postembryonic roots emerging from the shoot take over the anchorage, water, and nutritional requirements of the plant at later developmental stages (Feldman, 1994). Organized in two or three whorls of aboveground (prop or brace roots) and six whorls of belowground (crown roots), a total of 70 roots emerge from the shoot (Kiesselbach, 1999; Foth, 1960). As the crown roots follow a gravitropic vector after initially elongating horizontally and bending, lateral roots form from brace roots typically of the first two whorls that penetrate the soil, holding the plant against lodging (Feldman, 1994; Lynch, 2013). Of lateral roots, nutrient and water uptake is more efficient under a late open metaxylem but with a

characteristic short determination interval and increased response to drying through transpiration (Wang *et al.,* 2002).

The collection of meristematic cells at the shoot and root apices of immature maize embryos is essential for the growth and development of maize. The shoot apical meristem (SAM) is a domed structure positioned just above the most recent leaf primordium and consists of about two thousand cells in their embryonic stage (Johnston *et al.,* 2015). Largely, SAM's initiation is influenced by the conditions of growth and the genetic makeup of the seed (Bommineni *et al.,* 1995; Randolph, 1936). Leaf initiation in maize occurs singly in consecutive stages, forming a distichous phyllotaxy with each leaf emerging from opposite sides of the SAM (Abbe *et al.,* 1951). The leaf initiation process or plastochron takes the position P1, where a neoteric leaf is initiated or P0 where an adjacent leaf will form (Kaplan, 2001). Expansion of SAM post-leaf initiation events causes retraction as cells congregate into primordia (Johnston *et al.,* 2015; Kaplan, 2001) (Figure 2.2: a,b,c).

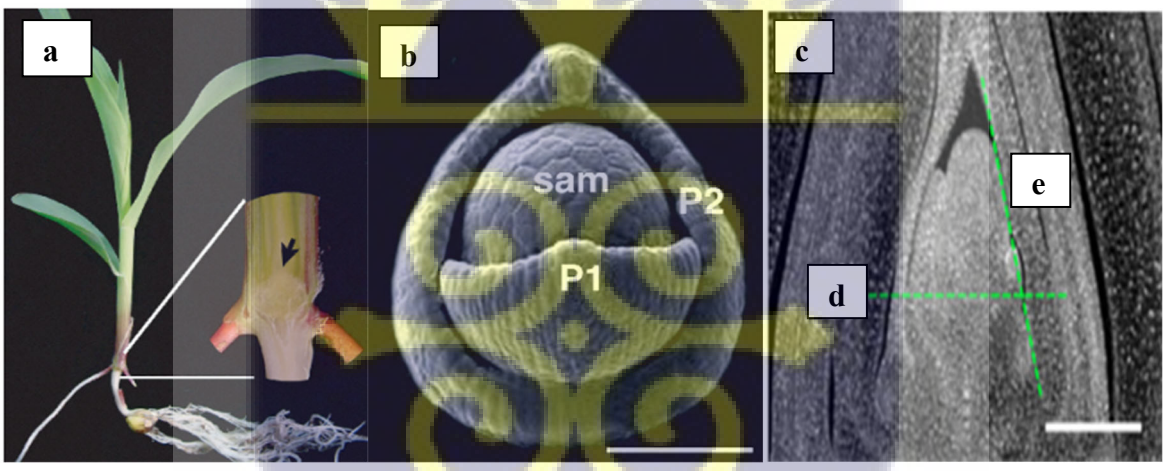


Figure 2.2. a Germinated maize seed at 10 days with about four visible leaves. b Visible SAM after dissection and removal of most of the leaf primordia, showing SAM, P1, and P2. c Longitudinal view of SAM, green dotted lines show succeeding sections plane of optical panels. d Paramarginal view of P2 primordium of SAM apex . e Transverse view of P2 primordium. (Jackson & Hake, 2009; Johnston et al., 2015). Scale bar = 100 µm (a,b), 5 µm (c).

With each leaf initiation, axillary shoot cells form the shoot meristem of the internode facing the midrib of newly initiating leaf (Johnston *et al.,* 2015). The phytomer, a repetitive unit is then formed

from the combination of the axillary meristem, bract, and stem driving plant shoot development (Brutnell & Langdale, 1998).

In the first few weeks, there is little expansion of the maize stem, and the root-shoot junction houses the SAM. The SAM is elevated as the floral internodes expand at the initiation of floral transition, refashioning the SAM into an apical meristem of the inflorescence generating the tassel. Majorly, the shoot meristems remain dormant during the seed development stage except under special conditions (McSteen & Hake, 2001; Hubbard *et al.,* 2002). The genes *barren inflorscence2* and *teonsite branched1* selected from teonsite during maize domestication suppress the axillary branches (McSteen & Hake, 2001). The meristematic similarities that exist between the ear and tassel result from a common development program, however, these complex structures occur as distinct male and female flowers (McSteen & Hake, 2001; Zhang & Yuan, 2014). The ears form from pistillate flowers at the apex of a compressed branch emanating from the axil of one or more leaves and terminate all lateral branches but tillers. In addition, there is the absence of a diverse number of long branches in ears which are traditionally present at the base of tassels (Thompson, 2014).

Subsequently, another abortion occurs at the entire lower end of each ear spikelet immediately after floral organ primordia initiate, forming a monoecious plant with differentiated male and female inflorescences (Smith & Zhao, 2016) (Figure 2.3).

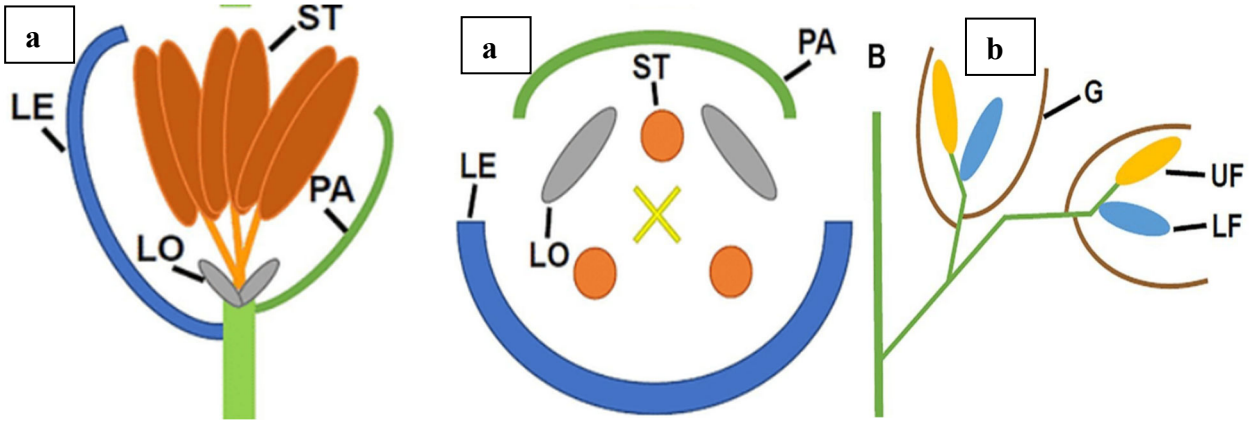


Figure 2.1 **a** Longitudinal view of the upper floret of mature maize. **b** Cross-sectional view of male maize flower. **c** Magnified view of male florets in the tassel showing upper florets (yellow), lower florets (blue), and glumes (brown) (LE, lemma; ST, stamen; LO, lodicule; PA, palea; G, glumes; UF, upper floret; LF, lower floret) (Smith & Zhao, 2016; Bortiri & Hake, 2007).

A key stage in the maize plant's transition from vegetative to reproductive growth is the floral transitioning stage. This stage is noticed when the SAM is reprogrammed which mainly determines when flowering occurs. During floral transitioning, leaf formation ceases, SAM elongates, and tassel primordium forms; ear formation follows a similar process, transforming axillary meristems into leaf primordia (Camus-Kulandaivelu *et al.,* 2006; Hake, 2009). A regulator coding for negative regulation of gibberellic acid signaling located in the polymorphic *dwarf8* (*d8*) locus controlled variation in plant height and flowering time (Thornsberry *et al.,* 2001; Camus-Kulandaivelu *et al.,* 2006). The photoreceptor phytochrome member *phytochromeB* (*phyB*) sub-family *phyB2* is known to repress flowering in long and short-day photoperiods in maize (Zhao *et al.,* 2022). Additionally, *phyB2* has a naturally occurring deletion allele known to regulate flowering time in flint maize. *Indeterminate1* (*id1*) is a homozygous-loss-of-function gene encoding a zinc finger protein localized to the nucleus and regulating transcription of other genes controlling flowering time (Colasanti *et al.,* 2006; Kozaki *et al.,* 2004). Minor effect mutations, *delayed flowering1* (*dlf1*), and *Leafy* (*Lfy*) are also noted for the delay in flowering. The maize leaf is responsible for photosynthetic processes that support the plant from germination through flowering to physiological maturity.

The simplicity of maize leaf arrangements organizes it into three main compartments: the lower sheath, the upper blade, and joined ligule-auricle. The shapes and sizes of leaf cells vary as does their functionality because of their arrangement in files parallel to the leaf shape (Feldman, 1994). Their large sizes, defined by spatial developmental gradients instilled by their growth from SAM, however, make maize leaf cells comparatively easy to study (Kynast, 2012). The maize C4 photosynthetic leaf supports plant biomass and reproductive development such that the blade contains leaf cells and tissues and the lower sheath provides structural support (Hake, 2009). The leaf blade is projected in one and other primordia at an angle optimal for light entrapment by the ligule-auricle junction (Mitkovski & Sylvester, 2003). The cellular structure of the leaf is linear owing to oriented patterns of cell division followed by directional expansion (Kynast, 2012; Mitkovski & Sylvester, 2003). Of the leaf blade, the mesophyll and vascular tissues are enclosed by the abaxial and adaxial epidermal tissues (Kynast, 2012; Hake, 2009).

Epidermal cells are of two major groups: specialized cells including stomatal complexes and three hair types (bicellular hairs, micro hairs, and macro hairs) combining to serve water regulation and protective functions and non-specialized intercostal cells (Hake, 2009). Epidermal groups of cells are distinguished by being boxed in varying levels of cuticular and epicuticular waxing interspersed by stomata complexes for protection and water and gas exchange respectively (Scanlon & Takacs, 2009). As stomata are dispersed over the surfaces of both abaxial and adaxial cells, specialized cells are limited to the adaxial epidermis only (Győri, 2010). The kernel formed from fertilization and fed by the photosynthetic processes of the leaf cells is a single-seeded endosperm-persistent fruit, enclosing a large embryo by the ovary wall (Scanlon & Takacs, 2009). Its histological simplicity and developmental precociousness are represented in only four tissue types in the endosperm: aleurone outer layer, basal endosperm transfer layer (BETL), starchy endosperm and the embryo-surrounding region (ESR) (Győri, 2017; 2010). A shoot meristem, 5-6 small leaf primordia enclosed in the coleoptile, and a root meristem are in the embryo of mature maize seed. As the coleoptile encloses leaf

primordia, so does the coloerhiza enclose the embryonic root (Győri, 2017). Scutellum, a highly modified spade-shaped structure performs digestive functions post-germination of seed. Whereas the coleoptile forms the sheathing cotyledonary base, the scutellum, in differentiating from the embryonic shoot may comprise the upper component of the cotyledon (García-Lara *et al.,* 2019; Scanlon & Takacs, 2009).

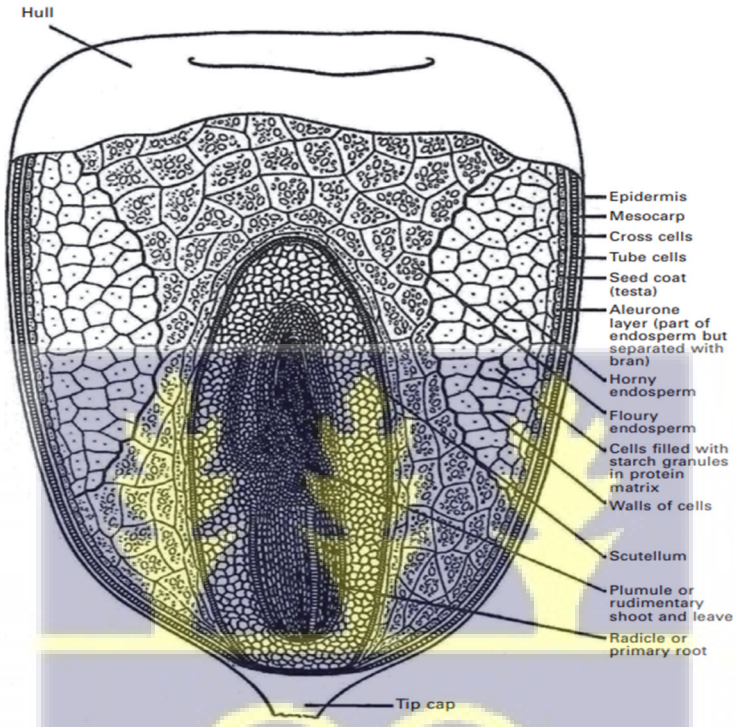


Figure 2.2 Longitudinal view of mature maize kernel (Lasztity, 2017).

Within the first three days of fertilization, several mitotic divisions occur in the triploid nucleus without cytokinesis, forming the syncytium. The plasma membrane surrounds each nucleus to form unique cells. Mitotic divisions cease after 72 hours of fertilization and the radial microtubule system (RMS) elongates from the nuclear membranes of the coenocyte (Lasztity, 2017).

The fusion of daughter and non-daughter nuclei triggered by the absence of mitosis causes free-growing cell walls to accumulate. Alveoli are formed from phragmoplast deposition between RMS and open into a central vacuole. Periclinal cell wall deposition comes with the resumption of mitotic

divisions, moving in a centripetal fashion and beginning from the outer endosperm and terminating toward the kernel until complete cellularization is achieved. This process is followed by tissue differentiation to form the four tissue types of the endosperm. Cellular division and elongation then take over and terminate initially in the central endosperm and later in the kernel periphery (Lopes & Larkins, 1991). Maize has important uses both industrially and at the home. Its importance has been further established by the effects of climate change, the COVID-19 pandemic and in recent times the Ukraine-Russia conflict (Mustafa, 2022; Agyei *et al.,* 2021).

In sub-Saharan Africa, maize is a staple food in most homes and a larger part of the everyday diet has a component of maize or maize products in it. Apart from serving as food for humans, a significant proportion of maize serves as animal feed, for example, the poultry industry depends on maize as a component of feed formulations providing carbohydrates and essential minerals (Győri, 2017). Lipids in maize are of the unsaturated group which is healthy for human consumption, and rich in linoleic and oleic acids. As the most nutritive part of the plant, the kernel contains vitamins B1 (thiamine), B2 (niacin), B3 (riboflavin), B5 (panthothenic acid), B6 (pyridoxine), vitamins C, E, K, potassium, N-ferrulyl and N-p-coumaryl tryptamine (Kumar & Jhariya, 2013).

Naturally present carotenoids and phytochemicals in maize are potential elements for reducing chronic diseases as do phytosterols and phenolic compounds (Lopez-Martinez *et al.,* 2009). B-complex vitamins are good for the skin, proper digestion, heart, hair, and brain and improve joint motility. Immune system and thyroid gland functioning are boosted by B-carotene, selenium, and vitamins A, C, and K. In countries like China, Greece, France, and Spain, the silk is used for the treatment of kidney stones, improving blood pressure, urinary tract infections and ulcers (Kumar & Jhariya, 2013). Vitamin E has antioxidant properties that inhibit atherosclerosis development and promulgation of oxidative stresses (Lemcke-Norojarvi *et al.,* 2001). The alcohol-soluble prolamine is used in the nutraceutical and pharmaceutical industries for the development of nanocomposite antibacterial agents, coat

nanoparticles, package food, provide targeted delivery with controlled release and encapsulate nutrients (Luo *et al.,* 2011; Sanchez-Garcia *et al.,* 2010).

High amylose maize or resistant starch (RS) from maize is beneficial in the diet as it escapes digestion and is capable of altering microbial populations, promoting fecal excretion, increasing fermentation and production of short-chain fatty acids, and lowering cholesterol, therefore, reducing complications related to obesity and cecal cancer (Wang *et al.,* 2002; Murphy *et al.,* 2008). Yellow maize contains a higher proportion of carotenoid pigments. The carotene content of stalklage, maize silage, and yellow maize is 6.5 mg/kg, 17.3 mg/kg, and 22 mg/kg respectively. Provitamin A activity of alpha and beta carotene enhances the antioxidant properties and induces apoptosis of leukemia cells, colon cancer cells, melanoma cancer cells, and gastric cancer cells for the latter (Palozza *et al.,* 2003; Jang *et al.,* 2009). Xanthophylls (lutein and zeaxanthin) and anthocyanins also have very relevant biological functions. The anti-carcinogenic, anti-diabetic, lipid-lowering, and antimicrobial properties of anthocyanins are well documented (Ghosh & Konishi, 2007). It also improves immune system response, reduces the fragility and permeability of capillaries, and inhibits aggregation of blood platelets (Ghosh & Konishi, 2007). Lutein supplementation was noted to reduce the occurrence of palpable tumor, promotes the proliferation of lymphocytes, inhibits damage to cells by anti-oxidants, and inhibits tumor growth in mammals. In addition, lutein prevents the development of cancerous cells and subsequent disease proliferation (Moreno *et al.,* 2007).

2.2 Production and Distribution

In SSA, maize is mainly cultivated on small scales by smallholder farmers in rainfed environments. Maize cultivation in rural West and Central Africa (WCA) was reported to be around 85% and has displaced pearl millet and sorghum in certain areas (Badu-Apraku *et al.,* 2013a; Fakorede *et al.,* 2003). Nigeria remains the highest producer in West Africa (https://www.iita.org/cropsnew/maize/). Maize production constitutes 50-60% of cereal production in Ghana and covers more than a million hectares of arable land (Obour *et al.,* 2022). More than 80% of Ghana's maize production is concentrated in the

forest and savannah agroecological zones though, with the remaining 20% scattered across the other agro-ecologies (Wongnaa *et al.,* 2019; Obour *et al.,* 2022).

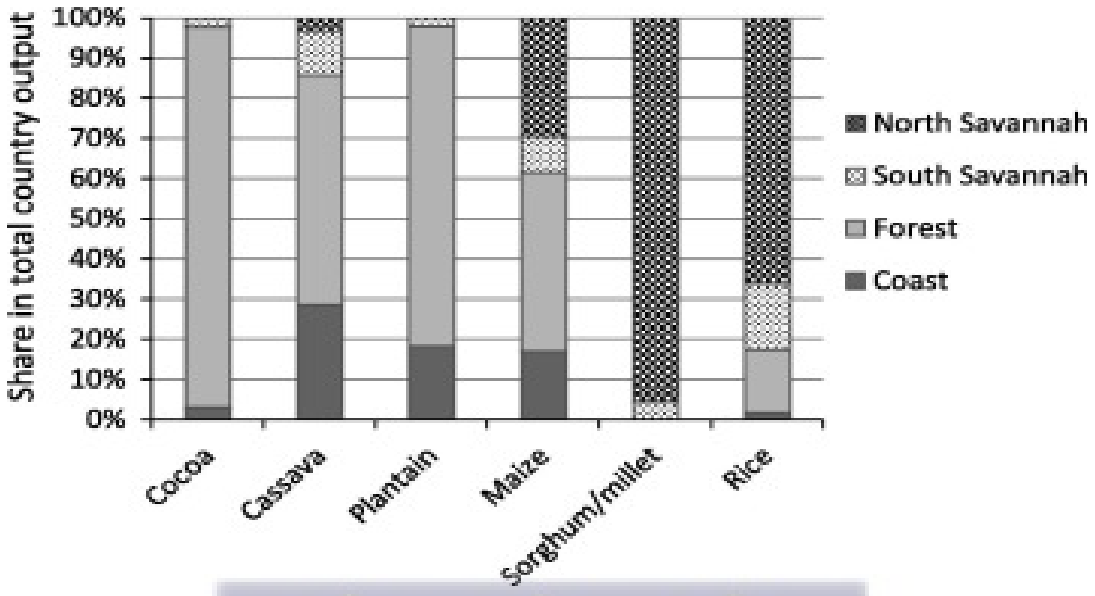


Figure 2. 3 Major crops cultivated in the main agroecological zones of Ghana (Nin-Pratt & McBride, 2014).

Maize varieties come in red, white, yellow, brown, or near-black colors. The choice of cultivation of a particular variety over another is influenced by many factors such as yield, color, maturity period, and purpose (Ifie *et al.,* 2022). White maize, for instance, is 85-95% more consumed in West Africa than yellow maize. Despite national and international interventions to increase the yield of maize from the present 1.7 t/ha in Ghana, not much success has been realized. Drought, poor soil fertility, crop nutrient deficiencies, lack of access to farmer inputs, erratic rainfall, low farmer adaptation of improved cultivars, insect pests, and diseases have been implicated as responsible for the low yield of maize (Obour *et al.,* 2022). The adoption of hybrid maize varieties by farmers has the potential of increasing the yield and commercial value of maize in Ghana.

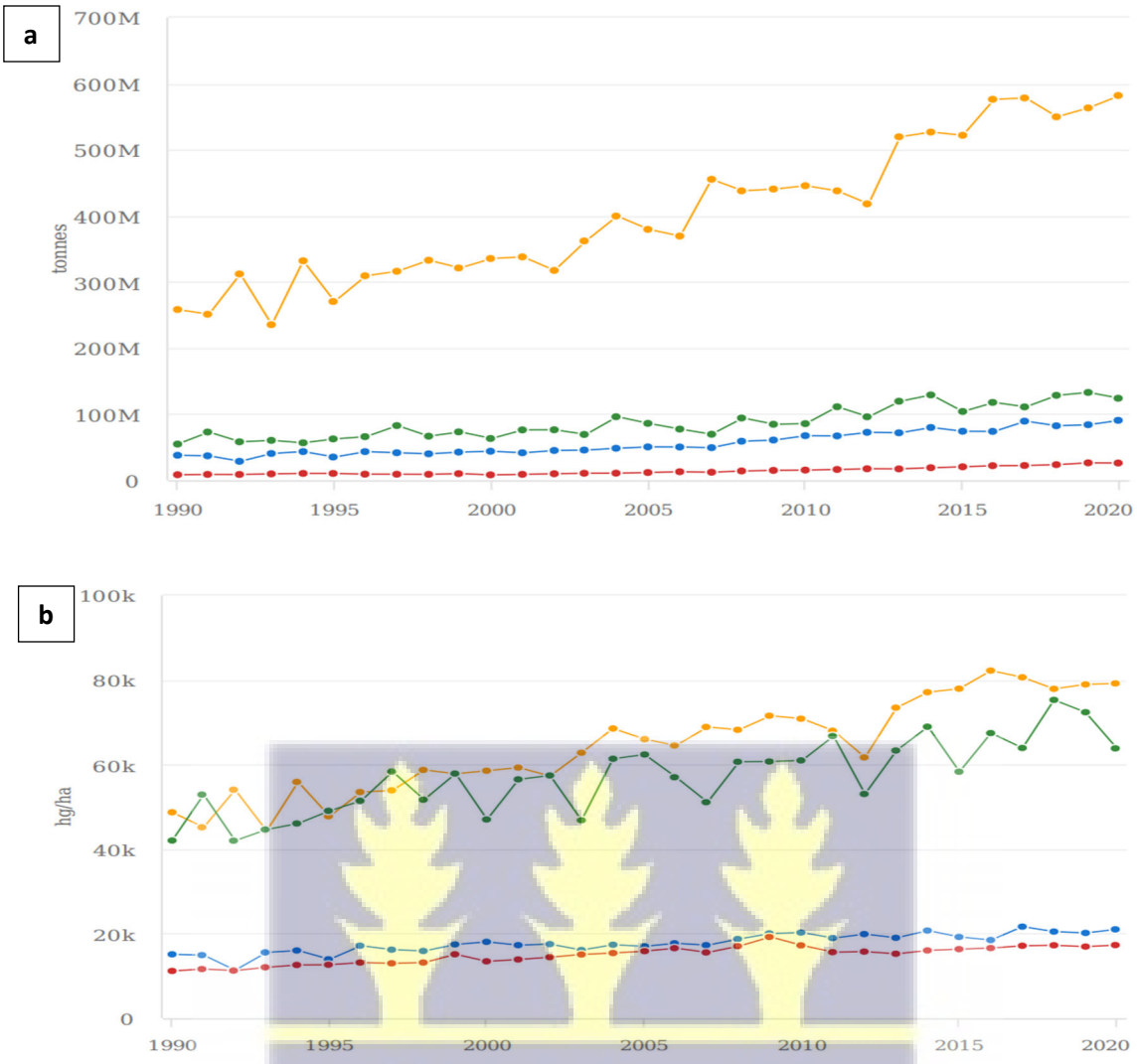


Figure 2.4 **a** Maize production quantity of four regions: Europe [green], Americas [yellow], Africa [blue], and West Africa [red] between 1990 to 2020. **b** Yield of maize in four regions: Europe [green], Americas [yellow], Africa [blue], and West Africa [red] between 1990 to 2020 (FAOSTAT, 2022).

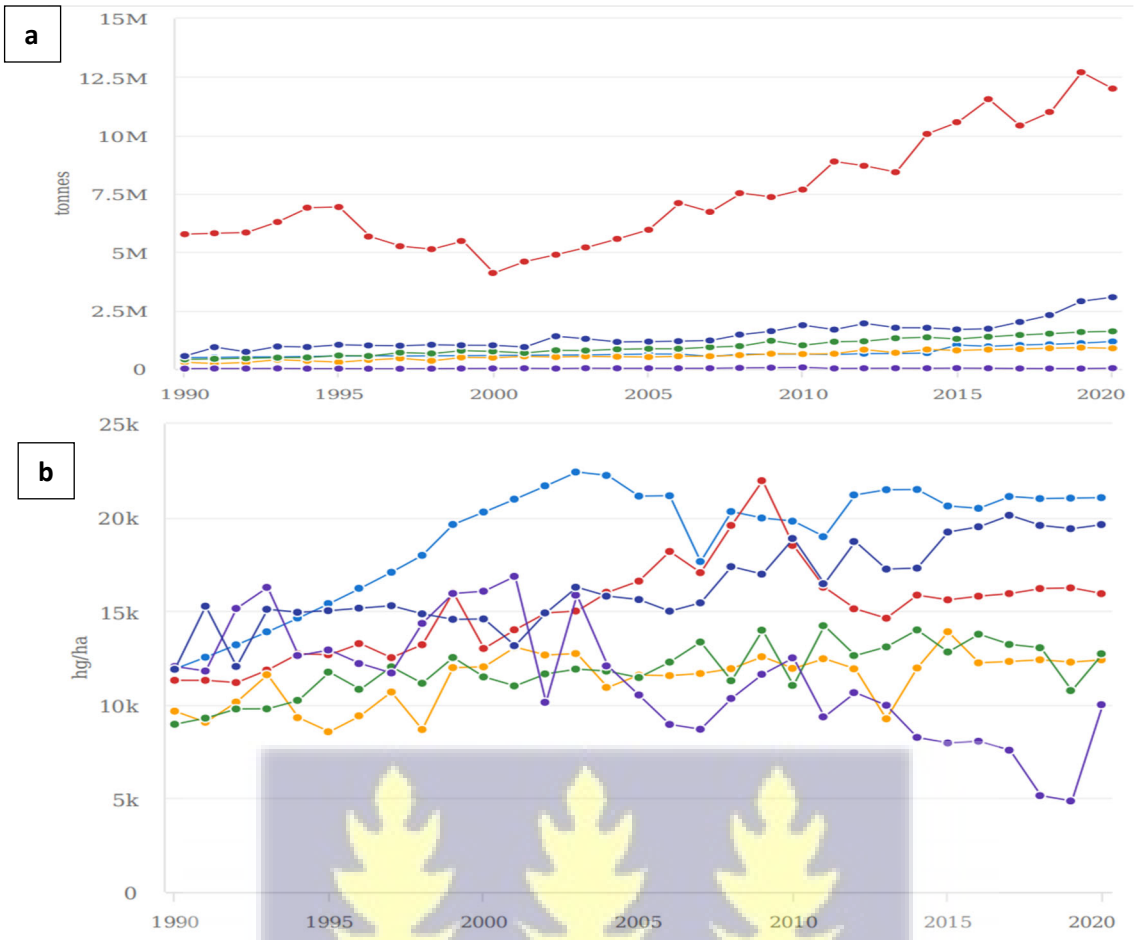


Figure 2.5 **a** Maize production quantity of five West African countries: Cote D'Ivoire [**blue**], Nigeria [**red**], Togo [**yellow**], Benin [**green**], Gambia [**violet**], Ghana [**dark blue**], **b** Yield of maize in four regions: Europe [**green**], Americas [**yellow**], Africa [**blue**], and West Africa [**red**] between 1990 to 2020 (FAOSTAT, 2022).

From Figure 2.7 (a,b) though Nigeria has the highest production in West Africa, its yield is low compared to other countries. Cote D'Ivoire has consistently recorded the highest maize yield in SSA irrespective of its relatively lower production volume whereas Ghana's yield has been increasing gradually over the years. This means there is potential for yield increment and the factors limiting the same must be addressed to push the yield limits forward.

2.3 Maize Breeding in Ghana

Since the introduction of maize breeding some 100 years ago, much has been done concerning breeding for various traits of importance in maize breeding programs (Shull, 1909). The development

of new and superior genotypes is pushing the limits of maize breeding research. The values and impact breeding methods and newly developed lines are having on maize research keep improving as advances in molecular genetics improve (Muntean *et al.,* 2022). This however has not completely taken the place of traditional breeding methodologies, especially in Africa where the low level or lack of improved technologies and funding are major factors limiting maize breeding research (Shiferaw *et al.,* 2011). The green revolution that increased crop yield in Asia failed in its implementation in Africa not only for issues related to inadequate access to fertilizer by farmers alone. Farmer adoption of improved varieties and limited extension services are also major challenges (Donkoh *et al.,* 2011; Ragasa & Chapoto, 2017). Ghana has formulated policies for the adoption of transgene crops in its bid to tackle food insecurity. The Biosafety Act 831, 2011 permits the release, use, importation, and marketing of genetically modified organisms (GMOs). As field trials of GM cowpea are completed, it is hoped that maize breeders will use the technology for increasing yield and other traits of interest (Akinbo *et al.,* 2021). The low rate of farmer adoption of improved varieties and the effects of biotic and abiotic stresses still limit maize yield. Farmers in Ghana cultivate more open-pollinated varieties (OPVs) and landraces than hybrids (Ifie *et al.,* 2022). There are 55 developed and released maize varieties in Ghana. Of the 55 released varieties, 29 are hybrid varieties mostly bred for high yield, quality protein, and resistance to MSV (CSIR-CRI, 2019). Though these hybrids have the potential for improving maize productivity in Ghana for attaining food and nutrition insecurity, farmer adoption and use has been relatively low owing to the high cost of seeds and rejection of certain verities which according to farmers are not tolerant to the local climate (Harou *et al.,* 2017; Ifie *et al.,* 2022). Farmer adoption and use of hybrid maize varieties in Ghana stand at 83% and 22.5% respectively in 2020 (Ifie *et al.,* 2022). Moving forward three things should drive the maize breeding industry in Ghana: demand-led breeding, farmer extension education, use of both conventional and molecular breeding technologies, and access to production utilities by farmers. Research intensification must accompany

these actions steps if high-yielding and environmentally adapted varieties are focus points for maize breeding in Ghana.

2.4 Leafhopper Morphobiology

The mesophyll or phloem tissues of infected maize harbor MSV. The virus is acquired through feeding from the plant sap after which it becomes persistent in the gut of the vector making it capable of infecting multiple maize plants, a contributing factor to building an epidemic in susceptible genotypes (Bosque-Perez, 2000). When the vector feeds from highly chlorotic areas of an infected leaf, the acquisition feeding period may be shorter (Oluwafemi & Jackai, 2013). Different species of *Cicadulina* can be distinguished using the pygophore shape and the size and shape of the aedeagus (Ruppel, 1965). As with organisms of different species, there are variations in the life cycles of *Cicadulina* species. Generally, the life cycle of *C. mbila* is temperature dependent, between 22 to 45 days. Its life cycle is distinguished into three stages of development: the egg, nymph, and adult. After oviposition in leaf tissues, the nymphal stage is completed in 5-8 days in five instars contingent on weather parameters such as rainfall, humidity, and temperature (Webb, 1987). Averagely, females lay 129 eggs and live up to 30 ± 3 days. Both nymphs and adults feed by piercing through the phloem or mesophyll of maize tissues. In infested maize, uninfected *C. mbila* can acquire MSV within 15 seconds of feeding from infested chlorotic regions (Storey, 1938). Lower temperatures stretch the development and population increment whereas higher temperatures promote egg laying and population increment. In most rearing experiments, the ideal temperature is capped between 25- 35 ºC. Graham (1979) found that cold immobilization of *C. mbila* for 30 minutes at temperatures of 3-5 ºC resulted in 10% mortality. High rainfall may cause insect mortality and the washing away of eggs. At the end of the rainy season leafhopper population peaks in suitable environments (Bosque-Perez & Alam, 1992). Interestingly, no relationship was found between leafhopper intensity and incidence and severity of MSV disease in Reunion Island, however, studies in Nigeria found significant relationships between

leafhopper populations, plant age at infection, MSV incidence, and temperature (Alegbejo & Banwo, 2005).

Figure 2. 6 Morphological comparison between *C. mbila* and *C. storeyi*, pictorial view of *Cicadulina mbila* **a.** adult *C.mbila* **b**. pygophore **c.** ventral view of aedeagus **d.** lateral view of the aedeagus.

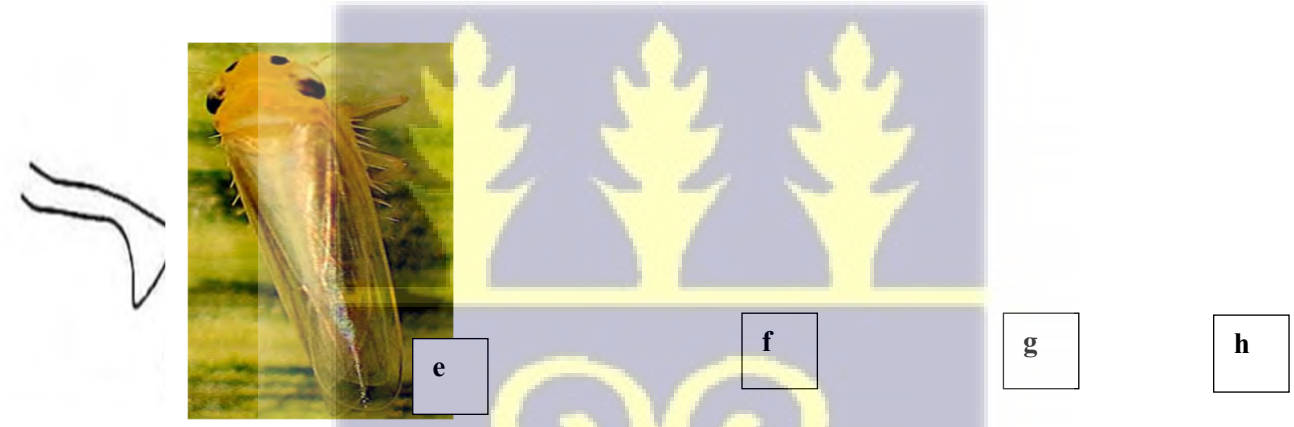


Figure 2. 7 Pictorial view of *Cicadulina storeyi* **e**. adult *C. storeyi* **f**. pygophore **g.** ventral view of aedeagus **h.** lateral view of the aedeagus.

Cicadulina species enter maize fields and feed on them mainly for the convenience of mate location. Females move away from the maize plant to oviposit as they do not prefer to lay eggs on maize plants (Rose, 1978; Cooter, 2009). Once on the maize plants, females hide in the whorls but the males stay at the base of the plant. Mate-seeking is initiated by male repeated acoustic signaling through the maize stalk which is responded to by the females. *Cicadulina spp.* show preference feeding for weaker plants and plants within heights of 25- 45cm (Cooter, 2009). Thus acoustic suitability of maize plants may be

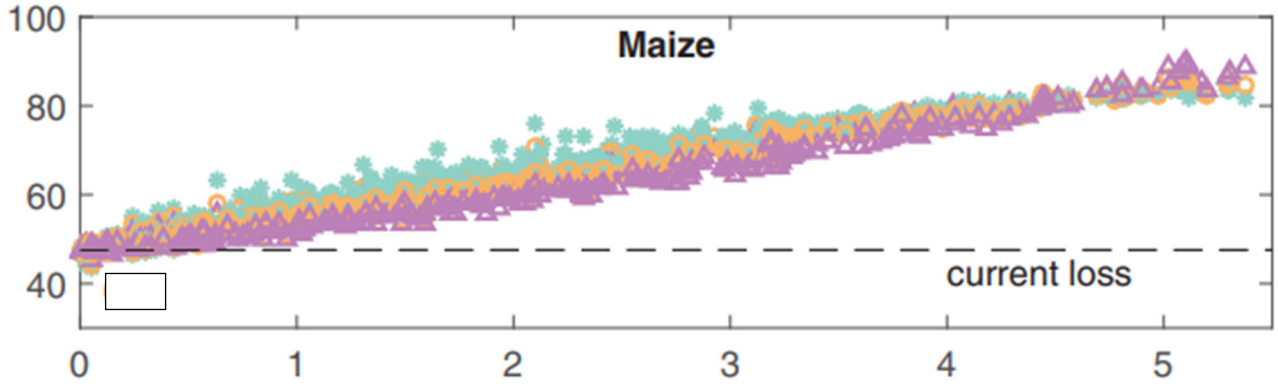
central to plant choice for feeding and mating, influencing the MSD distribution in farmers' fields where slender stem genotypes and nutrient-deficient or etiolated plants are found (Rose, 1978). In an experiment to test the acoustic suitability of maize plants for preference on *Cicadulina* mating, significant differences were found in plants with sticks leaning against them and the incidence of MSD compared with the control, maize plants with no stick leaning against them (Cooter, 2009).

2.5 Leafhopper Distribution and Damage

The low yield of maize in most African countries is aggravated by two means: indirect reduction that arises from the aversion of associated risks and direct losses of yield with the possibility of complete failure of crops (Efron *et al.,* 1989). Fuller (1901) first recorded MSV in South Africa from where the disease spread toward West Africa. Apart from tropical West Africa, the disease was found in other sub-tropical regions as far as Re-Union Islands. The International Institute of Tropical Agriculture (IITA), Ibadan-Nigeria was the first research institute in West Africa to initiate a program to tackle the MSV problem in 1975. The evasive and stubborn nature of the virus revealed that the development of resistant germplasm was the most effective way to tackle the problem. The grassland insect species, *Cicadulina* leafhoppers are generally considered confined to the tropical agroclimatic. Of the 22 species of *Cicadulina* that are known, 18 are present in Africa, 10 of which reportedly cause MSV (Oluwafemi *et al.,* 2011; Webb, 1987). Insects of the genera *Cicadulina* of the species *C. mbila* (Naude), *C. storeyi* or *triangula* (China), *C. bipunctata* (Melichar), *C. latens* (Fennah), *C. parazeae* (Ghauri), *C.arachidis* (China), *C. similis* (China) and *C. ghaurii* (Dabrowski) are the known vectors of MSV. Species are identified and differentiated by the pygophore processes shape as well as the shape and size of the aedeagus (Bosque-Perez & Alam,1992). Surveys of MSV and its vectors have been conducted in Nigeria where differences in qualitative and quantitative properties have been found (Taiwo *et al.,* 2006), however, such a nationwide study has not been conducted in Ghana, except for the predominantly maize-growing agroecological zones (Oppong *et al.,* 2015; Asare-Bediako *et al.,* 2017). Given that *Cicadulina spp* affects other grass species and some grasses serve as alternative

hosts, there is the need to undertake a national survey to differentiate which species of MSV causing *Cicadulina spp* are present in which of the agro climates in Ghana (Bosque-Perez & Buddenhagen, 1999). Five of the ten *Cicadulina spp* present in Africa were found in Nigeria, where *C. mbila* was the most common species. *C. arachis* was poor at transmitting MSV (15% maximum transmission) than *C. mbila* and *C. storeyi* (between 40 – 45%) although transmission efficiency was generally proportional to the length of the viral acquisition period (Bosque-Perez & Alam, 1992; Bosque-Perez & Buddenhagen, 1999). The persistent manner in which *Cicadulina* species transmit MSV and the erratic nature of the virus can reduce maize yield up to 70% to 100% (2.10 a) in very susceptible varieties (Buddenhagen & Bosque-Perez, 1999). However, MSV infestation after eight weeks only results in symptom expression but no significant loss in yield. Apart from maize other crops native to Africa like pearl millet (*Pennisetum glaucum*), sorghum (*Sorghum bicolor*), finger millet (*Eleusine coracona*), rice (*Oryza sativa*), sugarcane (*Saccaharum officinarum*), wheat (*Triticum aestivum*) and oats (*Avena sativa*). The vectors also find certain grasses suitable hosts or such hosts may harbor MSV inoculum at varying levels and could express the same under controlled environments such as *Axonopus compresus*, *panicum maximum*, *Setaria babarta*, *Bracharia spp,* and *Digitaria spp* (Mesfin *et al.,* 1991). Though virulent strains of MSV were not found in any of the weeds surveyed, both MSV and vectors were found to survive in both weeds and maize in areas where weeds grew close to maize plants (Buddenhagen & Bosque-Perez, 1999). This makes MSV more threatening to the object of realizing food security in a climate-fluctuating agrosystem (2.10 a,b). *C. storeyi* was more attracted to uninfected maize seedlings than to *C. storeyi*-infested maize seedlings in olfactometer tests (Oluwafemi *et al.,* 2011).

a



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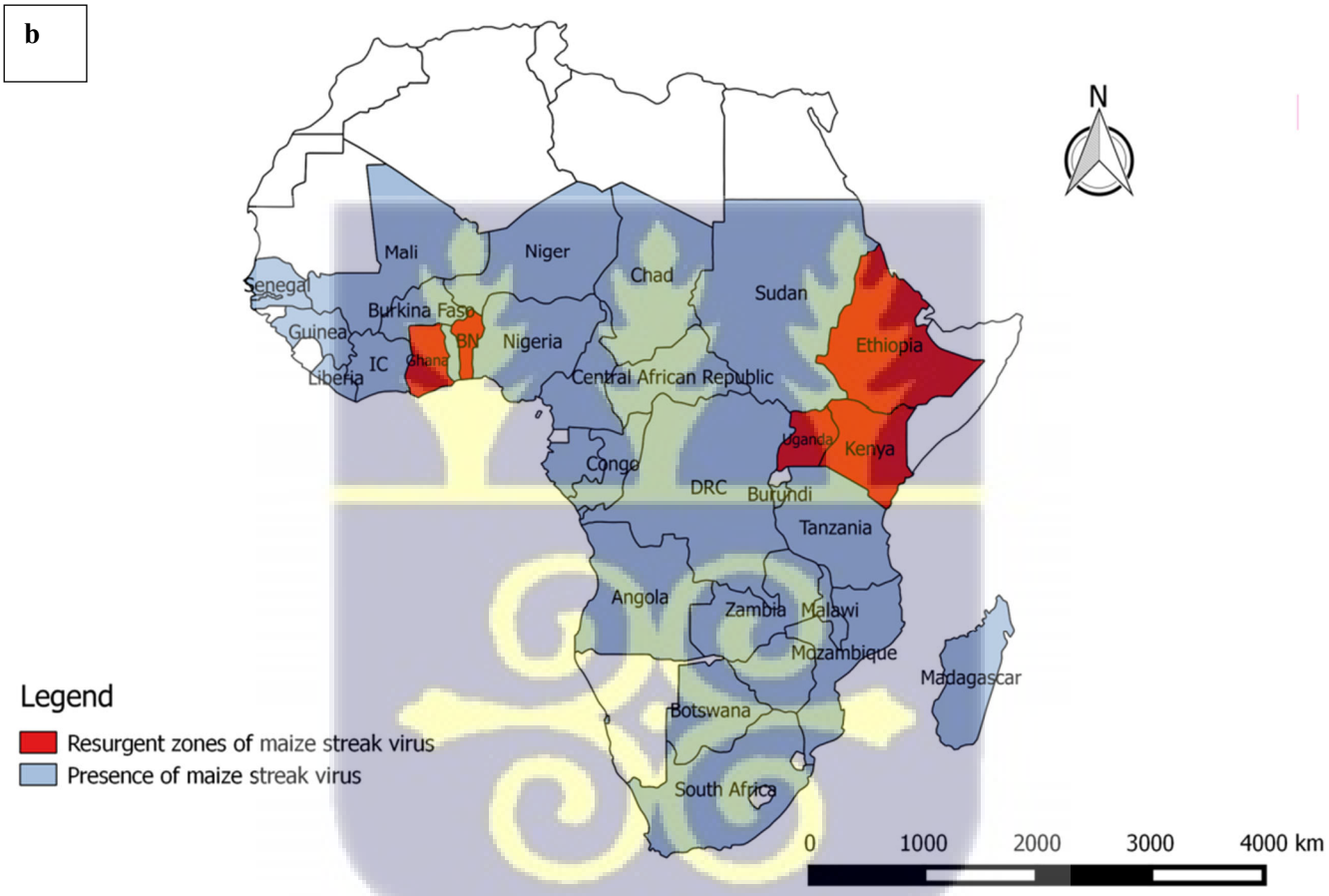


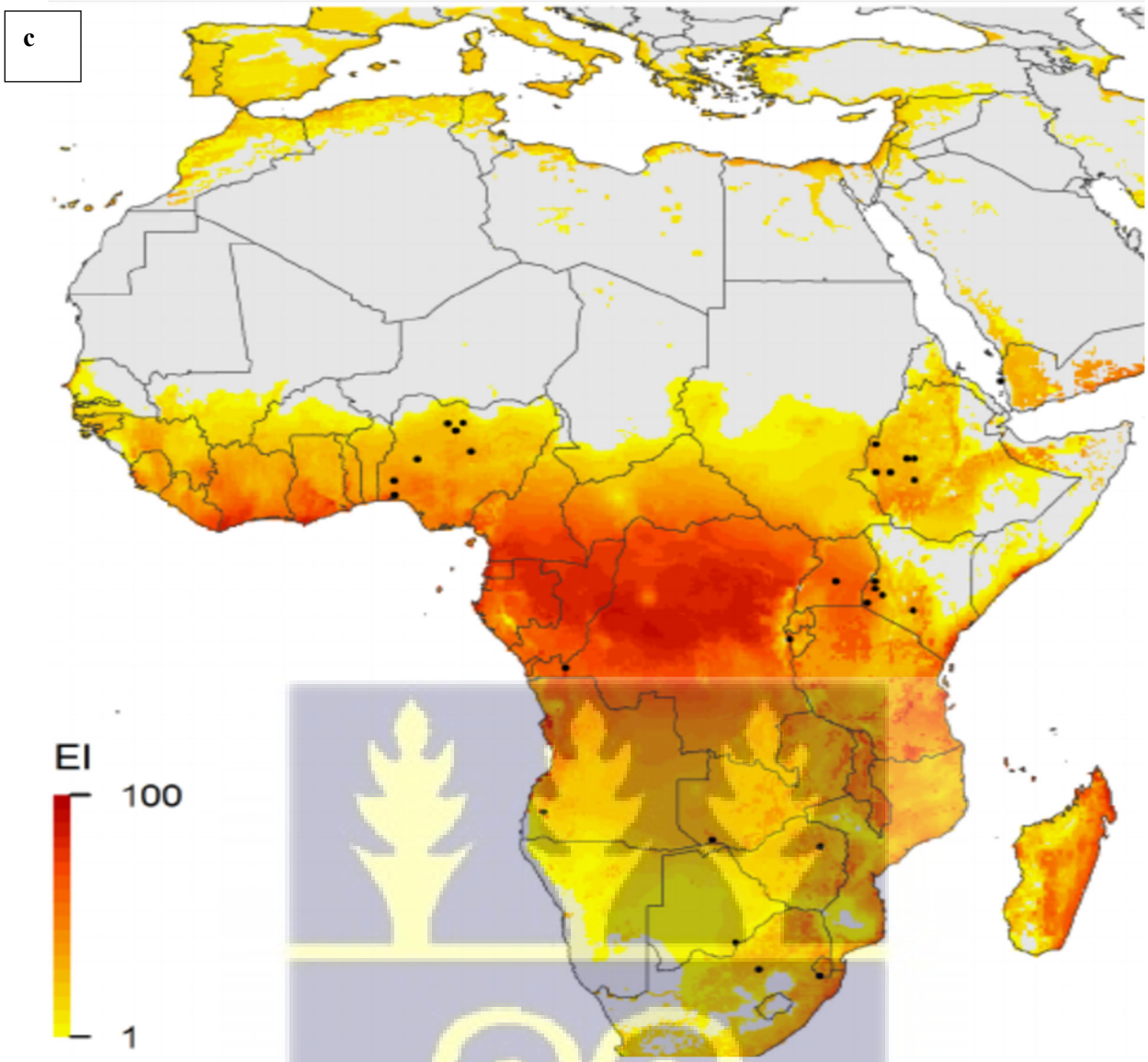


Figure 2. 8 **a** Global impact of climate change on insect pests promotes crop loss in maize. **b** Summary data on *Cicadulina mbila* distribution in Africa depicting zones of MSV presence and resurgence. **c** Climate suitability for *Cicadulina mbila* under irrigation and natural rainfall (Emeraghi *et al.,* 2021; Mylonas *et al.,* 2014; Deutsch *et al.,* 2018). Not drawn to scale.

2.6 Area Under the Disease Progress Curve

Epidemics are produced when favorable conditions are present for viruses to infect, colonize, and spread in a host plant (Ziebell & Carr, 2010; Madden *et al.,* 2007). The study of disease progress allows for timely, efficient, and economical disease management (Alves & Del Ponte, 2021). The

progress of a disease in a plant population can be followed once the amount of disease is assessed over a known period. The results from such analysis can be leveraged not only for developing control mechanisms but also for understanding the disease epidemic processes (Kranz, 2003; Helfer, 2004). Comparing disease progress results from different periods or environments helps in estimating and planning control measures. The area under the disease progress curve (AUDPC) quantifies disease resistance over repeated periods. Field assessment of quantitative disease progress and assessment of crop loss has been calculated using the AUDPC with important application in several varieties with resistance or tolerance (Ferrandino & Elmer, 1992; Royle, 1994). Alves & Del Ponte (2021) concluded that at least two evaluations are necessary to provide a significant estimate of the AUDPC. However, for proper communication of the data in MSD evaluation, it is the author's opinion that evaluations should be recorded over 5-7 time periods. This is based on the finding according to Bosque-Pérez (2000) that MSD development has a negligible effect on maize grain yield after the plant is 8 weeks old. The AUDPC is part of the sigmoidal family of curves specifically a sigmoidal growth function which calculates the area under the function by taking the definite integral between the last and first periods (Alves & Del Ponte, 2021; Kranz, 2003).

2.7 Maize Streak Disease Resistance

Tropical countries like those in sub-Saharan Africa have climatic environments that favor disease development and proliferation resulting in loss of yield plunging the region into food shortages and malnutrition. High temperatures with high relative humidity are particularly noted to promote disease development and severity (Agrios, 2005). Continuous use of the same land for farming increase the potential risks of disease epidemics accelerated by the relationship between ecology, varieties, ecology, varieties and the prevailing environmental conditions (Zhu *et al.,* 2021; Yang *et al.,* 2017). Hight throughput agricultural systems have effective control mechanisms for promoting economic investment in resistant germplasm development. In some countries in SSA where agricultural systems are undeveloped the potential of disease epidemic outbreaks is even higher. Gichuru *et al.* (2011)

studied the reaction of six inbred lines to MSV using half diallel mating design. Results showed that two general combiners (CML 197 and C92) were resistant to MSV. Twelve genotypes were identified as partially resistant whereas five genotypes were found to exhibit mild to severe reactions to MSV. The partially resistant genotypes were also identified to be high-yielding (Asare-Bediako *et al.,* 2021). In a related study using 45 single cross hybrids generated from 10 parental lines, three inbred lines (TL2012-41, TL2012-1, and TL2012-42) were observed as the best combiners for MSV resistance (Nyaligwa *et al.,* 2017). Another study identified three exotic inbred lines (CLM 444, CLM 442, and TZEI17) as high yielding and resistant and/or tolerant to MSV (Oppong *et al.,* 2019).

2.8 Management of Maize Streak Virus Disease

MSD resistance is centered around the development of resistant varieties, mainly hybrids. While this is in the right direction, it is not the only alternative that can be explored. Male sterile insects can be genetically modified to reduce the population of *Cicadulina spp* and effectively reduce the damage caused by MSV (Alphey *et al.,* 2010). In the meantime, intercropping with finger millet and beans and/or with beans and millet reduced the incidence of MSD by 14.9% and 17.4% respectively. The trade-off between maize yield penalty in intercrops however must be factored in such programs (Cooter, 2009). Breeders must select maize genotypes with resistance to MSV or breed for plant structures such as trichomes. Trichome density increases in early vegetative growth, where the impact of MSV is highest. Micro-hairs produced on maize leaves, regulated by the microhairless1 (*mh1*) locus, promote micro-hair initiation and encourage insect resistance (Moose *et al.,* 2004). Selection for trichome density in future maize breeding programs may provide a fraction of the solution. MSV resistance decline in farmer-saved seeds has also been reported, and tolerant or resistant hybrid varieties should be the seed choice for farmers. Extensive extension education on MSD including predisposing factors like weedy fields, planting susceptible varieties, planting under shade, etc should be promoted. Factors that discourage *Cicadulina* infestation such as early planting, planting resistant varieties and intercropping can provide better alternatives to managing MSVD (Cooter, 2009).

Generally, broadleaved plants are not affected by MSV, cowpea, groundnuts, cotton, tobacco, and soybean are non-hosts for *Cicadulina spp* (Charles, 2014). Chemical control methods may also be employed for controlling *Cicadulina spp*. Application of carbofuran, aldicarb, imidalcropid, endosulphan, dimethoate carbosulfan, and dimethoate can control the vectors as well as other insects common to maize but their environmental impact should be properly analyzed. Genetic manipulation could also be explored, dominant negative mutants of the gene replication-associated protein (*rep*) of MSV to develop MSV transgenic resistant maize (Shepherd *et al.,* 2010; Charles, 2014). Over-dependence on the *Msv1* gene should be avoided to prevent the event of a breakdown resulting in an epidemic, thus necessitating the need for MSV research intensification. The best management method in the field is an integration of two or more methods within the resources of the farmer.

2.9 Combining Ability

The ability of a genotype to pass intended traits to its offspring is referred to as combining ability (Kearsey *et al.,* 1997). It is important in finding which parents are better combiners in the development of crosses in breeding programs (Falconer & Mackay, 1983). Analysis of better combiners in breeding programs gives useful information on the genetic architecture of distantly related traits as well as general and specific combining abilities that can be employed in future crop improvement programs (Begna, 2021). The concept of combining ability in maize was first established by Sprague & Tatum (1942) and was adopted for use in other crops (Shamuyarira *et al.,* 2022; Mangena *et al.,* 2022; Azad *et al.,* 2022). Parents with higher general combining ability values imply the involvement of additive gene effects while higher specific combining abilities are indicative of dominance gene effects (Sprague & Tatum, 1942;). If both additive and epistatic gene effects are not significant, then epistatic gene effects may be cited for regulating the genetic effects of traits (Mangena *et al.,* 2022).

Creating a wide genetic pool is a prerequisite for any successful breeding program. The extent and nature of such genetic diversity largely determine the availability of genes regulating such traits. On the one hand, differences in specific combining ability (SCA) are related to variances in the non-

additive genetic effect. Further, additive, additive × additive, and additive genetic effects of higher-order interactions in the reference population are indicative of the general combining ability (GCA). The mean contribution in a series of hybrid combinations of inbred lines to the performance of hybrids is the general combining ability whereas the specific combining ability is the deviation from the mean performances of crossings from the averages of two parental lines. To assess the GCA of an inbred line, it is crossed with other inbred lines all of which possess particular traits of interest followed by comparing the performances of the single cross progenies (Griffing, 1956).

GCA as a selection tool has been applied from F_1 to F_n populations. Practically, low GCA values explain that the variance of the mean of one parent in combining with the other parent is not large in comparison to the general mean of the crosses irrespective of the operational sign on the value. A high GCA, in contrast, is indicative of an inferior or superior parental mean compared to the general mean of the crosses and makes a strong case for gene flow from parents to offspring (Fasahat *et al.,* 2016). Again, it validates the high intensity, high heritability, low environmental variance, and high concentration of additive gene effects (Fasahat *et al.,* 2016; Yu *et al.,* 2020; Begna, 2021). In an experiment to determine good general and specific combining ability for grain yield and yield-related components in 16 three-way hybrids, six lines were identified as good general combiners for grain yield and eight hybrids as good specific combiners for grain yield (Elmyhun *et al.,* 2020). Similarly, Gissa *et al.* (2007) evaluated the performance of eight selected inbred lines for yield and yield components. Results showed three lines, Gutto LMS5, CML 202, and CML 387 are good combiners for days to maturity, plant height, and ear height. The best combiner for grain yield was identified as line 143-5-i.

In another experiment, 170 F_1s developed from crossing five testers to four lines evaluated for yield and yield components showed tester CM 500 was a good combiner for yield and yield attributes. Further, it identified six inbred lines as good general combiners for yield and yield components (Kage *et al.,* 2013). Identifying and understanding the function of the gene expressing a trait(s) is important

for selection in breeding programs (Grami *et al.,* 1977). GCA and SCA values from combining ability analysis are important as they can lead to the identification and management of breeding populations for the selection of traits of economic importance in future breeding programs.

2.10 Heterosis and Heterotic Groupings

Heterosis measures the ability of the hybrid to perform better or worse that its parents in relevant traits of a breeding program (Acquaah, 2012). It is of significant importance in plant breeding research particularly in hybrid development for non-additive gene effect traits (Duvick, 2001). A heterotic group is defined as the combining ability and heterotic response displayed when groups of genotypes from related or unrelated populations are crossed with genotypes from distinctly related germplasm (Singh e*t al.,* 2013; Melchinger, & Gumber, 1998). Identifying heterotic groups points to suitable hybrid parents by performing combining ability analysis. Information from SCA effects of grain yield, HSGCA, and HGCAMT are approaches employed in classifying germplasm into distinct heterotic groups and selecting parents which pass for crosses (Badu-Apraku *et al.,* 2013). For efficiency in breeding programs, it is better to organize germplasm into distinct heterotic groups (Reif *et al.,* 2007). This promotes the effective creation of genetic pools needed for hybrid creation. Further, crosses from these distinct heterotic groups show higher heterosis than crosses from the same heterotic groups. These different sets of heterotic groups, exhibiting higher heterosis and high hybrid performance in their hybrid crosses are termed heterotic patterns (Fan *et al.,* 2008). Here, germplasm for hybrid development is subdivided into at least two distinct populations. The use of heterotic groups and patterns allows for consistency and efficiency in hybrid development as well as germplasm organization and maximization.

Relatively high numbers of hybrids can be generated when germplasm is sorted into heterotic groups and patterns than otherwise. The genetic basis of heterosis comes from epistasis, overdominance, or dominance effects according to quantitative genetics theory (Falconer & Mackay, 1983). Studies of these theories explain that the derived superiority of a hybrid is influenced by positive alleles dominant

to negative recessive alleles (Bruce, 1910). In an experiment to use ear photometry (EP) to determine the performance of inbred lines in a testcross, 274 drought-tolerant maize and 298 public and ex-plant variety protection (PVP) inbred lines were crossed to Iodent and/or Stiff Stalk testers. When testers crossed lines in the same heterotic group, there was a significant reduction in many ear-related yield components (Tolley *et al.,* 2021). Generally, the use of heterotic groups and heterotic patterns in breeding seeks to improve the performance of hybrids and mean heterosis, maximize new germplasm and broaden the genetic base, reducing the variance due to SCA and lowering the GCA/SCA variance ratio, saving time and resources by avoiding crosses that will not pass for the intended traits through germplasm classification into heterotic groups. Good heterotic groups identify superior performing lines in inter-heterotic groups than within the same heterotic groups. Thus heterotic patterns largely determine the extent of genetic variability and the type of germplasm used in breeding pipelines (Meena *et al.,* 2017).

CHAPTER THREE

MATERIALS AND METHODS

3.1 Location of Experiments

Crossing blocks were established at the WACCI Teaching and Research Farm (Figure 3.1) of the University of Ghana, (5° 36N, 0° 10W, and 68° ASL). The experimental location lies in the coastal savanna agroecological zone of Ghana. It has two rainfall seasons; the minor season starts from September to December and the major season starts from April to July each year.

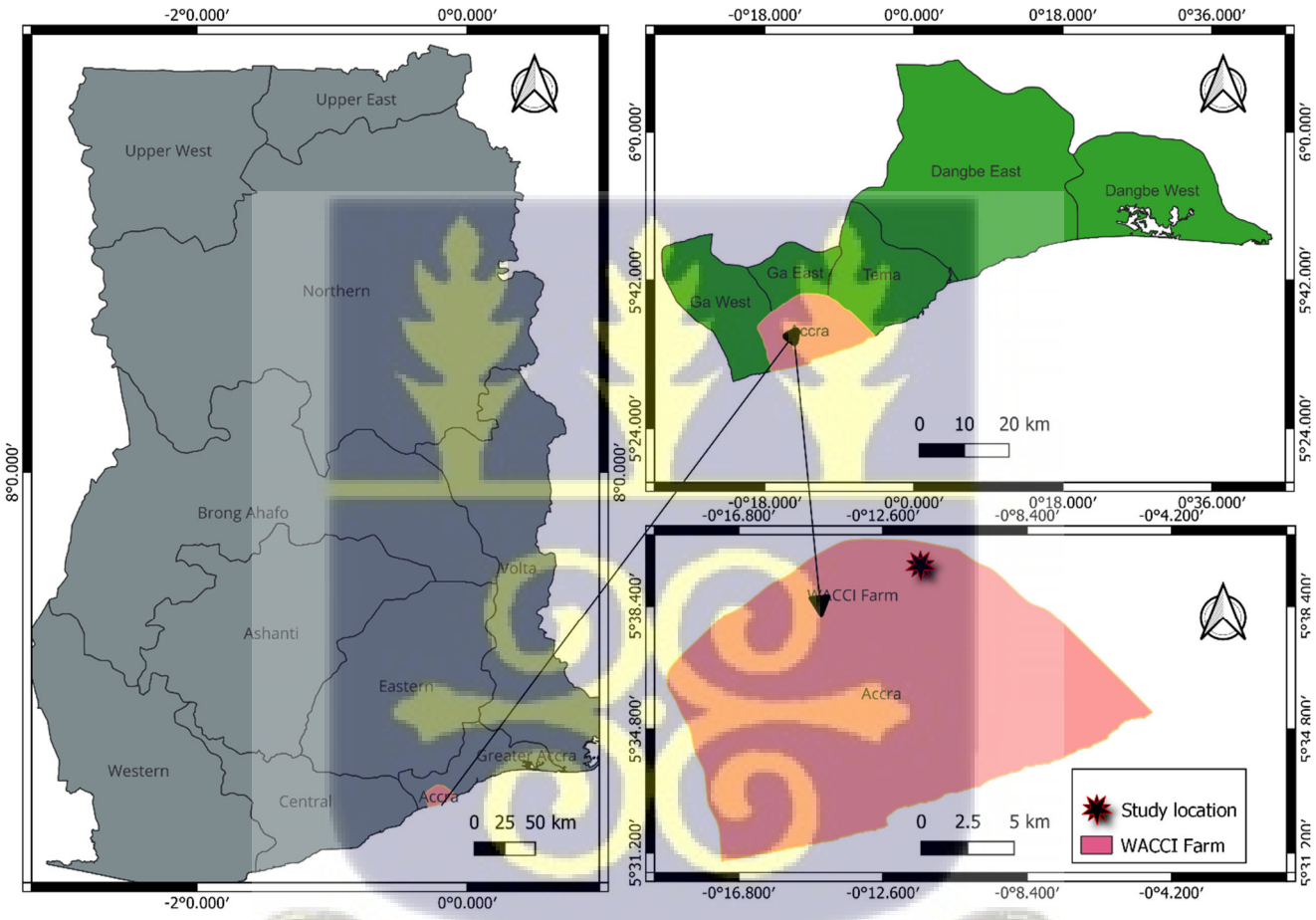


Figure 3.1 Map of the location of the experiment.

3.2 Germplasm description and generation of crosses

Initially, fourteen selected yellow maize inbred lines selected for their resistance to MSV were used for the generation of diallel crosses using half diallel mating design in the WACCI-Maize Improvement Program. At the end of the crossing cycle, eight inbred lines produced enough seeds for the

experiment, the remaining six did not properly nick and were discarded. Griffing's half-diallel mating design (method II, model I) was used to generate 28 F_1 single-cross hybrids (Griffing, 1956). The planting distance used was 0.75m × 0.25m in two-row plots. Each block measured 4 meters and had 1-meter alleys between blocks. Bulk pollen was collected from each parent and then crossing it with all other parents.

Table 3. 1 Germplasm used in the study.

Source	Genotype	Pedigree	Maturity	Heterotic group	Colour
WACCI	WYML 6	HP020-5/2(A)/1 S5(4)	Early	U	Yellow
WACCI	WYML 8	HP020-4/3/1-5 S5(4)	Intermediate	U	Yellow
WACCI	WYML 9	HP020-1/3(10)/6 S5(8)	Intermediate/Late	U	Yellow
WACCI	WYML 10	HP020-5/1(B)/1 S5(8)	Early	U	Yellow
WACCI	WYML 11	HP020-2/3/5 S5(3)	Intermediate/Late	U	Yellow
WACCI	WYML 12	HP020-2/5(9)/1 S5(5)	Early	U	Yellow
WACCI	WYML 15	HP020-6/2(9)/9 S5(5)	Late	U	Yellow
IITA	9450	-	Intermediate	U	Yellow
CSIR-CRI	PIONEER (CHECK 1)	-	-	U	Yellow
CSIR-CRI	AHUOFE (CHECK 2)	-	-	U	Yellow
CSIR-CRI	DZIFO (CHECK 3)	-	-	U	Yellow
CSIR-CRI	LAKE 606 (CHECK 4)	-	-	U	Yellow

WACCI = West Africa Center for Crop Improvement; U = Unknown heterotic group; CSIR-CRI= Council for Scientific and Industrial Research, Crop Research Institute, IITA = International Institute for Tropical Agriculture.

3.3 Experimental design and field layout.

A total land area of 285 m^2 measuring 19 m × 15m was ploughed and harrowed to loosen the soil. It was then divided into 16 blocks and each block was divided into four plots, thus each plot measured 5m × 3m. An alley of 1m was left between blocks. In the control environment (greenhouse), seedlings were transplanted into 5 – liter pots containing worked soil to one-third of it. One seedling per hill was planted in each plot and pot in all three environments. Agronomic practices were done including weeding by hoe and spraying of weedicide. N.P.K (15-15-15) was applied at a rate of 250 kg/ha when seedlings were three weeks old. Top dressing followed basal application with urea at five weeks after transplanting. Drip irrigation was employed in both artificial MSV-infested and natural MSV-infested environments whereas sprinkler irrigation was used in the control environment. For artificial and natural environments, hybrids were evaluated using 8×4 alpha lattice design with two replications. Adjacent to the hybrid plots in each environment, inbred lines were also evaluated using randomized complete block design (RCBD) with two replications, whereas completely randomized design (CRD) was used in the control environment. Planting was done in 4-meter row plots at a spacing of 0.75m× 0.20m, one seed per hill and one row per genotype making a plant population of 66,667 plants per hectare. Border rows were planted around experimental fields to avoid biases.

3.3 Rearing *Cicadulina mbila* Leafhoppers and Artificial of Maize Plants with MSV

Leafhoppers were sourced from the Center for Scientific and Industrial Research, Soil Research Institute (CSIR-SRI) Kwadaso and transported to WACCI Teaching and Research Farm, the University of Ghana in specialized cages (Figure 3.3 c) for rearing and population increment. Before that, pearl millet plants were grown in pots and kept in a cage constructed for rearing *Cicadulina mbila* leafhoppers (Figure 3.3d). The leafhoppers were released into these cages and fed with pearl millet to increase their population. When their population reached about 500 leafhoppers, they were starved for 24 hours and then fed to MSV-infected maize plants harvested from farmers' fields for viral acquisition (Shepherd et al. 2010). A viral acquisition period of 72 hours was allowed then

pregerminated maize seedlings nursed in trays were introduced to the leafhoppers. The seedlings were between the 2nd and 5th leaf stages and grouped according to genotypes. After three days access feeding period, leafhoppers were brushed off the maize seedlings and sprayed with lambda-cyhalothrin-based insecticide at a rate of 1.5 g/litre (Soto *et al.,* 1982). Infected maize seedlings were transported and transplanted to the evaluation fields.

Table 3.2 MSV severity rating scale for the study.

One-point severity rating scale	Interpretation
1	No symptoms present on leaves (no disease)
2	Light streak on older leaves gradually decreasing on young leaves (mild infection)
3	Moderate streaks on old and young leaves (moderate infection)
4	Severe streaking on 60% of leave area, plants stunted (severe infection)
5	Severe streaking on 75% or more of leave area, plants severely stunted, dying or dead (very severe infection)

(Soto *et al.,* 1982).

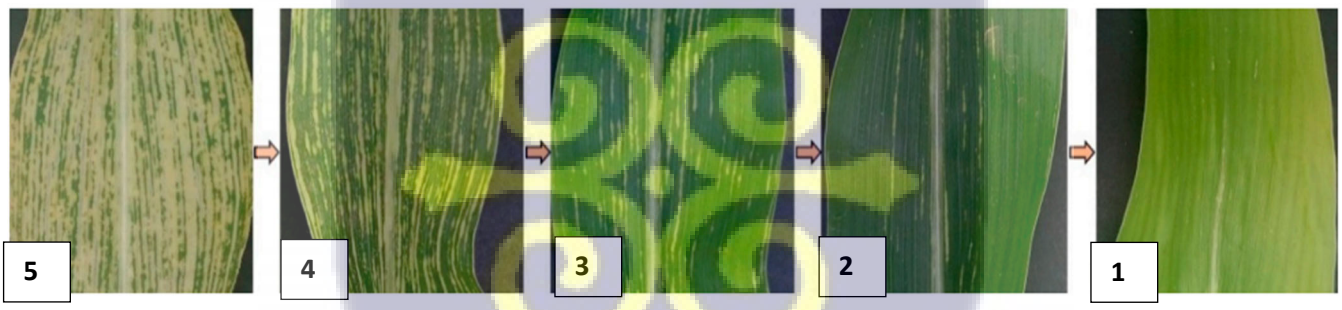


Figure 3.2 MSVD symptom severity scoring sheet where 1 = no disease, 2 = mild-infection, 3 = severe infection and 5 = very severe infection (Oppong *et al.,* 2020).

Figure 3.3 **a.** Field set up for collection of *Cicadulina mbila* leafhoppers **b.** *Cicadulina mbila* collection using aspirator **c.** transport cage for collected *C. mbila* insects containing pearl millet (*Pennisetum glaucum*) in a pot, **d.** constructed cage for *C.mbila* population increment, infection, and transfer of MSV to healthy maize seedlings (Author).

3.4 Germplasm evaluation

Evaluations were conducted in three environments; artificially infested environment, naturally infested environment, and control environment. In the artificially infested field, 28 F1 yellow hybrids generated

from the crossing blocks (Table 3.2) and four yellow hybrid checks were pregerminated and exposed to a population of *Cicadulina mbila* previously fed to MSV-infected maize plants (Soto *et al.,* 1982). This was done when the seedlings were at the 3-leaf stage in a controlled environment (Figure 3.3 d). In the naturally infested environment, pregerminated seedlings were transplanted directly to the field at the same time as seedlings in the infested environment. Thus the seedlings were exposed to possible infestation by *C. mbila* spp. present in the study environment. Evaluation in the control environment was done in a greenhouse structure, sheltering the seedlings from MSV infestation. In the control environment, the plants died due to high humidity and high temperature after data on incidence and severity were collected. Therefore in subsequent calculations, this environment was eliminated for lack of data on yield and yield-related parameters.

Table 3. 3 Germplasm used in the study showing single-cross hybrids and parental inbred lines

×	WYML 6	WYML 8	WYML 9	WYML 10	WYML 11	WYML 12	WYML 15	9450
WYML 6	WYML 6× WYML 6							
WYML 8	WYML 8 × WYML 6	WYML8× WYML 8						
WYML 9	WYML 9× WYML 6	WYML 9 × WYML 8	WYML 9× WYML 9					
WYML 10	WYML 10× WYML 6	WYML 10× WYML 8	WYML 10× WYML 9	WYML 10× WYML 10				
WYML 11	WYML 11× WYML 6	WYML 11× WYML 8	WYML 11× WYML 9	WYML 11× WYML 10	WYML 11× WYML 11			
WYML 12	WYML 12× WYML 6	WYML 12× WYML 8	WYML 12× WYML 9	WYML 12× WYML 10	WYML 12× WYML 11	WYML 12× WYML 12		
WYML 15	WYML 15× WYML 6	WYML 15× WYML 8	WYML 15× WYML 9	WYML 15× WYML 10	WYML 15× WYML 11	WYML 15× WYML 12	WYML 15× WYML 15	
9450	9450× WYML 6	9450× WYML 8	9450× WYML 9	9450× WYML 10	9450× WYML 11	9450× WYML 12	9450× WYML 15	9450×9450

3.5 Agronomic data collection

Data were collected on plants in all three environments; artificially infested MSV field, naturally infested MSV field, and control fields for 29 agronomic parameters. These were plant stand (PLT ST) determined by counting the number of plants per genotype, leaf count (LC) determined by counting the number of leaves per plant from 1 week after planting (WAP) to 7WAP, days to tasseling (DYTS)

was determined as the number of days taken for 50% of plant in a plot to start tasseling. Days to anthesis (DYAN) was determined as the number of days when 50% of plants in a plot started shedding pollen, and days to silking (DYSK) was determined as the number of days taken for 50% of silks of plants in a plot to start emerging. Anthesis silking interval (ASI) is determined as the number of days between DYAN and DYSK. Plant height (PH) was determined by measuring the height of plants in cm. Ear height (EH) is measured as the height from the base of the plant to the upper-most bearing node after pollen shedding and just before harvesting in cm, plant aspect (PASP) is determined by scoring the overall plant architecture on a scale of 1-5 where 1= excellent and 5 = poor. Husk cover (HC) was determined by scoring the number of plants based on the condition of the husk cover of the ears on a scale of 1-5 where 1 = tightly wrapped husks that extend beyond the tip of the ear and 5 = ear tips exposed from husks. Root lodging (RL) was determined by the percentage of plants floored from the roots. Stalk lodging (SL) was determined as the number of plants broken below or at the highest ear node. Plant harvest (PHARV) was determined by counting the total number of plants per plot at harvest time, including barren plants. Ear aspect (EASP) was scored on a scale of 1 - 5 based on an assessment of the general appearance of the ear where 1 = uniform, clean, fully-filled, and large ears and 5 = non-uniform, small, and randomly filled ears. Field weight (FWT) was measured as the total weight of all dehusked cobs in a plot to the nearest tenth of a kg. Grain weight per plot (GWPP) was measured as the total weight of grains of all plants in a plot in grams. Ear harvest (EHARV) was determined by counting the total number ear bearing kernels including the first and second ears. Ear diameter (ED) was determined by measuring the diameter of harvested ears in centimeters. Ear length (EL) was determined by measuring the perpendicular length of harvested ears in centimeters. Days to physiological maturity (DM) was measured as the number of days from emergence to when 50% of plants in a plot have a dark layer at the tip of the cob. Ear position (EPO) was calculated by dividing EH by PH. Row number (RN) was measured as the average number of rows per ear. Stem girth (STM GD) was determined by measuring the diameter at the base of plants, closer to the ground. Chlorophyll

content (CHLO) was determined by measuring the photosynthetic potential of plants in each plot using a spad meter (SPAD-502, Konica Monolta Inc., Japan). Moisture content (MOI) was determined with a moisture meter (Dickey-john, Auburn, Illinois, U.S.A) to determine the moisture content of grains. Grain number per row (GNPR) was determined as the average number of rows of randomly selected ears. Grain number per ear (GNPE) was determined as the average number of grains per row of randomly selected ears. Hundred-grain weight (HGW) was measured by taking a random sample of hundred grains and weighing them in grams.

Grain Yield (kg/ha) = $fwt \times \frac{(100-m)}{85} \times \frac{10000}{(8 \times \Phi)} \times 0.8$; where,

fwt = field weight of harvested ears per plot (kg),

m = grain moisture content at harvest 10,000= land area per hectare (m^2),

8= land area per plot (0.75 m x 0.4 m),

ϕ = number of hills/plot (11) and

0.80 = 80% shelling percentage

Disease incidence (*Vi*) per plot was estimated as the percentage of plants on each plot that displayed MSD symptoms. Disease incidence and disease severity (*Vs*) were scored at 1WAP -7WAP. *Vi* was measured by counting and expressing as a percentage the number of infected plants per plot, whereas *Vs* was measured by scoring each plant on a scale of 1-5, where 1 = no disease, 2 = mild infection, 3 = moderate infection, 4 = severe infection, and 5 = very severe infection (Nelson *et al.,* 1999; Oppong *et al.,* 2020).

$Vi = \frac{n}{N} \times 100$ where,

Vi is virus incidence,

n is the number of diseased plants and,

N is the total number of plants assessed.

$$Vs = \frac{1\times P1+2\times P2+3\times P3+4\times P4+5\times P5}{N(G-1)} \times 100 \text{ where}$$

Vs is the severity index of the virus, P_1 to P_5 is the total number of observed plants per rating of disease symptom in each evaluation field, G is the number of gradings (5) and, N is the total number of observations.

3.6 Statistical Analyses

3.6.1 Incidence and severity

All statistical analyses were performed in R Studio (R Studio Team, 2020). Data for mean incidence was tested for homogeneity of variances using Levene's test (Levene, 1960). Levenes' test statistic (W) is equivalent to the F-statistic produced using analysis of variance (ANOVA) as defined below:

$$W = \frac{(N-k)}{(k-1)} \frac{\sum_{i=1}^{k} \mathrm{N(Z}i-\mathrm{Z,.)\hat{}2}}{\sum_{i=1}^{k}, \sum_{j=1}^{Ni} \mathrm{N(Z}ij-\mathrm{Z}i)\hat{}2};$$

Where:

k = number of different groups to which the sample cases belong

Ni = the number of cases in the *ith* group

N = total number of cases across all groups

Yij = value of the measured variable for the *jth* case from the *ith* group

Zij = | Y*ij* - $\bar{Y}$ *i.* |; where *Yi* = mean of the *ith* subgroup.

The test was significant thus the incidence data was arc-sine transformed to homogenize the variances (Legendre & Legendre, 2012).

The area under the disease progress curve (AUDPC) was calculated according to Madden *et al.* (2007) to quantify the *Vs* into a single value using the midpoint method expressed below:

$$A_{tk} = \sum_{i=1}^{Ni-1} \frac{(yi+yi+1)}{2} (t_{i+1} - t_i)$$

Where:

A_{tk} = the total area under the disease progress curve (AUDPC)

y = disease severity (*Vs*)

t = evaluation dates ie weeks after planting (WAP)

3.6.2 Multivariate Analyses

ANOVA, pairwise correlation analysis, cluster analysis, structural equation modeling (path analysis), principal component analysis, and principal component biplots were done in R Studio. A pairwise correlation was used to identify the strength and direction of association between the yield and yield-related traits as well as the contributions of *Vi* and *Vs* to the total variation in yield of the naturally and artificially infested environments. Principal component analysis (PCA) was employed to estimate the percentage contribution of each quantitative trait to the total genetic variation. PCAs which returned eigenvalues greater than 1 and traits with a co-efficient greater than 0.3 were selected to have contributed significantly to the observed genetic variation. PCA biplots were computed for a graphical appreciation of the relationship between genotypes and traits. Path analysis was computed to determine the pattern of relationships among variables, their causal relationships, and variance due to error and unmeasured variables. Models were specified, estimated, identified, and plotted. Grain yield was regressed on other yield-related traits to determine their total contribution to grain yield. Cluster analysis was performed such that observations were grouped into distinct clusters using Ward's minimum variance distance. A dendrogram was plotted from the calculated similarity indices to present the relationship existing between genotypes.

3.6.3 Genetic parameter analyses

Genotypic and phenotypic analyses were performed on all traits to estimate the genotypic and phenotypic variances, genetic advance, broad sense heritability, and genotypic and phenotypic correlations. Traits that returned negative GCV were eliminated from this analysis because their residual mean squares were greater than their genotype mean squares. ANOVA was used to test their significance at $p \leq 0.05$. Estimates of the genotypic variance, phenotypic variance, and environmental variance with their respective coefficients of variation were used to determine genetic variability between traits and the type of gene action involved (Ewool & Akromah, 2017).The following formulae were adapted from (Ewool & Akromah, 2017; Belay & Fischa, 2020)

1. Genotypic Variance

$GV = (MSg - MSe)r$; where MSg = mean square of genotypes, MSe = Error mean square, and r = number of replications;

2. Phenotypic Variance,

$PV = GV + MSe$; where GV = genotypic variance and MSe = Error mean square;

3. Genotypic Coefficient of Variation

$GCV\ (\%) = \frac{\sqrt{\delta 2g}}{\bar{X}} \times 100$; where $\delta^2 g$ = genotypic variance and $\bar{X}$ =grand mean of the trait;

4. Phenotypic Coefficient of Variation,

$PCV\ (\%) = \frac{\sqrt{\delta 2p}}{\bar{X}} \times 100$; where $\delta^2 p$ = phenotypic variance and $\bar{X}$ = mean of the character;

5. Broad sense heritability (h^2) of traits was calculated as the ratio of the genotypic variance to the phenotypic variance expressed as a percentage (Singh, 1985)

$h^2 = \frac{\delta 2g}{\delta 2p} \times 100$; where $\sigma^2 g$ and $\sigma^2 p$ are the respective genotypic and phenotypic variances.

6. Genetic Advance (GA) for selection intensity (k) at 5% was determined below (Allard, 1960)

$GA = k\sigma^2 ph^2$; where, GA = expected genetic advance; k = 2.06 at 0.05 intensity of selection

$\sigma^2 p$ = phenotypic standard deviation; ; h^2 = broad sense heritability.

7. Genetic advance as a percentage of population means (GAM) was also estimated as:

GAM (%) = $\frac{GA}{\bar{X}}$ x 100; where GA = genetic advance, and $\bar{X}$ = population mean

3.6.4 Diallel analysis

Griffing's diallel mating design (Model 2, Method 1) was used to generate the 28 F1 hybrids from 8 inbred lines (Table 3.2). The model for fixed effects is given by (Fahasat *et al.,* 2016):

$Yij = \mu + g_i + g_j + s_{ij} + {}^{1}/_{bc}\sum\sum e_{ijkl}$; where μ = mean of the population; g_i and g_j = GCA effect of the i^{th} and j^{th} parents ; s_{ij} = SCA effects of the cross generated from the i^{th} and j^{th} parents; b = block number; c = number of crosses generated; and e_{ijkl} = environmental variance associated with the $ijkl^{th}$ observation.

The ratio of the combining ability variances (predictability ratio) was calculated as follows:

$${}^{2(\delta 2gca)}/_{2(\delta 2gca) + \ \delta 2sca}$$; where $\delta 2gca$ = GCA variance and $\delta 2sca$ = SCA variance

Diallel analysis was performed to classify genotypes into distinct heterotic groups based on their SCA and GCA estimates. Heterotic groupings were determined based on the SCA effects of grain yield. General and specific combining abilities were calculated according to Fan *et al.* (2008) as follows:

GCA = M-μ; where M = the mean for the hybrid crosses and μ is the population mean.

SCA = HP - μ - GCA_1 – GCA_2 where, HP = hybrid parent

GCA_1 and GCA_2 = general combining abilities for the crosses.

Heterosis was calculated for mid-parent and better-parent as follows:

Mid-parent heterosis (MPH) = $\frac{F1-MP}{MP} \times 100$

Better-parent heterosis (BPH) = $\frac{F1-BP}{BP} \times 100$; where F_1 = the mean of F_1 hybrid performance and MP = $(P_1 + P_2)/2$ where P_1 and P_2 are the respective means of the inbred parents, and BP = the mean of the best parent.

3.6.5 Principal component analysis

Data were scaled to a mean of zero and a standard deviation of 1 (0,1) by setting the scale. = TRUE function in R version 4.2.1 (2022-06-23 ucrt). The principal component analysis (PCA) was computed using the prcomp() function in R while the variance retained by each principal component was calculated by the function get_eigenvalue() for identification of the most important parameters which explain much of the variability observed in the PCA using the fviz_contrib() function.

3.6.7 Path coefficient analysis

Path coefficient analysis was computed according to Dewey & Lu (1959) using the GCV as;

$r_{ij} = P_{ij} + \sum r_{rk} P_{kj}$, where;

rij = association between yield-related trait (independent character, *i*) and grain yield (dependent character, *j*,

pij = direct and indirect effect of *i* on j,

$\sum r_{rk} P_{kj}$ = summation of components of indirect effects of *i* on a given *j* through all other indirect characters *k*.

The contribution of the remaining unknown characters is given by

$PR = \sqrt{(1- \sum r_{rk} P_{kj})}$

Data from genotypic and phenotypic correlation was subjected to path analysis in R. Model was specified using a linear model where grain yield was used as the explanatory variable and regressed on yield-related traits. The model was estimated and identified using the sem() function in lavaan package. Path diagrams were constructed using the semPaths() function in the semPlot package. The output was presented in a path diagram that explains the contribution of each trait to grain yield and their related variances.

CHAPTER FOUR

RESULTS

4.1 Hybrid performance in the naturally infested environment.

In the naturally infested environment, grain yield ranged from 6317.88 kg/ha for PIONEER to 1851.79 kg/ha for AHOUFE with a mean of 4101kg/ha (Table 4.1). Days to anthesis ranged from 70.5 days for WYML 15 × 9450 to 59.5 days for WYML6 × 9450, PIONEER, and WYML 6 × WYML 12 with a mean of 62.5 days. Days to silking ranged from 72 days for WYML 15 × 9450 to 58.5 days for WYML 6 × WYML 12 with a mean of 63.32 days. Number of grains per row and number of grains per ear ranged from 38 for WYML 6 × WYML 9 to 26.5 for WYML 8 × WYML 15 with a mean of 33.12 and from 2112 for WYML 6 × WYML 15 to 329.5 for WYML 8 × WYML 15 with a mean of 492.79 respectively. Plant aspect ranged from 1 for 9450 × WYML 9, WYML 8 × WYML 10, PIONEER, and WYML 15 × WYML 9 with a mean of 2.14. Ear diameter was highest for AHOUFE, 5.10 cm, and lowest for WYML 8 × WYML9, 3.95 cm with a mean of 4.51 cm. Chlorophyll content ranged from 41.15 for 9450 × WYML 10 to 26.65 for DZIFO with a mean of 34.85. Incidence ranged from 71.42 % for DZIFO to 22.91% for WYML 8 × WYML 9 with a mean value of 41.20%. Severity ranged from 100 % for WYML 15 × WYML 12, WYML 8 × 9450, WYML 8 × WYML 11, and WYML 12 × WYML 10 to 50 % for WYML 15 × WYML 12, 9450 × WYML 10, and WYML 8 × WYML 9 with a mean of 77.10 %. The best performing hybrids in the naturally infested environments include PIONEER, 9450 × WYML 10, WYML 15 × WYML 10, and WYML 11 × WYML 10. On the contrary, WYML 15 × 9450, WYML 11 × WYML 9, and WYML 8 × WYML 15 were selected as hybrids that performed poorly.

4.2 Hybrid performance in the artificially infested environment.

Grain yield in the artificially infested environment ranged from 6406.28 kg/ha for WYML 6 × WYML 8 to 1897.01 for WYML 15 × WYML 11 with a mean of 3941.48 kg/ha (Table 4.2). The hybrid check LAKE 606 outperformed the other three checks (PIONEER, AHOUFE, and DZIFO) with a yield of 5814.65 kg/ha compared to AHOUFE which recorded 2146.14 kg/ha. Hundred-grain weight ranged from 57 grams for DZIFO to 39.5 grams for PIONEER with a mean of 48.80 grams. Grain number per ear ranged from 646.5 for 9450 × WYML 12 to 255.5 for WYML 15 × WYML 11. Days to anthesis ranged from 61 days for DZIFO to 53 days for 9450 × WYML 11 with a mean of 56.42 days. WYML 15 × 9450 recorded the longest number of days to silking of 64 days whereas WUML 12 × WYML 9 recorded the least number of days to silking of 53 days with a mean of 57.76 days. Chlorophyll content ranged from 44.15 for WYML 6 × WYML 8 to 25.1 for WYML 8V WYML9 with a mean of 35.78. MSV incidence ranged from 100% for WYML 6 × WYML 11 to 0% in DZIFO and WYML 12 × WYML 11 with a mean of 53.84. MSV severity was highest in 9450 × WYML 10 recording 42.7% and lowest in WYML 12 × WYML 11, LAKE 606, and DZIIFO, all recording 12.42% with a mean of 25.11%. Comparatively, the checks recorded lower MSD severities than the F1 hybrids. The top performing hybrids include WYML 6 × WYML 8, LAKE 606, WYML 12 × WYML 9, and WYML 11 × WYML 10. Of the top-performing hybrids, only one check, LAKE 606, was selected. The worst-performing hybrids are WYML 8 × WYML 9, WYML 8 × WYML 11, WYML 10 × WYML 9, AHUOFE, and WYML 15 × WYML 11. These were selected based on grain yield, incidence, and severity.

4.3 Hybrid performance in the combined environments.

Grain yield across all environments ranged from 5461.86 kg/ha for WYML 6 × WYML 8 to 2625 kg/ha for WYML 8× WYML 9 with a mean of 4021.35 kg/ha (Table 4.3). Grain yield for the checks (AHUOFE, LAKE 606, and DZIFO) showed smaller variations except for PIONEER which had a relatively high value of 5071.21 kg/ha. Days to anthesis ranged from 68 days for WYML 15 × 9450 to 57.75 days for WYML 12 × WYML 9, WYML 6 × WYML 12, and 9450 × WYML 11 with a mean of 59.46 days while days to silking ranged from 68 days for WYML 15 ×9450 to 57.75 days for WYML 12 × WYML 9, 9450 × WYML 11, and WYML 6× WYML 12 with a mean of 60.54 days. Smaller variations were observed for anthesis silking interval and plant aspect for the checks, however, PIONEER had the highest value of 4.92 cm for ear diameter than the remaining three checks; AHUOFE, 4.42 cm; LAKE 606, 4.42 cm; DZIFO, 4.27 cm. It was the highest among all hybrids while WYML 8 ×WYML9 recorded the least value of 4.00 cm with an overall mean of 4.42cm. Chlorophyll content had the highest value of 41.04 for WYML 11× WYML 10 and 30.62 for AHOUFE with a mean of 35.31. Grain number per row ranged from 40 for WYML 6× WYML 9 to 28 for WYML 8 × WYML 15 with a mean of 33.23. MSVD incidence ranged from 72.12% for WYML 11 × WYML 9 to 15.47% for WYML 12 × WYML 11 with a mean of 47.52%. MSVD severity was highest in WYML 12 × WYML 10, 67.85%, and lowest in WYML 15 ×WYML 10, 36.25% with a mean of 51.11%. Based on the mean grain yield, percentage incidence, and severity values, WYML 6 ×WYML8, 9450 × WYML 10, PIONEER, WYML 12 × WYML 9, and 9450 × WYML 11 were selected as the best performing hybrids across all environments whereas WYML 10 × WYML 9, WYML 8 × WYML 11, WYML 8 × WYML 15, WYML 15 × WYML 11, and WYML 8 × WYML 9 were selected as the poorest performing hybrids across all environments (Table 4.7).

Table 4.1 Mean performance of the 28 F1 hybrids for grain yield and yield related components for naturally infested environment.

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	INC	SEV	EASP	CHLO	HC	ED
9450 × WYML 9	4644.97	50.5	366.0	30.5	2734	63.5	65.5	2.0	1.0	52.08	70.0	2.0	36.72	2.5	4.65
WYML 15 × WYML 12	4375.10	47.5	459.0	35.5	2856	63.0	64.5	1.5	2.5	47.91	100.0	2.5	36.70	2.5	4.25
WYML 11 × WYML 9	3251.52	52.0	390.0	32.5	2686	62.0	64.5	2.5	3.0	71.42	90.0	2.5	33.72	4.0	4.20
9450 × WYML 11	4744.18	44.5	483.0	34.5	2116	62.5	62.5	0.0	3.0	43.75	80.0	1.5	35.82	2.5	4.85
WYML 8 × WYML 12	4004.83	48.5	373.5	30.0	2555	63.0	64.5	1.5	3.0	50.00	70.0	2.5	27.45	3.0	4.45
WYML 15 × WYML 10	5134.12	51.0	438.0	29.0	2560	63.5	64.5	1.0	1.5	20.53	50.0	3.0	38.54	2.5	4.25
WYML 15 × WYML 11	4007.10	54.0	342.0	28.5	2373	62.5	63.5	1.0	2.0	26.78	70.0	3.5	35.27	1.5	4.30
9450 × WYML 12	3861.98	53.0	460.0	35.0	2226	63.0	64.5	1.5	2.5	40.17	87.5	3.0	31.42	2.5	4.35
WYML 12 × WYML 11	4680.53	44.0	417.5	33.5	2166	61.0	63.0	2.0	2.0	30.95	80.0	3.0	35.32	3.0	4.75
WYML 8 × 9450	4426.40	47.0	454.0	35.0	2176	63.0	64.0	1.0	3.0	57.14	100.0	2.5	29.72	3.5	4.85
WYML 6 × WYML 10	4083.87	54.5	412.0	31.5	2952	62.5	64.0	1.5	1.5	42.85	60.0	3.0	39.40	2.5	4.55
WYML 8 × WYML 11	3378.67	52.0	401.0	31.5	2498	64.5	65.0	0.5	3.0	47.32	100.0	3.5	29.07	2.5	4.35
9450 × WYML 10	6030.88	49.0	432.0	36.0	1892	61.0	61.5	0.5	2.5	25.00	50.0	3.5	42.15	4.0	4.30

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	INC	SEV	EASP	CHLO	HC	ED
WYML 12 × WYML 10	3569.69	48.0	428.0	30.5	2365	62.0	59.5	2.5	2.0	57.14	100.0	2.0	28.95	3.0	4.35
WYML 6 × 9450	4402.50	47.0	490.0	38.0	2212	59.5	59.5	0.0	2.0	28.57	80.0	1.5	33.40	2.5	4.55
WYML 15 × 9450	3287.74	50.0	384.0	29.5	2018	70.5	72.0	1.5	2.5	27.67	60.0	2.5	34.82	3.0	4.50
WYML 8 × WYML 10	4322.51	49.5	477.0	37.0	1908	62.0	62.5	0.5	1.0	25.89	70.0	2.5	32.07	3.0	4.60
WYML 6 × WYML 8	4517.44	49.0	555.0	37.0	2671	62.5	63.5	1.0	2.0	31.25	70.0	2.5	37.42	2.0	4.85
CHECK 1: POINEER	6317.88	42.0	504.0	36.0	2529	59.5	60.0	0.5	1.0	25.89	70.0	1.0	40.75	1.0	4.80
CHECK 2: AHOUFE	5105.47	44.5	574.5	35.0	2399	60.0	62.0	2.0	1.5	42.85	90.0	3.0	33.65	1.0	5.10
CHECK 4: LAKE 606	1851.79	54.0	418.0	30.5	2311	65.5	65.5	1.0	2.5	58.75	80.0	2.0	35.27	1.5	4.35
WYML 6 × WYML 12	3766.07	50.5	542.0	36.0	3488	59.5	58.5	1.0	2.0	33.33	60.0	1.5	38.50	2.5	4.40
CHECK 3: DZIFO	3310.80	46.5	472.0	32.5	2400	62.0	63.5	1.5	3.0	71.42	80.0	3.0	26.65	1.5	4.30
WYML 11 × WYML 10	3549.70	49.0	462.0	33.5	3006	63.0	62.0	1.0	2.0	53.57	70.0	3.0	39.52	4.0	4.80
WYML 15 × WYML 9	3846.75	49.0	375.0	28.5	2385	64.5	65.0	0.5	1.0	40.17	60.0	2.0	34.82	1.0	4.30
WYML 12 × WYML 9	4447.63	47.5	457.0	35.0	2687	61.0	62.5	1.5	1.5	53.57	90.0	2.0	41.05	2.5	4.75

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	INC	SEV	EASP	CHLO	HC	ED
WYML 8 × WYML 9	2262.81	51.5	450.5	31.0	2192	65.5	65.5	0.0	2.5	32.50	50.0	2.5	40.05	3.0	3.95
WYML 6 × WYML 9	4362.38	46.5	456.0	38.0	2977	62.0	62.0	0.0	2.5	44.28	90.0	1.0	30.87	2.5	4.65
WYML 10 × WYML 9	3813.94	53.0	408.0	34.0	2336	62.5	64.5	3.0	2.0	33.03	90.0	2.0	37.30	4.5	4.05
WYML 6 × WYML 11	4293.81	45.5	447.0	34.5	2821	60.0	60.5	0.5	2.5	40.17	60.0	2.0	31.87	3.5	5.00
WYML 6 × WYML 15	4801.88	52.5	2112.0	34.0	2796	61.0	62.0	2.0	2.0	39.58	80.0	2.5	36.87	3.5	4.60
WYML 8 × WYML 15	2784.30	55.5	329.5	26.5	2423	62.5	64.5	2.0	2.5	22.91	80.0	2.5	35.70	3.0	4.35
Mean	**4101.23**	**49.32**	**492.79**	**33.12**	**2491.06**	**62.5**	**63.32**	**1.20**	**2.14**	**41.20**	**77.10**	**2.42**	**34.85**	**2.65**	**4.51**
Lsd	**2678.57**	**8.28**	**796.06**	**11.91**	**934.56**	**6.06**	**8.24**	**3.52**	**1.89**	**36.66**	**46.63**	**2.27**	**12.65**	**2.04**	**0.87**
Cv	**30.95**	**7.96**	**76.56**	**17.04**	**17.78**	**4.59**	**6.17**	**138.71**	**41.93**	**42.17**	**28.66**	**44.56**	**17.21**	**36.54**	**9.18**

GRY = grain yield; HGW = hundred grain weight; GNPE = gain number per ear; GWPP = grain weight per plant; DYAN = days to anthesis; ASI = anthesis silking interval; PASP = plant aspect; SEV = severity; EASP = ear aspect; CHLO = chlorophyll content; HC = husk cover; ED = ear diameter; Lsd = least significant difference; Cv = coefficient of variation

Table 4.2 Mean performance of the 28 F1 hybrids for grain yield and yield related components for artificially infested environment.

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	INC	SEV	EASP	CHLO	HC	ED
9450 × WYML 9	4382.10	49.0	462.0	38.5	1816	55.0	55.5	0.5	3.0	71.42	22.51	2.0	41.850	3.0	4.10
WYML 15 × WYML 12	3506.18	49.0	432.0	32.0	1347	57.0	59.0	2.0	3.0	18.75	24.06	3.5	30.850	2.0	4.60
WYML 11 × WYML 9	4255.96	45.5	435.0	29.0	1516	54.0	55.0	1.0	2.5	72.91	32.60	3.0	40.850	3.0	4.20
9450 × WYML 11	4912.14	43.0	516.0	40.0	1458	53.0	53.0	0.0	2.0	43.75	23.29	1.5	30.500	3.0	4.65
WYML 8 × WYML 12	4169.37	49.0	402.5	32.5	1635	53.0	53.5	0.5	2.0	50.00	27.95	2.5	33.050	3.0	4.70
WYML 15 × WYML 10	3438.71	46.5	404.0	32.5	1248	54.5	55.5	1.0	3.0	64.58	22.51	3.5	35.925	3.0	3.90
WYML 15 × WYML 11	1897.01	52.0	255.5	20.5	1325	56.5	62.0	5.5	5.0	50.00	29.50	3.5	40.875	2.0	4.15
9450 × WYML 12	3450.87	48.5	646.5	40.5	1345	57.5	60.5	3.0	4.0	42.85	25.62	4.0	31.275	3.0	4.15
WYML 12 × WYML 11	4074.11	44.0	420.0	30.0	1536	54.5	56.0	1.5	2.5	0.00	12.42	2.5	40.325	1.0	5.00
WYML 8 × 9450	3202.85	50.0	423.0	35.0	1255	60.5	61.0	0.5	3.5	40.00	24.06	3.5	32.725	2.5	4.15
WYML 6 × WYML 10	4509.02	48.0	366.0	30.5	1586	53.0	54.0	1.0	3.0	80.35	27.17	3.0	38.650	2.5	4.50
WYML 8 × WYML 11	2926.63	46.5	512.0	34.0	1349	53.5	56.5	3.0	4.0	85.71	25.62	3.5	35.100	2.0	4.40

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	INC	SEV	EASP	CHLO	HC	ED
9450 × WYML 10	4405.42	50.5	476.0	37.0	1296	53.5	55.0	1.5	2.5	75.00	42.70	4.0	35.825	3.0	4.10
WYML 12 × WYML 10	3638.27	53.5	382.0	26.0	1390	60.0	63.0	3.0	4.0	64.28	35.71	2.0	37.200	1.5	4.15
WYML 6 × 9450	3949.05	51.5	404.0	32.5	1489	57.0	57.5	0.5	3.0	81.25	34.16	1.0	35.450	2.0	4.20
WYML 15 × 9450	3900.04	48.5	444.0	30.5	1432	59.0	64.0	5.0	4.5	31.25	27.17	2.5	36.575	2.5	4.20
WYML 8 × WYML 10	4643.10	47.5	468.0	39.0	1499	56.0	57.5	1.5	3.5	43.75	16.30	2.0	39.925	2.5	4.40
WYML 6 × WYML 8	6406.28	54.5	529.5	39.5	1670	62.0	61.0	4.0	2.5	31.25	19.40	3.0	44.150	2.0	4.05
CHECK 1: POINEER	3824.53	39.5	375.0	28.5	1465	57.0	59.0	2.0	4.5	54.76	27.95	1.0	28.925	2.0	5.05
CHECK 2: AHOUFE	2146.14	53.5	541.0	37.0	1377	58.0	59.5	1.5	3.0	80.00	25.62	3.5	27.600	3.0	3.75
CHECK 4: LAKE 606	5814.65	47.5	520.0	35.0	1421	59.5	60.5	1.0	2.0	37.50	12.42	1.5	34.725	3.5	4.50
WYML 6 × WYML 12	3555.45	45.5	377.0	29.0	1773	55.0	57.0	2.0	2.5	50.00	35.71	2.5	32.100	2.0	4.50
CHECK 3: DZIFO	3858.36	57.0	615.0	37.0	1228	61.0	62.5	1.5	3.0	0.00	12.42	3.5	43.000	2.5	4.25
WYML 11 × WYML 10	5038.95	47.5	414.0	32.0	1672	55.0	55.5	0.5	1.5	31.25	22.51	3.5	42.650	2.5	4.75
WYML 15 × WYML 9	3615.82	50.5	406.0	29.0	1436	56.0	58.0	2.0	2.0	66.07	24.84	2.0	42.050	1.5	4.05

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	INC	SEV	EASP	CHLO	HC	ED
WYML 12 × WYML 9	5442.20	46.5	574.0	37.0	1643	53.5	53.0	0.5	2.0	87.50	36.49	2.0	30.400	1.0	4.55
WYML 8 × WYML 9	2988.04	55.5	393.0	28.0	1015	62.0	62.5	0.5	3.5	73.21	24.84	3.0	25.100	3.0	4.05
WYML 6 × WYML 9	4631.41	45.5	547.0	42.0	1794	57.5	55.5	2.0	2.0	52.67	20.18	1.5	32.525	2.0	4.30
WYML 10 × WYML 9	2896.70	49.5	390.0	30.0	1427	55.0	59.5	4.5	3.5	37.50	19.40	2.5	38.300	2.5	4.15
WYML 6 × WYML 11	3909.31	47.0	519.0	37.0	1347	56.5	56.5	0.0	3.0	100.00	26.39	1.5	35.425	3.5	4.40
WYML 6 × WYML 15	3508.51	44.5	476.0	36.5	1754	54.0	54.0	0.0	3.0	42.85	20.18	2.5	32.175	3.0	4.30
WYML 8 × WYML 15	3230.06	42.5	383.5	29.5	1522	56.0	56.0	0.0	3.0	62.50	17.08	3.0	38.950	3.0	4.10
Mean	**3941.48**	**48.40**	**453.39**	**33.34**	**1470.81**	**56.42**	**57.76**	**1.65**	**3.01**	**53.84**	**25.11**	**2.62**	**35.78**	**2.45**	**4.33**
Lsd	**2611.29**	**10.86**	**180.36**	**10.59**	**577.89**	**4.92**	**4.51**	**3.34**	**2.02**	**51.16**	**19.79**	**2.52**	**18.94**	**1.55**	**0.64**
Cv	**31.40**	**10.64**	**18.85**	**15.06**	**18.13**	**4.13**	**3.70**	**95.78**	**31.81**	**45.03**	**37.37**	**45.66**	**14.30**	**30.09**	**7.06**

GRY = grain yield; HGW = hundred grain weight; GNPE = gain number per ear; GWPP = grain weight per plant; DYAN = days to anthesis; ASI = anthesis silking interval; PASP = plant aspect; SEV = severity; EASP = ear aspect; CHLO = chlorophyll content; HC = husk cover; ED = ear diameter; Lsd = least significant difference; Cv = coefficient of variation.

Table 4.3 Mean performance of the 28 F1 hybrids for grain yield and yield related components for combined environments

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	INC	SEV	EASP	CHLO	HC	ED
9450 × WYML 9	4513.53	49.75	414.00	34.50	2275.0	59.25	60.50	1.25	2.00	61.75	46.25	2.00	39.28	2.75	4.37
WYML 15 × WYML 12	3940.64	48.25	445.50	33.75	2101.5	60.00	61.75	1.75	2.75	33.33	62.03	3.00	33.77	2.25	4.42
WYML 11 × WYML 9	3753.74	48.75	412.50	30.75	2101.0	58.00	59.75	1.75	2.75	72.17	61.30	2.75	37.28	3.50	4.20
9450 × WYML 11	4828.16	43.75	499.50	37.25	1787.0	57.75	57.75	0.00	2.50	43.75	46.25	1.50	33.16	2.75	4.37
WYML 8 × WYML 12	4087.10	48.75	388.00	31.25	2095.0	58.00	59.00	1.00	2.50	50.00	48.97	2.50	30.25	3.00	4.57
WYML 15 × WYML 10	4286.42	48.75	421.00	30.75	1904.0	59.00	60.00	1.00	2.25	42.55	36.25	3.25	37.23	2.7	4.07
WYML 15 × WYML 11	2952.05	53.00	298.75	24.50	1849.0	59.50	62.75	3.25	3.50	38.39	49.75	3.50	38.07	1.75	4.22
9450 × WYML 12	3656.42	50.75	553.25	37.75	1785.5	60.25	62.50	2.25	3.25	41.51	56.56	3.50	31.35	2.75	4.25
WYML 12 × WYML 11	4377.32	44.00	418.75	31.75	1851.0	57.75	59.50	1.75	2.25	15.47	46.21	2.75	37.82	2.00	4.87
WYML 8 × 9450	3814.62	48.50	438.50	35.00	1715.5	61.75	62.50	0.75	3.50	48.57	62.03	3.00	31.22	3.00	4.50
WYML 6 × WYML 10	4296.45	51.25	389.00	31.00	2269.0	57.75	59.00	1.25	2.25	61.60	43.58	3.00	39.02	2.50	4.52
WYML 8 × WYML 11	3152.65	49.25	456.50	32.75	1923.5	59.00	60.75	1.75	3.50	66.51	62.81	3.50	32.08	2.25	4.37
9450 × WYML 10	5218.15	49.75	454.00	36.50	1594.0	57.25	58.25	1.00	2.50	50.00	46.35	3.75	38.98	3.50	4.20

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	INC	SEV	EASP	CHLO	HC	ED
WYML 12 × WYML 10	3603.98	50.75	405.00	28.25	1877.5	61.00	61.25	2.75	3.00	60.71	67.85	2.00	33.07	2.25	4.25
WYML 6 × 9450	4175.78	49.25	447.00	35.25	1850.5	58.25	58.50	0.25	2.50	54.91	57.08	1.25	34.42	2.25	4.37
WYML 15 × 9450	3593.89	49.25	414.00	30.00	1725.0	64.75	68.00	3.25	3.50	29.46	43.58	2.50	32.86	2.75	4.35
WYML 8 × WYML 10	4482.81	48.50	472.50	38.00	1703.5	59.00	60.00	1.00	2.25	34.82	43.15	2.25	36.00	2.75	4.50
WYML 6 × WYML 8	5461.86	51.75	542.25	38.25	2170.5	62.25	62.25	2.50	2.25	31.25	44.70	2.75	40.78	2.00	4.50
CHECK 1: POINEER	5071.21	40.75	439.50	32.25	1997.0	58.25	59.50	1.25	2.75	40.32	48.97	1.00	34.83	1.50	4.92
CHECK 2: AHOUFE	3625.81	49.00	557.75	36.00	1888.0	59.00	60.75	1.75	2.25	61.42	57.81	3.25	30.62	2.00	4.42
CHECK 4: LAKE 606	3833.22	50.75	469.00	32.75	1866.0	62.50	63.00	1.00	2.25	48.12	46.21	1.75	35.00	2.50	4.42
WYML 6 × WYML 12	3660.76	48.00	459.50	32.50	2630.5	57.25	57.75	1.50	2.25	41.66	47.85	2.00	35.30	2.25	4.45
CHECK 3: DZIFO	3584.58	51.75	543.50	34.75	1814.0	61.50	63.00	1.50	3.00	35.71	46.21	3.50	34.82	2.00	4.27
WYML 11 × WYML 10	4294.32	48.25	438.00	32.75	2339.0	59.00	58.75	0.75	1.75	42.41	46.25	3.25	41.08	3.25	4.77
WYML 15 × WYML 9	3731.28	49.75	390.50	28.75	1910.5	60.25	61.50	1.25	1.50	53.12	42.42	2.00	38.43	1.25	4.17
WYML 12 × WYML 9	4944.92	47.00	515.50	36.00	2165.0	57.25	57.75	1.00	1.75	70.53	63.24	2.00	35.72	1.75	4.65

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	INC	SEV	EASP	CHLO	HC	ED
WYML 8 × WYML 9	2625.43	53.50	421.75	29.50	1603.5	63.75	64.00	0.25	3.00	52.85	37.42	2.75	32.57	3.00	4.00
WYML 6 × WYML 9	4496.89	46.00	501.50	40.00	2385.5	59.75	58.75	1.00	2.25	48.48	57.42	1.25	31.70	2.25	4.47
WYML 10 × WYML 9	3355.32	51.25	399.00	32.00	1881.5	58.75	62.00	3.75	2.75	35.26	54.70	2.25	37.80	3.50	4.10
WYML 6 × WYML 11	4101.56	46.25	483.00	35.75	2084.0	58.25	58.50	0.25	2.75	70.08	58.19	1.75	33.65	3.50	4.95
WYML 6 × WYML 15	4155.20	48.50	1294.00	35.25	2275.0	57.50	58.00	1.00	2.50	41.22	50.09	2.50	34.52	3.25	4.45
WYML 8 × WYML 15	3007.18	49.00	356.50	28.00	1972.5	59.25	60.25	1.00	2.75	42.70	48.54	2.75	37.32	3.00	4.22
Mean	**4021.35**	**48.86**	**473.09**	**33.23**	**1980.93**	**59.46**	**60.54**	**1.42**	**2.57**	**47.52**	**51.11**	**2.52**	**35.31**	**2.55**	**4.42**
Lsd	**1850.65**	**6.20**	**406.05**	**7.10**	**439.82**	**3.86**	**4.70**	**2.19**	**35.74**	**30.00**	**21.88**	**1.24**	**9.42**	**1.17**	**0.48**
Cv	**32.58**	**8.98**	**60.77**	**15.13**	**15.72**	**4.59**	**5.50**	**108.84**	**1.30**	**44.70**	**30.31**	**34.98**	**18.90**	**32.52**	**7.80**

GRY = grain yield(kg/ha); HGW = hundred grain weight; GNPE = gain number per ear; GWPP = grain weight per plant; DYAN = days to anthesis; ASI = anthersis silking interval; PASP = plant aspect; SEV = severity; EASP = ear aspect; CHLO = chlorophyll content; HC = husk cover; ED = ear diameter; Lsd = least significant difference; Cv = coefficient of variation.

4.4 Variation and performance of hybrids under the naturally infested environment.

Significant differences were found in the mean squares for replication for husk cover and hundred-grain weight but for grain yield, grain number per ear, grain number per row, days to anthesis, days to silking, anthesis silking interval, plant aspect, ear aspect and ear diameter (Table 4.4). Again significant differences were found in the blocks for husk cover alone. For genotypes, there were significant differences in grain yield, ear diameter, grain weight per plot, and hundred-grain weight. GCA showed significant differences for ear diameter, husk cover, days to silking, and grain weight per plant. GCA for grain yield did not show a significant difference as was hundred-grain weight, days to anthesis, and plant aspect. However, significant differences were shown for SCA for grain yield, hundred-grain weight, grain weight per plant, plant aspect, and ear diameter.

The genotypic and phenotypic correlation among traits for hybrids in the naturally-infested environment (Table 4.5, 4.6). Negative genotypic variances from the association and variability analysis were eliminated because they produced errors i.e, not a number (NaN). The significance of both genotypic and phenotypic correlations was tested using a two-tailed t-test. Grain yield showed significant differences for ear height, field weight, stem girth, ear diameter, and hundred-grain weight. Grain yield showed significant differences for ear height, field weight, stem girth, ear diameter, hundred-grain weight, grain weight per plot, ear position, number of rows, and grain number per ear (Table 4.5). The strongest significant genotypic correlation was between grain yield and stem girth (0.87)

There were no significant differences between grain yield and grain weight per plot whereas ear position and number of rows showed negative and no significant relationship with grain yield (Table 4.6).. Field weight, ear position, ear diameter, and hundred-grain weight also showed significant relationships while the rest of the traits did not show significant relationships. The strongest positive

genotypic correlation was shown between grain yield and field weight (0.99) whereas the weakest genotypic correlation(-0.0065) was shown between grain yield and grain number per row.

The environmental variance, genotypic variance, phenotypic variance, environmental coefficient of variation, genotypic coefficient of variation, broad-sense heritability, genetic advance, and genetic advance as a percentage of the mean for yield, and yield-related traits under naturally infested environment (Table 4.7). Broad-sense heritability for grain yield recorded 0.03. Environmental variance ranged from 1591608.03 for grain yield to 0.00 for ear position. Genotypic variance ranged from 62058.29 for grain yield to 0.00 for root lodging, stalk lodging, field weight, ear diameter, and ear position. Phenotypic variance was highest for grain yield (1653666.32) followed by grain weight per plot (209323.95) and lowest for ear position (0.00). Genetic advance ranged from 174.58 for grain weight per plot to 0.00 for root lodging and stalk lodging.

Table 4.4 Mean squares of combining abilities for naturally infested environment.

SV	Df	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
Rep	3	4250162	78.77*	62938	49.00	320922	33.06	9.76	0.39	1.26	0.76	16.00***	0.31
Block	14	1386869	16.22	169459	12.79	326175	5.78	6.54	1.97	1.58	1.14	2.63*	0.07
Geno	31	1797098	22.33	182325	23.83	163742	12.05	16.93	1.44	1.47	0.93	0.82	0.15
GCA	7	836061.50	30.75	133680.88	48.91	646764.84***	14.93	32.42*	2.69	0.55	1.28	2.09*	0.49***
SCA	28	2576849.60**	36.21**	180449.48	25.90	334043.28***	11.61	17.46	2.01	2.14***	1.42	1.17	0.27**
Error	83	1142777.77	15.19	138522.92	31.00	94713.53	8.22	12.36	2.82	0.67	1.17	0.92	0.11

*=significant at $p \leq 0.05$; ** = significant at $p < 0.01$; GRY= grain yield; HGW= hundred grain weight; GNPE= grain number per ear; GNPR= grain number per row; GWPP= grain weight per plot; GNPR= grain number per row; DYAN= days to 50% anthesis; DYSK=days to 50% silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; ED= ear diameter; SV= source of variation; Df= degree of freedom; Rep = replication; Gen = genotype; GCA= general combining ability; SCA=specific combining ability.

Table 4.5 Genotypic correlations for naturally infested environments

	EH	FWT	GWPP	STM GD	ED	EPO	RN	GNPE	HGW	GRY
EH	1 **	-0.54 **	-0.59 **	0.12 ns	-0.68 **	0.15 **	-0.27 **	-0.11 **	0.00 ns	-0.61 **
FWT	-0.54 **	1 **	-0.78 **	0.72 **	0.09 **	-0.90 **	0.34 **	0.76 **	-0.30 **	0.45 **
GWPP	0.55 ns	-0.78 **	1 **	0.79 **	-0.38 *	0.17 ns	1.33 **	1.14 **	0.82 **	-0.94 **
STM GD	-0.59 **	0.72 **	0.79 **	1 **	0.40 *	-0.51 **	-0.88 **	-0.33**	-0.50 **	0.87 **
ED	-0.67 **	0.08 **	-0.37 *	0.40 *	1 **	-0.51 **	0.21 ns	0.68 **	-0.16 **	0.98 **
EPO	0.15 **	-0.89 **	0.17 ns	-1.50 **	-0.50 **	1 **	-0.50 **	-0.34**	-0.26 ns	-0.91 **
RN	-0.27 **	0.34 **	0.33 **	-0.88**	0.20 ns	-0.50 **	1 **	0.59 **	0.68 **	0.50 **
GNPE	-0.11 **	0.76 **	0.14 **	-0.33 **	0.67 **	-0.34 **	0.05 **	1 **	0.42 *	0.88 **
HGW	0.00 ns	-0.30 **	0.82 **	-0.50 **	-0.16 **	-0.26 ns	0.68 **	0.45 *	1 **	-0.32 **
GRY	-0.62 **	0.00 **	-0.94 **	0.87 **	0.98 **	-0.91 **	0.50 **	0.88 **	-0.32 **	1 **

*=significant at $p \leq 0.05$; ** = significant at $p < 0.01$; ns= not significant; EH= ear height ; FWT = field weight; GWPP = grain weight per plot; STM GD = stem girdth; ED= ear diameter; EPO = ear position; RN= row number; GNPE= grain number per ear; HGW= hundred grain weight; GRY = grain yield.

Table 4.6 Phenotypic correlations for naturally infested environment.

	EH	FWT	GWPP	STM GD	ED	EPO	RN	GNPE	HGW	GRY
EH	1 **	0.26 *	-0.16 ns	0.13 ns	0.17 ns	0.68 **	0.07 ns	0.09 ns	-0.17 ns	0.259 *
FWT	0.2637 *	1 **	0.1493 ns	0.2926 *	0.418 **	-0.0627 ns	-0.0016 ns	0.0671 ns	-0.51 **	0.99 **
GWPP	-0.16 ns	0.14 ns	1 **	0.02 ns	0.18 ns	-0.25 *	0.06 ns	0.07 ns	-0.06 ns	0.14 ns
STM GD	0.12 ns	0.29 *	0.02 ns	1 **	0.12 ns	0.02 ns	0.17 ns	0.19 ns	-0.16 ns	0.29 *
ED	0.17 ns	0.42 **	0.18 ns	0.13ns	1 **	0.08 ns	0.08 ns	0.11 ns	-0.56 **	0.41 **
EPO	0.68 **	-0.06 ns	-0.25 *	0.02 ns	0.08 ns	1 **	-0.02 ns	-0.03 ns	-0.07 ns	-0.06 ns
RN	0.07 ns	-0.00 ns	0.06 ns	0.17 ns	0.08 ns	-0.02 ns	1 **	0.98 **	0.08 ns	-0.00 ns
GNPE	0.09 ns	0.06 ns	0.07 ns	0.19 ns	0.11 ns	-0.03 ns	0.98 **	1 **	0.02 ns	0.06 ns
HGW	-0.17 ns	-0.51 **	-0.06 ns	-0.16 ns	-0.56 **	-0.07 ns	0.08 ns	0.02 ns	1 **	-0.51 **
GRY	0.25 *	0.99 **	0.14 ns	0.29 *	0.41 **	-0.06 ns	-0.00 ns	0.06 ns	-0.51 **	1 **

*=significant at $p \leq 0.05$; ** = significant at $p < 0.01$; ns= not significant; EH= ear height ; FWT = field weight; GWPP = grain weight per plot; STM GD = stem girdth; ED= ear diameter; EPO = ear position; RN= row number; GNPE= grain number per ear; HGW= hundred grain weight; GRY = grain yield.

Table 4.7 Estimates of genotypic and phenotypic variances for yield and yield-related traits in naturally infested environment

PARAMETER	EH	HC	RL	SL	FWT	GWPP	STMGD	ED	EPO	RN	GNPE	HGW	GRY
Grand Mean	78.29	2.65	0.03	0.03	0.35	2491.06	23.99	4.51	0.47	14.93	492.79	49.32	4101.23
SEM	9.03	0.68	0.12	0.12	0.25	292.01	2.35	0.25	0.02	8.75	279.12	2.78	892.07
EV	163.13	0.93	0.03	0.03	0.13	170549.08	11.06	0.13	0.00	153.25	155817.94	15.50	1591608.03
GV	14.48	0.32	0.00	0.00	0.00	38774.87	0.74	0.00	0.00	8.03	12645.57	3.54	62058.29
PV	177.61	1.26	0.03	0.03	0.14	209323.95	11.81	0.14	0.00	161.28	168463.51	19.05	1653666.32
ECV	16.31	36.41	556.48	556.48	30.46	16.57	13.86	8.13	8.54	82.87	80.10	7.98	30.76
GCV	4.86	21.61	0	0	6.32	7.90	3.60	2.04	6.63	18.97	22.81	3.81	6.07
H^2	0.08	0.26	0.00	0.00	0.04	0.18	0.06	0.05	0.37	0.04	0.07	0.18	0.03
GA	2.23	0.60	0.00	0.00	0.03	174.58	0.44	0.04	0.03	1.30	63.46	1.67	99.41
GAM	2.85	22.72	0.00	0.00	2.65	7.00	1.87	1.02	8.30	8.72	12.87	3.39	2.42
P-value	**0.32**	**0.07**	**0.5**	**0.05**	**0.40**	**0.15**	**0.36**	**0.37**	**0.01***	**0.39**	**0.33**	**0.14**	**0.41^{ns}**

EH= ear harvest; HC= husk cover; RL= root lodging; SL = stalk lodging; FWT = field weight; GWPP = grain weight per plot; STMGC= stem girth; ED = ear diameter; EPO = ear position; RN = number of rows; GNPE= grain number per row; HGW= hundred grain weight; GRY = grain yield; SEM= standard error of the mean; EV = environmental variance; GV =genotypic variance; PV= phenotypic variance; ECV = environmental coefficient of variation; H^2 = broad sense heritability; GA= genetic advance; GAM= genetic advance as percentage of mean.

4.5 Variation and performance of hybrids under artificially infested environment.

Significant differences were shown in the mean squares for replication for grain weight per plot and days to silking (Table 4.8). Apart from days to anthesis, days to silking, and anthesis silking interval which showed significant differences in the block, no significant difference was shown for the remaining traits under study. The mean square for the genotypes ranged from 1987060 for grain yield to 0.15 for ear diameter and showed significance only for days to silking. GCA mean squares were significant for grain number per row, grain number per ear, grain weight per plot, husk cover, and ear diameter and ranged from 129745.64 for grain weight per plot to 0.65 for ear diameter. SCA means squares were not significant for hundred-grain weight, days to anthesis, days to silking, anthesis silking interval, and ear aspect, whereas the remaining traits, were significant. SCA values ranged from 2923000.55 for grain yield to 1.58 for ear aspect.

The genotypic and phenotypic correlation among traits for hybrids under the artificially infested environment are presented in Table 4.9-10. Negative genotypic variances from the association and variability analysis were eliminated because they produced errors i.e, not a number (NaN). The significance of both genotypic and phenotypic correlations was tested using a two-tailed t-test. Grain yield showed a significant correlation for all traits that were considered. Genotypic correlation was strongest between root lodging and leaf count (-0.38) and weakest between days to maturity and plant aspect (0.03). Plant height showed significant correlations with all traits except for ear diameter, ear position, and row number. Chlorophyll content ranged from 0.01 for root lodging to 0.11 for ear length. There were significant differences between chlorophyll content and most traits except for plant aspect and ear length. Phenotypic correlations for grain yield ranged from 0.99 for field weight to 0.03 for root lodging. Grain yield showed significant differences only for plant height, leaf count, plant

aspect, ear harvest, field weight, and chlorophyll content. Root lodging showed no significant relationship with all traits except for ear height.

Environmental variance was highest for grain yield (3941.48), followed by grain number per ear (453.39), and lowest for husk cover (2.45). Genotypic variance ranged from 69235.39 for grain yield to 0.28 for husk cover (Table 4.11). Genotypic coefficient of variation ranged from 18.80 for ear length to 2.76 for leaf count. Phenotypic variance was lowest in ear diameter and highest in grain yield and lowest in plant aspect. Ear length showed the highest broad-sense heritability estimate of 0.58 and plant aspect recorded the least broad-sense heritability of 0.21. The genetic advance made by grain yield is 107.06, translating into 2.71% genetic advance as a percentage of the mean. Husk cover recorded the highest genetic advance as a percentage of the mean of 22.0% compared to 0.68% recorded by leaf count.

Table 4.8 Mean squares of combining abilities for artificially infested environment.

SV	Df	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
Rep	3	3832796	1.56	11104	60.06	1177225**	0.39	50.77**	16.00*	0.14	1.56	0.14	0.00
Block	14	1598214	36.67	8002	31.42	75975	53.68***	64.93***	9.88**	1.75	1.46	0.74	0.16
Gen	31	1987060	21.07	11843	41.47	62721	7.78	10.51*	3.52	1.11	1.18	0.64	0.15
GCA	7	990635.55	39.39	12810.69*	78.42***	129745.64*	20.21	26.21	0.72	1.78	2.25	1.47**	0.65***
SCA	28	2923000.55**	41.59	16703.35***	66.57***	202812.08***	23.79	24.69	5.86	1.67*	1.58	1.04*	0.26***
Error	83	1393358.61	25.31	4853.85	20.49	49925.46	27.92	27.43	4.06	0.88	1.21	0.53	0.06

*=significant at $p \leq 0.05$; ** = significant at $p < 0.01$; ns= not significant; GRY= grain yield; HGW= hundred grain weight; GNPE= grain number per ear; GNPR= grain number per row; GWPP= grain weight per plot; GNPR= grain number per row; DYAN= days to 50% anthesis; DYSK=days to 50% silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; ED= ear diameter; SV= source of variation; Df= degree of freedom; Rep = replication; Gen = genotype; GCA= general combining ability; SCA=specific combining ability.

Table 4.9 Genotypic correlations artificially infested environment.

	LC	PH	EH	PASP	HC	HGW	GRY	RL	EHARV	FWT	EASP	ED	EL	CHLO	DM	EPO	RN
LC	1 **	-0.49 **	-0.74 **	-0.85 **	-0.15 ns	-0.39 **	0.21 **	-0.38 **	0.73 **	0.69 **	0.13 **	0.29 ns	0.88 **	-0.74 **	-0.69 **	-0.51 **	-0.64 **
PH	-0.49 **	1 **	0.97 **	-0.64 **	0.50 **	0.83 **	0.31 **	0.01 **	0.37 **	0.21 **	-0.03 **	-0.10 ns	0.67 **	-0.38 *	0.67 **	0.23 ns	0.19 ns
EH	-0.74 **	0.97 **	1 **	-0.67 **	0.25 ns	0.75 **	0.66 **	0.73 **	0.62 **	0.61 **	-0.94 **	0.06 ns	0.65 **	-0.98 **	0.57 **	0.44 *	0.52 **
PASP	-2.85 **	-0.64 **	-0.67 **	1 **	-0.59 **	-0.04 ns	-0.50 **	0.97 **	-0.52 **	-0.35 **	0.44 *	0.09 ns	-0.86 **	-0.27 ns	0.03 ns	-0.44 *	0.43 *

	LC	PH	EH	PASP	HC	HGW	GRY	RL	EHARV	FWT	EASP	ED	EL	CHLO	DM	EPO	RN
HC	-0.15 ns	0.50 **	0.25 ns	-0.59 **	1 **	-0.19 ns	0.69 **	0.29 **	0.81 **	0.56 **	0.80**	-0.25 ns	0.48 **	-0.63 **	-0.39 *	-0.67 **	-0.11 ns
HGW	-0.39 **	0.83 **	0.75 **	-0.04 ns	-0.19 ns	1 **	-1.08 **	0.81 **	0.41 *	-0.92 **	0.62 **	-0.30 **	-0.24 ns	-0.71 **	0.06 ns	0.06 ns	0.22 ns
GRY	0.21 **	0.31 **	0.66 **	-0.50 **	0.69 **	-0.08 **	1 **	0.78 **	0.47**	0.00 **	-0.57 **	0.26 **	0.83 **	-0.54 **	0.24 **	-0.52 **	-0.87 **
RL	-0.3898 **	0.01 **	0.73 **	0.97 **	0.29 **	0.81 **	0.78 **	1 **	0.97 **	0.61 **	-0.47 **	0.02 ns	0.55 **	0.01 **	0.59 **	-0.58 **	0.10 **
EHARV	0.72 **	0.37 **	0.62 **	-0.52 **	0.81 **	0.41 *	0.47 **	0.97**	1 **	0.51 **	-0.81 **	0.31 ns	0.32 **	-0.42 **	-0.51 **	-0.58 **	-0.40 **
FWT	0.69**	0.20 **	0.61 **	-0.35 **	0.56 **	-0.92 **	0.00 **	0.61 **	0.51 **	1 **	-0.14 **	0.15 **	0.70 **	-0.48 **	0.07 **	-0.22 **	-0.79 **
EASP	0.12 **	-0.03 **	-0.94 **	0.44 *	0.80 **	0.62 **	-0.57 **	-0.47 **	-0.81 **	-0.14 **	1 **	-0.26 **	-0.69 **	0.72 **	0.19 ns	0.51 **	0.25 **
ED	0.29 ns	-0.10 ns	0.06 ns	0.09 ns	-0.25 ns	-0.30 **	0.26 **	0.02 ns	0.31 ns	0.15 **	-0.26 **	1 **	0.41 *	-0.71 **	0.07 ns	0.66 **	-0.32 ns
EL	0.88 **	0.67 **	0.65 **	-0.86 **	0.48 **	-0.24 ns	0.83 **	0.55 **	0.32 **	0.70 **	-0.69 **	0.41 *	1 **	-0.11 ns	0.15 ns	0.18 ns	0.10 ns
CHLO	-0.74 **	-0.38 *	-0.98 **	-0.27 ns	-0.63 **	-0.71 **	-0.54 **	-0.01 **	-0.42 **	-0.48 **	0.72 **	-0.71 **	-0.11 ns	1 **	-0.33 ns	-0.00 **	-0.47 **
DM	-0.69 **	0.67 **	0.57 **	0.03 ns	-0.39 *	0.06 ns	0.24 **	0.59 **	-0.51 **	0.07 **	0.19 ns	0.07 ns	0.15 ns	-0.33 ns	1 **	-0.35 *	0.78 **
EPO	-0.51 **	0.23 ns	0.44 *	-0.44 *	-0.67 **	0.06 ns	-0.52 **	-0.58 **	-0.58 **	-0.22 **	0.51 **	0.66 **	0.18 ns	-0.00 **	-0.35 *	1 **	0.73 **
RN	-0.64 **	0.19 ns	0.52 **	0.43 *	-0.11 ns	0.22 ns	-0.87 **	0.10 **	-0.40 **	-0.79 **	0.25 **	-0.32 ns	0.10 ns	-0.47 **	0.78 **	0.73 **	1 **

*=significant at $p \leq 0.05$; ** = significant at $p < 0.01$; ns= not significant; LC= leaf count; PH=plant height; EH= ear height; PASP = plant aspect; HC= husk cover; HWG = hundred grain weight; GRY = grain yield; RL = root lodging; EHARV= number of ears harvested; FWT = field weight; EASP= ear aspect; ED= ear diameter; CHLO= chlorophyll content; DM = days to physiological maturity; EPO= ear position

Table 4.10 Phenotypic correlations for artificially infested environment.

LC	PH	EH	PASP	HC	HGW	GRY	RL	EHARV	FWT	EASP	ED	EL	CHLO	DM	EPO	RN

LC	1 **	0.07 ns	0.10 ns	-0.34 **	0.06 ns	-0.24 ns	0.11 ns	0.07 ns	0.00 ns	0.12 ns	-0.08 ns	0.15 ns	-0.02 ns	0.11 ns	-0.41 **	0.14 ns	0.09 ns
PH	0.07 ns	1 **	0.83 **	-0.56 **	0.04 ns	0.04 ns	0.54 **	0.19 ns	0.55 **	0.55 **	-0.15 ns	0.08 ns	0.29 *	0.03 ns	-0.15 ns	0.01 ns	0.18 ns
EH	0.10 ns	0.83 **	1 **	-0.42 **	-0.00 ns	0.12 ns	0.51 **	0.29 *	0.49 **	0.51 **	-0.13 ns	0.08 ns	0.11 ns	0.15 ns	-0.06 ns	0.52 **	0.30 *
PASP	-0.34 **	-0.56 **	-0.42 **	1 **	0.10 ns	0.16 ns	-0.55 **	-0.03 ns	-0.51 **	-0.55 **	0.13 ns	-0.28 *	-0.15 ns	-0.09 ns	0.25 *	-0.01 ns	-0.12 ns
HC	0.06 ns	0.04 ns	-0.00 ns	0.10 ns	1 **	0.03 ns	-0.12 ns	-0.01 ns	-0.03 ns	-0.12 ns	0.02 ns	-0.17 ns	0.25 *	-0.10 ns	0.17 ns	-0.10 ns	-0.07 ns
HGW	-0.24 ns	0.04 ns	0.12 ns	0.16 ns	0.03 ns	1 **	-0.07 ns	-0.06 ns	0.09 ns	-0.07 ns	0.03 ns	-0.39 **	-0.12 ns	0.24 *	0.24 ns	0.16 ns	0.22 ns
GRY	0.11 ns	0.54 **	0.51 **	-0.55 **	-0.12 ns	-0.07 ns	1 **	-0.03 ns	0.86 **	0.99 **	-0.12 ns	0.23 ns	0.12 ns	0.32 **	-0.11 ns	0.10 ns	0.13 ns
RL	0.07 ns	0.19 ns	0.29 *	-0.03 ns	-0.01 ns	-0.06 ns	-0.03 ns	1 **	-0.05 ns	-0.03 ns	-0.19 ns	0.04 ns	-0.08 ns	-0.14 ns	0.12 ns	0.21 ns	-0.05 ns
EHARV	0.00 ns	0.55 **	0.49 **	-0.50 **	-0.03 ns	0.09 ns	0.86 **	-0.05 ns	1 **	0.86 **	-0.11 ns	0.06 ns	0.07 ns	0.39 **	-0.13 ns	0.08 ns	0.05 ns
FWT	0.12 ns	0.55 **	0.51 **	-0.55 **	-0.12 ns	-0.07 ns	0.99 **	-0.03 ns	0.86 **	1 **	-0.14 ns	0.24 ns	0.12 ns	0.33 **	-0.11 ns	0.10 ns	0.13 ns
EASP	-0.08 ns	-0.15 ns	-0.13 ns	0.12 ns	0.02 ns	0.03 ns	-0.12 ns	-0.19 ns	-0.11 ns	-0.14 ns	1 **	-0.22 ns	0.05 ns	-0.08 ns	0.04 ns	-0.03 ns	-0.05 ns
ED	0.15 ns	0.08 ns	0.08 ns	-0.28 *	-0.17 ns	-0.39 **	0.23 ns	0.04 ns	0.06 ns	0.24 ns	-0.22 ns	1 **	0.27 *	-0.02 ns	-0.02 ns	-0.03 ns	0.05 ns
EL	-0.03 ns	0.29 *	0.12 ns	-0.15 ns	0.25 *	-0.12 ns	0.12 ns	-0.08 ns	0.07 ns	0.12 ns	0.05 ns	0.27 *	1 **	-0.29 *	0.16 ns	-0.21 ns	-0.03 ns
CHLO	0.11 ns	0.04 ns	0.15 ns	-0.09 ns	-0.10 ns	0.25 *	0.33 **	-0.14 ns	0.39 **	0.33 **	-0.09 ns	-0.02 ns	-0.29 *	1 **	-0.07 ns	0.23 ns	0.09 ns

	LC	**PH**	**EH**	**PASP**	**HC**	**HGW**	**GRY**	**RL**	**EHARV**	**FWT**	**EASP**	**ED**	**EL**	**CHLO**	**DM**	**EPO**	**RN**
DM	-0.42	-0.16	-0.06	0.25 *	0.17	0.24 ns	-0.11	0.13 ns	-0.13 ns	-0.11	0.03 ns	-0.02	0.16 ns	-0.07	1 **	0.03 ns	0.10 ns

	**	ns	ns		ns		ns			ns		ns		ns		
EPO	0.14 ns	0.01 ns	0.52 **	-0.01 ns	-0.10 ns	0.16 ns	0.10 ns	0.22 ns	0.08 ns	0.11 ns	-0.03 ns	-0.03 ns	-0.21 ns	0.22 ns	0.03 ns	1. **	0.26 *
RN	0.09 ns	0.18 ns	0.30 *	-0.12 ns	-0.07 ns	0.23 ns	0.13 ns	-0.05 ns	0.05 ns	0.13 ns	-0.05 ns	0.05 ns	-0.03 ns	0.09 ns	0.10 ns	0.26 *	1 **

*=significant at $p \leq 0.05$; ** = significant at $p < 0.01$; ns= not significant; LC= leaf count; PH=plant height; EH= ear height; PASP = plant aspect; HC= husk cover; HWG = hundred grain weight; GRY = grain yield; RL = root lodging; EHARV= number of ears harvested; FWT = field weight; EASP= ear aspect; ED= ear diameter; CHLO= chlorophyll content; DM = days to physiological maturity; EPO= ear position.

Table 4.11 Estimates of genotypic and phenotypic variances for yield and yield-related traits in artificially infested environment

PARAMETER	**LC**	**PH**	**PASP**	**HC**	**EASP**	**ED**	**EL**	**EH**	**CHLO**	**RN**	**GNPR**	**GNPE**	**HGW**	**GRY**
Grand Mean	8.82	152.95	3.01	2.45	2.62	4.33	19.62	73.07	35.78	13.57	33.34	453.39	48.40	3941.48
SEM	1.41	10.17	3.01	0.46	0.75	0.20	2.21	6.53	4.69	0.87	3.31	54.92	3.31	923.36
EV	4.00	206.90	0.94	0.43	1.14	0.08	9.83	85.43	44.13	1.53	21.99	6032.40	21.98	1705212
GV	0.05	252.12	0.26	0.20	0.17	0.05	13.61	69.94	2.04	0.68	12.75	3700.13	4.11	69235.39
PV	4.06	459.03	1.20	0.64	1.31	0.14	23.44	155.38	46.18	2.21	34.74	9732.53	26.09	1774447
ECV	22.68	9.40	32.27	26.76	40.73	6.78	15.98	12.65	18.56	9.11	14.06	17.13	9.68	33.13
GCV	2.76	10.38	16.91	18.66	15.72	5.42	18.80	11.44	3.99	6.10	10.70	13.41	4.18	6.67
H^2	0.01	0.54	0.21	0.32	0.12	0.39	0.58	0.45	0.04	0.30	0.36	0.38	0.15	0.03
PARAMETER	LC	PH	PASP	HC	EASP	ED	EL	EH	CHLO	RN	GNPR	GNPE	HGW	GRY

GA	0.06	24.24	0.48	0.53	0.30	0.30	5.79	11.55	0.61	0.95	4.45	77.26	1.65	107.06
GAM	0.68	15.84	16.17	22.00	11.66	6.98	29.51	15.81	1.72	7.00	13.36	17.04	3.42	2.71
P-value	**0.46^{ns}**	**0.00*** **	**0.11 ^{ns}**	**0.03***	**0.23**	**0.01***	**0.00*** **	**0.00** **	**0.40^{ns}**	**0.03***	**0.01***	**0.01***	**0.19^{ns}**	**0.41^{ns}**

DYAN= days to anthesis; DYSK=days to silking; PASP= plant aspect; HC = husk cover; EASP= ear aspect; ED =ear diameter; GWPP = grain weight per plant; GNPE= grain number per ears; HGW = hundred grain weight; GRY= grain yield; SEM= standard error of the mean; EV = environmental variance; GV =genotypic variance; PV= phenotypic variance; ECV = environmental coefficient of variation; H^2 = broad sense heritability; GA= genetic advance; GAM= genetic advance as percentage of mean.

4.6 Variation and performance of hybrids under combined environments.

No significant differences were shown for mean squares for block ear diameter, grain yield, hundred-grain weight, grain number per ear, and grain number per plot. Only ear aspect showed a significant difference for the genotype mean square (Table 4.12). GCA ranged from 557189.89 for grain yield to 0.74 for plant aspect, showing significance for grain number per row and ear diameter. SCA mean squares on the other hand were not significant for grain yield, ranging from 2353558.15 for grain yield to 0.24 for ear diameter. grain number per row, grain yield, and ear diameter were significant for SCA mean squares.

Negative genotypic variances from the association and variability analysis were eliminated because they produced errors i.e, not a number (NaN). The significance of both genotypic and phenotypic correlations was tested using a two-tailed t-test. Grain yield showed a significant correlation for all traits that were considered. Grain yield recorded a significant genotypic correlation with most traits except for husk cover and grain number per plot (Table 4.13). There was no significant genotypic correlation between hundred-grain weight and husk cover. Husk cover showed significance only with days to silking and days to anthesis. The strongest genotypic correlation is showed between plant aspect and days to anthesis (4.3587) whereas the weakest correlation was showed between grain number per ears and plant aspect (-0.0297). In Table 4.14, grain yield showed a significant correlation with most traits except for husk cover (-0.08) and grain number per ear (0.0949). Grain number per ear did not show significance with most traits except for grain number per row (0.2363). Days to silking and days to anthesis showed the strongest phenotypic correlation of 0.882 whiles the weakest correlation existed between grain number per ear and ear aspect (0.0066).

Environmental, phenotypic and genotypic variances were highest for grain yield, 1695256.47, 1714056.62, and 18800.14 whilst the lowest values recorded were 0.77 for husk cover, 0.14 for ear

diameter, and 0.01 for plant aspect respectively (Table 4.15). Broad-sense heritability estimates ranged from 0.29 for ear aspect to 0.01 for grain yield. Genetic advance was highest for grain yield of 29.58 and lowest for ear diameter of 0.16. Ear aspect recorded the highest score for genetic advance as a percentage of the mean (25.95%) whereas days to anthesis recorded the lowest score (0.37%).

Table 4.12 Mean squares for combining abilities for combined environments.

SV	Df	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
Rep	3	2966533	35.84	41244	36.86	11602423***	405.2***	350.2***	7.65*	8.63***	1.22	5.82***	0.42*
Block	14	1044193	19.35	97370	29.96	265036**	33.3***	33.6**	5.25*	1.54*	2.31**	1.99**	0.17
Gen	31	1907166	25.96	102893	43.59*	171817	11.7	15.0	2.80	0.94	1.91**	0.83	0.21
GCA	7	557189.89	23.52	43494.07	53.94*	327779.02	15.25	25.27	1.01	0.74	1.72	1.18	0.46***
SCA	28	2353558.15**	27.43	55733.25	37.59*	236942.35	13.27	14.78	1.87	1.32	1.38*	0.67	0.24***
Error	83	1173981.32	21.73	73889.10	23.99	423776.52	28.36	30.72	3.32	1.03	0.85	1.07	0.10

*=significant at $p \leq 0.05$; ** = significant at $p < 0.01$; ns= not significant; GRY= grain yield; HGW= hundred grain weight; GNPE= grain number per ear; GNPR= grain number per row; GWPP= grain weight per plot; GNPR= grain number per row; DYAN= days to 50% anthesis; DYSK=days to 50% silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; ED= ear diameter; SV= source of variation; Df= degree of freedom; Rep = replication; Gen = genotype; GCA= general combining ability; SCA=specific combining ability.

Table 4.13 Genotypic correlations for combined environments

	DYAN	DYSK	PASP	HC	GWPP	EASP	ED	GNPR	GNPE	HGW	GRY
DYAN	1 **	0.07 **	0.35 **	-0.53 **	-0.07 **	0.38 *	-0.32 **	-0.43 **	-0.93 **	0.68 **	0.05 **
DYSK	0.07 **	1 **	0.67 **	-0.43 *	-0.19 **	0.79 **	-0.16 **	-0.71 **	-0.82 **	0.21 **	-0.36 **
PASP	0.35 **	0.67 **	1 **	0.29 ns	-0.98 **	0.25 **	-0.24 ns	-0.81 **	-0.02 ns	0.70 **	-0.02**
HC	-0.53 **	-0.43 *	0.29 ns	1 **	-0.14 ns	0.27 ns	-0.10ns	0.21 ns	0.18 ns	0.20 ns	-0.2 ns
GWPP	-0.07 **	-0.19 **	-0.98 **	-0.14 ns	1 **	-0.39 *	0.60 **	0.14 ns	0.71 **	-0.38 *	0.17 ns
EASP	0.38 *	0.79 **	0.25 **	0.27 ns	-0.39 *	1 **	-0.55 **	-0.17 ns	-0.08 ns	0.34 **	-0.34 **
ED	-0.32 **	-0.16**	-0.24 ns	-0.10 ns	0.60 **	-0.55 **	1 **	0.80 **	0.22 ns	-0.56 **	0.53 **
GNPR	-0.45**	-0.71 **	-0.81 **	0.21 ns	0.14 ns	-0.17 ns	0.80 **	1 **	0.98 **	-0.49 **	0.81 **
GNPE	-0.93 **	-0.82**	-0.02 ns	0.18 ns	0.71 **	-0.08 ns	0.23 ns	0.98 **	1 **	-0.65 **	0.32 **
HGW	0.68 **	0.21 **	0.70 **	0.21 ns	-0.38 *	0.34 **	-0.56**	-0.49 **	-0.65 **	1 **	-0.45 **
GRY	-0.05 **	-0.36 **	-0.02 **	-0.23 ns	0.17 ns	-0.34 **	0.53 **	0.81 **	0.31 **	-0.45 **	1 **

*=significant at $p \leq 0.05$; ** = significant at $p < 0.01$; NS= not significant; GRY= grain yield; HGW= hundred grain weight; GNPE= grain number per ear; GNPR= grain number per row; GWPP= grain weight per plot; GNPR= grain number per row; DYAN= days to 50% anthesis; DYSK=days to 50% silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; ED= ear diameter.

Table 4.14 Phenotypic correlations for combined environments

	DYAN	DYSK	PASP	HC	GWPP	EASP	ED	GNPR	GNPE	HGW	GRY
DYAN	1 **	0.88 **	0.19 *	0.00 NS	-0.26 **	0.04 NS	-0.17 *	-0.10 NS	-0.06 NS	0.30 **	-0.22 *
DYSK	0.88 **	1 **	0.34 **	0.00 NS	-0.29 **	0.11 NS	-0.25 **	-0.22 *	-0.13 NS	0.37 **	-0.30 **
PASP	0.19 *	0.34 **	1 **	0.18 *	-0.20 *	0.24 **	-0.27 **	-0.20 *	-0.08 NS	0.19 *	-0.47 **
HC	0.00 NS	0.00 NS	0.18 *	1 **	-0.01 NS	0.13NS	-0.13 NS	0.04 NS	0.15 NS	0.11 NS	-0.08 NS
GWPP	-0.26 **	-0.29 **	-0.203 *	-0.01 NS	1 **	-0.14 NS	0.13 NS	0.09 NS	0.06 NS	-0.13 NS	0.27 **
EASP	0.04 NS	0.11 NS	0.24 **	0.13 NS	-0.14 NS	1 **	-0.26 **	-0.17 *	0.00 NS	0.17 NS	-0.19 *
ED	-0.17 *	-0.25 **	-0.27 **	-0.13 NS	0.13 NS	-0.26**	1 **	0.04 NS	0.07 NS	-0.47 **	0.32 **
GNPR	-0.10 NS	-0.22 *	-0.20 *	0.04 NS	0.09 NS	-0.17 *	0.04NS	1 **	0.23 **	-0.22 *	0.37 **
GNPE	-0.06 NS	-0.13 NS	-0.08 NS	0.15 NS	0.06 NS	0.00 NS	0.07 NS	0.23 **	1 **	0.02 NS	0.09 NS

	DYAN	DYSK	PASP	HC	GWPP	EASP	ED	GNPR	GNPE	HGW	GRY
HGW	0.30 **	0.37 **	0.19 *	0.10 NS	-0.13 NS	0.17 NS	-0.47**	-0.22 *	0.02 NS	1 **	-0.27 **
GRY	-0.22 *	-0.30 **	-0.47 **	-0.08 NS	0.27 **	-0.18 *	0.32 **	0.37 **	0.09 NS	-0.27 **	1 **

*=significant at $p \leq 0.05$; ** = significant at $p < 0.01$; NS= not significant; GRY= grain yield; HGW= hundred grain weight; GNPE= grain number per ear; GNPR= grain number per row; GWPP= grain weight per plot; GNPR= grain number per row; DYAN= days to 50% anthesis; DYSK=days to 50% silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; ED= ear diameter

Table 4.15 Estimates of genotypic and phenotypic variances for yield and yield-related traits in combined environments

PARAMETER	DYAN	DYSK	PASP	HC	EASP	ED	GWPP	GNPR	GNPE	HGW	GRY
Grand Mean	59.46	60.54	2.57	2.55	2.52	4.42	1980.93	33.23	473.09	48.86	4021.35
SEM	1.81	2.04	0.51	0.44	0.45	0.16	164.16	2.37	145.22	2.28	651.01
EV	13.14	16.72	1.04	0.77	0.83	0.11	107794.02	22.6	84359.95	20.79	1695256.47
GV	0.4	0.92	0.01	0.18	0.34	0.03	31411.79	6.54	4738.07	1.77	18800.14
PV	13.54	17.65	1.05	0.95	1.17	0.14	139205.82	29.14	89098.02	22.57	1714056.62
ECV	6.09	6.75	39.73	34.51	36.19	7.58	16.57	14.30	61.39	9.33	32.37
GCV	1.06	1.58	3.80	16.40	23.28	3.92	8.94	7.69	14.54	2.72	3.40
H^2	0.02	0.05	0.01	0.18	0.29	0.21	0.23	0.22	0.05	0.08	0.01

PARAMETER	DYAN	DYSK	PASP	HC	EASP	ED	GWPP	GNPR	GNPE	HGW	GRY
GA	0.22	0.45	0.02	0.37	0.65	0.16	173.43	2.5	32.69	0.77	29.58
GAM	0.37	0.74	0.74	14.5	25.95	3.7	8.75	7.51	6.91	1.57	0.73
P-value	**0.32**	**0.23**	**0.43**	**0.009****	**0.0001*****	**0.004****	**0.002****	**0.002****	**0.23**	**0.14**	**0.42**

DYAN= days to anthesis; DYSK=days to silking; PASP= plant aspect; HC = husk cover; EASP= ear aspect; ED =ear diameter; GWPP = grain weight per plant; GNPE= grain number per ears; HGW = hundred grain weight; GRY= grain yield; SEM= standard error of the mean; EV = environmental variance; GV =genotypic variance; PV= phenotypic variance; ECV = environmental coefficient of variation; H^2 = broad sense heritability; GA= genetic advance; GAM= genetic advance as percentage of mean

4.7 Path diagrams for grain yield and yield-related traits.

In the linear model (Table 4.16, Fig 4.1), grain yield, the dependent variable, was explained by ear diameter, row number, grain number per ear, and hundred-grain weight as independent variables (GRY ~ ED + RN + GNPE + HGW). These parameters were selected as grain-related traits from the genotypic and phenotypic correlation analysis presented in Table 4.5 - 4.6. Negative covariances (dashed lines) between grain weight per plot and hundred-grain weight (-39.10) and ear diameter and hundred-grain weight (-0.98). Positive covariances were shown between row number and hundred-grain weight (6.29), row number and grain weight per pot (465.54), grain weight per plot and grain number per ear (16261.59), grain number per ear and ear diameter (14.62), ear diameter and row number (0.29), hundred-grain weight and grain number per ear (80.25). Variances (curved arrows) were shown for grain weight per plant (207797.00), grain number per ear (16482.44), row number (157.96), hundred-grain weight (9.69), ear diameter (0.14), and grain yield (1021267.39). The contributions of the explanatory variables to grain yield are largest for ear diameter (639.81) and smallest for row number (-192.91). Row number ($b = -192.908$, $p < 0.05$) and hundred-grain weight are statistically significant and negative. Grain weight per plot ($b = 0.174$, $p > 0.05$) and row number ($b = -192.908$, $p < 0.05$) were not significant and positive. Only grain weight per ear was significant and positive ($b = 6.025$, $p < 0.05$). The unadjusted R^2 value was 38.8%. The determinants of model fit ie. Root mean square of approximation (RMSEA) and Comparative Fit Index (CFI) recorded 0.00 and 1.00 respectively.

In the linear model (Table 4.17, Fig 4.2) parameters for the path diagram in Figure 4.2 under the artificially infested environment. In the linear model, grain yield, the dependent variable, was explained by hundred-grain weight, ear diameter, row number, grain number per ear, and grain number per row as independent variables (GRY ~ HGW + ED + RN + GNPE + GNPR). These parameters

were selected as grain-related traits from the genotypic and phenotypic correlation analysis presented in Table 4.10 - 4.11. Negative covariances (dashed lines) were shown between hundred-grain weight and ear diameter (-0.74), ear diameter and grain number per ear (-0.16), and hundred-grain weight and grain number per ear (-2.39), and grain number per ear and ear diameter (-0.74). Variances (curved arrows) were shown for row number (2.15), hundred-grain weight (25.30), grain number per row (34.60), ear diameter (0.14), grain yield (1276800.79), grain number per ear (9601.89), and hundred-grain weight (25.30). Hundred-grain weight ($b = 24.604$, $p > 0.05$) was not statistically significant and positive. Ear diameter ($b = 1222.588$, $p < 0.05$), row number ($b = 1966.398$, $p<0.05$), and grain number per row ($b = 792.309$, $p<0.05$) were positive and significant. Only grain number per ear ($b = -53.057$, $p<0.05$) was shown to be negative and significant. The unadjusted R^2 value was 28.2%. The determinant of model fit ie. Root mean square of approximation (RMSEA) and Comparative Fit Index (CFI) recorded 0.00 and 1.00 respectively. In the linear model (Table 4.18, Fig 4.3), grain yield, the dependent variable, was explained by grain weight per plot, ear diameter, grain number per row, grain number per ear, and hundred-grain weight as independent variables (GRY ~ GWPP + ED + GNPR + GNPE + HGW). These parameters were selected as grain-related traits from the genotypic and phenotypic correlation analysis presented in Table 4.13 and Table 4.14. Negative covariances (dashed lines) were shown for hundred-grain weight and ear diameter (- 0.82) and grain number per row and hundred-grain weight (-0.62). Variances (curved arrows) were shown for row grain number per row (29.10), grain weight per plot (406787.43), grain number per ear (87280.38), grain yield (1244200.83), ear diameter (0.15), and hundred-grain weight (22.71).

Grain weight per plant ($b = 0.280$, $p < 0.05$) was positive and significant. Hundred-grain weight ($b = -21.079$, $p>0.05$) and grain number per ear ($b = -0.099$, $p>0.05$) were negative and not significant. Ear diameter ($b = 878.777$, $p<0.05$) and grain number per row ($b = 88.977$, $p<0.05$) were positive and

significant. The unadjusted R^2 value was 28.1%. The determinant of model fit ie. Root mean square of approximation (RMSEA) and Comparative Fit Index (CFI) recorded 0.00 and 1.00 respectively.

Table 4.16 Path diagram model for selected parameters under naturally infested environment.
Model: GRY ~ ED + RN + GNPE + HGW

Parameter	Intercept (b)	Std.Err	z-value	P(>|z|)
GWPP	0.174	0.282	0.617	0.537
ED	639.814	421.682	1.517	0.129
RN	-192.908	72.709	-2.653	0.008
GNPE	6.025	2.241	2.688	0.007
HGW	-87.512	38.755	-2.258	0.024
Variances:				
GRY	1244201	155525.1	8	0
Root mean square of approximation (RMSEA) = 0.000				
Comparative Fit Index (CFI) = 1.000				
R-Square = 0.388				

FWT= field weight; ED = ear diameter; RN= row number; GNPE= grain number per ear; GRY= grain yield; GWPP = rain weight per plot; ED= ear diameter; HGW = hundred-grain weight; Std.Err = standard error.

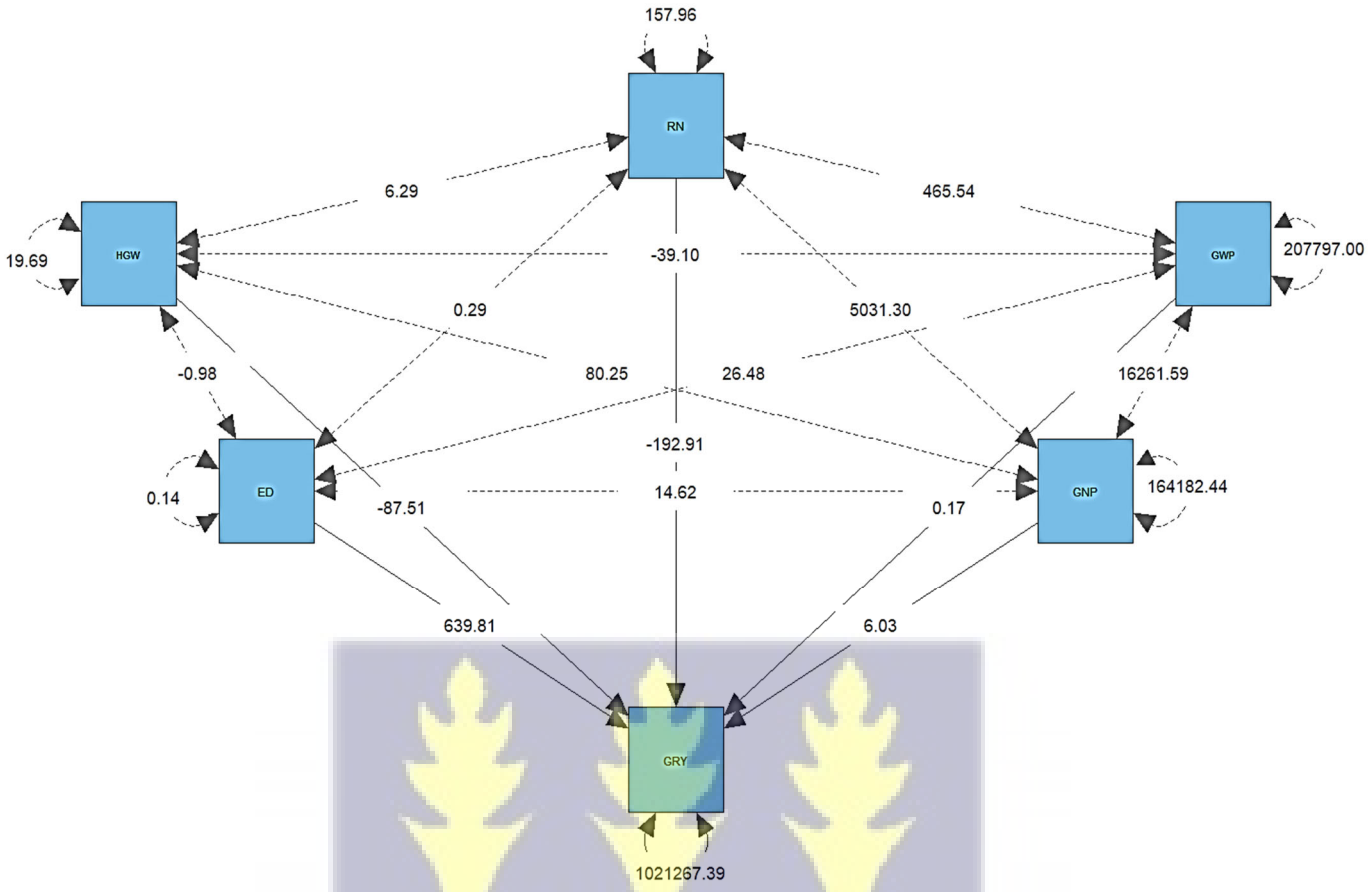


Figure 4.1 Path biplot showing the relationship between grain yield and yield related traits under naturally infested environment. FWT= field weight; ED = ear diameter; RN= row number; GNPE= grain number per ear; GRY= grain yield; GWPP = rain weight per plot; ED= ear diameter; HGW = hundred-grain weight.

Table 4.17 Path diagram model for selected parameters under artificially infested environment.
Model : GRY ~ HGW + ED + RN + GNPE + GNPR

Parameter	Intercept (b)	Std.Err	z-value	P(>|z|)
HGW	24.604	32.281	0.762	0.446
ED	1222.588	430.297	2.841	0.004
RN	1966.398	716.576	2.744	0.006
GNPE	-53.057	19.804	-2.679	0.007
GNPR	792.309	265.641	2.983	0.003
Variances:				
GRY	1276800.793	225708.625	5.657	0
Root mean square of approximation (RMSEA) = 0.000				
Comparative Fit Index (CFI) = 1.000				
R-Square = 0.282				

HGW = hundred grain weight; FWT= field weight; ED = ear diameter; RN= row number; GNPR= grain number per row; GNPE= grain number per ear; GRY= grain yield; Std.Err = standard error.

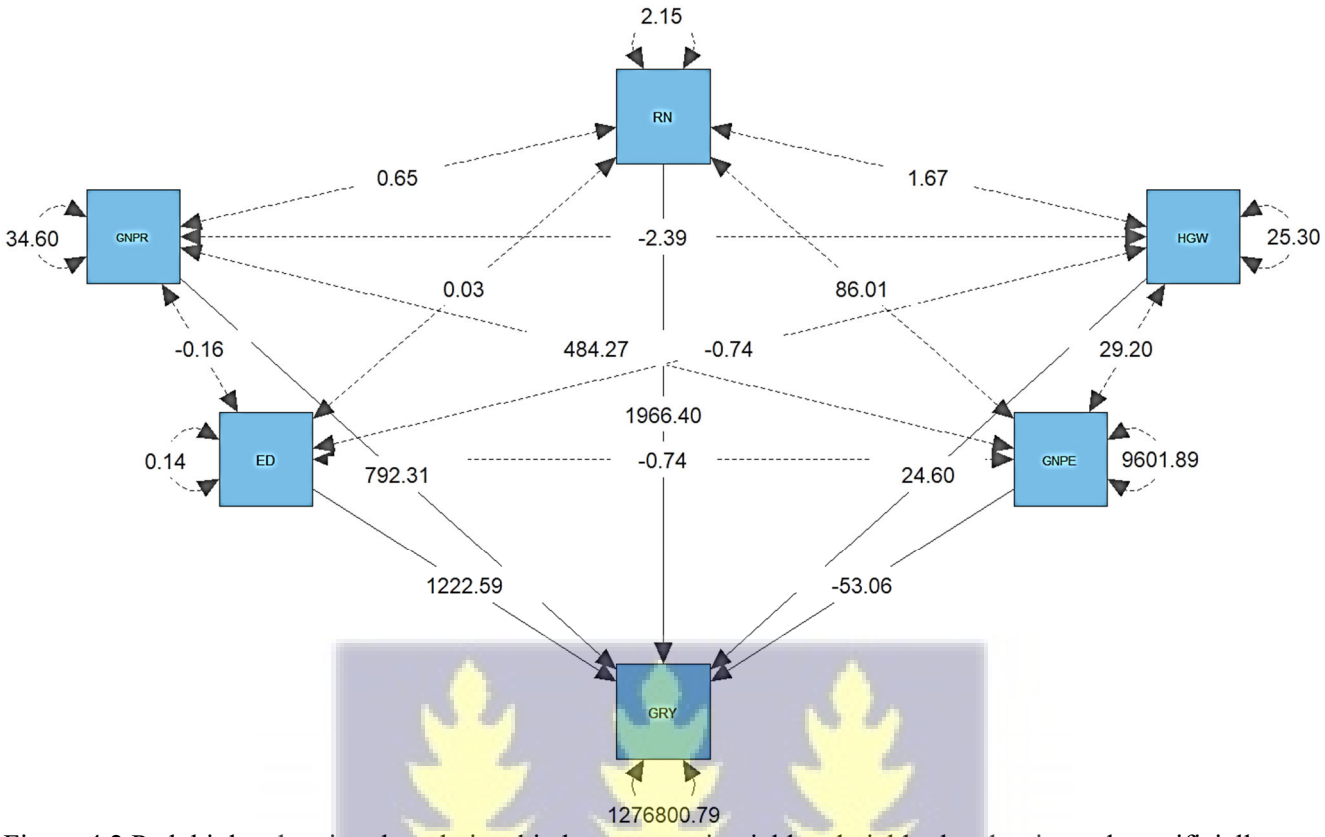


Figure 4.2 Path biplot showing the relationship between grain yield and yield related traits under artificially infested environment. HGW = hundred grain weight; FWT= field weight; ED = ear diameter; RN= row number; GNPR= grain number per row; GNPE= grain number per ear; GRY= grain yield.

Table 4.18 Path diagram model for selected parameters under combined environments.
Model : GRY ~ GWPP + ED + GNPR + GNPE + HGW

Parameter	Intercept (b)	Std.Err	z-value	P(>|z|)
GWPP	0.280	0.162	1.728	0.084
ED	878.777	301.308	2.917	0.004
GNPR	88.977	19.494	4.564	0.000
GNPE	-0.099	0.348	-0.284	0.776
HGW	-21.079	24.364	-0.865	0.387
Variances:				
GRY	1244200.828	155525.1	8	0
Root mean square of approximation (RMSEA) = 0.000				
Comparative Fit Index (CFI) = 1.000				
R-Square = 0.281				

GNPE= grain number per ear; GWPP= grain weight per plot; ED = ear diameter; HGW = hundred grain weight; GNPR= grain number per row; GRY= grain yield; Std.Err = standard error.

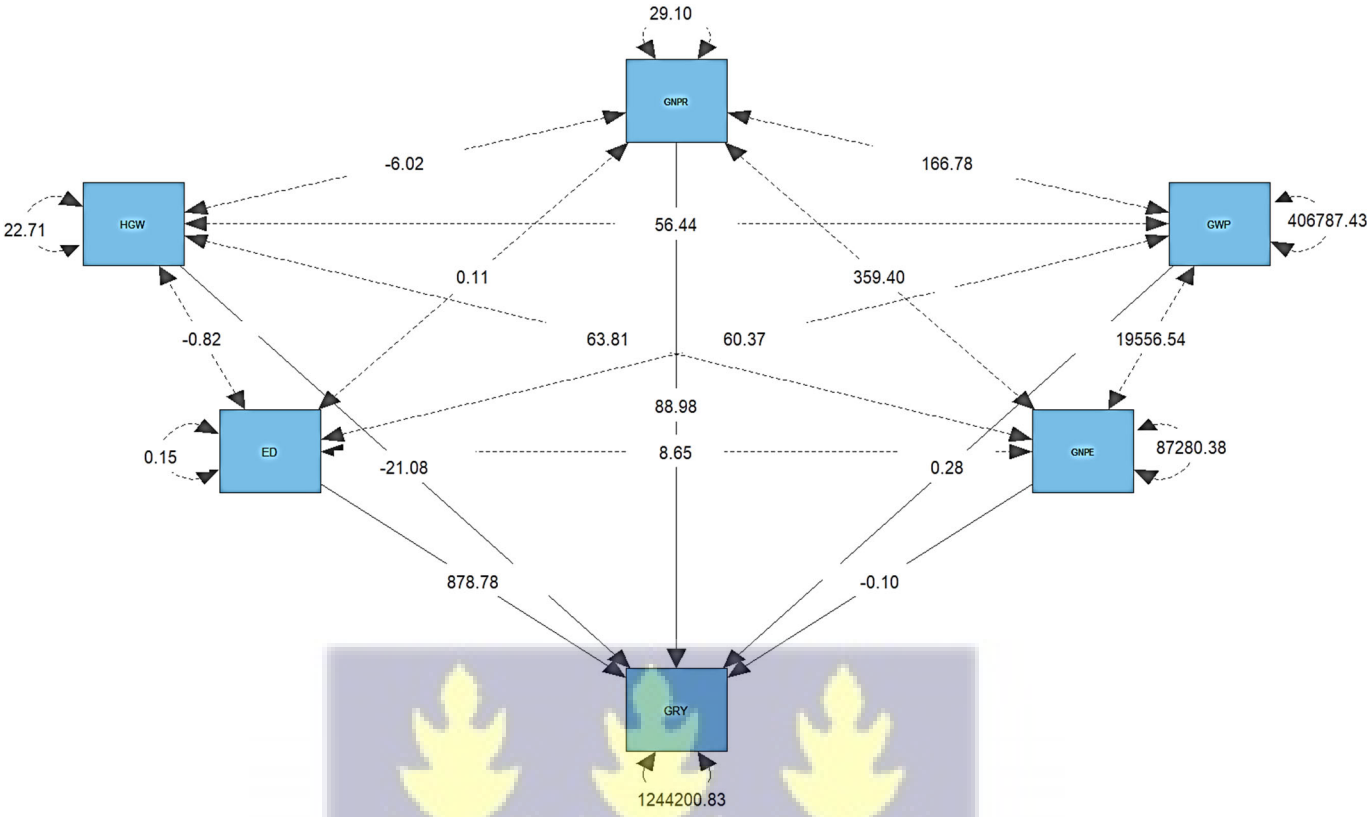


Figure 4.3 Path biplot showing the relationship between grain yield and yield related traits under combined environments. GNPE= grain number per ear; GWPP= grain weight per plot; ED = ear diameter; HGW = hundred grain weight; GNPR= grain number per row; GRY= grain yield.

4.8 Top 10 and bottom 5 genotypes for grain yield, MSV incidence and severity.

Ten hybrids including one check were selected for high grain yield. 9450 × WYML 10 was the highest performing hybrid with a grain yield of 6030.88 kg/ha with an incidence of 25.89% and severity of 27.95% (Table 4.19). The least performing hybrid for grain yield among the top 10 hybrids was WYML 6 × 9450 which recorded a grain yield of 4402.50 kg/ha with an incidence of 31.25% and severity of 19.40%. The bottom 5 hybrids ranged from WYML 8 × WYML 11 which recorded a grain yield of 3378.67 kg/ha, an incidence of 33.68% and severity of 70.18% to WYML 8 × WYML 9 which recorded a grain yield of 2262.81 kg/ha, the incidence of 80% and severity of 50%. The relative percentage contributions are shown in Figure 4.4.

In the artificially infested environment (Table 4.20), the hybrid WYML 6 × WYML 8 outperformed all other hybrids with a grain yield of 6406.28 kg/ha, an incidence of 31.25%, and a severity of 19.40%. The worst-performing hybrid among the top 10 hybrids, WYML 11 × WYML 9, recorded a grain yield of 4255.96 kg/ha, an incidence of 72.91%, and a severity of 32.60%. Among the bottom 5 hybrids, WYML 8 × 9450 recorded a grain yield of 3202.85 kg/ha, an incidence of 40.00%, and a severity of 24.06%. WYML 15 × WYML 11 was the worst performing hybrid in the bottom 5 hybrids and recorded a grain yield of 1897.01 kg/ha, incidence of 50%, and severity of 29.50%. Their relative percentage contributions are shown in Figure 4.5.

Across all environments (Table 4.21), WYML 6 × WYML 8 was the top-performing hybrid among the top 10 hybrids. It recorded a grain yield of 5461.86 kg/ha, an incidence of 31.25%, and a severity of 44.70%. The least performing hybrid among the top 10 hybrids was WYML 11 × WYML 10 which recorded a grain yield of 4294.32 kg/ha, an incidence of 42.41%, and a severity of 46.25%. For the bottom 5 hybrids, WYML 10 × WYML 9 recorded a grain yield of 3355.32 kg/ha, an incidence of 35.36%, and a severity of 54.70 %. On the other hand, WYML 8 × WYML 9 was the worst-performing hybrid among the bottom 5 hybrid with a grain yield of 2625.43 kg/ha, an incidence of 52.85%, and severity of 37.42%. Their relative percentage contributions are shown in Figure 4.6.

Table 4.19 Top 10 and bottom 5 genotypes for yield and yield-related components in naturally infested environment.

Genotype	GRY	INCI	SEV	Genotype	GRY	INCI	SEV
Top 10				**Bottom 5**			
9450 × WYML 10	6030.88	25.89	27.95	WYML 8 × WYML 11	3378.67	33.68	70.18
WYML 15 × WYML 10	5134.12	25	42.7	WYML 15 × 9450	3287.74	27.67	60.0
WYML 6 × WYML 15	4801.88	20.53	22.51	WYML 11 × WYML 9	3251.52	71.42	90.0
9450 × WYML 11	4744.18	53.57	22.51	WYML 8 × WYML 15	2784.30	37.5	80.0
WYML 12 × WYML 11	4680.53	42.85	20.18	WYML 8 × WYML 9	2262.81	80.00	50.0
9450 × WYML 9	4644.971	39.58	23.29				
WYML 6 × WYML 8	4517.44	43.75	12.42				
WYML 12 × WYML 9	4447.63	30.95	22.51				
WYML 8 × 9450	4426.40	52.08	19.40				
WYML 6 × 9450	4402.50	31.25	23.45				

GRY = grain yield; INCI = incidence; SEV = severity.

Table 4.20 Top 10 and bottom 5 genotypes for yield, incidence, and severity in artificially infested environment.

Genotype	GRY	INCI	SEV	Genotype	GRY	INCI	SEV
Top 10				**Bottom 5**			
WYML 6 ×WYML 8	6406.28	31.25	19.40	WYML 8 × 9450	3202.85	40	24.06
WYML 12 × WYML 9	5442.20	87.50	36.49	WYML 8 × WYML 9	2988.045	73.21	24.84
WYML 11 × WYML 10	5038.95	31.25	22.51	WYML 8 × WYML 11	2926.635	85.71	25.62
9450 × WYML 11	4912.14	43.75	23.29	WYML 10 × WYML 9	2896.704	37.5	19.40

WYML 8 × WYML 10	4643.10	43.75	16.30	WYML 15 × WYML 11	1897.016	50	29.50
WYML 6 × WYML 9	4631.41	52.67	24.84				
WYML 6 × WYML 10	4509.02	80.35	27.17				
9450 × WYML 10	4405.42	75.00	42.70				
9450 × WYML 9	4382.10	71.42	22.51				
WYML 11 × WYML 9	4255.96	72.91	32.60				

GRY = grain yield; INCI = incidence; SEV = severity.

Table 4.21 Mean performance of top 10 and bottom 5 genotypes for yield, incidence, and severity in combined environments

Genotype	**GRY**	**INCI**	**SEV**	**Genotype**	**GRY**	**INCI**	**SEV**
Top 10				**Bottom 5**			
WYML 6 ×WYML 8	5461.86	31.25	44.70	WYML 10 × WYML 9	3355.32	35.26	54.70
9450 × WYML 10	5218.15	50	46.35	WYML 8 × WYML 11	3152.65	66.51	62.81
WYML 12 × WYML 9	4944.92	70.53	63.24	WYML 8 × WYML 15	3007.18	42.70	48.54
9450 × WYML 11	4828.16	43.75	51.64	WYML 15 × WYML 11	2952.05	38.39	49.75
9450 × WYML 9	4513.539	61.75	46.25	WYML 8 × WYML 9	2625.43	52.85	37.42
WYML 6 × WYML 9	4496.89	48.48	57.42				
WYML 8 × WYML 10	4482.81	34.82	43.15				
WYML 12 × WYML 11	4377.32	15.47	46.21				
WYML 6 × WYML 10	4296.45	61.60	43.58				
WYML 11 × WYML 10	4294.32	42.41	46.25				

GRY = grain yield; INCI = incidence; SEV = severity.

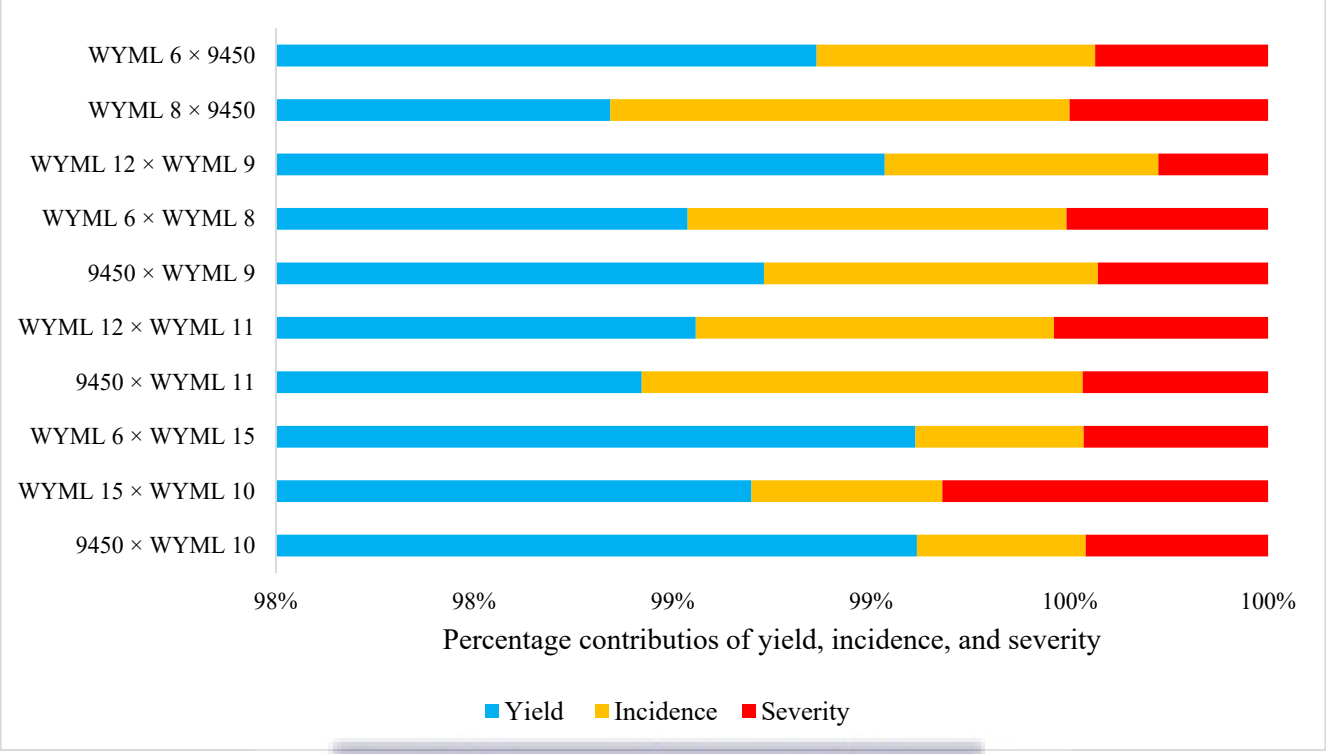


Figure 4.4 Performance of the top 10 genotypes under naturally infested environment.

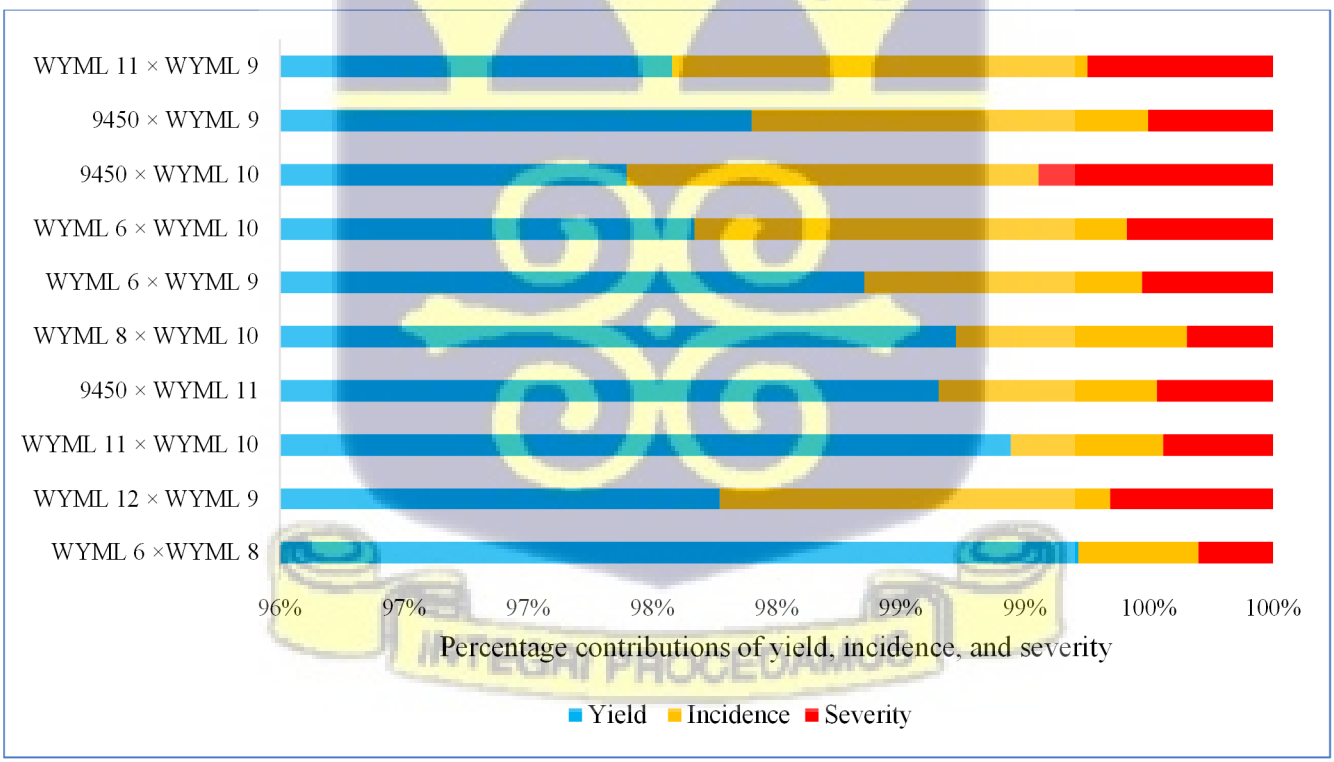


Figure 4.5 Performance of the top 10 genotypes under artificially infested environment.

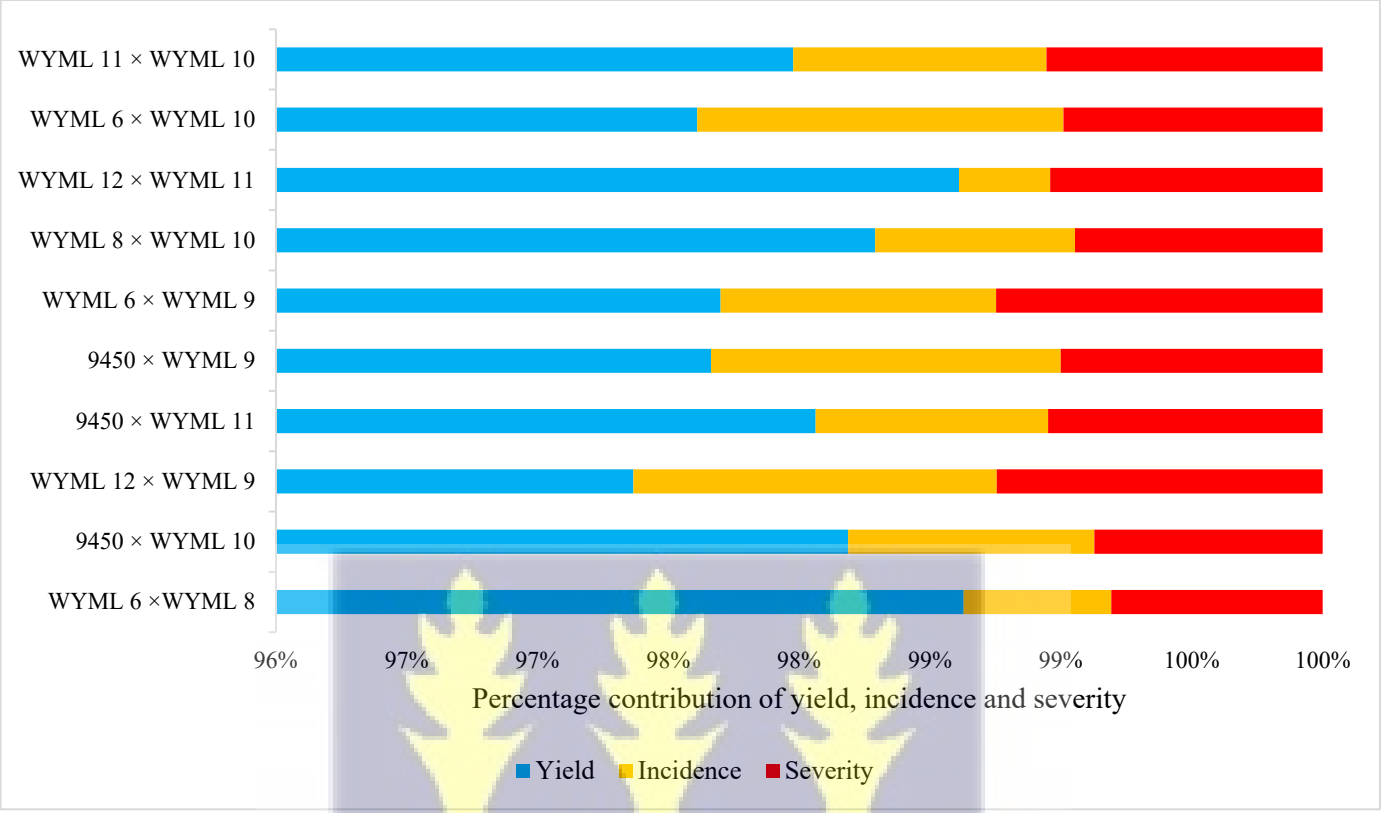


Figure 4.6 Performance of the top 10 genotypes under combined environments

4.9 Correlation between traits and principal component analysis

A correlation plot was done to determine the strength and direction of the relationship between traits (Figure 4.7). Of these, yield and yield-related traits were selected for PCA (Figure 4.8). For dimension 1, grain yield recorded the highest contribution whereas ear aspect recorded the least contribution. In all, the traits contributed 19.46% (Figure 4.10, Figure 4.11) to the variance observed in dimension 1 (Table 4.21). Days to anthesis, grain weight per plot, severity, and days to silking were the traits that contributed most to the total variation of 18.84 % (Figure 4.10, Figure 4.11) in dimension 2 (Figure 4.12). Cumulatively dimensions 1 and 2 contributed a total of 38.30 % to the variation observed (Figure 4.9, Figure 4.12). Variables that are correlated to each other fall within the same dimension (Table 4.22). Days to anthesis, days to silking, and severity are positively correlated. Ear diameter is negatively correlated to plant aspect, grain yield is negatively correlated to anthesis silking interval. Incidence showed a weak positive correlation with severity.

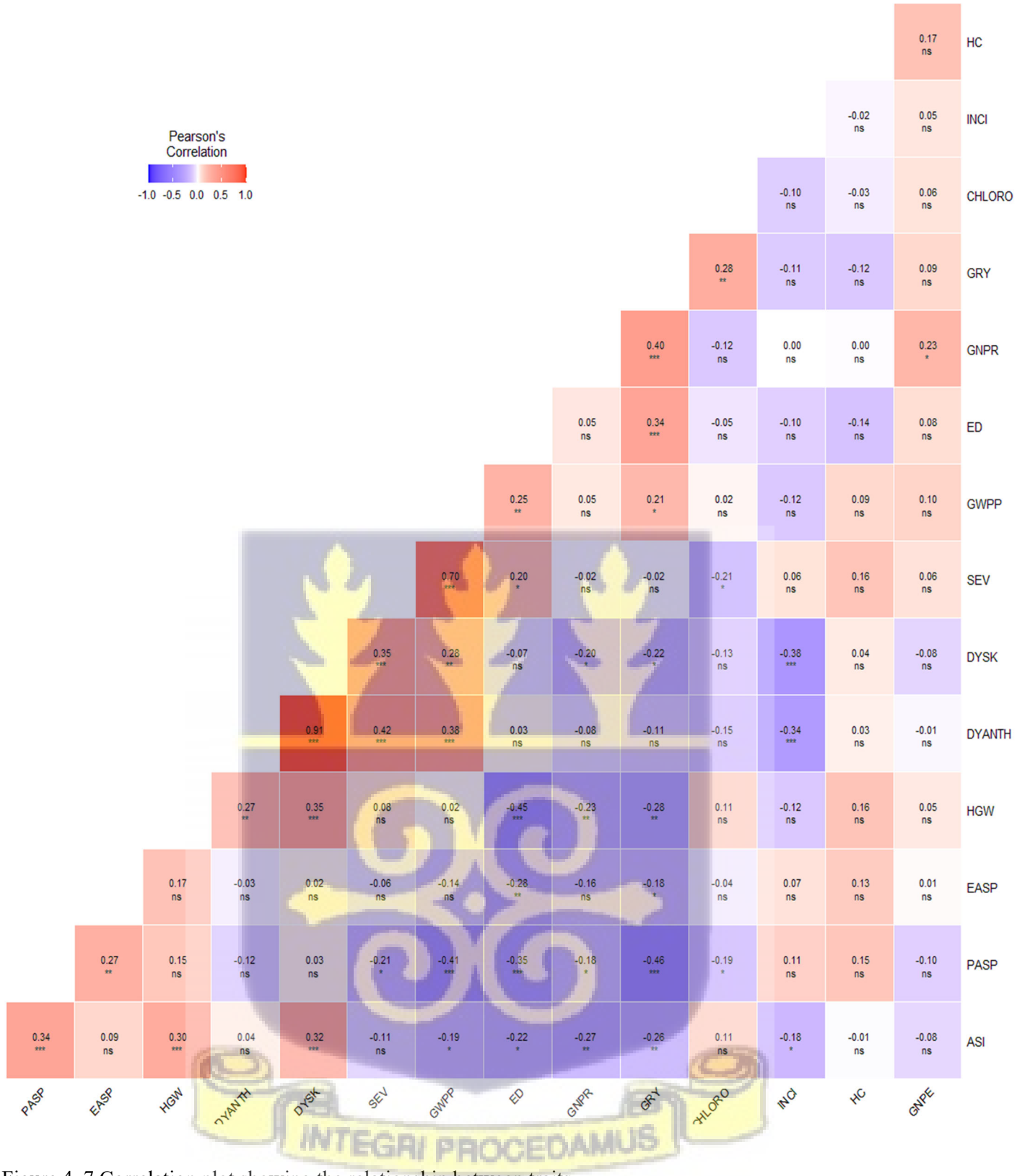


Figure 4. 7 Correlation plot showing the relationship between traits

*** = significant at p≤ 0.001; **= significant at p≤ 0.01; * significant at p≤ 0.05; ns = not significant; DYANTH= days to anthesis; DYSK = days to silking; PASP = plant aspect; HC= husk cover; INCI = incidence; SEV= severity; GWPP =grain weight per plot; EASP= ear aspect; ED= ear diameter; CHLORO= chlorophyll

content; GNPR= grain number per row; GNPE= grain number per ear; HGW= hundred grain weight; GRY= grain yield.

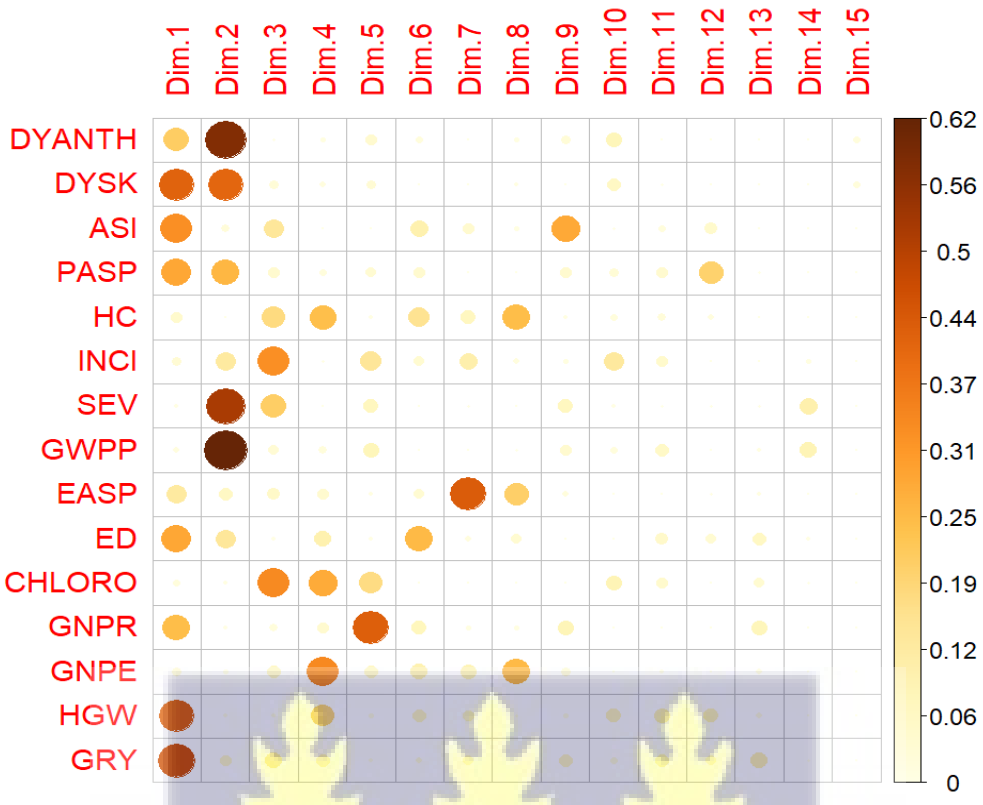


Figure 4.8 Correlation plot showing the total contribution of each trait to each dimension.
DYANTH= days to anthesis; DYSK = days to silking; ASI = anthesis silking interval; PASP = plant aspect; HC= husk cover; INCI = incidence; SEV= severity; GWPP =grain weight per plot; EASP= ear aspect; ED= ear diameter; CHLORO= chlorophyll content; GNPR= grain number per row; GNPE= grain number per ear; HGW= hundred grain weight; GRY= grain yield.

Table 4.22 Eigenvalues and variance contributions to each dimension

Dimension	Eigenvalue	Variance (%)	Cumulative variance (%)	Standard deviation
Dim.1	2.91904027	19.4602685	19.46027	1.70852
Dim.2	2.82718925	18.8479283	38.3082	1.681425
Dim.3	1.54519964	10.3013309	48.60953	1.243061
Dim.4	1.3657673	9.1051153	57.71464	1.168661
Dim.5	1.10607286	7.3738191	65.08846	1.0517
Dim.6	0.8991666	5.994444	71.08291	0.948244
Dim.7	0.85539585	5.702639	76.78555	0.924876
Dim.8	0.79378619	5.2919079	82.07745	0.890947
Dim.9	0.6882512	4.5883413	86.66579	0.829609
Dim.10	0.5365015	3.5766767	90.24247	0.732463
Dim.11	0.45380533	3.0253689	93.26784	0.673651
Dim.12	0.42156109	2.8104072	96.07825	0.649277
Dim.13	0.32717201	2.1811467	98.25939	0.57199
Dim.14	0.22178129	1.4785419	99.73794	0.470937
Dim.15	0.03930961	0.2620641	100	0.198267

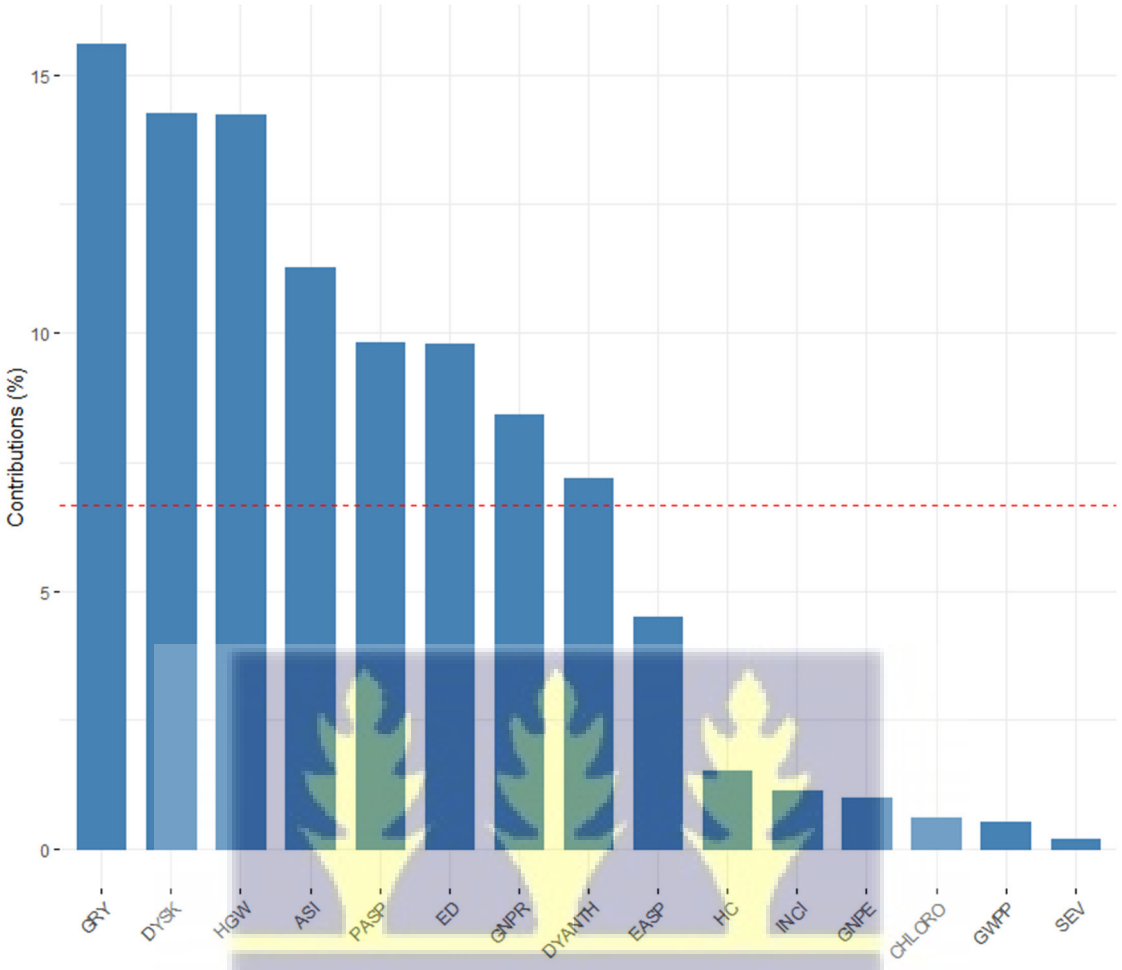


Figure 4.9 Contribution of the variables to the first principal component. GRY = grain yield; DYSK= days to silking; ASI= anthesis silking interval; PASP= plant aspect; ED= ear diameter; GNPR= grain number per ear; DYANTH= days to anthesis; HC= husk cover; INCI= disease incidence; GNPE= grain number per ear; CHLORO = chlorophyll content; GWPP= grain weight per plant; SEV= disease severity.

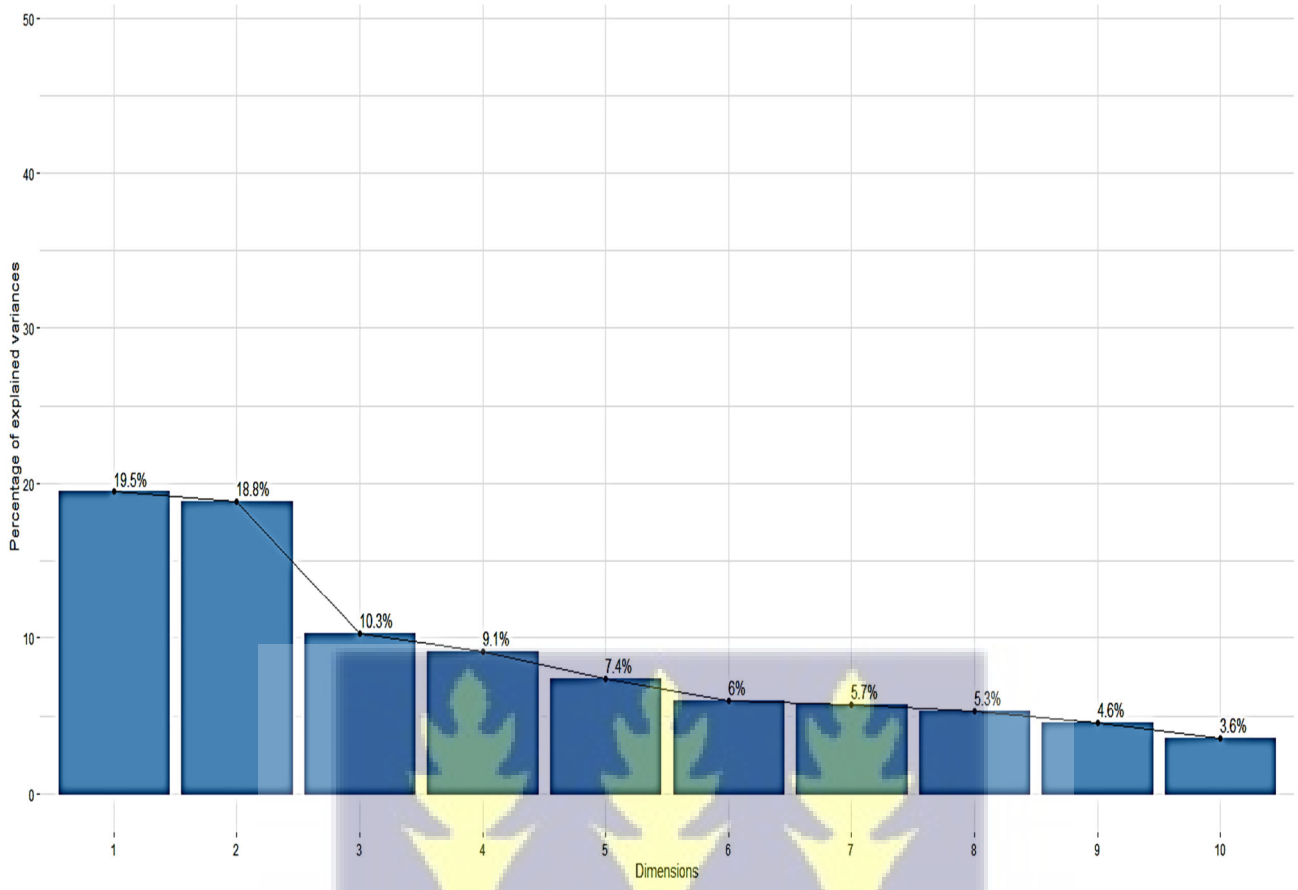


Figure 4.10 Scree plot showing the percentage of variance explained by each dimension.

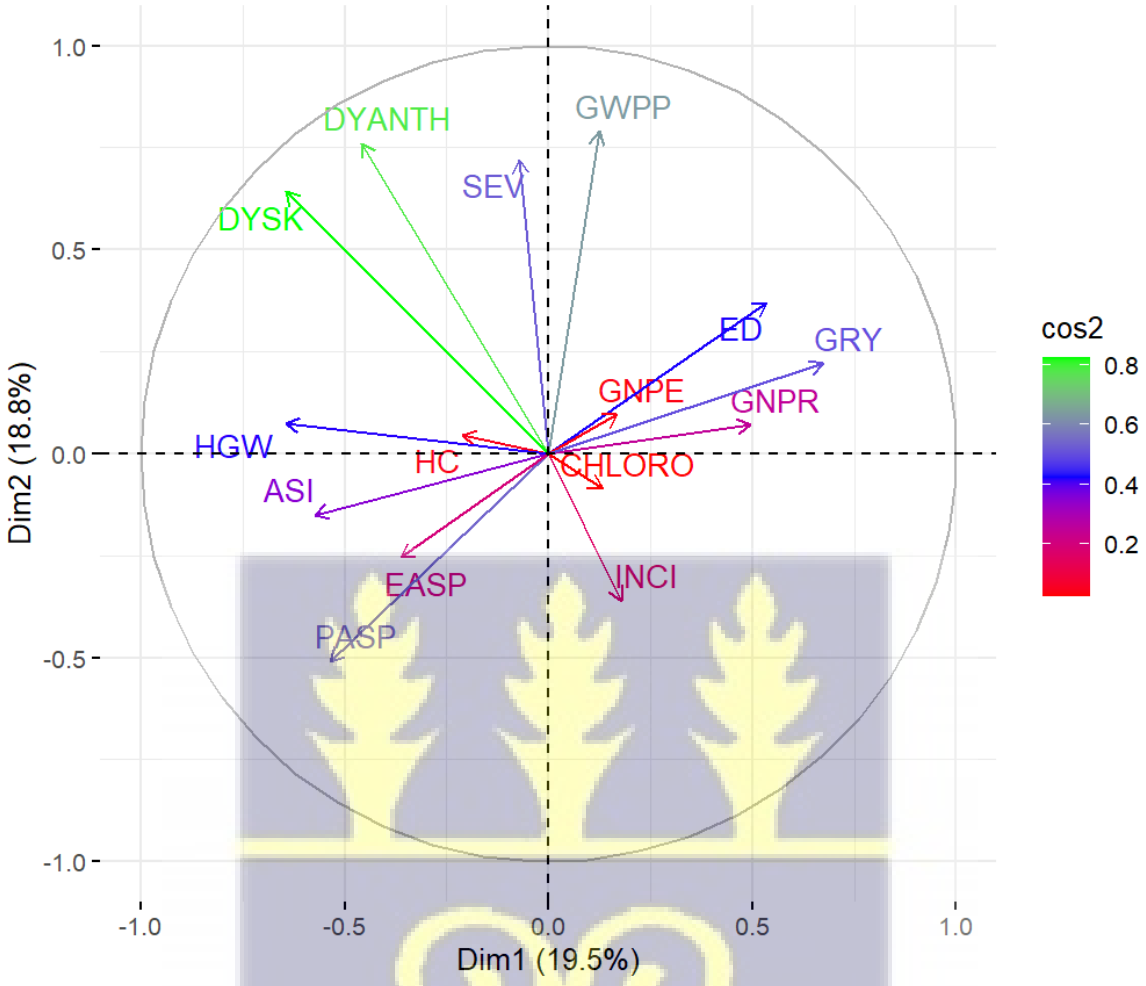


Figure 4.11 PCA biplot showing the variances explained by the first two principal components . GRY = grain yield; DYSK= days to silking; ASI= anthesis silking interval; PASP= plant aspect; ED= ear diameter; GNPR= grain number per ear; DYANTH= days to anthesis; HC= husk cover; INCI= disease incidence; GNPE= grain number per ear; CHLORO = chlorophyll content; GWPP= grain weight per plant; SEV= disease severity.

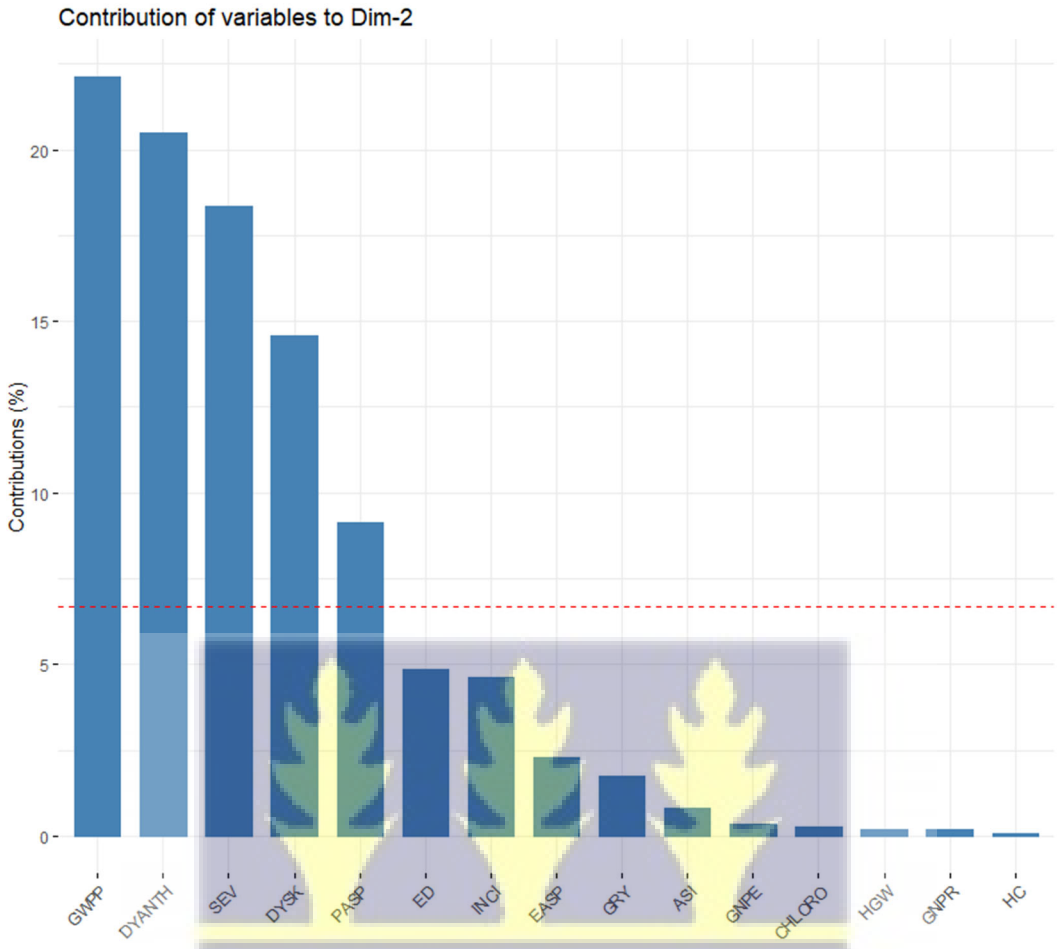


Figure 4.12 Contribution of the variables to the second principal component. GRY = grain yield; DYSK= days to silking; ASI= anthesis silking interval; PASP= plant aspect; ED= ear diameter; GNPR= grain number per ear; DYANTH= days to anthesis; HC= husk cover; INCI= disease incidence; GNPE= grain number per ear; CHLORO = chlorophyll content; GWPP= grain weight per plant; SEV= disease severity.

4.10 Combining abilities for yield and yield-related traits under naturally infested environment

Specific combining abilities for grain yield were significant and varied from 1999.78 for WYML 10 × WYML 9 to -465.57 in WYML 10 × WYML 12. WYML 6 × WYML 10 showed the highest SCA value for hundred-grain weight whereas WYML 11 × WYML 15 was the least SCA value (Table 4.23). However, WYML 11 × WYML 15 and WYML 11 × WYML 12 were the only hybrids with significant SCA values for hundred-grain weight. SCA for grain number per ear ranged from 1407.57

for WYML 6 × WYML 15 (being the only significant value for this trait) to -170.27 for WYML 6 × WYML 10. SCA for grain number per row ranged from 4.98 for WYML 15 × WYML 12 to -3.36 for WYML 8 × WYML 12. SCA for grain weight per plot was significant for WYML 6 × WYML 10, WYML 6 × WYML 12, WYML 9 × 9450, and WYML 10 × WYML 11 and ranged from 769.27 for WYML 10 × WYML 11 to -337.52 for WYML 11 × WYML 12. SCA for days to anthesis ranged from 5.62 for WYML 15 × 9450 (significant) to -2.92 for WYML 6 × 9450. SCA for days to silking was significant for WYML 6 × 9450 and ranged from 6.06 to -3.53 for WYML 10 × WYML 12. SCA for plant aspect was significant for WYML 8 × WYML 10, WYML 9 × 9450, and WYML 10 × WYML 11. It ranged from 1.22 for WYML 8 × WYML 11 to -1.7 for WYML 10 × WYML 11. SCA for ear diameter ranged from 0.51 for WYML 9 × WYML 12 to -0.21 for WYML 8 × WYML 9.

GCA for grain yield ranged from 195.00 for WYML 12 to -302.54 for WYML 9 (Table 4.24). Hundred-grain weight GCA was significant for WYML 11 and WYML 15, values ranged from 2.06 for WYML 15 to -1.98 for WYML 11. GCA for grain number per ear ranged from 164.81 for WYML 6 to -68.33 for WYML 9. GCA for WYML 15 was the only significant value for grain number per row, where values ranged from 1.92 for WYML 6 to -3.02 for WYML 15 (significant). GCA for days to anthesis was significant for only WYML 6. GCA for days to silking ranged from 1.9 for WYML 9 to -2.25 for WYML 6. It showed significance for WYML 6 and WYML 9. GCA for ear diameter was significant for WYML 6, WYML 9, WYML 11, and WYML 15. GCA values for ear diameter varied from 0.19 for WYML 6 to -0.23 for WYML 15. Variance ratios for GCA and SCA are shown in Table 4.25. GCA/SCA ratios ranged from 0.47 for husk cover to -0.03 for grain yield.

Table 4.23 Specific combining ability effects for grain yield and yield related traits for naturally infested environment

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 6 × WYML 8	1023.75	-2.48	-27.92	3.38	109.97	0.67	0.96	0.05	-0.85	-0.11	-1.11	0.33
WYML 6 × WYML 9	883.04	-4.38	-97.12	4.33	269.17	-0.92	-2.03	-1.45	-0.09	-1.26	-0.31	0.26
WYML 6 × WYML 10	133.28	3.21	-170.27	-2.46	399.17*	0.72	2.36	0.6	-1	0.43	-1.16	0.10
WYML 6 × WYML 11	539.02	-3.18	-115.32	1.73	150.87	-1.37	-1.38	-0.45	0.1	-0.16	0.58	0.27
WYML 6 × WYML 12	-210.81	-0.08	-76.17	0.53	668.37***	-1.77	-2.78	0.05	-0.5	-0.61	-0.51	-0.18
WYML 6 × WYML 15	1067.09	-0.23	1407.57***	3.23	111.77	-1.77	-1.28	1.15	-0.45	0.08	0.98	0.28
WYML 6 × 9450	429.78	-2.58	-92.17	3.63	-180.92	-2.92	-3.03	-0.35	-0.8	-0.61	-0.46	-0.10
WYML 8 × WYML 9	-818.00	-0.73	100.72	-0.56	-90.62	1.07	-1.18	-2.1	-0.25	-0.51	0.08	-0.21
WYML 8 × WYML 10	770.44	-3.13	98.07	5.13	-219.62	-1.27	-1.78	-1.05	-1.65***	-0.81	-0.76	0.37
WYML 8 × WYML 11	22.40	1.96	42.02	0.83	253.07	1.62	0.46	-1.1	1.22	0.58	-0.51	-0.15
WYML 8 × WYML 12	426.47	-3.43	-41.32	-3.36	160.57	0.22	0.56	-0.1	0.45	-0.36	-0.11	0.08
WYML 8 × WYML 15	-551.96	1.41	-171.57	-2.16	163.97	-1.77	-1.43	0.50	0.35	-0.66	0.38	0.25

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 8 × 9450	852.19	-3.93	75.17	2.73	208.27	-0.92	-1.18	0.00	-0.1	-0.36	0.43	0.41
WYML 9 × WYML 10	276.23	0.96	58.87	2.08	61.57	-1.87	-1.28	0.95	0.05	2.33	1.03	-0.04
WYML 9 × WYML 11	-90.38	2.56	60.82	1.78	294.27	-1.97	-1.53	0.4	-0.4	-0.96	1.28*	-0.16
WYML 9 × WYML 12	883.63	-3.83	71.97	1.58	145.77	-2.87	-2.93	-0.6	0.7	-0.06	-0.31	0.51**
WYML 9 × WYML 15	524.84	-4.48	-96.27	-0.21	-20.82	-0.87	-2.43	-1.5	-0.9	-0.51	-1.31*	0.35
WYML 9 × 9450	1085.12	0.16	16.97	-1.81	619.47***	-1.52	-1.18	0.5	-1.35**	-0.81	-0.26	0.36
WYML 10 × WYML 11	-263.46	-0.83	103.67	2.48	769.27***	0.17	-1.63	-0.55	-1.7***	-0.51	0.43	0.05
WYML 10 × WYML 12	-465.57	-3.73	13.82	-3.21	-21.22	-0.72	-3.53	0.95	-0.2	0.13	-0.66	0.22
WYML 10 × WYML 15	1340.95	-2.88	-62.42	-0.01	309.17	-0.72	-0.53	-0.45	-0.3	-0.81	-0.66	-0.06
WYML 10 × 9450	1999.78**	-1.73	53.82	3.38	-67.52	-2.87	-2.78	-0.45	-0.75	-0.11	0.38	0.22
WYML 11 × WYML 12	841.07	-5.13*	23.27	0.98	-337.52	-1.32	-0.28	0.4	-0.1	0.68	0.08	0.17
WYML 11 × WYML 15	409.74	2.71	-138.47	0.68	4.87	-1.32	-1.78	-0.5	-0.2	0.58	-0.91	0.00
WYML 11 × 9450	908.89	-3.63	124.77	3.08	39.17	-0.97	-2.03	-1	-0.15	0.78	-0.36	0.21

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 12 × WYML 15	555.64	-5.68*	-77.32	4.98	338.37	-0.72	-0.18	0.00	0.5	-0.91	-0.01	0.09
WYML 12 × 9450	-195.40	2.96	45.92	0.88	-0.32	-0.37	0.56	0	0.25	0.63	-0.46	-0.15
WYML 15 × 9450	-527.55	-2.18	-116.32	0.08	-72.92	5.62***	6.06**	0.6	-0.05	-0.16	0.53	0.27

Table 4.24 General combining abilities of 8 inbred lines for yield and yield-related traits in the naturally infested environment

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 6	110.33	-0.53	164.81	1.92	314.37***	-1.51*	-2.25**	-0.53	0.1	-0.4	0.01	0.19*
WYML 8	-288.18	0.81	-38.53	-0.17	-110.82	-0.01	0.4	0.11	0.25	0.35	0.11	-0.03
WYML 9	-302.54	0.21	-68.33	-0.12	35.97	1.08	1.9*	0.61	0	0	-0.18	-0.16*
WYML 10	168.71	0.61	-39.18	0.17	-119.02	-0.06	-0.5	0.06	-0.1	0.3	0.66**	-0.1
WYML 11	-27.09	-1.98*	-59.13	-1.02	-1.72	-0.46	-0.25	0.11	-0.2	-0.1	-0.08	0.17*
WYML 12	195.00	-0.08	-3.28	1.67	147.77*	-0.56	-0.85	0.11	-0.1	-0.15	0.01	0.04
WYML 15	-47.08	2.06*	82.96	-3.02*	12.37	0.93	1.15	0.01	-0.15	0.15	-0.48*	-0.23**
9450	190.84	-1.08	-39.28	0.57	-278.92***	0.58	0.4	-0.48	0.2	-0.15	-0.04	0.11

Table 4.25 Ratios of combining ability variance components in naturally infested environments

Component	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
GCA	-19012.41	0.77	-242.10	0.82	25839.15	0.33	1.00	-0.01	-0.01	0.01	0.06	0.02
SCA	680270.00	10.40	20963.28	-3.26	102030.70	1.60	2.55	-0.40	0.73	0.13	0.12	0.08
GCA/ SCA	-0.03	0.07	-0.01	-0.25	0.25	0.20	0.39	0.02	-0.01	0.04	0.47	0.24

4.11 Combining abilities for yield and yield-related traits under artificially infested environment

SCA values for grain yield were significant for WYML 6 × WYML 8 and WYML 9 × WYML 12.SCA values ranged from 2689.29 for WYML 6 × WYML 8 to -1128.61 for WYML 11 × WYML 15 (Table 4.25). SCA for hundred-grain yield varied from 4.47 to -8.22 for WYML 8 × WYML 15. SCA for grain number per ear was significant for WYML 6 × WYML 8, WYML6 × WYML 9, WYML 6 × WYML 11, WYML 6 × WYML 12, WYML 8 × WYML 11, WYML 9 × WYML 12, WYML 11× WYML 15, and WYML 12 × 9450. SCA values varied from 176.47 for WYML 12 × 9450 to -112.82 for WYML 11 × WYML 15. SCA for grain number per row ranged from 8.69 for WYML 8 × WYML 10 to -6.55 for WYML 11 × WYML 15. SCA for days to anthesis and days to silking ranged from 5.15 for WYML 6 × WYML 8 to -6.55 for WYML 11 × WYML 15. SCA for days to silking ranged from 4.87 for WYML 10 × WYML 12 to -5.12 for WYML 9 × WYML 12. SCA for ear diameter was significant for WYML 6 × WYML 10, WYML 6 × WYML 11, WYML 8 × WYML 10, WYML 8 × WYML 12, WYML 10 × WYML 11, WYML 12 × WYML 15, and WYML 15 × 9450. Its values ranged from 0.43 for WYML 10 × WYML 11 to -0.003 for WYML 8 × WYML 9.

GCA for grain yield ranged from 309.94 for WYML 6 to -438.54 for WYML 15 (Table 4.26). GCA for hundred-grain weight ranged from 1.45 for WYML 10 to -2.25 for WYML 12. GCA for grain number per ear was significant for WYML 6 and 9450 and ranged from 34.52 for WYML 6 to -22.97 for WYML 11. GCA for ear diameter ranged from 0.28 for WYML 11 to -0.17 for WYML 15. GCA for ear diameter was significant for WYML 10, WYML 11, WYML 12, WYML 15, and 9450. GCA/SCA ratios was highest for ear diameter (0.30) and lowest for anthesis silking interval (-0.21).

Table 4.26 Specific combining effects for grain yield and yield related traits for artificially infested environment

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 6 × WYML 8	2689.29***	4.37	87.62*	5.89*	197.02	5.15	4.42	3.09*	-0.59	0.30	-0.47	-0.11
WYML 6 × WYML 9	631.77	-4.47	95.77*	8.19**	267.02	0.15	-1.67	0.99	-0.79	-0.84	-0.17	0.05
WYML 6 × WYML 10	558.80	-2.27	-66.72	-2.85	150.52	-3.64	-3.17	-0.20	0.25	0.30	0.07	0.38*
WYML 6 × WYML 11	135.19	-0.32	88.42*	5.19	-117.77	2.05	1.67	-1.05	0.30	-0.54	1.52***	0.34**
WYML 6 × WYML 12	-312.84	-1.17	-94.32*	-4.95	182.42	-0.49	1.12	0.84	0.05	0.35	0.37	-0.01
WYML 6 × WYML 15	108.08	-4.02	50.17	4.59	249.92	-3.24	-4.02	-1.45	-0.19	0.00	0.82	0.19
WYML 6 × 9450	95.85	1.72	-82.77	-4.75	42.02	0.30	0.47	-0.50	-0.14	-1.09	-0.17	0.07
WYML 8 × WYML 9	-579.64	3.32	-12.02	-2.75	-314.37*	3.45	3.67	-0.55	0.05	-0.29	0.32	-0.003
WYML 8 × WYML 10	1124.82	-4.97	81.47	8.69**	261.12	-1.84	-1.32	0.24	0.10	-1.64*	-0.42	0.47***
WYML 8 × WYML 11	-415.54	-3.02	127.62*	5.24	81.82	-2.14	0.02	1.89	0.65	0.50	-0.47	0.03
WYML 8 × WYML 12	733.00	0.12	-22.62	1.59	242.02	-3.69	-4.02	-0.70	-1.09	-0.59	0.87	0.38**
WYML 8 × WYML 15	261.57	-8.22**	3.87	0.64	215.52	-2.44	-3.67	-1.50	-0.84	-0.44	0.32	0.18
WYML 8 × 9450	-218.39	-1.97	-17.57	0.79	5.62	2.60	2.32	-0.55	0.20	0.45	-0.17	0.21

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 9 × WYML 10	-904.21	-2.82	-5.87	-0.50	135.12	-3.34	0.07	3.14*	0.40	-0.79	-0.12	0.14
WYML 9 × WYML 11	631.12	-3.87	41.27	0.04	194.82	-2.14	-2.07	-0.20	-0.54	0.35	0.82	-0.24
WYML 9 × WYML 12	1723.18*	-2.22	139.52**	5.89*	196.02	-3.69	-5.12	-0.80	-0.79	-0.74	-0.82	0.15
WYML 9 × WYML 15	364.68	-0.07	17.02	-0.05	75.52	-2.94	-2.27	0.39	-1.54**	-1.09	-0.87	0.06
WYML 9 × 9450	678.20	-2.82	12.07	4.09	512.62***	-3.39	-3.77	-0.65	-0.49	-0.69	0.62	0.08
WYML 10 × WYML 11	1463.53	-2.17	38.77	3.49	442.32**	-0.44	-1.57	-0.90	-1.49**	0.50	0.07	0.43**
WYML 10 × WYML 12	-31.32	4.47	-33.97	-4.65	34.52	3.50	4.87	1.49	1.25*	-1.09	-0.57	-0.11
WYML 10 × WYML 15	236.99	-4.37	33.52	3.89	-20.97	-3.74	-4.77	-0.80	-0.49	0.05	0.37	-0.11
WYML 10 × 9450	750.92	-1.62	44.57	3.04	84.12	-4.19	-4.27	0.14	-0.94	0.95	0.37	0.21
WYML 11 × WYML 12	580.60	-2.07	6.17	0.89	151.22	0.20	0.22	0.14	-0.19	0.05	-0.62	0.29
WYML 11 × WYML 15	-1128.61	4.07	-112.82**	-6.55*	26.72	0.45	4.07	3.84***	1.55**	0.70	-0.17	-0.15
WYML 11 × 9450	1433.74	-6.17	86.72	7.59**	216.82	-2.49	-3.92	-1.20	-1.39*	-0.89	0.82	0.32
WYML 12 × WYML 15	386.36	1.72	22.92	2.79	-77.07	-0.09	0.02	0.24	-0.19	0.60	0.17	0.34*

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 12 × 9450	-121.71	-0.02	176.47***	5.94*	-21.97	0.95	2.52	1.69	0.85	1.50*	1.17**	-0.12
WYML 15 × 9450	795.33	-1.87	19.47	-2.00	151.52	0.70	3.87	3.39**	0.60	-0.34	0.12	0.32*

GRY= grain yield; HGW= hundred grain weight; GNPE = grain number per ear; GNPR= grain number per row; DYAN= days to anthesis; DYSK= days to silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; HC= husk cover; ED= ear diameter.

Table 4.27 General combining abilities of 8 inbred lines for yield and yield-related traits in the artificially infested environment

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 6	309.94	-0.9	34.52*	2.61*	156.52**	-0.65	-1.52	-0.22	-0.37	-0.53*	-0.15	0.08
WYML 8	-121.99	1.3	-11.67	-0.43	-41.07	0.55	0.12	-0.17	0.27	0.41	0.35*	-0.10
WYML 9	160.65	1.15	-2.32	-0.23	12.92	1.05	0.72	-0.07	-0.02	0.06	0.05	-0.03
WYML 10	111.24	1.45	-20.82	-0.68	-78.57	0.35	0.72	0.12	-0.07	0.41	0.30	-0.15*
WYML 11	-64.85	-1.5	-22.97	-2.23*	-49.27	-1.85	-1.62	-0.02	-0.12	-0.23	-0.15	0.28***
WYML 12	29.33	-2.15	17.77	-0.08	76.52	-0.8	-0.57	0.07	-0.37	-0.13	-0.5**	0.23***
WYML 15	-438.54	-0.3	-27.72	-2.13*	-9.97	0.95	1.57	0.37	0.37	0.21	0.05	-0.17**
9450	14.22	0.95	33.22*	3.21*	-67.07	0.4	0.57	-0.07	0.32	-0.18	0.05	-0.14*

GRY= grain yield; HGW= hundred grain weight; GNPE = grain number per ear; GNPR= grain number per row; DYAN= days to anthesis; DYSK= days to silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; HC= husk cover; ED= ear diameter.

Table 4.28 Ratios of combining ability variance components in artificially infested environments

Component	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
GCA	-31764.08	0.70	397.84	2.90	3416.51	-0.39	-0.06	-0.18	0.04	0.05	0.05	0.03
SCA	648541.70	8.14	5924.75	23.04	70698.32	-2.07	-1.37	0.82	0.39	0.19	0.25	0.10
GCA/ SCA	-0.05	0.09	0.07	0.13	0.05	0.19	0.04	-0.21	0.11	0.28	0.19	0.30

GRY= grain yield; HGW= hundred grain weight; GNPE = grain number per ear; GNPR= grain number per row; DYAN= days to anthesis; DYSK= days to silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; HC= husk cover; ED= ear diameter.

4.12 Combining abilities for yield and yield-related traits under combined environments

SCA values for grain yield ranged from 1856.52 for WYML 6 × WYML 8 to -698.82 for WYML 8 × WYML 9. WYML 6 × WYML 8 and WYML 10 × 9450 (Table 4.28). SCA foe hundred-grain weight ranged from 3.39 for WYML 11 × WYML 15 to -4.90 for WYML 11 × 9450. SCA for grain yield per ear showed significance for WYML 6 × WYML 15 and ranged from 728.87 to -125.65 for WYML 11 × WYML 15. SCA for grain number per row was significant for WYML 6 × WYML 9 and WYML 8 × WYML 10. SCA for grain yield per ear ranged from 6.91 for WYML 8 × WYML 10 to -2.93 for WYML 11× WYML. SCA for days to anthesis was highest for WYML6 × WYML 8 (2.91) and lowest for WYML 10 × 9450 (-3.53). SCA for days to silking ranged from 2.69 for WYML 6 × WYML 8 to -4.03 for WYML 9 × WYML 12. SCA for ear diameter was significant for WYML 8 × WYML 10 and WYML 10 × WYML 11 and ranged from 0.42 for WYML 8 × WYML 10 to -0.20 for WYML 9 × WYML 11.

GCA for grain yield ranged from 210.04 for WYML 6 to -242.81 for WYML 15 (Table 4.29). GCA for hundred-grain weight varied from 1.05 for WYML 8 to -1.74 for WYML 11. GCA for grain yield for rows ranged from 99.66 for WYML 6 to -35.33 for WYML 9. GCA for grain number per row was not significant for all inbred lines except for WYML 15 (-2.58). Values ranged from 2.26 for WYML 6 to -2.58 for WYML 15. GCA for ear diameter was significant for both WYML 11 and WYML 15 where values ranged from 0.23 to -0.20 respectively. GCA/SCA ratios are presented in Table 4.30. Ear diameter recorded the highest GCA/SCA ratio of 0.26, whiles the lowest ratio was recorded by husk cover of -0.03.

Table 4.29 Specific combining effects for grain yield and yield related traits for combined environments

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 6 × WYML 8	1856.52**	0.94	29.84	4.64	153.5	2.91	2.69	1.57	-0.72	0.09	-0.79	0.10
WYML 6 × WYML 9	757.41	-4.42	-0.67	6.26*	268.1	-0.38	-1.85	-0.22	-0.44	-1.05	-0.24	0.16
WYML 6 × WYML 10	346.04	0.47	-118.50	-2.65	274.85	-1.45	-0.40	0.19	-0.37	0.36	-0.54	0.24
WYML 6 × WYML 11	337.10	-1.75	-13.45	3.46	16.55	0.34	0.14	-0.75	0.20	-0.35	1.05	0.30
WYML 6 × WYML 12	-261.83	-0.62	-85.25	-2.20	425.4	-1.13	-0.83	0.44	-0.22	-0.13	-0.07	-0.10
WYML 6 × WYML 15	587.58	-2.12	728.87***	3.91	180.85	-2.50	-2.65	-0.15	-0.32	0.04	0.90	0.24
WYML 6 × 9450	262.81	-0.42	-87.47	-0.55	-69.44	-1.30	-1.28	-0.42	-0.47	-0.85	-0.32	-0.01
WYML 8 × WYML 9	-698.82	1.29	44.34	-1.65	-202.5	2.26	1.24	-1.32	-0.09	-0.40	0.20	-0.10
WYML 8 × WYML 10	947.63	-4.05	89.77	6.91*	20.75	-1.55	-1.55	-0.40	-0.77	-1.23*	-0.59	0.42*
WYML 8 × WYML 11	-196.57	-0.52	84.82	3.04	167.45	-0.25	0.24	0.39	0.55	0.54	-0.49	-0.06
WYML 8 × WYML 12	579.74	-1.65	-31.97	-0.88	201.3	-1.73	-1.73	-0.40	-0.37	-0.48	0.38	0.23
WYML 8 × WYML 15	-145.19	-3.40	-83.85	-0.75	189.75	-2.10	-2.55	-0.50	-0.47	-0.55	0.35	0.22
WYML 8 × 9450	316.89	-2.95	28.79	1.76	106.95	0.84	0.56	-0.27	0.13	0.04	0.13	0.31

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 9 × WYML 10	-313.99	-0.92	26.49	0.79	98.34	-2.60	-0.60	2.04	0.00	-0.88	0.45	0.05
WYML 9 × WYML 11	270.37	-0.65	51.04	0.91	244.55	-2.05	-1.80	0.09	0.07	0.14	1.05	-0.20
WYML 9 × WYML 12	1303.40	-3.02	105.74	3.74	170.9	-3.28	-4.03	-0.70	-0.84	-0.63	-0.56	0.33
WYML 9 × WYML 15	444.76	-2.27	-39.62	-0.13	27.34	-1.90	-2.35	-0.55	-1.44*	-0.95	-1.09	0.20
WYML 9 × 9450	881.66	-1.32	14.52	1.14	566.05	-2.45	-2.48	-0.07	-1.09	-0.60	0.18	0.22
WYML 10 × WYML 11	600.03	-1.50	71.22	2.99	605.8	-0.13	-1.60	-0.72	-0.84	0.31	0.25	0.39*
WYML 10 × WYML 12	-248.44	0.37	-10.07	-3.93	6.65	1.39	0.66	1.22	0.47	-0.95	-0.61	-0.03
WYML 10 × WYML 15	788.97	-3.62	-14.45	1.94	144.1	-2.23	-2.65	-0.62	-0.62	-0.03	-0.14	0.13
WYML 10 × 9450	1375.35*	-1.67	49.19	3.21	8.30	-3.53	-3.53	-0.15	-0.52	0.81	0.38	0.07
WYML 11 × WYML 12	710.84	-3.60	14.72	0.94	-93.15	-0.55	-0.03	0.27	-0.19	0.31	-0.26	0.23
WYML 11 × WYML 15	-359.43	3.39	-125.65	-2.93	15.80	-0.43	1.14	1.67	0.70	0.74	-0.54	-0.07
WYML 11 × 9450	1171.31	-4.90	105.74	5.34	128	-1.73	-2.98	-1.10	-0.44	-0.90	0.23	0.26
WYML 12 × WYML 15	471.00	-1.97	-27.20	3.89	130.65	-0.40	-0.08	0.12	0.02	0.21	0.08	0.21

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 12 × 9450	-158.55	1.47	111.19	3.41	-11.15	0.29	1.54	1.09	0.37	1.06	0.35	-0.14
WYML 15 × 9450	133.89	-2.02	-48.42	-0.95	39.30	3.16	2.09	1.99	0.27	-0.25	0.33	0.29

GRY= grain yield; HGW= hundred grain weight; GNPE = grain number per ear; GNPR= grain number per row; DYAN= days to anthesis; DYSK= days to silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; HC= husk cover; ED= ear diameter.

Table 4.30 General combining abilities of eight inbred lines for yield and yield-related traits across environments

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
WYML 6	210.14	-0.71	99.66	2.26	235.45	-1.08	-1.88	-0.38	-0.13	-0.46*	-0.06	0.14
WYML 8	-205.08	1.05	-25.10	-0.30	-75.95	0.26	0.26	-0.03	0.26	0.38	0.23	-0.06
WYML 9	-70.94	0.68	-35.33	-0.18	24.45	1.06	1.31	0.26	-0.01	0.03	-0.06	-0.09
WYML 10	139.97	1.03	-30.00	-0.25	-98.8	0.14	0.11	0.09	-0.08	0.35	0.48	-0.13
WYML 11	-45.97	-1.74	-41.05	-1.63	-25.5	-1.15	-0.93	0.04	-0.16	-0.16	-0.11	0.23**
WYML 12	112.16	-1.11	7.24	0.79	112.15	-0.68	-0.71	0.09	-0.23	-0.14	-0.24	0.14
WYML 15	-242.81	0.88	27.61	-2.58*	1.2	0.94	1.36	0.19	0.11	0.18	-0.22	-0.20**

GENOTYPE	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
9450	102.53	-0.06	-3.03	1.89	-173	0.49	0.48	-0.28	0.26	-0.16	0.01	-0.01

GRY= grain yield; HGW= hundred grain weight; GNPE = grain number per ear; GNPR= grain number per row; DYAN= days to anthesis; DYSK= days to silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; HC= husk cover; ED= ear diameter.

Table 4.31 Ratios of combining ability variance components for combined environments

Component	GRY	HGW	GNPE	GNPR	GWPP	DYAN	DYSK	ASI	PASP	EASP	HC	ED
GCA	-34693.97	0.08	-1519.75	1.50	-4799.88	-0.66	-0.27	-0.12	-0.01	0.04	0.01	0.02
SCA	551244.40	2.72	-9077.92	6.80	-93417.09	-7.54	-7.97	-0.81	0.14	0.26	-0.20	0.07
GCA/ SCA	-0.06	0.03	0.17	0.22	0.05	0.09	0.03	0.15	-0.10	0.16	-0.03	0.26

GRY= grain yield; HGW= hundred grain weight; GNPE = grain number per ear; GNPR= grain number per row; DYAN= days to anthesis; DYSK= days to silking; ASI= anthesis silking interval; PASP= plant aspect; EASP= ear aspect; HC= husk cover; ED= ear diameter.

4.13 Heterosis and heterotic grouping

Hybrids were ranked according to their grain yield SCA values under naturally infested, artificially infested, and combined environments (Table 4.31). In the naturally infested environment, the best 10 hybrids recorded the following values: WYML 6 × WYML 8, SCA = 2689.29, rank = 1; WYML 9 × WYML 12, SCA = 1723.18, rank = 2; WYML 10 × WYML 11, SCA = 1463, rank = 3; WYML 11 × 9450, SCA = 1433.74, rank = 4; WYML 8 × WYML 12, SCA = 1124.82, rank = 5; WYML 15 × 9450, SCA = 795.33, rank = 6; WYML 10 × 9450, SCA = 750.92, rank = 7; WYML 8 × WYML 12, SCA = 733.00, rank = 8; WYML 9 × 9450, SCA = 678.20, rank = 9; WYML 6 × WYML 9, SCA = 632.77, rank = 10. In the artificially infested environment, the top 10 hybrids ranked as follows: WYML 10 × 9450, SCA = 1999.78, rank = 1; WYML 10 × WYML 15, SCA = 1340.95, rank = 2; WYML 9 × 9450, SCA = 1085.12, rank = 3; WYML 6 × WYML 15, SCA = 1067.09, rank = 4; WYML 6 × WYML 8, SCA = 1023.75, rank = 5; WYML 11 × 9450, SCA = 908.89, rank = 6; WYML 9 × WYML 12, SCA = 883.63, rank = 7; WYML 6 × WYML 9, SCA = 883.04, rank = 8; WYML 8 × 9450, SCA = 852.19, rank =9, and WYML 11 × WYML 12, SCA = 841.07, rank = 10. Under combined environments, the top 10 hybrids ranked as follows: WYML 6 × WYML 8, SCA = 1856.52, rank = 1; WYML 10 × 9450, SCA = 1375.35, rank = 2; WYML 9 × WYML 12, SCA = 1302.40, rank = 3; WYML 11 × 9450, SCA = 1171.31, rank = 4; WYML 8 × WYML 10, SCA = 947.63, rank = 5; WYML 9 × 9450, SCA = 881.66, rank = 6; WYML 10 × WYML 15, SCA = 788.97, rank = 7; WYML 6 × WYML 9, SCA = 757.41, rank = 8; WYML 11 × WYML 12, SCA = 710.84, rank = 9, and WYML 10 × WYML 11, SCA = 600.03, rank = 10.

Mid-parent heterosis (MPH) and better-parent heterosis (BPH) were calculated on grain yield for artificially infested, naturally infested, and combined environments (Table 4.32). Results in the artificially infested environment for MPH ranged from 247.85% for WYML 6 × WYML 8 to -9.43%

for WYML 15 × WYML 11 with a mean of 92.12%. BPH values ranged from 191.75% for WYML 6 × WYML 8 to -11.34% with a mean of 76.80%. Under the naturally infested environment, MPH values varied from 210.07% for 9450 × WYML 10 to 15.25% for WYML 8 × WYML 9 with a mean of 91.98%. BPH values ranged from 185.39% for 9450 × WYML 10 to 1.36% for WYML 8 × WYML 9 with a mean of 75.53%. For combined environments, MPH values ranged from 177.41% for WYML 6 × WYML 8 to 31.40% for WYML 8 × WYML 9 with a mean of 89.98%. BPH values ranged from 162.87% for WYML 6 × WYML 8 to 12.39% for WYML 15 × WYML 11 with a mean of 74.69%.

Inbred lines were classified into distinct heterotic groups based on their respective SCA values (Table 4.34). Inbred lines were classified into two heterotic groups based on significant SCA values. The classification was based on arbitrary heterotic groups A and B, for each environment because testers were not used in the study. In the artificially infested environment, WYML 6 and WYML 9 formed heterotic group A whereas WYML 8 and WYML 12 formed heterotic group B. In the naturally infested environment, WYML 10 formed heterotic group A and 9450 formed heterotic group B. In combined environments, WYML 6 and WYML 10 formed heterotic group A and WYML 8 and 9450 formed heterotic group B.

Table 4.32 Specific combining ability (SCA) for 28 F1 hybrids for grain yield evaluated in artificially infested, naturally infested and combined environments

Hybrid	Artificial Environment		Natural Environment		Combined Environments	
	SCA	Rank	SCA	Rank	SCA	Rank
WYML 6 × WYML 8	2689.29***	1	1023.75	5	1856.52**	1
WYML 6 × WYML 9	631.77	10	883.04	8	757.41	8
WYML 6 × WYML 10	558.80	13	133.28	19	346.04	15
WYML 6 × WYML 11	135.19	18	539.02	13	337.10	16
WYML 6 × WYML 12	-312.84	24	-210.81	23	-261.83	25
WYML 6 × WYML 15	108.08	19	1067.09	4	587.58	11
WYML 6 × 9450	95.85	20	429.78	15	262.81	19
WYML 8 × WYML 9	-579.64	27	-818.00	28	-698.82	28
WYML 8 × WYML 10	1124.82	5	770.44	11	947.63	5
WYML 8 × WYML 11	-415.54	25	22.40	20	-196.57	23
WYML 8 × WYML 12	733.00	8	426.47	16	579.74	12
WYML 8 × WYML 15	261.57	16	-551.96	27	-145.19	21
WYML 8 × 9450	-218.39	23	852.19	9	316.89	17
WYML 9 × WYML 10	-904.21	28	276.23	18	-313.99	26
WYML 9 × WYML 11	631.12	11	-90.38	21	270.37	18
WYML 9 × WYML 12	1723.18*	2	883.63	7	1303.40	3
WYML 9 × WYML 15	364.68	15	524.84	14	444.76	14

Hybrid	Artificial Environment		Natural Environments		Combined Environments	
	SCA	Rank	SCA	Rank	SCA	Rank
WYML 9 × 9450	678.20	9	1085.12	3	881.66	6
WYML 10 × WYML 11	1463.53	3	-263.46	24	600.03	10
WYML 10 × WYML 12	-31.32	21	-465.57	25	-248.44	24
WYML 10 × WYML 15	236.99	17	1340.95	2	788.97	7
WYML 10 × 9450	750.92	7	1999.78**	1	1375.35*	2
WYML 11 × WYML 12	580.60	12	841.07	10	710.84	9
WYML 11 × WYML 15	-1128.61	29	409.74	17	-359.43	27
WYML 11 × 9450	1433.74	4	908.89	6	1171.31	4
WYML 12 × WYML 15	386.36	14	555.64	12	471.00	13
WYML 12 × 9450	-121.71	22	-195.40	22	-158.55	22
WYML 15 × 9450	795.33	6	-527.55	26	133.89	20

SCA= specific combining ability

Table 4.33 Hybrids heterosis for grain yield under artificially infested, naturally infested and combined environments

Hybrids	Artificial Environment		Natural Environment		Combined Environments	
	GRY		GRY		GRY	
	MPH(%)	BPH(%)	MPH(%)	BPH(%)	MPH(%)	BPH(%)
9450 × WYML 9	97.91	69.99	167.64	161.42	128.55	111.31
WYML 15 × WYML 12	65.04	63.86	64.72	39.15	64.86	50.03
WYML 11 × WYML 9	83.96	65.10	57.54	33.60	71.50	67.46
9450 × WYML 11	151.92	139.67	173.36	167.00	138.12	115.40
WYML 8 × WYML 12	131.85	97.69	48.97	27.38	82.19	55.60
WYML 15 × WYML 10	60.25	59.81	139.89	136.81	100.84	63.19
WYML 15 × WYML 11	-9.43	-11.34	74.16	64.65	34.87	12.39
9450 × WYML 12	74.31	63.62	56.96	22.83	64.69	39.21
WYML 12 × WYML 11	95.94	93.17	67.83	48.87	79.84	66.65
WYML 8 × 9450	91.90	73.08	120.80	98.27	107.67	105.08
WYML 6 × WYML 10	107.43	105.34	100.54	93.26	104.09	101.48
WYML 8 × WYML 11	65.49	42.81	44.81	38.82	53.73	40.64
9450 × WYML 10	120.15	104.74	210.07	185.39	164.47	144.70
WYML 12 × WYML 10	70.77	69.08	35.80	13.53	51.46	37.21
WYML 6 × 9450	95.19	79.84	135.65	124.66	114.62	100.98
WYML 15 × 9450	95.48	82.27	66.68	51.65	81.98	36.83

Hybrids	Artificial Environment		Natural Environment		Combined Environments	
	GRY		GRY		GRY	
	MPH(%)	BPH(%)	MPH(%)	BPH(%)	MPH(%)	BPH(%)
WYML 8 × WYML 10	155.17	115.78	98.93	93.61	124.56	110.22
WYML 6 × WYML 8	247.85	191.75	115.52	102.35	177.41	162.87
WYML 6 × WYML 12	65.18	61.91	47.58	19.78	55.64	39.38
WYML 11 × WYML 10	139.89	134.18	56.13	45.86	96.36	91.58
WYML 15 × WYML 9	53.29	40.26	99.20	77.43	74.68	42.06
WYML 12 × WYML 9	132.23	111.12	83.85	41.46	107.65	88.26
WYML 8 × WYML 9	47.00	15.91	15.25	1.36	31.40	22.91
WYML 6 × WYML 9	94.04	79.66	138.78	122.61	113.43	110.53
WYML 10 × WYML 9	22.49	12.37	100.34	80.48	57.21	57.08
WYML 6 × WYML 11	84.17	78.03	95.46	76.43	89.92	82.98
WYML 6 × WYML 15	61.85	59.78	132.67	121.49	97.22	94.53
WYML 8 × WYML 15	78.10	50.96	26.54	24.72	50.51	40.78
Mean	**92.12**	**76.80**	**91.98**	**75.53**	**89.98**	**74.69**
Maximum	**247.85**	**191.75**	**210.07**	**185.39**	**177.41**	**162.87**
Minimum	**-9.43**	**-11.34**	**15.25**	**1.36**	**31.40**	**12.39**

GRY = grain yield; MPH= mid-parent heterosis; BPH = better-parent heterosis

Table 4.34 Heterotic grouping of inbred lines

Environment	Heterotic group	
	A	**B**
Artificially infested environment	WYML 6	WYML 8
	WYML 9	WYML 12
Naturally infested environment	WYML 10	9450
Combined environments	WYML 6	WYML 8
	WYML 10	9450

4.14 Performance of genotypes for incidence across environments

The mean performance of the 28 F1 hybrids and four standard checks are presented for incidence over 7 WAP across all environments (Table 4.35). In the artificially infested environment at 1WAP, incidence ranged from 29% for WYML 8 × WYML 15 to 50% for 9450 × WYML 10 with a mean of 38%. Incidence progressed from 33% for DZIFO to 72% for WYML 6 × WYML 11 at 4WAP with a mean of 52%. At 7WAP, incidence ranged from 33% for DZIFO and WYML 12 × WYML 11 to 79% for WYML 12 × WYML 9 with a mean of 61%. In the naturally infested environment, incidence at 1WAP ranged from 28% for WYML 8 × WYML 12 and WYML 15 × 9450 to 50% for DZIFO with a mean of 36%. At 4WAP, incidence values ranged from 34% for WYML 8 × WYML 9 to 69% for WYML 11 × WYML 9 and DZIFO with a mean of 48%. At 7WAP, incidence values ranged from 41% for WYML 15 × WYML 10 to 70% for 9450 × WYML 10 and DZIFO with a mean of 52%. The

control environment recorded 0% across all 7 weeks for all hybrids. Incidences for the performance of hybrids across all environments are shown in Table 4.36. In the artificially infested environment at 1WAP, incidence varied from 32% for WYML 11 to 51% for WYML 6 with a mean of 41%. At 4WAP, incidence ranged from 44% for WYML 12 to 66% for WYML 6 and WYML 15with a mean of 56%. At 7WAP, incidence ranged from 52% for 9450 to 76% for WYML 15 with a mean of 67%. In the naturally infested environment, incidence ranged from 29% for WYML 9, WYML 11, and WYML 12 to 47% for WYML 10 with a mean of 35%. At 4WAP, incidence ranged from 38% for WYML 11 to 59% for WYML 6 with a mean of 47%. At 7WAP, incidence ranged from 42% in WYML 11 to 68% in WYML 6 with a mean of 53%. In the control environment, an incidence was 0% for all inbred lines.

Table 4.35 Mean incidence of maize streak disease in hybrid genotypes across all environments from 1-7 weeks after planting (WAP).

Mean Incidence (%)

Hybrid	Artificially Infested Environment							Naturally Infested Environment							Control
	1WAP	2WAP	3WAP	4WAP	5WAP	6WAP	7WAP	1WAP	2WAP	3WAP	4WAP	5WAP	6WAP	7WAP	1-7WAP
9450 × WYML 9	0.32 bc	0.33 ij	0.41 e-i	0.50 c-j	0.61 a-e	0.65a-d	0.70 a-e	0.33 ab	0.36 d-g	0.36 d-f	0.50 bc	0.50 b-d	0.54 a-c	0.58 a-c	0.00
WYML 15 ×WYML 12	0.32 bc	0.36 f-j	0.36 g-i	0.39 h-j	0.39 f-h	0.39 e-g	0.47 f-h	0.45 ab	0.45 a-f	0.45 b-e	0.53 a-c	0.53 a-d	0.56 a-c	0.56 a-c	0.00
WYML 11 × WYML 9	0.33bc	0.41 d-i	0.49 a-f	0.58 a-g	0.62 a-e	0.70 a-d	0.70 a-e	0.37 ab	0.56 ab	0.60 ab	0.69 a	0.70 a	0.70 a	0.70 a	0.00
9450 × WYML 11	0.42 a-c	0.43 b-h	0.50 a-f	0.64 a-d	0.72 ab	0.75 ab	0.79 ab	0.37 ab	0.47 a-f	0.47 b-e	0.54 ab	0.54 a-d	0.54 a-c	0.54 a-c	0.00
WYML 8 × WYML 12	0.40 a-c	0.40 e-i	0.44 d-i	0.48 d-j	0.53 b-h	0.57 b-e	0.61 b-f	0.28 b	0.33 e-g	0.37 d-f	0.45 bc	0.57 ab	0.57 a-c	0.57 a-c	0.00
WYML 15 ×WYML 10	0.32 bc	0.36 g-j	0.44 e-i	0.48 d-j	0.51b-h	0.51d-g	0.61 b-f	0.33 ab	0.33 e-g	0.33 ef	0.36 bc	0.37 cd	0.40 c	0.41 c	0.00
WYML 15 ×WYML 11	0.39 a-c	0.43 b-h	0.47 b-g	0.54 b-i	0.57 a-f	0.57 b-e	0.57 b-f	0.29 b	0.29 g	0.36 d-f	0.44 bc	0.44 b-d	0.44 bc	0.44 bc	0.00
9450 × WYML 12	0.33 bc	0.37 g-j	0.40 e-i	0.49 c-j	0.53 b-h	0.53b-g	0.53 c-h	0.44 ab	0.44 a-f	0.48 b-d	0.52 a-c	0.52 a-d	0.52 a-c	0.53 a-c	0.00
WYML 12 ×WYML 11	0.33 bc	0.33 h-j	0.33 hi	0.33 j	0.33 gh	0.33 fg	0.33 gh	0.33 ab	0.41 b-g	0.46 b-e	0.46 bc	0.46 b-d	0.46 bc	0.46 bc	0.00
WYML 8 × 9450	0.40 a-c	0.44 b-g	0.44 e-i	0.46 f-j	0.51 b-h	0.51 d-g	0.51 d-g	0.49 a	0.53 a-c	0.53 a-c	0.53 a-c	0.53 a-d	0.57 a-c	0.61 a-c	0.00
WYML 6 × WYML 10	0.36 a-c	0.36 g-j	0.39 f-i	0.43 g-j	0.51 c-h	0.54 b-g	0.54 c-h	0.33 ab	0.41c-g	0.41 c-f	0.49 bc	0.53 a-d	0.53 a-c	0.53 a-c	0.00
WYML 8 × WYML 11	0.37 a-c	0.37 f-j	0.46 c-g	0.59 a-g	0.63 a-e	0.68 a-d	0.73 a-e	0.37 ab	0.44 a-f	0.48 b-d	0.48 bc	0.48 b-d	0.56 a-c	0.56 a-c	0.00
9450 × WYML 10	0.50 a	0.50 a-d	0.58 ab	0.67 ab	0.67 a-d	0.72 a-d	0.75 a-c	0.36 ab	0.36 d-g	0.39 c-f	0.43 bc	0.43 b-d	0.43 bc	0.43 b-c	0.00
WYML 12 ×WYML 10	0.41 a-c	0.49 b-e	0.57 a-c	0.61 a-f	0.65 a-d	0.65 a-d	0.74 a-d	0.41 ab	0.45 a-f	0.49 b-d	0.53 a-c	0.57 ab	0.61 ab	0.61 a-d	0.00
WYML 6 × 9450	0.42 a-c	0.51 a-c	0.56 a-d	0.66 a-c	0.69 b-d	0.75 ab	0.75 a-c	0.41 ab	0.41 c-g	0.45c-e	0.45 bc	0.45 b-d	0.45 bc	0.45 bc	0.00
WYML 15 × 9450	0.39 a-c	0.43 b-g	0.47 b-g	0.47 e-j	0.51 c-h	0.51 d-g	0.51 e-h	0.28 b	0.29 g	0.37 d-f	0.40 bc	0.40 b-d	0.44 bc	0.44 bc	0.00
WYML 8 × WYML 10	0.34 bc	0.38 f-j	0.41e-i	0.45 f-j	0.52 b-h	0.56 b-f	0.59 b-f	0.33 ab	0.33 e-g	0.33 ef	0.40 bc	0.43 b-d	0.43 bc	0.43 b-f	0.00
WYML 6 × WYML 8	0.40 a-c	0.40 e-i	0.40 e-i	0.43 g-j	0.43 e-h	0.51 d-g	0.51 e-h	0.32 ab	0.36 d-g	0.43 c-f	0.43 bc	0.47 b-d	0.47 bc	0.47 bc	0.00
CHECK 1: POINEER	0.38a-c	0.42 e-i	0.50 a-f	0.55 b-h	0.55 b-f	0.60 a-e	0.64 a-f	0.29 b	0.36 d-g	0.39 c-f	0.43 bc	0.43 b-d	0.43 bc	0.43 bc	0.00
CHECK 2: AHOUFE	0.34 bc	0.52 ab	0.52 a-e	0.69 ab	0.69 a-d	0.74 a-c	0.74 a-c	0.33 ab	0.41c-g	0.45 c-e	0.53 a-c	0.53 a-d	0.53 a-c	0.53 a-c	0.00
CHECK 4: LAKE 606	0.36 a-c	0.41 d-i	0.44 e-i	0.47 d-j	0.51 b-h	0.51 d-g	0.55 c-h	0.34 ab	0.47 a-e	0.47 b-e	0.47 bc	0.50 a-d	0.51 a-c	0.62 ab	0.00
WYML 6 × WYML 12	0.41 a-c	0.41 d-i	0.44 e-i	0.53 b-i	0.57 a-f	0.57 b-e	0.57 b-f	0.36 ab	0.39 c-g	0.39 c-f	0.43 bc	0.43 b-d	0.48 bc	0.48 bc	0.00
CHECK 3: DZIFO	0.33 bc	0.33 h-j	0.33 i	0.33 j	0.33 h	0.33 g	0.33 h	0.50 a	0.58 a	0.65 a	0.69 a	0.69 a	0.70 a	0.70 a	0.00
WYML 11 ×WYML 10	0.45ab	0.49 b-e	0.49 a-f	0.53 b-i	0.56 a-f	0.56 b-e	0.56 b-g	0.40 ab	0.44 a-f	0.48 b-d	0.48 bc	0.55 a-c	0.55 a-c	0.59 a-c	0.00

	Artificially Infested Environment							Naturally Infested Environment							Control
	1WAP	2WAP	3WAP	4WAP	5WAP	6WAP	7WAP	1WAP	2WAP	3WAP	4WAP	5WAP	6WAP	7WAP	1-7WAP
WYML 15 × WYML 9	0.36 a-c	0.36 g-j	0.36 g-i	0.43 g-j	0.51 c-h	0.54 b-g	0.62 b-f	0.40 ab	0.43 a-f	0.44 c-e	0.48 bc	0.51 a-d	0.52 a-c	0.52 a-c	0.00
WYML 12 × WYML 9	0.39 a-c	0.47 b-f	0.47 b-g	0.57 a-g	0.64 a-d	0.72 a-d	0.79 ab	0.40 ab	0.46 b-f	0.48 b-e	0.51a-c	0.55 a-c	0.55 a-c	0.59 a-c	0.00
WYML 8 × WYML 9	0.37 a-c	0.48 b-e	0.52 a-e	0.63 a-e	0.70 a-c	0.71 a-d	0.71 a-e	0.29 b	0.29 g	0.29 f	0.34 c	0.34 d	0.42 bc	0.47 bc	0.00
WYML 6 × WYML 9	0.43 a-c	0.43 b-g	0.51 a-e	0.55 b-h	0.55 b-f	0.59 a-e	0.59 b-f	0.48 a	0.48 a-d	0.54 a-c	0.54 ab	0.54 a-c	0.54 a-c	0.54 a-c	0.00
WYML 10 × WYML 9	0.42 a-c	0.42 c-i	0.45d-h	0.49 d-j	0.49 d-h	0.52 c-g	0.56 c-g	0.39 ab	0.39 c-g	0.43 c-f	0.43 bc	0.43 b-d	0.48 bc	0.48 bc	0.00
WYML 6 × WYML 11	0.50 a	0.59 a	0.59 a	0.72 a	0.76 a	0.81 a	0.86 a	0.32 ab	0.32 g	0.44 c-e	0.48 bc	0.51 a-d	0.52 a-c	0.52 a-c	0.00
WYML 6 × WYML 15	0.37 a-c	0.41 d-i	0.41 e-i	0.45 f-j	0.54 b-f	0.54 b-g	0.58 b-f	0.33 ab	0.33 e-g	0.43 c-f	0.47 bc	0.46 b-d	0.46 bc	0.51 a-c	0.00
WYML 8 × WYML 15	0.28 c	0.28 j	0.49 a-f	0.53 b-i	0.57 a-d	0.61 a-e	0.64 a-f	0.29 b	0.42b-g	0.42 c-f	0.42 bc	0.41 b-d	0.42 bc	0.42 bc	0.00
Mean	**0.38**	**0.42**	**0.46**	**0.52**	**0.56**	**0.59**	**0.61**	**0.36**	**0.41**	**0.44**	**0.48**	**0.56**	**0.51**	**0.52**	**0.00**
Lsd	**0.15**	**0.09**	**0.12**	**0.17**	**0.21**	**0.23**	**0.23**	**0.18**	**0.09**	**0.15**	**0.19**	**0.21**	**0.20**	**0.21**	**0.00**

Means in the same columns having different letters are not significantly different ($p<0.05$).

Table 4.36 Mean incidence of MSD in inbreds across all environments from 1-7 weeks after planting (WAP).

Mean Incidence (%)

	Artificially Infested Environment							**Naturally Infested Environment**							**Control**
Inbred Line	**1WAP**	**2WAP**	**3WAP**	**4WAP**	**5WAP**	**6WAP**	**7WAP**	**1WAP**	**2WAP**	**3WAP**	**4WAP**	**5WAP**	**6WAP**	**7WAP**	**1-7WAP**
WYML 15	0.48 ^{ab}	0.48 ^{a}	0.57 ^{ab}	0.66 ^{a}	0.67 ^{ab}	0.76 ^{a}	0.76 ^{a}	0.33 ^{ab}	0.37 ^{a}	0.48 ^{a}	0.48 ^{a}	0.48 ^{a}	0.48 ^{a}	0.48^{a}	0.00
WYML 11	0.32 ^{c}	0.44 ^{a}	0.49 $^{a-c}$	0.52 ^{ab}	0.52 ^{c}	0.60 ^{ab}	0.63 ^{ab}	0.29 ^{b}	0.29 ^{a}	0.33 ^{a}	0.38 ^{a}	0.38 ^{a}	0.42 ^{a}	0.42^{a}	0.00
WYML 12	0.36 ^{bc}	0.40 ^{a}	0.44 ^{bc}	0.44 ^{b}	0.52 ^{c}	0.59 ^{ab}	0.63 ^{ab}	0.29 ^{b}	0.43 ^{a}	0.43 ^{a}	0.43 ^{a}	0.43 ^{a}	0.51 ^{a}	0.51^{a}	0.00
WYML 8	0.42 $^{a-c}$	0.42 ^{a}	0.51^{a-c}	0.60 ^{a}	0.64 ^{b}	0.69 ^{ab}	0.69 ^{ab}	0.40 ^{ab}	0.44 ^{a}	0.44 ^{a}	0.45 ^{a}	0.45 ^{a}	0.48 ^{a}	0.48^{a}	0.00
WYML 10	0.42 $^{a-c}$	0.42 ^{a}	0.51 $^{a-c}$	0.57 ^{ab}	0.60 ^{bc}	0.69 ^{ab}	0.70 ^{ab}	0.47 ^{a}	0.51 ^{a}	0.51 ^{a}	0.51 ^{a}	0.55 ^{a}	0.55 ^{a}	0.55 ^{a}	0.00
WYML 6	0.51 ^{a}	0.51 ^{a}	0.62 ^{a}	0.66 ^{a}	0.78 ^{a}	0.71 ^{ab}	0.75 ^{ab}	0.46 ^{a}	0.51 ^{a}	0.55 ^{a}	0.59 ^{a}	0.60 ^{a}	0.60 ^{a}	0.68^{a}	0.00
9450	0.38 ^{bc}	0.38 ^{a}	0.43 ^{c}	0.52 ^{ab}	0.52 ^{c}	0.52 ^{b}	0.52 ^{b}	0.34 ^{ab}	0.40 ^{a}	0.40 ^{a}	0.40 ^{a}	0.44 ^{a}	0.50 ^{a}	0.50^{a}	0.00
WYML 9	0.40 $^{a-c}$	0.45 ^{a}	0.49 $^{a-c}$	0.57 ^{ab}	0.61^{bc}	0.69 ^{ab}	0.69 ^{ab}	0.29 ^{b}	0.42 ^{a}	0.42 ^{a}	0.55 ^{a}	0.55 ^{a}	0.55 ^{a}	0.58 ^{a}	0.00
Mean	**0.41**	**0.44**	**0.51**	**0.56**	**0.61**	**0.66**	**0.67**	**0.35**	**0.42**	**0.44**	**0.47**	**0.48**	**0.51**	**0.53**	**0.00**
Lsd	**0.12**	**0.14**	**0.14**	**0.14**	**0.11**	**0.18**	**0.23**	**0.16**	**0.31**	**0.29**	**0.31**	**0.28**	**0.32**	**0.29**	**0.00**

Means in the same columns having different letters are significantly different ($p<0.05$).

4.15 Performance of genotypes for severity across environments

In the artificially infested environment (Table 4.37), severity scores at 1WAP ranged from 1.0 for WYML 8 × WYML 15 to 2.5 for WYML6 × WYML 12 with a mean of 1.7. At 4WAP, severity ranged from 1.5 for WYML 8 × 9450 to 4.0 for 9450 × WYML 11 with a mean of 2.59. At 7WAP, severity scores ranged from 0.5 for WYML 12 × WYML 11 to 7.0 for 9450 × WYML 11 with a mean of 3.96. In the naturally infested environment, severity scores ranged from 1.0 for WYML 8 × WYML9 to 2.5 for WYML 10 × WYML 9 with a mean of 1.65 at 1WAP. At 4WAP, severity scores ranged from 1.5 for WYML 8 × WYML 9 to 4.0 for AHOUFE with a mean of 3.01. At 7WAP, severity scores varied from 2.5 for WYML 8 × WYML 9 to 5.0 for 9450 × WYML 12 with a mean of 3.92. In the control environment, 0% severity was recorded for all hybrids over 1WAP – 7WAP. For the inbred lines, at 1WAP severity varied from 1.5 for WYML 11 to 2.5 for WYML 6 with a mean of 2.0 (Table 4.38). At 4WAP, severity ranged from 2.0 for WYML 11 to 4.0 for WYML 6 with a mean of 2.93. At 7WAP, severity ranged from 2.5 for WYML 11 to 5.0 for WYML 6 with a mean of 3.75. In the naturally infested environment, severity ranged from 1.0 for WYML 9 to 2.5 with a mean of 1.56% at 1WAP. At 4WAP, severity ranged from 1.5 for WYML 11 to 3.5 for WYML 6 with a mean of 2.68. At 7WAP, severity ranged from 3.0 for WYML 15 to 5.0 for WYML 6 with a mean of 3.81. In the control environment, severity was 0% from 1WAP-7WAP for all inbred lines.

Table 4.37 Mean severity scores of MSD in hybrid genotypes across all environments from 1-7 weeks after planting (WAP).

Mean Severity Score

	Artificially Infested Environment							**Naturally Infested Environment**							**Control**
Hybrid	**1WAP**	**2WAP**	**3WAP**	**4WAP**	**5WAP**	**6WAP**	**7WAP**	**1WAP**	**2WAP**	**3WAP**	**4WAP**	**5WAP**	**6WAP**	**7WAP**	**1-7WAP**
9450 × WYML 9	1.5 ab	1.5 bc	2.0 ab	3.0 ab	3.0 abc	3.0 ab	5.0 abc	1.5 ab	2.0 bcd	2.5 bcd	2.5 abc	2.5 abc	3.5 abc	3.5 ab	0.00
WYML 15 × WYML 12	1.5 ab	2.0 abc	2.0 ab	2.5 ab	2.5 abc	3.0 ab	3.0 abc	2.0 ab	2.0 bcd	2.0 cde	3.0 abc	3.5 abc	4.5 ab	5.0 a	0.00
WYML 11 × WYML 9	1.5 ab	2.0 abc	2.5 ab	2.5 ab	3.5 abc	4.0 ab	5.0 abc	2.0 ab	3.0ab	3.5 ab	4.0 a	4.0 ab	4.0 abc	4.5 ab	0.00
9450 × WYML 11	2.0 ab	2.0 abc	2.0 ab	2.5 ab	2.5 abc	4.0 ab	7.0 a	2.0 ab	2.5 abc	2.5 bcd	3.0 abc	3.0 abc	4.0 abc	4.0 ab	0.00
WYML 8 × WYML 12	2.0 ab	2.0 abc	2.5 ab	3.0 ab	3.0 abc	3.5 ab	4.0 abc	1.0 b	1.5 cd	2.0 cde	3.0 abc	3.0 abc	3.0 abc	3.5 ab	0.00
WYML 15 × WYML 10	1.5 ab	1.5 bc	2.0 ab	2.0 ab	2.0 bc	2.5 ab	3.0 abc	1.5 ab	1.5 cd	1.5 de	1.5 c	2.0 bc	2.5 bc	2.5 b	0.00
WYML 15 × WYML 11	2.0 ab	2.0 abc	2.0 ab	2.5 ab	3.0 abc	4.0 ab	4.0 abc	1.0 b	1.0 d	2.5 bcd	3.0 abc	4.0 ab	4.0 abc	4.0 ab	0.00
9450 × WYML 12	1.5 ab	2.0 abc	2.0 ab	3.0 ab	3.0 abc	3.0 ab	3.0 abc	2.0 ab	2.5 abc	3.0 abc	3.5 ab	4.0 ab	4.5 ab	5.0 a	0.00
WYML 12 × WYML 11	1.5 ab	1.5 bc	1.5 b	1.5 b	1.5 c	1.5 b	2.5 abc	1.5 ab	2.0 bcd	2.0 cde	3.0 abc	3.5 abc	3.5 abc	4.0 ab	0.00
WYML 8 × 9450	1.5 ab	1.5 bc	1.5 b	1.5 b	1.5 c	1.5 b	2.0 bc	2.0 ab	2.0 bcd	3.0 abc	4.0 a	4.0 ab	5.0 a	5.0 a	0.00
WYML 6 × WYML 10	1.5 ab	1.5 bc	2.0 ab	2.5 ab	3.0 abc	3.0 ab	3.5 abc	1.5 ab	2.0 bcd	2.0 cde	2.0 bc	2.0 bc	2.5 bc	3.0 ab	0.00
WYML 8 × WYML 11	2.0 ab	2.0 abc	2.5 ab	2.5 ab	2.5 abc	3.0 ab	5.0 abc	2.0 ab	3.0 ab	3.5 ab	4.0 a	4.0 ab	5.0 a	5.0 a	0.00
9450 × WYML 10	1.5 ab	3.0 a	3.0 ab	4.0 a	4.5 a	4.5 a	5.5 ab	1.5 ab	2.0 bcd	3.0 abc	3.0 abc	3.0 abc	3.0 abc	3.0 ab	0.00
WYML 12 × WYML 10	2.0 ab	2.0 abc	2.5 ab	3.0 ab	3.0 ab	3.5 ab	5.5 ab	2.5 a	2.5 abc	3.0 abc	4.0 a	4.0 ab	4.5 ab	5.0 a	0.00
WYML 6 × 9450	2.0 ab	2.0 abc	2.5 ab	2.5 ab	3.0 ab	3.5 ab	5.0 abc	2.0 ab	2.0 bcd	2.5 bcd	2.5 abc	3.0 abc	3.0 abc	4.0 ab	0.00
WYML 15 × 9450	1.5 ab	2.0 abc	2.0 ab	2.0 ab	2.5 ab	2.5 ab	3.0 abc	1.0 b	1.0 d	1.5 de	3.0 abc	3.0 abc	3.5 abc	3.5 ab	0.00
WYML 8 × WYML 10	1.5 ab	2.0 abc	2.0 ab	2.5 ab	2.5 abc	3.0 ab	4.0 abc	1.5 ab	1.5 cd	1.5 de	2.5 abc	3.0 abc	3.5 abc	3.5 ab	0.00
WYML 6 × WYML 8	2.0 ab	2.0 abc	2.0 ab	2.5 ab	2.5 abc	3.0 ab	3.0 abc	1.5 ab	2.0 bcd	2.0 cde	3.0 abc	3.0 abc	3.5 abc	3.5 ab	0.00
CHECK 1: POINEER	2.0 ab	2.0 abc	2.5 ab	2.5 ab	3.0 abc	3.5 ab	4.0 abc	1.0 b	1.5 cd	2.0 cde	3.0 abc	3.0 abc	3.5 abc	3.5 ab	0.00

	Artificially Infested Environment							Naturally Infested Environment							Control
	1WAP	**2WAP**	**3WAP**	**4WAP**	**5WAP**	**6WAP**	**7WAP**	**1WAP**	**2WAP**	**3WAP**	**4WAP**	**5WAP**	**6WAP**	**7WAP**	**1-7WAP**
CHECK 2: AHOUFE	1.5 ab	2.5 ab	3.0 ab	3.5 ab	3.5 abc	4.0 ab	4.0 abc	1.5 ab	2.0 bcd	3.0 abc	4.0 a	4.0 ab	4.5 ab	4.5 ab	0.00
CHECK 4: LAKE 606	1.5 ab	2.0 abc	2.0 ab	2.5 ab	3.0 abc	3.0 ab	3.5 abc	1.5 ab	2.0 bcd	2.5 abc	2.5 abc	3.5 abc	3.5 abc	4.0 ab	0.00
WYML 6 × WYML 12	2.5 a	2.5 ab	2.5 ab	3.5 ab	3.5 abc	4.0 ab	3.5 abc	1.5 ab	2.0 bcd	2.0 cde	2.0 bc	2.5 abc	3.0 abc	3.0 ab	0.00
CHECK 3: DZIFO	1.5 ab	1.5 bc	1.5 b	1.5 b	1.5 c	1.50 b	2.0 bc	1.5 b	2.0 bcd	3.0 abc	3.0 abc	3.5 abc	4.0 abc	4.0 ab	0.00
WYML 11 × WYML 10	2.0 ab	2.5 ab	2.5 ab	2.5 ab	3.0 abc	3.0 ab	3.0 abc	2.0 ab	2.5 abc	3.0 abc	3.5 ab	3.5 abc	3.5 abc	3.5 ab	0.00
WYML 15 × WYML 9	1.5 ab	1.5 bc	2.0 ab	2.0 ab	2.5 abc	3.0 ab	4.5 abc	2.0 ab	2.0 bcd	2.0 cde	2.5 abc	2.5 abc	3.0 abc	3.0 ab	0.00
WYML 12 × WYML 9	2.0 ab	2.5 ab	3.0 ab	3.5 ab	4.0 ab	4.5 a	7.0 a	2.0 ab	2.5 abc	2.5 bcd	3.5 ab	4.0 ab	4.5 ab	4.5 ab	0.00
WYML 8 × WYML 9	1.5 ab	2.0 abc	2.5 ab	3.0 ab	3.0 ab	3.0 ab	5.5 ab	1.0 b	1.0 abc	1.0 e	1.5 c	1.5 c	2.0 c	2.5 b	0.00
WYML 6 × WYML 9	2.0 ab	2.0 abc	2.5 ab	2.5 ab	2.5 abc	3.0 ab	4.0 abc	2.5 a	2.5 abc	2.5 bcd	4.0 a	4.0 ab	4.5 ab	4.5 ab	0.00
WYML 10 × WYML 9	2.0 ab	2.0 abc	2.0 ab	2.0 ab	2.5 abc	2.5 ab	3.5 abc	2.5 a	3.5 a	4.0 a	4.0 a	4.5 a	4.5 ab	4.5 ab	0.00
WYML 6 × WYML 11	1.50 ab	2.50 ab	3.5 a	3.5 ab	3.5 abc	4.5 a	6.5 ab	1.5 ab	2.0 bcd	2.5 bcd	3.0 abc	4.0 ab	4.5 ab	4.5 ab	0.00
WYML 6 × WYML 15	1.5 ab	1.5 bc	1.5 b	2.5 ab	3.0 abc	3.5 ab	3.5 abc	1.5 ab	1.5 cd	2.0 cde	3.0 abc	3.0 abc	3.5 abc	4.0 ab	0.00
WYML 8 × WYML 15	1.0 b	1.0 c	2.0 ab	3.0 ab	2.0 bc	3.0 ab	4.5 abc	1.0 b	2.5 abc	2.5 bcd	2.5 abc	2.5 abc	3.5 abc	4.0 ab	0.00
Mean	**1.70**	**2.00**	**2.23**	**2.59**	**2.78**	**3.18**	**3.96**	**1.65**	**2.04**	**2.45**	**3.01**	**3.26**	**3.73**	**3.92**	**0.00**
Lsd	**1.20**	**1.12**	**1.56**	**2.06**	**2.00**	**2.72**	**4.69**	**1.21**	**1.29**	**1.42**	**1.76**	**2.07**	**2.07**	**2.03**	**0.00**

Means in the same columns having different letters are significantly different ($p<0.05$). MSD symptom severity score: 1 = no infection; 2= mild infection; 3= moderate infection; 4 = severe infection; 5 = very severe infection.

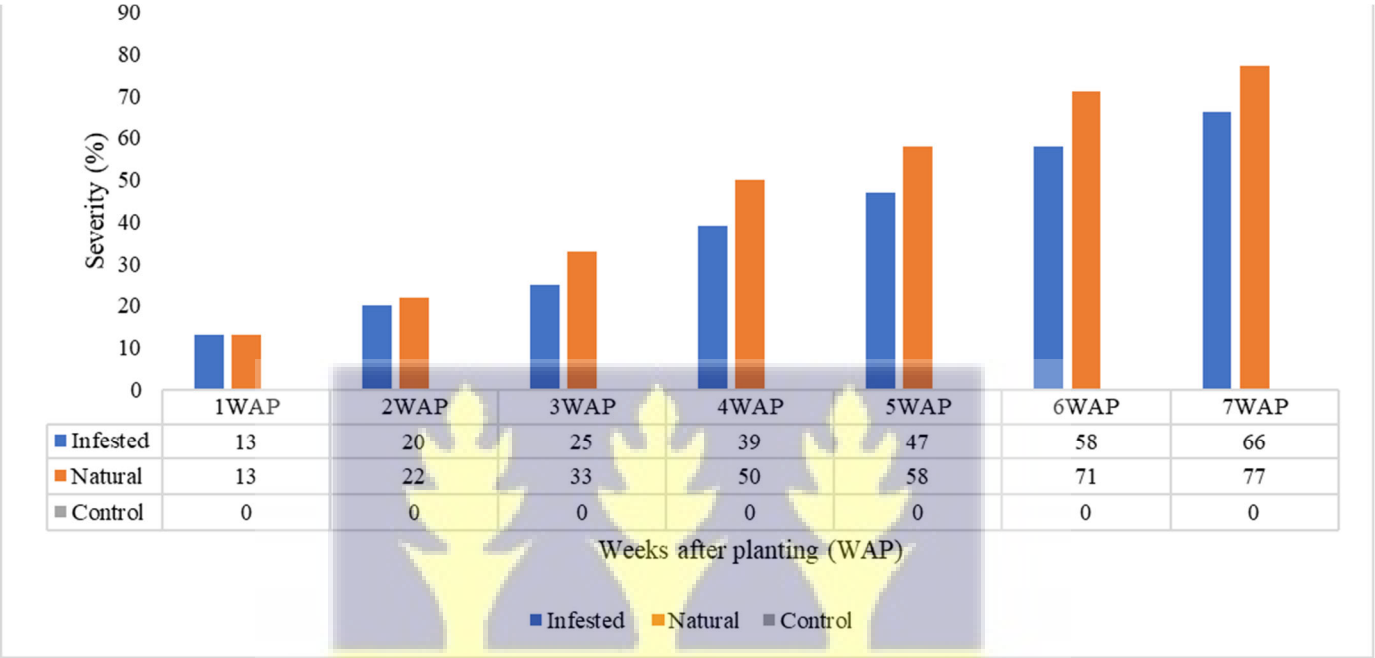
Table 4.38 Mean severity scores of MSD in inbreds across all environments from 1-7 weeks after planting (WAP).

Inbred Line	Mean Severity Score														
	Artificially Infested Environment							Naturally Infested Environment							Control
	1WAP	2WAP	3WAP	4WAP	5WAP	6WAP	7WAP	1WAP	2WAP	3WAP	4WAP	5WAP	6WAP	7WAP	1-7WAP
WYML 15	2.0 ab	3.0 a	3.0 ab	3.5 a	3.5 ab	4.0 ab	4.5ab	1.5 ab	1.5 bc	2.0 abc	2.5 a	2.5 ab	2.5 a	3.0 a	0.0
WYML 11	1.5 b	2.0 b	2.0 b	2.0 b	2.0 d	2.5 b	2.5 b	1.0 b	1.0 c	1.0 c	1.5 a	1.5 b	3.0 a	3.0 a	0.0
WYML 12	2.0 ab	2.0 b	2.5 ab	3.0 ab	3.0 bc	3.0 b	3.5 ab	1.0 b	1.5 bc	1.5 bc	2.0 a	2.5 ab	3.5 a	3.5 a	0.0
WYML 8	2.0 ab	2.5 ab	3.0 ab	3.0 ab	3.5 ab	4.0 ab	4.0 ab	2.0 ab	2.5 ab	2.5 abc	3.0 a	3.0 ab	3.5 a	4.0 a	0.0
WYML 10	2.0 ab	2.5 ab	2.5 ab	3.0 ab	3.5 ab	3.5 ab	3.5ab	2.5 a	3.0 a	3.0 ab	3.0 a	4.0 ab	4.0 a	4.0 a	0.0
WYML 6	2.5 a	3.0 a	3.5 a	4.0 a	4.0 a	5.0 a	5.0 a	2.0 ab	3.0 a	3.5 a	3.5 a	4.5 a	5.0 a	5.0 a	0.0
9450	2.0 ab	2.0 b	2.0 b	2.0 b	2.0 d	2.5 b	3.0 ab	1.5 ab	1.5 bc	2.0 abc	2.5 a	3.0 ab	3.0 a	3.0 a	0.0
WYML 9	2.0 ab	2.0 b	3.0 ab	3.0 ab	3.0 bc	4.0 ab	4.0 ab	1.0 b	2.5 ab	3.5 a	3.5 a	4.0 ab	5.0 a	5.0 a	0.0
Mean	**2.00**	**2.37**	**2.68**	**2.93**	**3.00**	**3.56**	**3.75**	**1.56**	**2.06**	**2.37**	**2.68**	**3.12**	**3.68**	**3.81**	**0.0**
Lsd	**0.77**	**0.77**	**1.07**	**1.24**	**0.89**	**1.98**	**2.14**	**1.07**	**1.39**	**1.73**	**2.88**	**2.52**	**2.51**	**2.74**	**0.0**

Means in the same columns having different letters are significantly different ($p<0.05$).

4.16 Effect of MSD on the performance of hybrid and inbred lines across environments.

Severity increased steadily from 13% at 1WAP to 39% at 4WAP and then to 66% at 7WAP under the artificially infested environment (Figure 4.13). For the natural environment, severity increased from 13% at 1WAP to 50% at 4WAP and 77% at 7WAP. In the control environment, there was no severity from 1WAP-7WAP. The correlation was strongly positive and significant between incidence and severity in the artificially infested environment (Figure 4.14a). The correlation between incidence and hundred-grain weight was negative. In Figure 4.14b severity was negatively and significantly correlated to chlorophyll content and plant height was negatively correlated to plant height and incidence. In the naturally infested environment leaf count was positively and significantly correlated to chlorophyll content (Figure 4.15a). Incidence was negatively correlated to leaf count. Among the inbreds, incidence was positively and significantly correlated to incidence (Figure 4.15b). Figure 4.38 showed the AUDPC for each environment estimated using the severity scores from 1WAP – 7WAP. Of the total area of 4200, the AUDPC ranged from 1953 for naturally infested environment (Figure 4.16a); 1809.5 for combined environments (Figure 4.16c), and 1564.5 under artificially infested environment (Figure 4.16b).



	1WAP	2WAP	3WAP	4WAP	5WAP	6WAP	7WAP
Infested	13	20	25	39	47	58	66
Natural	13	22	33	50	58	71	77
Control	0	0	0	0	0	0	0

Figure 4.13 Graph of MSD severity scores for across naturally infested, artificially infested and control environments

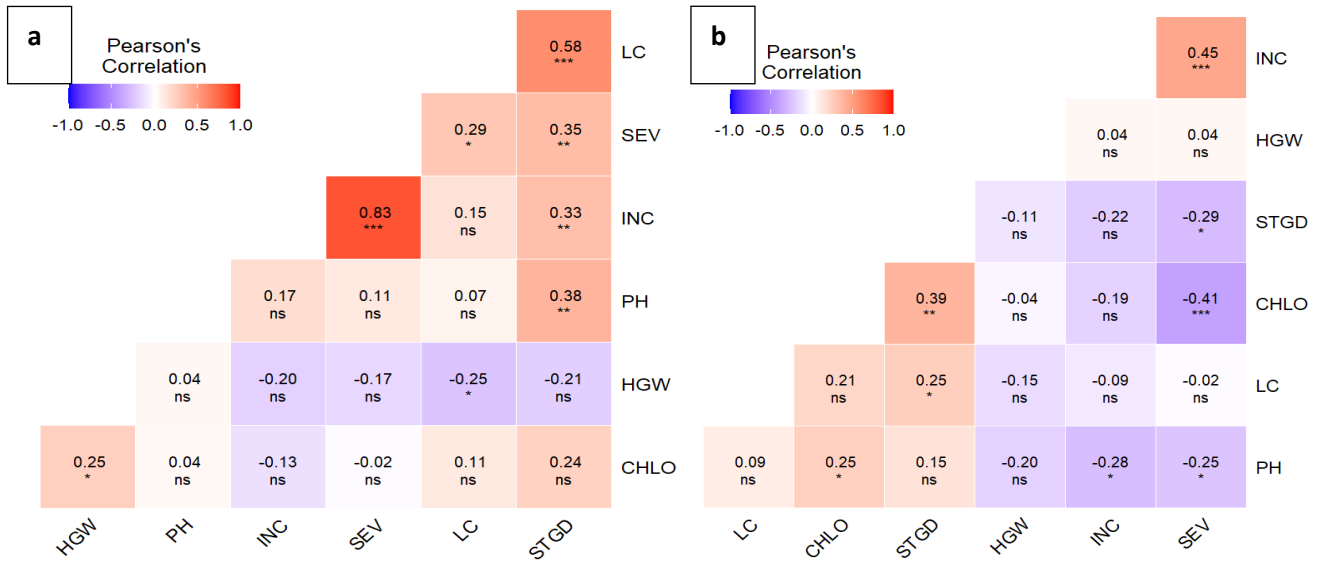


Figure 4.14 Correlation plot of MSD incidence(INC) and severity(SEV) on PH = Plant height, HGW= Hundred grain weight; LC= Leaf count; ST GD= Stem girdth; CHLORO = Chlorophyll content. **a** Correlation between traits in hybrids in artificially infested environment; **b** Correlation between traits of inbreds in artificially infested environment. ns p> = 0.05; * p< 0.05; **p<0.01; and ***p<0.001.

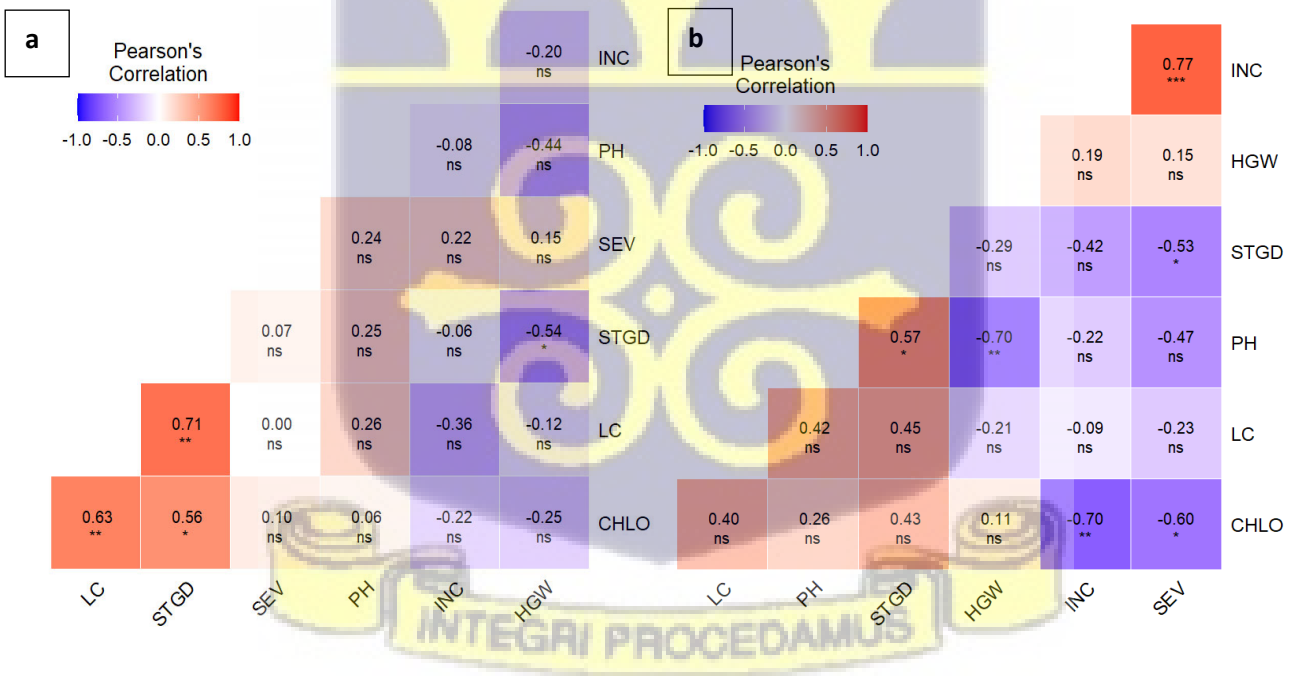
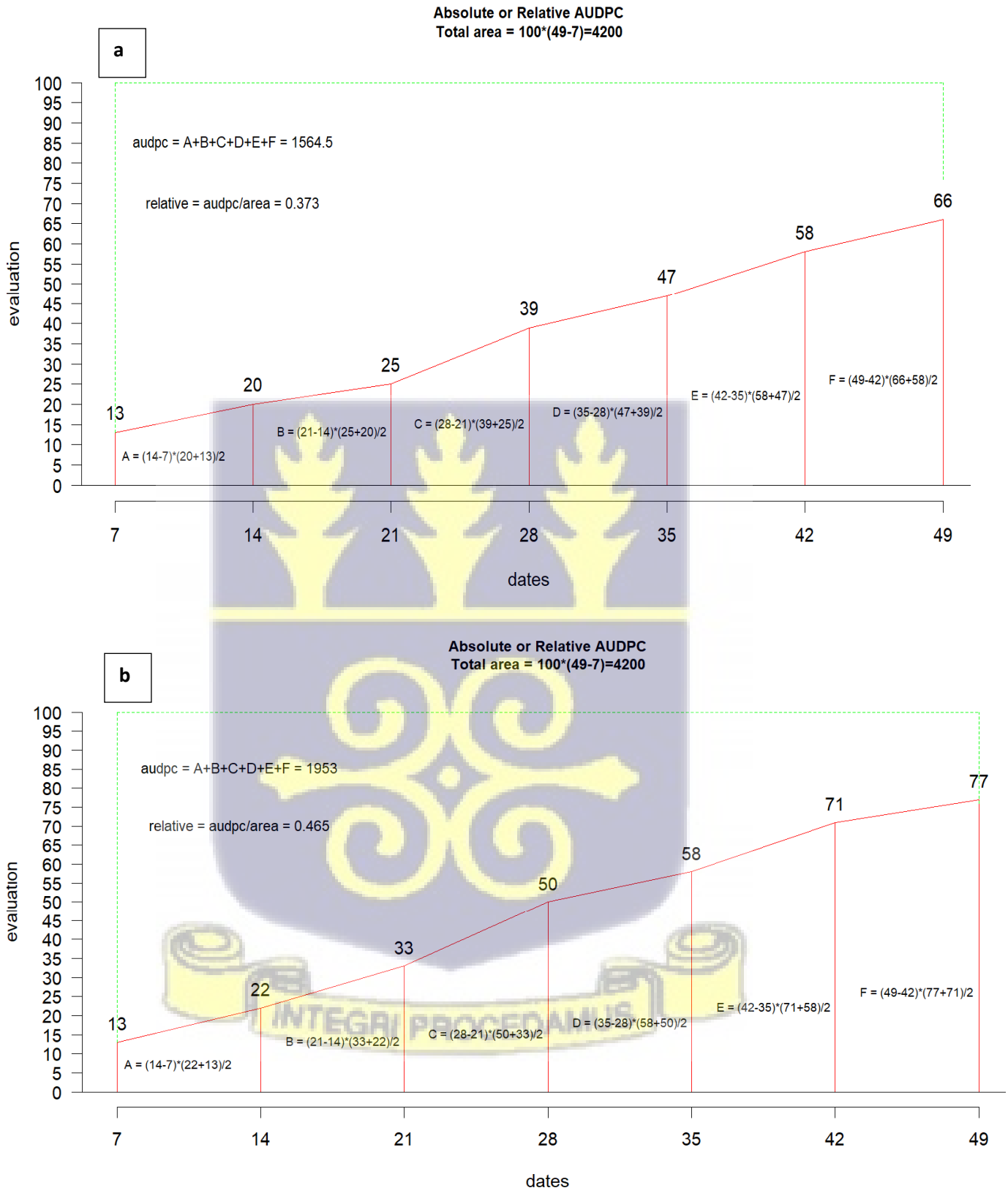


Figure 4.15 Correlation plot of MSD incidence(INC) and severity(SEV) on PH = Plant height, HGW= Hundred grain weight; LC= Leaf count; ST GD= Stem girth; CHLORO = Chlorophyll content in inbred. **a** Correlation between traits of hybrids in naturally infested environment; **b** Correlation among traits in inbreds naturally infested environment. ns p> = 0.05; * p< 0.05; **p<0.01; and ***p<0.001.

Table 4.39 Table showing AUDPC in artificially infested, naturally infested, control and across all environments

	Weeks after planting (WAP)							AUDPC						Total
ENV	**1WAP**	**2WAP**	**3WAP**	**4WAP**	**5WAP**	**6WAP**	**7WAP**	**1-2WAP**	**2-3WAP**	**3-4WAP**	**4-5WAP**	**5-6WAP**	**6-7WAP**	**Total Area = 4200**
ART	13	20	25	39	47	58	66	50.5	157.5	224	301	367.5	434	1564.5
NAT	13	22	33	50	58	71	77	122.5	192.5	290.5	378	451	518	1953
CTR	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00
CMB	13	22	28	45	56	65	72	122.5	175	255.5	353.5	423.5	479.5	1809.5

ENV= environment; INF= infested environment; NAT= natural environment; CTR = control environment; CMB= combined environments



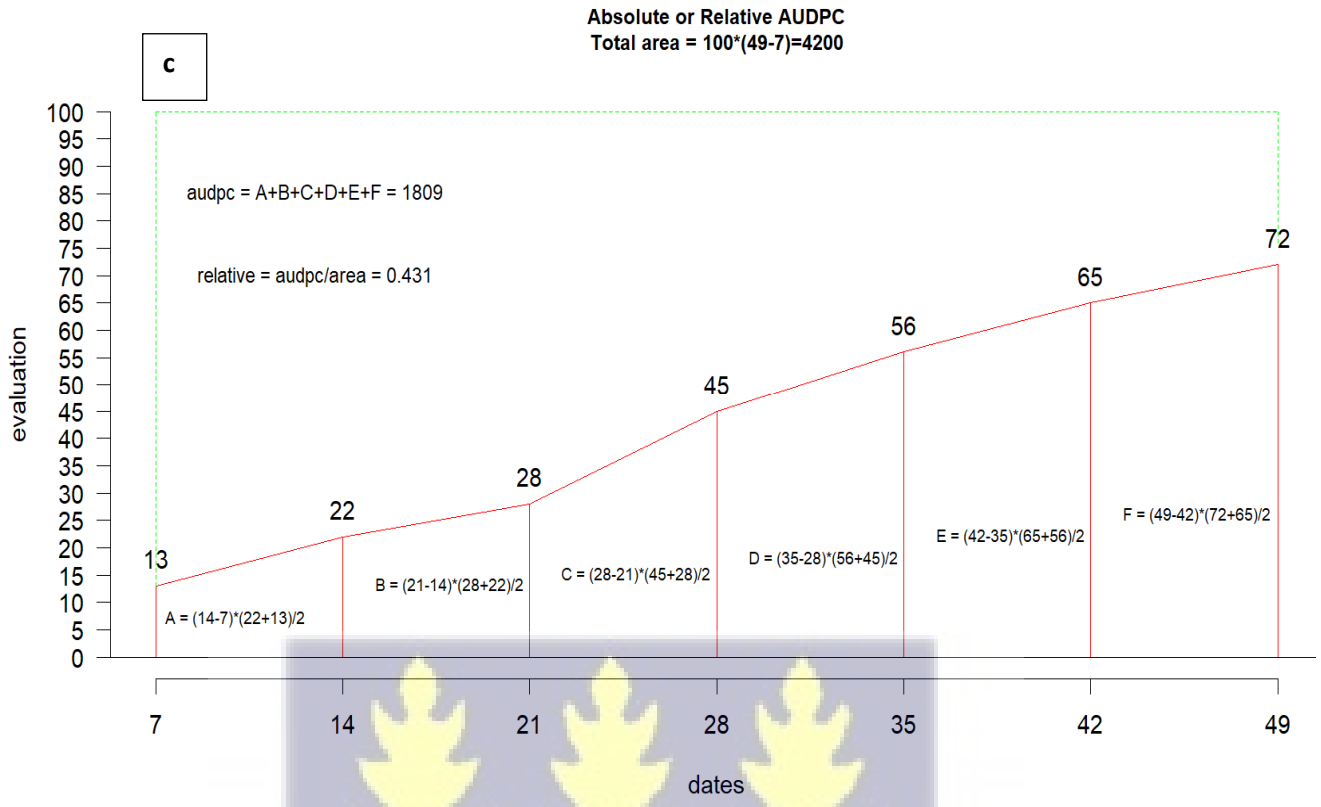


Figure 4.16 Graph of the Area Under the Disease Progress Curve. **a** MSD severity under naturally infested environment. **b** MSD severity under artificially infested environment. **c** MSD severity under combined environments. Evaluation = percentage severity scores; dates = from 1 week after planting (1WAP – 7WAP)

CHAPTER FIVE

DISCUSSION

Significant positive SCA is indicative of non-additive gene action therefore, its exploitation is limited for trait improvement. Significant positive GCA explains the inheritance of these traits in terms of additive gene action. Similar findings were reported by Oppong *et al.* (2015, 2020) and Fato *et al.* (2012). The general analysis of variance showed that in the naturally infested environment, genotype was not significant for most of the traits except for grain yield, ear diameter, grain weight per plot, hundred-grain weight, and plant aspect. Under the artificially infested environment, genotype was found to be significant for ear diameter, husk cover, plant aspect, grain number per ear, grain number per row, and grain weight per plot, there was no significance indicated for grain yield. In the combined environments, most traits were not significant except for grain yield, hundred-grain weight, and plant aspect. These findings indicate that the performance of genotypes differed for traits in different environments, emphasizing the need to test genotypes in multiple environments to ascertain the extent to which traits varied (Falconer & Mackay, 1983). Generally, crosses involving the inbred line WYML 6 produced the highest yields. The yield performance of the hybrids was highest for the artificially infested environment for WYML 6 × WYML 8 (6406.28kg/ha) compared to the standard check PIONEER (6317.88 kg/ha). This is in contravention to the findings by Abebe *et al.* (2018), who investigated combining ability and heterosis in maize inbred lines and reported that all hybrid crosses outperformed the checks for grain yield. Further in combined environments WYML 6 × WYML 8 had the highest yield of 5461.86 kg/ha. In the naturally infested environment, though WYML 6 × WYML 8 was the 10th highest for grain yield, the marginal difference between the 1st and 10th hybrids was 16.3%. Comparatively, the differences between the marginal difference between the

1st and 10th best hybrids for grain yield was 18.78% for the artificially infested environment and 11.92% for combined environments. For the checks, PIONEER was the highest for grain yield across all environments. These show genetic variability exists among genotypes, which can be harnessed for the improvement of grain yield in maize breeding programs. Similar findings were reported in studies by Oppong *et al.* (2019), Elmyhun *et al.* (2020), and Prasanna (2012). WYML 8, WYML 12, and 9450 were the top-performing inbred lines across all environments.

Genotypic correlations were significant and positive for grain yield and grain number per ear in the naturally-infested environment. However, hundred-grain yield and grain weight per plot were found to be negatively correlated. This means that increase in the yield of grains relates to a decrease in the weight of grain influenced by the genes regulating grain yield or grain weight. Genotypic correlations are free of environmental effects, thus grain number per ear is the best trait to select for improvement of grain yield. This finding is in agreement with reports by Aman *et al.* (2021) who reported a positive genotypic correlation with grain yield. If the genes were determined to be additive, such lines can be eliminated from breeding programs. Phenotypic correlations were significant for grain weight and ear diameter but not significant for grain yield and hundred-grain weight. Low broad-sense heritability estimates suggest that genotype plays a smaller role in determining the phenotype compared to environmental factors. Therefore, it is advisable to employ synthetic breeding methods rather than relying solely on natural processes (Egesel *et al.,* 2003; Kearsey & Pooni, 1997; Grüneberg *et al.,* 2005). For all hybrids, PV was higher than GV and GCV for the studied traits under consideration which suggests the influence of environmental factors on the traits (Rafiq *et al.,* 2010). Low heritability, high GCV, and low GAM values showed that such traits may be additive in nature but additivity may be masked, rendering the trait ineffective for selection thus hybridization may be exploited (Bello *et al.,* 2012).

In the artificially infested environment, gain yield showed a significant negative relationship with hundred-grain weight and a significant positive relationship with ear length. Thus an increase in grain yield translates into a decrease in the weight of grain whereas an increase in grain yield translates into a corresponding increase in ear length. This agrees with the study by Gissa *et al.* (2007) who reported that grain yield and ear length had a significant positive relationship. GV and GCV values were shown to be lower than PV, EV, and ECV values. In addition, low GA values due to low heritability estimates are indicative of non-additive gene action, reducing the efficiency of selection (Larik *et al.,* 2000). The results of this finding do not agree with the findings of Ewool & Akromah, (2017) who reported low heritability and low GA for grain yield.

Path coefficient analysis has been widely used in breeding programs for determining the relative contribution of yield-related components to grain yield. It partitions the genotypic correlation between two variables into direct and indirect effects of yield-related components on grain yield (Shengu, 2017). The results of the genotypic path analysis in the naturally infested environment revealed that row number per ear, grain number per ear, and hundred-grain weight have significant effects on grain yield. The highest direct positive effect on grain yield was contributed by ear diameter, grain weight per plot, and grain number per ear. This finding is in agreement with the findings by Rafiq *et al.* (2010) but contradicts with findings reported by Bello *et al.* (2012) who observed negative direct effects of kernel number on grain yield. On the other hand, row number and hundred-grain weight contributed significant negative direct genotypic effects. This finding is in agreement with the negative genotypic correlation between grain yield and hundred-grain weight above. Hundred-grain weight had negligible indirect effect via row number on grain yield. The indirect effect contributed by grain weight per ear via grain number per ear was large. Overall, grain number per ear was the only positive and significant trait with grain yield. This implies that

selection based on grain number per ear would be effective (Aman *et al.,* 2020). The model perfectly explains the data where CFI >0.95 and RMSEA was <0.08.

In the artificially infested environment, hundred-grain weight, ear diameter, row number, and grain number per row showed positive direct genotypic effects on grain yield. Of these, ear diameter, row number, and grain number per ear showed a significant correlation with grain yield. These findings are in agreement with the findings reported by Aman *et al.* (2020). Hundred-grain weight and row number had positive indirect effects on grain yield via grain number per ear and grain number per row respectively (Aman *et al.,* 2020; Munawar *et al.,* 2013). Selection based on grain number per ear would negatively impact grain yield. For improvement in grain yield, selection should be based on hundred-grain weight, grain number per row, row number, and ear diameter. The most important traits that could potentially contribute to improved grain yield are row number and ear diameter which have relatively larger and significant direct genotypic effects.

Merging the results of both environments, grain weight per plant, ear diameter, and grain number per ear had significant positive direct effects on grain yield. Grain number per ear and hundred-grain weight had negative direct effects on grain yield. Grain number per row recorded a negative indirect effect on grain yield via ear hundred-grain weight. Thus, selection based on grain number per row should be made with caution. Similar results were observed by Beulah *et al.* (2018) and Jakhar *et al.* (2017). Generally, the R^2 values ranged from 38.8%, 28.2%, and 28.1% for the naturally infested, artificially infested, and combined environments respectively. These represent the correlation and intercorrelation that exist between the independent variables and grain yield for each environment. Overall, 28.1% of the total variation in grain yield is explained by the dependent variables, leaving the remaining 71.9% of the variability unexplained. This finding is in contravention to observations by Aman *et al*. (2020) who reported that 79.1% of the variability in

grain yield was explained by the independent variables. Even though R^2 values were relatively smaller, the model perfectly fits the data as observed from the RMSEA and CFI values. The lower R^2 values could be attributed to the fact that grain yield is a quantitative trait and could best be explained by the additive effect of all traits under investigation. However, only a few traits were used as explanatory variables, hence their minimal effect on the R^2 value. This finding is in an opposite direction compared to findings by Sibley *et al.* (2014) who ascribed lower R^2 values to models that poorly described the data.

A correlation plot between all traits (Figure 4.7) showed that cobs that recorded larger ear diameter values produced smaller weights per 100 kernels, the same findings were established between ear diameter and plant aspect. A strong positive correlation between days to silking and days to anthesis could be used for selecting hybrids as it indicates that the emergence of silk and pollen shed would occur together which could increase the nicking rate. Disease incidence is negatively correlated with hundred-grain weight, chlorophyll content, grain yield, days to silking, and days to anthesis. Particularly, the negative relationship between disease incidence and days to anthesis and days to silking could infer a mechanism of resistance employed by the hybrids to evade the disease. However, once the severity starts increasing, days to anthesis and days to silking were positively correlated with severity. Grain yield showed a weak negative relationship which was also observed in Figure (4.4 – 4.6). This explains the marginal yield increase across environments irrespective of the high incidence and severity levels. MSV resistance genes may be present in such genotypes which can be harnessed for resistance breeding. Several studies agree with this finding (Oppong *et al.,* 2015; Almekinders *et al.,* 1994; Martin & Shepherd, 2009; Asare-Bediako *et al.,* 2021). Principal component analysis was computed for dimensions having eigenvalues >1. The total variation accounted for the first and second dimensions were shown to be 19.5% and 18.8%

respectively. The PCA was computed by eigenvalue decomposition of the covariance matrix of the data. The first PCA explains 19.5% of the variability present in the data and the second PCA accounted for 18.8%. Cumulatively, the first 3 PCAs explain about 50% of the variation in the data, leaving the remaining 50% to the last 12 PCAs. The point of inflection in Figure 4.10 showed that approximately 3 components were retained without significant loss of data. The results from Figure 4.9 showed that grain yield, days to silking, hundred-grain weight, anthesis silking interval, plant aspect, ear diameter, grain number per row, and days to anthesis showed the maximum positive contribution to the divergence in PC1. In PC2, grain weight per plot, days to anthesis, disease severity, days to silking, and plant aspect were the major contributors to the divergence observed. The findings by Saleh *et al.* (2022) agree with this finding. Hierarchical clustering was performed using Euclidean distance and distinguished hybrids into 3 clusters. Clusters of the same group had similar relationships for agronomic traits. Shrestha (2016) observed similar findings where maize inbred lines were classified into distinct groups for agronomic traits using cluster analysis.

GCA and SCA effects are associated with additive and non-additive (dominance or epistasis) genetic effects. GCA/SCA ratio was used to determine the type of gene action that influenced the performance of traits across individual environments. Ratios closer to unity imply a preponderance of GCA effects indicating the trait is under additive gene action. Values closer to zero imply SCA effects dominate GCA effects thus non-additive gene action controlled traits. In the naturally infested, artificially infested, and combined environments, all traits showed ratios closer to zero. Therefore, the traits were under the control of non-additive genes. Many authors reported findings that corroborate this finding (Derera *et al.,* 2008; Gissa *et al.,* 2007). Genetic variability can be maximized by crossing inbred lines from different heterotic groups. Lines of the same heterotic

groups that show favorable GCA effects can be used for developing synthetic varieties (Elmyhun *et al.,* 2020).

The performance of inbred lines is highly correlated with heterosis (Gissa *et al.,* 2007). Hybrids with negative heterosis for grain yield are not desirable as they would result in decreased yield when used in breeding programs. Hybrids with high heterosis are the most preferable for the improvement of grain yield. Heterotic groupings were performed based on significant SCA effects for grain yield (Elmyhun *et al.,* 2020). Six parental lines were grouped into two heterotic groups (A and B) based on significant SCA effects for the performance of grain yield under naturally infested, artificially infested, and combined environments. There were two inbred lines grouped into two heterotic groups under the naturally infested environment. Four inbred lines were grouped into two heterotic groups in the artificially-infested environment. In the combined environment, two heterotic groups containing four inbred lines were identified. Dosho (2019) classified inbred lines into three heterotic groups from a diallel analysis under low nitrogen, optimum nitrogen, and combined environments. It is worth noting that testers were not used in this study therefore the heterotic groupings are arbitrary rather than confirmatory.

Significant differences were observed in the genotypes for incidence and severity for all environments. In the artificially infested environment, the incidence was as high as 78% whereas the severity was 70.2%. Similarly, in the naturally infested incidence was 75% and severity was 50.3%. However, the highest grain yield recorded for the naturally-infested environment was lower (6317.88 kg/ha) compared to the artificially-infested environment (6406.28 kg/ha). This could be due to four reasons. Firstly, the differences observed in the genotypes could be due to differences in MSD resistance levels of inbred lines. Genes conditioning resistance or the genetic background's influence could be responsible for the observed differences as reported by some

authors (Gichuru, 2014; Asare-Bediako *et al.,* 2021; Oppong *et al.,* 2019). Secondly, *C. mbila* may have shown a selective preference for some genotypes. The inbred lines WYML 6, WYML 8, WYML 12, and 9450 were found to possess significant levels of resistance which culminated in high yield in their hybrid combinations. During the assessment of the incidence and severity scores in the infested environment, it was observed that genotypes that had high trichome density had relatively lower incidence compared to genotypes with lower trichome density. This finding corroborates with reports from Moose *et al.* (2004) who attributed trichome density in maize to insect resistance. Thirdly, weeds around the experimental field may serve as an alternate host for MSV, especially because the naturally infested field was closer to the boundaries of the research farm where grasses species such as *Axonopus compresus* and *panicum maximum* were found. Similar findings were established by Mesfin *et al.* (1992) and Bosque-Perez & Buddenhagen, (1999) who found that *C. mbila* and MSV inoculum were found on these grasses. Lastly, *C. mbila* feeding could be selective for plants that were not already carrying MSV than plants that were infested. Olfactometer studies by Oluwafemi *et al.* (2011), where *C. storeyi* affinity was higher for healthy maize seedlings than for MSV-infested maize seedings are in tandem with this finding.

Marginal yield reduction in the naturally infested environment could be attributed to possible mixed infections present in the evaluation environment. Though artificially *Cicadiluna* vectored inoculation more closely resembles natural inoculation in farmers' fields, differences may exist in the severity of the MSV isolates in the two environments. Similar results were reported by Mawere *et al.* (2006). Previous reports (unpublished) indicated the presence of MSD in the evaluation environment. Further, Oppong *et al.* (2015) detected that Ghanaian MSV isolates belonged to the highly virulent MSV-A_1 subtype. The observations above were again reflected in relatively low AUDPC values for the various environments. Of a total of 4200 m^2 MSD severity covered 37.7%,

46.5%, and 43.1% for naturally infested, artificially infested, and combined environments respectively.

CHAPTER SIX

CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

Genotype was not significant for the majority of the traits investigated under naturally infested, arterially infested, and combined environments. Correlations between grain yield and disease incidence and severity were negative. GCA/SCA ratio revealed that all traits were under the influence of non-additive genetic effects. This was supported by low heritability values, low GCV, and high PCV and ECV values. Genotypic correlations between some traits and grain yield revealed the additive genetic contribution of those traits to grain yield. The inbred lines WYML 6, WYML 8, WYML 12, and WYML 9 were shown to be the highest-yielding parents across all environments and had good potential for use in improving yield and yield-related components. Further, their hybrid combinations, especially WYML 6× WYML 8, WYML 12 × WYML 9 recorded higher heterosis and relatively lower incidence and severity levels under individual environments.

These inbred lines were classified into heterotic groups A and B which can be exploited in future maize breeding programs. Under the naturally infested environment, inbred lines WYML10 (group A) and 9450 (group B) were identified. In the artificially infested environment, inbred lines WYML 6 and WYML 9 (group A) and WYML 8 and WYML 12 (group B) were identified. In combined environments heterotic group A were identified to be inbred lines WYML 6 and WYML 10 and heterotic group B was made up of inbred lines WYML 8 and 9450.

Path analysis showed that ear diameter, grain number per ear, and grain number per row were the three most important traits that had direct significant positive effects on grain yield across all environments.

Inbred lines WYML 8, WYML 9, WYML 12 and 9450 and their hybrid combinations showed varying levels of tolerance and/or resistance to MSV. WYML 6 × WYML 8, WYML 9450 × WYML 10 and WYML 12 × WYML 9 showed the highest levels of resistance or tolerance against MSV across all environments. AUDPC for severity affected less than 50% of all fields, however, yields were still high mainly in the artificially infested environment. This suggests most genotypes were tolerant or resistant to MSV infection and are potentially important lines for developing resistance to MSV in future breeding programs. On the other hand, the decrease in the yield of the naturally infested environment suggests the presence of more virulent strains of MSV in the experimental location.

6.2 Recommendations

This study has demonstrated the yield potential for yellow maize hybrids in Ghana as well as developing MSV-resistant hybrids. Inbred lines WYML 6, WYML 8, WYML 12, and WYML 9 are recommended for high yielding hybrid development as due to their good combining ability for yield and yield related traits. Further, inbred lines 9540, WYML 8, WYML 9 and WYML 12 are recommended for developing MSV resistant hybrids. However, evaluation of these promising genotypes should be carried out in multiple environments to ascertain their stability for grain yield and MSV resistance and/or tolerance because the current study was carried out in only one location. It is recommended that MSV studies should be carried out at the study location to ascertain the virulence levels of MSV strains present. High-yielding and MSV-resistant hybrids

can then be developed out of these promising yellow maize inbred lines to support the food and feed industry in Ghana.

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APPENDICES

Appendix 1 ANOVA table for percentage incidence in infested and natural environments

Source of variation	Degree of freedom	Sum of squares	Mean square	F-value	P-value
Genotype	31	21180	683	1.226	0.232112
Replication	1	4	4	0.007	0.933069

Environment	1	7472	7472	13.410	0.000448 ***
Replication × Block	14	16506	1179	2.116	0.019184 *
Residuals	80	44578	557		

*Significant at $p < 0.05$; *** significant at $p < 0.001$.

Appendix 2 ANOVA table for severity scores in infested and natural environments

Source of variation	**Degree of freedom**	**Sum of squares**	**Mean square**	**F-value**	**P-value**
Genotype	31	43.97	1.418	1.064	0.40134
Replication	1	0.78	0.781	0.586	0.44630
Environment	1	10.13	10.125	7.592	0.00726 **
Replication × Block	14	33.90	2.422	1.816	0.05025
Residuals	80	106.69	1.334		

**Significant at $p < 0.01$; · significant at $p < 0.1$.

Appendix 3 ANOVA table for percentage mortality in infested and natural environments

Source of variation	Degree of freedom	Sum of squares	Mean square	F-value	P-value
Genotype	31	4755	153.4	1.263	0.22502
Replication	1	72	72.5	0.597	0.44279
Environment	1	98	98.0	0.807	0.37166
Replication × Block	14	4996	356.9	2.938	0.00122 **
Residuals	80	9717	121.5		

**Significant at $p < 0.01$