Adaptability and Stability Analysis of Commercial Cultivars, Experimental Hybrids and Lines under Natural Fall Armyworm Infestation in Zimbabwe Using Different Stability Models

Prince M. Matova 1,2,3,4, Casper N. Kamutando 5, Bruce Mutari 6, Cosmos Magorokosho 3 and Maryke Labuschagne 4,*

1 Former Department of Research and Specialist Services, Causeway, Harare P.O. Box CY550, Zimbabwe; matova_p@yahoo.com
2 Mukushi Seeds (Pvt) Ltd., Mt Humpden, Harare P.O. Box MP287, Zimbabwe
3 Former International Maize and Wheat Improvement Centre, Harare P.O. Box MP163, Zimbabwe; c.magorokosho42@gmail.com
4 Department of Plant Sciences, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa
5 Department of Plant Production Sciences and Technologies, University of Zimbabwe, Harare P.O. Box MP167, Zimbabwe; kamutandocn@gmail.com
6 International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bulawayo P.O. Box 776, Zimbabwe; brucemutari@gmail.com
* Correspondence: labuscm@ufs.ac.za

Abstract: Fall armyworm (Spodoptera frugiperda (J.E. Smith); FAW)-resistant cultivars and breeding lines have been identified in sub-Saharan Africa. However, these genotypes have not been evaluated for their stability across environments with natural FAW infestation. The objectives of this study were to: (i) identify hybrids/open pollinated varieties combining high grain yield (GYD) and stability across environments with natural FAW infestation, (ii) select maize inbred lines with high GYD and stable FAW resistance, and (iii) identify the most discriminating environments for GYD performance and foliar FAW damage (FFAWD) under natural FAW infestation. The additive main effect and multiplicative interaction (AMMI) model was used to detect the presence of genotype-by-environment interaction (GEI) for GYD, and foliar and ear FAW damage. Seven stability analysis models were used to analyse adaptation and stability of genotypes across environments. The hybrids Mutsa-MN521 and CimExp55/CML334 were the best, combining adaptation and stability across FAW infested environments. Other acceptable hybrids were identified as 113WH330, Manjanja-MN421, CML338/CML334 and PAN53. The local inbred lines SV1P and CML491 combined adaptability and stable FAW resistance across environments. The best exotic donor lines exhibiting stable FAW resistance were CML67, CML346, CML121 and CML338. Harare and Gwebi were identified as the most discriminating sites for GYD performance, while Kadoma and Rattray-Arnold Research Stations were identified for FFAWD among inbred lines.

Keywords: adaptation; fall armyworm; stability; stable FAW resistance

1. Introduction

The invasion of the sub-Saharan Africa (SSA) region by the fall armyworm (Spodoptera frugiperda (J.E. Smith); FAW) continues to threaten food security and livelihoods in the region [1,2]. Breeding efforts against the maize feeding pest are currently underway in SSA, and locally adapted genotypes with significant resistance to FAW have been identified [3,4]. The International Maize and Wheat Improvement Centre (CIMMYT) recently released hybrids with partial resistance to the pest [5]. Again, several studies in SSA have identified potential genotypes for use in breeding as well as recommendation to farmers in mitigating the effects of FAW in maize production [3,4].
However, varietal performance is largely determined by its genetics, production environment and the interaction between the two. This is commonly referred to as genotype-by-environment interaction (GEI) and in most cases it affects breeding decisions [6]. The same applies to the FAW resistant hybrids and lines that have been identified and released in SSA.

Breeding aims to enhance crop adaptation through improving yield, quality and other desirable agronomic traits. Adaptation has been defined as any characteristic of a living organism that gives it value under the prevailing environmental conditions [7]. In the present scenario, adaptation will mean a variety that is able to give the highest yield in a given production environment. This may not necessarily be across a set of different environments and that makes adaptation easier to compute compared to stability. However, superior yield performance should be stable across environments. Stability is described as the ability of a genotype to perform consistently across a range of environments [8]. Naturally the interaction of a genotype with a number of environments tends to result in differential performance across the environments. Genotypes that perform well and produce good yields across environments are considered adapted and stable. Resistance breeding is targeted at improving adaptation and stability of performance across environments. Testing of adaptation is relatively easy and straightforward compared to stability. Stability of performance is a complex trait that is often negatively affected by several production factors, chief among them being stresses in the production environment.

Several biometrical models have been developed for use in the analysis of GEI and partitioning of yield performance and adaptation with stability across environments [8,9]. However, one model may not be enough to explain the variation and identify the ideal genotype combining adaptation and stability across environments. In this study different statistical models were used to evaluate and dissect GEI, adaptation and stability of performance of candidate genotypes for FAW resistance and other local cultivars and lines across environments. The objectives of the study were to: (i) detect the presence of GEI among FAW resistant genotypes, (ii) identify the most adapted and stable resistant genotypes across environments with natural FAW infestation and (iii) identify the most discriminating environment for yield performance and foliar FAW damage (FFAWD) under natural FAW infestation. This information can guide breeding for stable FAW resistance in southern Africa.

2. Materials and Methods
2.1. Germplasm for Testing

Fifty two genotypes consisting of 26 hybrids/OPVs, and 26 inbred lines were evaluated. The genotypes were selected for FAW resistance and good GYD performance under FAW infestation and some for being susceptible to FAW [10]. Thirteen of the inbred lines were parental lines of the hybrids evaluated in this study. These were evaluated together with eleven other local and exotic lines with high yield and FAW resistance and two local FAW susceptible lines (Table 1).

The germplasm used were developed by the Crop Breeding Institute (CBI), International Maize and Wheat Improvement Centre (CIMMYT), HarvestPlus and various seed houses in Zimbabwe. Some of the lines and hybrids evaluated included cultivars and parental genotypes produced not only in Zimbabwe but across the East and Southern African (ESA) regions (Table 1).
Table 1. Description of genotypes evaluated for adaptation and stability of performance under natural fall armyworm infestation in Zimbabwe during the 2019–2020 summer seasons.

| Genotype Code | Name          | Source       | Year of Release | Production Region          | Line Code | Line Name  | Source         | Type | Status/Origin |
|---------------|---------------|--------------|-----------------|----------------------------|-----------|------------|----------------|------|---------------|
| G1            | Salisbury white | CBI          | Not Clear       | Zimbabwe and ESA           | G25       | CLHP0005   | HarvestPlus    | local|               |
| G6            | R215          | CBI          | 1974            | Zimbabwe                   | G27       | CML304     | CIMMYT         | local|               |
| G13           | ZS265         | CBI          | 2011            | Zimbabwe                   | G42       | CZL1227    | CIMMYT         | local|               |
| G14           | ZS269         | CBI          | 2014            | Zimbabwe                   | G28       | CML444     | CIMMYT         | local|               |
| G19           | SR52          | CBI          | 1962            | Zimbabwe and ESA           | G57       | CML543     | CIMMYT         | local|               |
| G20           | ZS242A        | CBI          | 2015            | Zimbabwe and ESA           | G34       | CML395     | CIMMYT         | local|               |
| G21           | ZS246A        | CBI          | 2016            | Zimbabwe and ESA           | G48       | CML334     | CIMMYT         | local|               |
| G24           | 113WH330      | CBI          | 2014            | Zimbabwe                   | G33       | CML312     | CIMMYT         | local|               |
| G29           | CZH1258       | CIMMYT       | Experimental    | N/A                        | G36       | CLHP00478  | HarvestPlus    | local|               |
| G30           | NTS51         | NTS          | 2014            | Zimbabwe                   | G51       | CML139     | CIMMYT         | local|               |
| G31           | PAN63         | PANNAR       | 2007            | Zimbabwe and ESA           | G52       | CML571     | CIMMYT         | local|               |
| G32           | PAN4M-23      | PANNAR       | -               | Zimbabwe and ESA           | G24       | CLHP0003   | HarvestPlus    | local|               |
| G33           | PAN-7M-81     | PANNAR       | 2013            | Zimbabwe and ESA           | G60       | CimExp54   | CIMMYT         | local|               |
| G34           | PHB30G19      | PIONEER      | 2008            | Zimbabwe and ESA           | G50       | CML67      | CIMMYT         | local|               |
| G39           | Manjanja MN421| Mukushi      | 2015            | Zimbabwe, South Africa, Zambia | G55 | CML121 | CIMMYT | Exotic |               |
| G40           | Mutsa MN521   | Mukushi      | 2014            | Zimbabwe, South Africa, Zambia | G47 | CML338 | CIMMYT | Exotic |               |
| G42           | Mukwa         | Mukushi      | 2016            | Zimbabwe, South Africa, Zambia | G53 | CML346 | CIMMYT | Exotic |               |
| G44           | ZAP61         | Agriseeds    | 2008            | Zimbabwe and ESA           | G9        | SV1P       | CBI-DR & SS    | local|               |
| G49           | CML338/CML334 | CIMMYT       | Experimental    | N/A                        | G49       | CML331     | CIMMYT         | Exotic|               |
| G52           | CIM52/CML139 | CIMMYT       | Experimental    | N/A                        | G30       | CML491     | CIMMYT         | local|               |
| G53           | CIM53/CML345 | CIMMYT       | Experimental    | N/A                        | G61       | CZL1112    | CIMMYT         | local|               |
| G54           | CIM54/CML334 | CIMMYT       | Experimental    | N/A                        | G38       | DPTY... *9 | HarvestPlus    | local|               |
| G55           | CIM55/CML334 | CIMMYT       | Experimental    | N/A                        | G46       | CML539     | CIMMYT         | local|               |
| G58           | CIM58/CML121 | CIMMYT       | Experimental    | N/A                        | G40       | CZL1315    | CIMMYT         | local|               |
| G59           | CML543/CML334 | CIMMYT       | Experimental    | N/A                        | G23       | WW01408    | CBI-DR & SS    | local|               |
| G60           | CML571/CML338 | CIMMYT       | Experimental    | N/A                        | G18       | HX482P     | CBI-DR & SS    | local|               |
2.2. Trial Sites, Experimental Design and Agronomic Management

Genotypes evaluated were established under natural FAW infestation across different sites in Zimbabwe during the 2019 and 2020 summer seasons, except for Harare, which had both natural infestation and managed FAW environments. Managed FAW environments were included for inbred lines because some inbred lines tend to suffer FAW damage even with FAW control. The trials under natural FAW infestation were raised without chemical control for the pest. The Chiredzi and Chisumbanje research stations are situated in the lowveld (altitude < 600 masl, average temperature 30 °C). These sites are characterized by low rainfall and high temperatures; thus, they naturally have a high and active infestation population of stem borers, FAW and other insect pests and have been traditionally used for maize stalk borer screening. Harare, Gwebi and Kadoma are active maize production zones, and they tend to have high and active FAW populations during maize growing seasons. The sites CIMMYT-Harare and Chisumbanje were used during the 2019 summer season, while Chiredzi, RARS and Kadoma-CRI were used in the 2020 summer season. The sites DR&SS-Harare and Gwebi VTC were used in the summer seasons of both years (Table 2).

| Location          | Management | Precipitation (mm) | Latitude | Longitude | 2018/2019 | 2019/2020 | Fertilisers (NPK) ha⁻¹ |
|-------------------|------------|--------------------|----------|-----------|-----------|-----------|-----------------------|
| CIM-Harare        | NI         | 1506               | 17°48′ S | 31°85′ E  | 557.2     | 547.3     | 166:24:5:23:2          |
| RARS              | NI         | 1341               | 17°14′ S | 31°14′ E  | 631.8     | 543.8     | 166:24:5:23:2          |
| Chisumbanje       | NI         | 421                | 20°05′ S | 32°15′ E  | 441.9     | 434.8     | 166:24:5:23:2          |
| Chiredzi          | NI         | 409                | 21°01′ S | 21°25′ E  | 416.5     | 419.2     | 166:24:5:23:2          |
| DR&SS-Harare      | NI + Managed | 1506             | 17°48′ S | 31°03′ E  | 502.7     | 436.3     | 166:24:5:23:2          |
| Gwebi VTC         | NI         | 1448               | 17°41′ S | 30°32′ E  | 571.5     | 542.5     | 166:24:5:23:2          |
| KD-CRI            | NI         | 1149               | 18°94′ S | 29°25′ E  | 555.6     | 474.8     | 28:24:5:23:2           |

CIM-Harare, CIMMYT-Harare; RARS, Rattray-Arnold Research Station; ART-Farm, Agriculture Research Trust Farm; CHS, Chisumbanje; CHZ, Chiredzi; DR&SS-Hre, DR&SS-Harare; Gwebi VTC, Gwebi Variety Testing Centre; KD-CRI, Kadoma Cotton Research Institute; NI, Natural Infestation.

The hybrid/OPV experiment was laid out in a 10 × 6 α (0, 1) lattice design, while the inbred line experiment was laid out in a 9 × 7 α (0, 1) lattice design. Both experiments had two replications at each testing site and one 4 m row plot for all environments except at DR&SS-Harare and CIMMYT-Harare that had 2 m row plots. Inter-row and intra-row spacing were 0.75 m and 0.25 m, respectively. Plants were thinned to one per planting station at two leaf stage (approximately three weeks after planting) to give a crop population density of 17 and 9 plants per row for the 4 m and 2 m rows, respectively, which translates to about 53,000 plants ha⁻¹. The plants in the experiments were raised using standard agronomic practices for maize production. Optimal fertiliser rates of 400 kg ha⁻¹ for both compound D (7N:14P:7K) basal applications and ammonium nitrate (34.5N) for top dressing were applied at all environments. Weeds were controlled using herbicides and hand weeding where necessary.

2.3. Data Collection and Analysis

The following data were recorded per plot: (i) foliar FAW damage (FFAWD) averaged for scores at 4, 8 and 12 week intervals from date of planting, (ii) ear FAW damage (EFAWD) and (iii) grain yield (GYD) per plot adjusted to 12.5% moisture content. FFAWD and EFAWD damage were recorded following the modified Davis scale [11] where scores 1–2 = resistant, 2–5 = partial resistance, 5–7 = susceptible, 7–9 = highly susceptible. All the other agronomic traits were recorded as described previously [12,13].

Individual site ANOVA for each trait was done to determine the existence of differences between genotypes using Genstat Discovery Software V18.0 and Multi-
environment Trials Analysis in R (META-R) V2.1 R package software. Best linear unbiased predictions (BLUPs) and broad sense heritability estimates ($H^2$) were performed with META-R. To reduce the confounding effect of error and environmental variances, sites with $H^2$ lower than 20% were excluded from the combined analysis. The Bartlett’s test was used to test for homogeneity of error variances for the evaluated traits in each environment. Across site ANOVA was carried out to test the effects and magnitude of genotypes (G), environments (E) and GE interactions using the additive main effect and multiplicative interaction (AMMI) analysis model in Genstat. Genotypes were considered fixed, while replications within environments and environments were considered random [14,15].

Both the genotype-by-environment analysis with R (GEA-R) V4.1 R package software and Genstat Discovery Software V18.0 were used to estimate adaptability and stability parameters of the genotypes across environments [9,14]. The AMMI model was used to assess GEI, adaptation and stability of the genotypes and environments. The first two principal components (PCs), interaction principal component axes (IPCA1 and IPCA2) of the AMMI model and PC1 and PC2 for GGE biplots were computed to visualise the GEI and adaptation of the genotypes to the test environments. However, the AMMI model on its own cannot effectively identify stable genotypes as it does not encompass a quantitative measure for stability [16,17]. Therefore, the AMMI stability value (ASV) [18] was employed to further analyse stability. The ASV measures stability in two dimensions using PC analysis of the scores of IPCA1 and IPCA2. It denotes the distance from zero in a scatter plot of IPCA1 and IPCA2. The IPCA1 contributes more to the total GEI sum of squares compared to IPCA2. There is therefore a proportional difference between the two PC scores, hence the need to balance the contribution of the two to the total GEI sum of squares. A genotype with the lowest ASV is the most stable [18].

In addition, the yield stability index (YSI) that gives a simultaneous single measure of yield and yield stability, was used. Genotypes with the lowest YSI are considered the most stable and high yielding [6,18]. The YSI sums up the ranks of yield and ranks of yield stability as follows: $YSI = \text{Rank of ASV} + \text{rank of yield}$.

Further analysis for adaptation and stability was done with the GGE biplots, cultivar superiority index, Eberhart and Russel’s coefficient of regression and Wricke’s ecovariance models [9,14,19]. The GGE biplots were used to visualise the most adapted and stable genotypes, the most discriminating environments as well as clustering the genotypes and environments based on the effects of FAW infestation on the GYD and FAW damage parameters.

3. Results

3.1. Analysis of Genotype by Environment Effects for Grain Yield, Fall Armyworm Resistance and Related Traits of Hybrids/OPVs Using the AMMI Model

The AMMI across environment ANOVA showed significant ($p < 0.001$) differences for genotypes, environments and GEI. The contribution of environmental variance to the total variance was higher than that of genotypes and GEI for all traits. The two interaction principal component axes (IPCA1 and IPCA2) were significant ($p < 0.05$) for all traits. For GYD the highest contribution to total variance came from the GEI (44.85%), while environments and genotypes contributed 36.97% and 18.18%, respectively (Table 3).

For FFAWD, environments made the largest contribution to total variance of 52.88% followed by GEI with 30.26% and lastly genotypes with 16.89%. Similarly, for EFAWD, environments made the largest contribution to the variance, which amounted to 42.22%, while GEI and G contributed 41.61% and 16.17%, respectively (Table 3).
Table 3. Analysis of genotype by environment effect for grain yield, fall armyworm resistance and related traits using the AMMI model for commercial cultivars, experimental hybrids and inbred lines under natural FAW infestation sites in Zimbabwe during the 2019 and 2020 summer seasons.

(A) Hybrids/OPVs

| Source of Variation | DF  | SS    | MS   | DF  | SS    | MS   | DF  | SS    | MS   |
|---------------------|-----|-------|------|-----|-------|------|-----|-------|------|
| Treatments          | 233 | 1405.5| 6.03 *** | 285 | 49,044| 172.10 *** | 155 | 565.6 | 3.65 *** |
| Genotypes           | 25  | 255.5 | 10.22 *** | 25  | 8283  | 331.30 *** | 25  | 91.5  | 3.66 *** |
| Environments        | 8   | 519.6 | 16.49 *** | 10  | 25,920| 2592.00 *** | 5   | 238.8 | 47.75 *** |
| Block               | 9   | 18    | 2.00 | 11  | 355   | 32.3 | 6   | 9.6   | 1.60 |
| Interactions        | 196 | 630.4 | 3.22 *** | 250 | 14841 | 59.40 **  | 123 | 235.4 | 1.91 *** |
| IPCA 1              | 32  | 283.7 | 8.86 *** | 34  | 4604  | 135.40 ** | 29  | 97.2  | 3.35 *** |
| IPCA 2              | 30  | 117.8 | 3.93 *** | 32  | 2901  | 90.60 *** | 27  | 61.8  | 2.29 ** |
| Residuals           | 134 | 229   | 1.71 | 184 | 7337  | 39.9 | 67  | 76.3  | 1.14 |
| Error               | 199 | 342.6 | 1.72 | 275 | 11,339| 41.2 | 147 | 150.9 | 1.03 |

(B) Inbred lines

| Source of Variation | DF  | SS    | MS   | DF  | SS    | MS   | DF  | SS    | MS   |
|---------------------|-----|-------|------|-----|-------|------|-----|-------|------|
| Treatments          | 181 | 99.47 | 0.55 *** | 259 | 1206.5| 4.66 *** | 129 | 375.3 | 2.91 ** |
| Genotypes           | 25  | 39.31 | 1.52 *** | 25  | 524.2 | 20.97 *** | 25  | 137   | 5.48 *** |
| Environments        | 6   | 23.2  | 1.37 *** | 9   | 427.8 | 47.54 *** | 4   | 60.4  | 15.11 *** |
| Block               | 7   | 3.08  | 0.44 | 10  | 18.4  | 1.84 *  | 5   | 0.9   | 0.19 |
| Interactions        | 136 | 36.96 | 0.27 | 224 | 254.4 | 1.36 *  | 94  | 177.8 | 1.89 |
| IPCA 1              | 30  | 14.71 | 0.49 * | 33  | 84.7  | 2.57 *** | 28  | 104.2 | 3.72 ** |
| IPCA 2              | 28  | 9.43  | 0.37 | 31  | 42.6  | 1.37 *  | 26  | 40    | 1.54 |
| Residuals           | 78  | 12.81 | 0.16 | 160 | 127.1 | 0.8   | 40  | 33.6  | 0.84 |
| Error               | 124 | 37.43 | 0.3  | 233 | 194.6 | 0.84 | 102 | 186.8 | 1.83 |

* p < 0.05; ** p < 0.01; *** p < 0.001; IPCA, interaction principal component axes; DF, degrees of freedom; SS, sum of squares; MS, mean squares; GYD, grain yield; FFAWD, foliar fall armyworm damage; EFAWD, ear fall armyworm damage.

3.2. Mean Grain Yield Performance of Hybrids/OPVs and Stability Analysis

GGE biplot analysis showed that the most adaptable and stable genotypes were G40 (Mutsa MN521), G42 (Mukwa) and G58 (CIM58/CML121) (Figure 1A). These combined high grain yield performance and stability, reflective of their large PC1 values and small PC2 values on the biplot. The genotype G40 (Mutsa MN521) was located on the first concentric ring, close to the position of the most ideal genotype, indicating that it is the most acceptable genotype, combining high GYD performance and stability, as identified by the biplot. The ideal genotype is the most preferred, as it combines adaptation and stability. The most stable genotypes were G54 (CIM54/CML334), G49 (CML338/CML334) and G53 (CIM53/CML345). These were located near the origin of the biplot, implying they had low PC1 and PC2 values. Genotype G49 (CML338/CML334) had GYD that was equal to the trial means, while G53 (CIM53/CML345) and G54 (CIM54/CML345) performed below the trial means as they were located below the average environmental coordination axis. The biplots explained 65.05% of the total variation observed, with PC1 contributing 46.72% and PC2 contributing 18.33% (Figure 1A).

The ranking biplot showed that the best grain yielder was G31 (PAN53), followed by G42 (Mukwa), G40 (Mutsa MN521) and G32 (PAN4M-23) (Figure 1B). However, genotypes G31 (PAN53) and G32 (PAN4M-23) were highly unstable, despite being high yielding as they were located further away from the x-axis. In contrast, genotypes G40 (Mutsa MN521) and G42 (Mukwa) were located closer to the x-axis, indicating low PC2 values. Combining that with their large PC1 values, the two were more stable and adaptable. Genotype G19 (SR52) was identified to be stable but it was very low-yielding (Figure 1B).
Figure 1. GGE biplots showing adaptation and stability of genotypes across nine environments. (A) A comparison GGE biplot (genotype scaling) showing adaptation and stability of genotypes across nine environments, (B) A ranking GGE biplot showing the mean grain yield performance of 26 maize hybrids/OPV produced across nine environments in Zimbabwe. Genotypes are identified by a code prefixed by an ‘x’. Environments are identified by a number prefixed by a ‘+E’: +E1 = Harare-DR&SS-2019; +E2 = Harare-CIMMYT-2019; +E3 = Gwebi-2019; +E4 = Chisumbanje-2019; +E5 = Panmure-2019; +E6 = Rattray-Arnold-2020; +E7 = Gwebi-2020; +E8 = Chiredzi-2020; +E9 = Harare-DR&SS-2020.

Further analysis with the covariance percentage (CV%) and coefficient of regression models identified G13 (ZS265), G31 (PAN53), G40 (Mutsa MN521) and G55 (CIM55/CML334) as the best genotypes selected by both models for combining good GYD performance with stability across environments. The plot of CV% vs. mean GYD-placed high yielding and stable genotypes in the 4th quadrant (Figure 2A). The plot of coefficient of regression (bi) vs. variability ($S^2_{di}$) separates genotypes into three categories (adapted, stable and adapted). When bi is close to 1 the genotypes are adaptable and when $S^2_{di}$ is near zero the genotypes are stable. If $S^2_{di}$ is low and the bi is high the genotypes will be adaptable and stable (Figure 2B). Simultaneous selection using AMMI mean yield performance and stability parameters (ASV and YSI) together with the Standard deviation (Sd), cultivar superiority (Cs), Eberhart and Russel (ER) and Wricke’s ecovalence (We) models identified the best genotypes as G24 (113WH330), G40 (Mutsa MN521), G39 (Manjanja MN421), G55 (CIM55/CML334) and G49 (CML338/CML334). The yield performance and stability ranks of the genotypes are shown in Table 4. The cultivar G6 (R215) showed good stability with the ASV, Sd, Ss and We models but failed to perform well on YSI and Cs indices and had poor per se performance for GYD. G31 (PAN53) and G42 (Mukwa) were the best on GYD per se performance across natural FAW environments but they lacked good stability (Table 4).
Table 4. Assessment of grain yield stability of hybrids and OPVs evaluated across nine natural fall armyworm infestation environments in Zimbabwe during the 2019–2020 seasons using different stability models. The shaded rows in gray highlight the selections made.

| Genotype Number | Genotype Code | Name             | IPCAg1 | IPCAg2 | Mean GYD | ASV Rank | ASV | YSI Rank | Sd Rank | Cultivar Superiority Cs Rank | Static Stability Ss Rank | Wricke’s Ecovalence We Rank |
|-----------------|---------------|------------------|--------|--------|----------|----------|-----|----------|---------|--------------------------------|---------------------------|---------------------------|
| 1               | G1            | Salisbury White  | −2.10  | 0.32   | 1.68     | 24       | 3.27 | 26       | 10.79   | 24                             | *                         | 53.19                     |
| 2               | G6            | R215             | −0.07  | −0.20  | 1.30     | 25       | 0.23 | 13       | 11.43   | 25                             | 0.65                      | 6.63                      |
| 3               | G13           | ZS265            | −0.45  | −0.46  | 3.29     | 9        | 0.84 | 12       | 3.42    | 5                              | 2.55                      | 6.73                      |
| 4               | G14           | ZS269            | −0.58  | −0.62  | 2.88     | 20       | 1.10 | 17       | 5.14    | 17                             | 2.11                      | 11.64                     |
| 5               | G19           | SB52             | −0.24  | 1.48   | 0.95     | 26       | 1.53 | 33       | 13.13   | 26                             | *                        | 19.95                     |
| 6               | G20           | ZS242A           | −0.43  | −0.56  | 3.05     | 17       | 0.86 | 13       | 13.13   | 26                             | *                        | 19.95                     |
| 7               | G21           | ZS246A           | −0.80  | −0.36  | 3.39     | 7        | 1.30 | 20       | 5.14    | 24                             | 10.56                     | 16                        |
| 8               | G24           | 113WH330         | 0.20   | 0.27   | 3.30     | 8        | 0.41 | 11       | 4.49    | 14                             | 0.86                      | 5.14                      |
| 9               | G29           | CZH128           | 0.75   | 0.04   | 3.72     | 4        | 1.19 | 19       | 3.90    | 9                              | 2.49                      | 9.66                      |
| 10              | G30           | NT551            | 0.35   | −0.17  | 2.77     | 21       | 0.57 | 6        | 5.50    | 19                             | 2.80                      | 7.69                      |
| 11              | G31           | PAN53            | 1.03   | −0.22  | 4.14     | 1        | 1.62 | 24       | 3.12    | 4                              | 5.12                      | 16.75                     |
| 12              | G32           | PAN4M-23         | −0.23  | −0.96  | 3.64     | 5        | 1.02 | 15       | 3.01    | 3                              | 2.98                      | 10.13                     |
| 13              | G33           | PAN7M-81         | 0.42   | 0.49   | 3.23     | 10       | 0.82 | 20       | 4.93    | 16                             | 3.69                      | 13.93                     |
| 14              | G34           | PHB30C19         | 0.44   | −0.09  | 2.60     | 23       | 0.68 | 7        | 5.87    | 22                             | 2.50                      | 3.53                      |
| 15              | G39           | Manjanja-MN421   | 0.07   | 0.44   | 3.22     | 13       | 0.45 | 17       | 4.20    | 11                             | 1.48                      | 6.07                      |
| 16              | G40           | Mutsa-MN521      | 0.44   | −0.01  | 3.91     | 3        | 0.68 | 8        | 2.41    | 1                             | 3.61                      | 6.32                      |
| 17              | G42           | Mukwa            | 0.56   | 0.75   | 4.08     | 2        | 1.15 | 18       | 2.95    | 2                              | 4.82                      | 19.98                     |
| 18              | G44           | ZAPw1            | 1.01   | −0.44  | 3.22     | 11       | 1.63 | 25       | 5.43    | 18                             | 5.14                      | 19.16                     |
| 19              | G49           | CML338/CML334    | −0.17  | 0.31   | 3.10     | 16       | 0.41 | 2        | 4.43    | 13                             | 1.37                      | 4.77                      |
| 20              | G52           | CimExp52/CML139  | −0.66  | 0.18   | 3.11     | 15       | 1.03 | 16       | 4.53    | 15                             | 1.06                      | 9.12                      |
| 21              | G53           | CimExp53/CML345  | −0.31  | 0.08   | 2.64     | 22       | 0.49 | 5        | 5.71    | 21                             | 1.38                      | 5.39                      |
| 22              | G54           | CimExp54/CML334  | −0.48  | 0.05   | 3.14     | 14       | 0.75 | 9        | 3.87    | 8                              | 1.39                      | 6.42                      |
| 23              | G55           | CimExp55/CML334  | 0.53   | 0.02   | 3.54     | 6        | 0.83 | 11       | 3.43    | 6                              | 3.56                      | 6.87                      |
| 24              | G58           | CimExp56/CML121  | 0.50   | −1.16  | 3.02     | 18       | 1.40 | 21       | 6.05    | 23                             | 4.22                      | 20.66                     |
| 25              | G59           | CML543/CML334    | 0.80   | 0.73   | 3.02     | 19       | 1.43 | 22       | 5.67    | 20                             | 3.98                      | 15.37                     |
| 26              | G60           | CML571/CML338    | −0.58  | 0.10   | 3.22     | 12       | 0.91 | 14       | 3.92    | 10                             | 2.50                      | 11.03                     |

*p < 0.05; IPCAg1 = interaction principal component axes for genotypes 1; IPCAg2 = interaction principal component axes for genotypes 2; GYD = grain yield; ASV = AMMI stability value; YSI = yield stability index; Sd = standard deviation; We = Wricke’s ecovalence.
Figure 2. Covariance percentage and coefficient of regression biplots showing adaptation and stability of genotypes across environments. (A) A biplot showing covariance percentage (CV%) against mean grain yield performance of 26 maize genotypes evaluated across nine environments in Zimbabwe. (B) A graphical presentation of the Eberhart and Russel coefficient of regression (bi) vs. variability (S<sup>2</sup>di) of mean grain yield for 26 maize genotypes evaluated across nine environments in Zimbabwe. The numbers represent the genotypes evaluated and these correspond with the genotype codes in Table 1.

3.3. Identification of the Best Screening Environments for Grain Yield Potential under Natural Fall Armyworm Infestation in Zimbabwe

The AMMI model biplot and the GGE biplot (Scatter plot) shown in Figure 3A,B, respectively, identified E1 as the most discriminating environment, followed by E7. The two had the longest vectors showing their high discriminating power. Environment E1 (Harare-DR&SS-2019) and E7 (Gwebi-2020) were not strongly associated with genotypes, while the other environments had associations with specific genotypes. The environments E2 (Harare-CIMMYT-2019), E3 (Gwebi-2019) and E4 (Chisumbanje-2019) were stable as they had short vectors and most of the genotypes were clustered around these environments (Figure 3A). This implies that these environments (E2, E3 and E4) may not be the best in screening genotypes for FAW resistance under natural FAW infestation conditions.

Further analysis with the scatter plot showed that genotypes G40 (Mutsa MN521), G42 (Mukwa), G31 (PAN53), G29 (CZH1258), G44 (ZAP61), G55 (CIM55/CML334), G58 (CIM58/CML121), G39 (Manjanja MN421) and G54 (CIM54/CML334) were clustered within the mega-environment including all the other environments except E1. The genotypes that were outside the mega-environments were G1, G19, G6, G59, G30, G54, G53, G19, G32, G21, G13, G14, G20 and G60. E2 formed its own mega-environment; however, this was circulated by the bigger mega-environment covering all the other environments besides E1. The mega-environment covering E1 was positioned further away from the other two mega-environments (Figure 3B).
Figure 3. Biplots showing the positions of genotypes and environments on the scatter-gram. (A) A comparison AMMI scatter biplot for grain yield (environment scaling) showing the positions of the 26 genotypes and nine environments on the two dimensional scatter-gram, (B) A GGE biplot showing mega-environments depicted by grain yield scores of 26 maize genotypes evaluated across nine environments in Zimbabwe during 2019–2020 seasons. Genotypes are identified by a genotype number (for Figure 3A) and a genotype code (for Figure 3B) prefixed by an ‘x’ all shown in Table 5. Environments are identified by a number prefixed by a ‘+E’, +E1 = Harare-DR&SS-2019; +E2 = Harare-CIMMYT-2019; +E3 = Gwebi-2019; +E4 = Chisumbanje-2019; +E5 = Panmure-2019; +E6 = Rattray-Arnold-2020; +E7 = Gwebi-2020; +E8 = Chiredzi-2020; +E9 = Harare-DR&SS-2020.

Table 5. Assessment of grain yield potential of inbred lines evaluated across six environments with natural fall armyworm infestation and one managed fall armyworm environment in Zimbabwe during the 2019–2020 seasons.

| Genotype Number | Genotype Code | Name         | Grain Yield | Grain Yield Rank |
|-----------------|---------------|--------------|-------------|-----------------|
| 1               | G9            | SV1P         | 1.37        | 1               |
| 2               | G18           | HX482P       | 0.10        | 25              |
| 3               | G23           | WW01408      | 0.07        | 26              |
| 4               | G24           | CLHP0003     | 0.52        | 15              |
| 5               | G25           | CLHP0005     | 0.60        | 12              |
| 6               | G27           | CML304       | 0.79        | 5               |
| 7               | G28           | CML444       | 0.31        | 21              |
| 8               | G30           | CML491       | 1.30        | 2               |
| 9               | G33           | CML312       | 0.45        | 18              |
| 10              | G34           | CML395       | 0.37        | 19              |
| 11              | G36           | CLHP00478    | 0.31        | 20              |
| 12              | G38           | DFTY . . . *9| 1.15        | 3               |
| 13              | G40           | CZL1315      | 0.71        | 8               |
| 14              | G42           | CZL1227      | 0.67        | 10              |
| 15              | G46           | CML539       | 0.49        | 17              |
| 16              | G47           | CML338       | 0.78        | 6               |
| 17              | G48           | CML334       | 0.71        | 7               |
| 18              | G49           | CML331       | 0.59        | 13              |
| 19              | G50           | CML67        | 0.63        | 11              |
| 20              | G51           | CML139       | 0.30        | 22              |
| 21              | G52           | CML571       | 0.26        | 23              |
| 22              | G53           | CML346       | 0.50        | 16              |
| 23              | G55           | CML121       | 0.88        | 4               |
| 24              | G57           | CML543       | 0.13        | 24              |
| 25              | G69           | CML60Exp     | 0.69        | 9               |
| 26              | G61           | CZL1112      | 0.54        | 14              |
3.4. Inbred Lines Exhibiting High Adaptation and Foliar Fall Armyworm Resistance Stability across Environments with Natural Fall Armyworm Infestation

The genotypes G9 (SV1P), G30 (CML491) and G38 (DPTY . . . *9) were the best for GYD performance across environments with mean yields of 1.37 t ha\(^{-1}\), 1.30 t ha\(^{-1}\) and 1.15 t ha\(^{-1}\), respectively (Table 5).

The ANOVA of the AMMI model showed significant \((p < 0.001)\) effects of genotypes and environments for GYD, FFAWD and EFAWD, while GEI was significant for FFAWD only. For this reason, only FFAWD was included for further analysis. The IPCA1 was significant for all traits while the IPCA2 was significant for FFAWD only. The dissection of the GEI variance for FFAWD showed that the genotypes made the largest contribution to total variance, which amounted to 43.45%, while environments and GEI contributed 35.46% and 21.09%, respectively (Table 3).

The most discriminating environments for FFAWD were identified as +7 (Kadoma) and +5 (Rattray-Arnold) for the 2020 season whilst +1 (Harare-DR&SS) and +2 (Harare-CIMMYT) were identified for the 2019 season. These had the longest vectors indicative of the high discriminating power of these environments. The environment +4 (Gwebi-2019) had the shortest vector, implying it was the least discriminating (Figure 4A).

Figure 4B showed that the inbred line G50 (CML67) had the lowest FFAWD scores, it had the smallest PC1 value followed by G53 (CML346), G55 (CML121), G9 (SV1P), G47 (CML338) and G30 (CML491) as some of the best performers for resistance to FFAWD.
The highest stability for FFAWD across the environments was exhibited by G53 (CML346), followed by G55 (CML121), G47 (CML338), G30 (CML491), G50 (CML67) and G9 (SV1P). The inbred lines G33 (CML312) and G49 (CML331) showed average performance on FFAWD resistance, but they were unstable as shown by their large PC2 values. The poor performers included genotypes G18 (HX482P), G57 (CML543), G28 (CML444) and G34 (CML395), these had large PC1 values indicating large FFAWD scores.

The biplot clustered the testing environments into three mega-environments based on FFAWD scores that were scored in those environments. The first mega-environment covered +2 (Harare-CIMMYT-2019), the second covered +1 (Harare-DR&SS-2019) and +3 (Harare-Managed FAW-2019) and the third mega-environment encompassed environments +4, +5, +6, +7, +8, +9 and +10 (Figure 4B).

4. Discussion

Breeding for yield stability in FAW infested environments is important, as it aims to guarantee the performance of cultivars and varieties recommended for production in such environments. A previous study [10] identified commercial cultivars, experimental hybrids and inbred lines with acceptable levels of FAW resistance. However, the performance of these genotypes needed to be evaluated for stability across environments with natural FAW infestation. These genotypes were evaluated in this study, and the significant GEI that was observed for hybrids/OPVs for all traits and for FFAWD for inbred lines indicates differential performance of the genotypes. This indicated that selection of the best genotypes across environments was not going to be easy, hence the need for a more refined analysis for increased screening efficiency and effective selection and cultivar recommendations.

Refined analysis for cultivar performance when GEI is present aims to check the adaptability and stability of genotypes across environments, as has been recommended [8,20]. Most of the variation observed for FFAWD and EFAWD on hybrids/OPVs across the environments was a result of the differences in the environments, as environments showed the largest percentages of the total sum of squares. This indicates that there were large differences in the mean performance of these traits for most of the environments. However, for GYD the greatest contribution to the observed variation came from GEI, implying that GYD performance was highly dependent on the response of the genotype to the production environment. This concurs with a previous study [8], which suggested that genotypic performance is determined by the environmental conditions.

Contrary to the above, the genotypes were responsible for most of the variation observed across inbred lines for GYD and FFAWD. This suggests that varietal performance was highly distinct and explicit such that the effects of the environments and GEI were overshadowed by genotypic effects. This could probably be the same reason for the lack of significance on GEI for GYD and EFAWD. However, though not significant, GEI contributed the largest effects to the variation that was observed for EFAWD on the inbred lines. This may relate to factors, such as husk cover, that may depend on genotypes and environmental factors that stress the plants or make them more attractive or delicious to the pest. Observations from a prior study [10] noted that genotypes with open husk cover tend to have more damage on the ears by the FAW. The GEI was significant for FFAWD only on inbred lines. This suggested the need to focus on only FFAWD for stability analysis. With regards to that, genotypes contributed 43.45% to the total sum of squares of the GEI, while environments and GEI contributed 35.46% and 21.09%, respectively (Table 1).

The GGE comparison and ranking biplots (PC1 vs. PC2) for hybrids and OPVs in Figure 1 showed that genotype effect scores were more scattered compared to the environmental effect scores. The same was observed on inbred lines (see Figure 4). This suggests that variability due to genotypes was greater than variability due to the environments as was shown by the contributions of the genotypes to total sum of squares of the variance components (Table 3). Adaptability is measured by PC1 in the positive direction of the x-axis, while stability is evaluated by PC2 along the y-axis on either side of the x-axis [18]. Accordingly, the hybrids G31 (PAN53), G42 (Mukwa), G40 (Mutsa MN521) and
G32 (PAN4M-23) were the highest yielders as they had the largest PC1 values. With regards to stability, genotypes G40 (Mutsa MN521) and G42 (Mukwa) were more stable, hence the two combined both stability and adaptability and that makes them acceptable. It was recommended [8] that cultivars should not only be high yielding but should have sustained yield superiority across environments.

The environments of Harare and Gwebi were observed to be highly discriminating for GYD performance in the hybrids/OPVs as they had the longest vectors. This implied that the sites Harare and Gwebi were able to differentiate GYD varietal performance under natural FAW infestation better than other sites. Similar results were reported in a study on cowpea [21], in which Harare was identified to be the most discriminating and representative site. A study on sorghum [22] identified the Rattray-Arnold Research Station as the most discriminating and representative site. High potential environments are the best in discriminating genotypic performance for GYD potential [21,22]. Again, these seem to concur with the findings of this study that observed Harare and Gwebi as the most discriminating environments. The two environments are in natural region 11, characterised by good soils and high rainfalls.

The hybrids G54 (CIM54/CML334), G49 (CML338/CML334) and G53 (CIM53/CML345) were the most stable for GYD performance across environments with natural FAW infestation; however, they had average to below-average GYD performance, and hence are not preferred. This concurs with other studies [8,23] that reported that the most stable genotypes are not necessarily the highest yielders. Genotypes that combined both adaptability (high GYD performance) and stability across environments are the most preferred by both seed producers and farmers. The GGE biplot analysis in the current study identified genotypes G40 (Mutsa MN521) and G42 (Mukwa) as the most preferred hybrids combining adaptability and stability. The hybrids G31 (PAN53) and G55 (CIM55/CML334) were also identified as acceptable genotypes. G31 (PAN53) had high GYD performance and relatively good stability, while G55 (CIM55/CML334) had good stability and acceptable GYD performance (see Figure 1).

These four hybrids (CIM55/CML334, Mutsa MN521, Mukwa and PAN53) were again identified as the best by the CV% stability model. The quadrant position of the hybrid G55 (CIM55/CML334) showed that the genotype is stable, but its GYD performance was relatively low compared to G40 (Mutsa MN521), G42 (Mukwa) and G31 (PAN53). This was also displayed by the GGE biplot in Figure 1. The Eberhart and Russel Coefficient of Regression model identified genotypes G40 (Mutsa MN521) and G55 (CIM55/CML334) as the best, combining adaptability and stability (Figure 2B). These results suggest that quick genetic gains for FAW resistance in locally adapted materials can be achieved if breeders focus on the improvement of the parents of the hybrids.

Different stability analysis methods were used in this study, as it is quite difficult to use only one method and come up with a correct conclusive decision. The same sentiments were echoed in previous studies [8,19], which stated that stability analysis is a complex phenomenon that remains a challenge to breeders in variety evaluation and recommendations. Additional stability methods were used to conclude the findings from the previous models that had collectively identified genotypes G55 (CIM55/CML334), G40 (Mutsa MN521), G42 (Mukwa) and G31 (PAN53) as the most adapted and stable performers under natural FAW infestation. These models included the ASV, YSI, mean square deviation, cultivar superiority index, static stability and Wricke’s ecovalence models (Table 4) [18,20]. The use of different stability models helped in reaching conclusive results, breeders should thrive to use different analysis models in stability analysis.

A simultaneous analysis of the results of the above models shown in Table 4 identified genotypes G24 (113WH330), G39 (Manjanja MN421), G40 (Mutsa MN521), G49 (CML338/CML334) and G55 (CIM55/CML334) as the most adapted and stable hybrids. Selection was primarily based on the ranks of ASV and YSI, which have the advantage of simultaneous selection for GYD performance and yield stability [6,18]. Rank inversions were noted across different models. A good example was cultivar G40 (Mutsa-MN521),
which was ranked second on the YSI of the AMMI model and was ranked number 18 with the static stability model (Table 4). Such rank inversions have also been reported previously [6] on fruit yield of yellow passion fruit. The models, AMMI1 and AMMI2 were giving opposing stability ranks of the yellow passion fruit varieties. However, the rank inversions exhibited by G40 (Mutsa-MN521) and G55 (CimExp55/CML334) suggests that the two may have dynamic stability. This implies that they are adapted to a wide range of environments hence they exhibit low GEI but are not as stable as genotypes with static stability. Genotypes with static stability have consistent performance across environments hence they tend to perform better in stressful environments [24].

The stability models shown in Table 4 brought in four new candidates that were not visible among the most adapted and stable genotypes with the first analysis models. These included G6 (R215), G24 (113WH330), G39 (Manjanja MN421) and G49 (CML338/CML334). The mean GYD performances of these genotypes were generally low, mostly average to below average. These were therefore easily eliminated from the top performers, initially by the GGE biplots, which placed them near or below the y-axis of the biplot (Figure 1). The CV% model identified them among the performers that combined good GYD and stability. However, their GYD performance was not preferred, as there were many cultivars with better GYD performance and stability (see Figure 2A). The coefficient of regression plot excluded these genotypes as they were labelled non-significant, implying they were not different from the other poor performers (see Figure 2B). Overall, this identifies the genotypes G40 (Mutsa MN521) and G55 (CIM55/CML334) as the most adapted and stable genotypes under natural FAW infestation, selected by all models.

With regards to the inbred lines, the genotype G9 (SV1P) exhibited the best GYD performance across the environments. The genotypes G30 (CML491) and G38 (DPTY . . . *9) were second and third in terms of grain yield rankings. The three genotypes are locally adapted lines bred by CBI-DR&SS, CIMMYT and HarvestPlus, respectively. The lines G9 (SV1P) and G30 (CML491) combined high GYD performance and FAW resistance as reported previously [4]. Again, the current study noted that the lines G9 (SV1P) and G30 (CML491) combined high GYD performance with stable FAW resistance across environments (see Table 5 and Figure 4). This suggests that the two local lines can be effectively used in further breeding for FAW resistance as they are likely to produce progenies that combine enhanced stable FAW resistance with adaptation. The exotic donor lines CML67, CML346, CML121 and CML338 exhibited very low FFAWD damage scores and their performance were consistent across environments (Figure 4). The lines can be good FAW donor lines in introgression of FAW resistance into local lines.

5. Conclusions

The commercial cultivar Mutsa-MN521 and the experimental hybrid CimExp55/CML334 were identified as the FAW resistant hybrids combining adaptation and stability across FAW infested environments. Other acceptable hybrids were identified as 113WH330, Manjanja-MN421, CML338/CML334 and PAN53. The local inbred lines SV1P and CML491 combined adaptability and stable FAW resistance across environments. The best exotic donor lines combining good FFAWD resistance with stable FFAWD resistance across environments were identified as CML67, CML346, CML121 and CML338. Harare and Gwebi were identified as the most discriminating and representative sites that can be used for quick screening of good GYD performers under natural FAW infestation for both lines and hybrids/OPVs. Kadoma and Rattray-Arnold Research Stations were identified as the most discriminating environments for FFAWD among inbred lines. Harare was also identified as a discriminating environment under both natural infestation as well as managed FAW conditions.
Author Contributions: Conceptualization, P.M.M., M.L. and C.M.; methodology, P.M.M., C.N.K. and B.M.; software, P.M.M. and C.N.K.; formal analysis, P.M.M.; investigation, P.M.M. and C.M.; resources, C.M.; data curation, P.M.M.; writing—original draft preparation, P.M.M.; writing—review and editing, P.M.M., C.N.K., B.M. and M.L.; supervision, C.N.K., C.M. and M.L.; project administration, P.M.M., C.M. and M.L.; funding acquisition, C.M. and M.L. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by the Stress Tolerant Maize for Africa (STMA, Grant No. OPP1134248) project, funded by the Bill and Melinda Gates Foundation and USAID, and the MAIZE CGIAR research program.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: The authors have complied with local and national regulations for using plants/seeds.

Data Availability Statement: Data is available from the main author.

Acknowledgments: We are grateful to the Crop Breeding Institute under the Department of Research and Specialist Services in the Ministry of Lands, Agriculture, Water, Climate and Rural Resettlement of Zimbabwe, CIMMYT, and various seed houses in Zimbabwe for providing germplasm and testing sites.

Conflicts of Interest: The authors declare no conflict of interest.

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