**Title:** GENETIC VARIABILITY OF EARLY MATURING INBRED MAIZE LINE INFESTATION OF FALL ARMYWORM (*Spodoptera frugiperda* J.E. Smith)

**Course title:** Bio 539- BIG DATA ANALYSIS

**Course Advisor**: Dr. Rachel Schwart

**INTRODUCTION.**

Maize (*Zea mays* L.) is one of the most important staple crops globally, serving as a primary source of food, feed, and industrial raw materials. However, its production faces significant challenges due to biotic stresses, with the fall armyworm (*Spodoptera frugiperda* J.E. Smith) emerging as a major threat to maize cultivation, particularly in sub-Saharan Africa. The fall armyworm (FAW) causes severe damage to maize plants by feeding on leaves, stems, and ears, leading to substantial yield losses if left unmanaged.

This study evaluates the genetic variability, combining ability, and performance of early-maturing maize hybrids under FAW pressure. Specifically, it investigates the response of these hybrids to artificial and natural infestations, assesses the relationship between agronomic traits and FAW resistance, and identifies promising hybrids and parental lines with favorable genetic attributes. The findings aim to provide valuable insights for maize breeding programs focused on enhancing resistance to FAW while maintaining high grain yield and other desirable agronomic traits.

**MATERIALS AND METHODS.**

Sixteen early maturing white maize inbred lines with different levels of resistance to FAW that constituted the genetic material for this study were obtained from the maize improvement program of IITA. Sixteen inbred lines were grouped into 4 sets and crossed using the North Carolina Design II scheme to generate 64 hybrids, which were evaluated under both infested (natural and artificial infestation) and control (non-infested) of fall armyworm infestation conditions at two locations. Field trials were conducted at two locations: Ile-Ife and Ikenne, Nigeria, during 2023. The experimental design consisted of a randomized complete block design with three replications per environment. Treatments included both infested and non-infested conditions.

The project analyzes the genetic performance of early-maturing maize hybrids under infested condition (natural or artificial infestation) by fall armyworm (FAW), using statistical tools like ANOVA, AMMI analysis, correlation studies, and mixed-effects models in R to evaluate variability, identify promising hybrids, assess trait relationships, and estimate GCA effects of parental lines, with results indicating significant genetic variability for FAW resistance (EASP) and grain yield (GY), identifying top-performing hybrids and parents, and highlighting key agronomic traits associated with resistance. Stability analysis using coefficient of variation (CV) and visualization tools such as violin plots, scatter plots, and lollipop charts were employed to evaluate hybrid performance across infested and non-infested environments. Multi-trait selection criteria were applied to identify promising hybrids that combine FAW resistance with desirable agronomic traits, such as grain yield and plant height.

The methodology facilitated a comprehensive evaluation of genotype-by-environment interactions, enabling the identification of stable performers under varying infestation scenarios. This approach provides valuable insights into the genetic variability of FAW resistance and its association with key agronomic traits in early maturing maize germplasm.

**RESULTS.**

**Table 1**

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The analysis of variance reveals strong evidence of genetic variability among hybrids for the trait being studied, indicating that some hybrids perform better than others; however, the environment (infested vs. controlled) does not significantly influence the trait, suggesting that hybrids respond similarly across conditions, and the lack of significant interaction between hybrids and environments implies that hybrid rankings remain consistent regardless of environmental conditions.

**table 2:A table with numbers and letters

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Table 2 highlights the General Combining Ability (GCA) effects of parents for fall armyworm resistance (EASP) under controlled and infested environments, with a combined measure (GCA\_Effect\_EASP\_Low) ranking parents based on resistance; notable findings include consistent performance by Parent 3 and Parent 14, making them promising for breeding programs, while Parent 5 shows susceptibility to FAW damage.

Fig 1: A screen shot of a graph

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Fig 1 reveals significant genetic variability in FAW resistance (EASP) among maize hybrids, with higher EASP values in infested environments indicating greater susceptibility, while hybrids like H1\_5, H10\_3, and H16\_2 consistently exhibit low EASP scores and stable performance across environments.

Fig 2 highlights that most parents exhibit consistent GCA effects for FAW resistance across control and infested environments, with notable performers like Parent 3 and Parent 14 showing robust resistance, while Parent 5 demonstrates susceptibility, emphasizing the importance of stability and genotype-by-environment interactions in selecting promising candidates for breeding programs.

**Fig 2:** A graph with red and blue lines

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**Fig 3:**

A graph with blue dots

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Fig 4:A graph with a red line

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Fig 3 and 4 reveal a negative correlation between plant height and FAW resistance, with taller plants showing better resistance, and identifies promising hybrids like H4-8, H10-9, and H13-3 that combine low EASP values (high resistance) with high grain yields, offering potential for breeding programs to improve both traits simultaneously.

Fig 5 shows the mean grain yield exhibits a strong negative correlation with **EASP**, indicating that hybrids with higher grain yield tend to have better FAW resistance. Notable positive correlations are observed for traits like **EHT** (mean ear height), **AS** (mean anthesis-silking interval), and **DS** (mean days to silking). Traits such as **PHT** (mean plant height) and **DA** (mean days to anthesis) show no significant correlation with **EASP**.

A graph with red dots

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**DISCUSSION**

From the finding in this study, the sixteen inbred maize line evaluated differed signaficantly for all yield and relative traits and this indicate that there is presence of variation among the trait. The GCA highlights significant genetic variability for FAW resistance among maize parents, with consistent performers like Parent 3 and Parent 14 showing promise for breeding programs, while the combined measure offers a practical tool for ranking parental lines; further research should validate these findings across environments and explore genomic approaches to enhance resistance through marker-assisted selection

Hybrids with consistently low EASP values (e.g., H1\_5, H10\_3) can be used as prime candidates for breeding programs due to their robust FAW resistance, emphasizing the need for multi-environment trials, genomic approaches, and further field validation to develop resilient maize varieties and enhance food security in regions affected by fall armyworms**.** demonstrating strong resistance and making them promising candidates for breeding programs aimed at improving FAW tolerance**.** the genetic basis for FAW resistance is relatively stable across environments, emphasizing the importance of selecting parents like hybrid 3 and14 with consistent GCA effects for breeding programs, while also underscoring the need to explore genotype-by-environment interactions, environmental factors, and genomic approaches to enhance resistance and ensure broad adaptability in maize hybrids.

Top-performing hybrids like H4-8, H10-9, and H13-3 demonstrate strong resistance and high grain yield, emphasizing the need for multi-trait selection strategies, further validation across environments, and genomic approaches to enhance breeding programs aimed at developing resilient maize line. The correlation between grain yield and EASP suggests that high-yielding hybrids may also exhibit better resistance to FAW. By prioritizing hybrids with favorable trait combinations, breeders can develop maize varieties better equipped to withstand fall armyworm challenges. Further validation in multi-environment trials and exploration of the genetic basis of these traits can enhance the reliability and applicability of the findings.