

# Genotype x Environment Interaction and Stability Analysis for Gran Yield of Diallel Cross Maize Hybrids Across Tropical Medium and Highland Ecologies

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**Abstract:** Genotype x environment (G x E) interaction is the differential performance of genotypes across environments, especially in the tropics where seasonal and spatial variability is large. This results in serious challenges of product selection across environments. The objectives of this study were to determine G x E interaction and yield stability of new diallel cross maize hybrids and to identify suitable genotypes for the medium and highland ecologies in Rwanda. Forty-five diallel cross maize hybrids and three commercial checks were evaluated in four locations representing the major agro-ecologies of Rwanda over three seasons. The data were subjected to genotype and genotype by environment interaction (GGE) biplot analysis, using Genstat statistical package. The analysis revealed two mega-environments which discriminated the hybrids. Two genotypes 3 (S1/S4) and 25 (S4/S5) displayed specific adaptation; qualifying them as candidates for further testing in respective mega-environments. Genotypes 3 (S1/S4) and 29 (S4/S9) demonstrated high yield and stability. Overall, the study revealed crossover interaction and there is need to breed for both broad and specific adaptation in these medium and high altitude environments.

**Keywords:** Biplot, Genotype by Environment Interaction, Grain Yield, Maize Hybrids, Stability

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## 1. Introduction

Maize is an important staple crop for Sub-Saharan Africa. It grows in a wide range of environmental conditions from sea level to highlands region [1-4]. More than half of the daily calorie and protein intake of the region's population is acquired from maize [5]. However, maize grain yield is highly influenced by genotype x environment interactions (GxE) [6-8]. It is therefore prudent to characterize the behavior of new experimental hybrids such as diallel cross hybrids in medium (800 - 1600 m above sea level) and highland (>1600 m) environments in East Africa. Similar maize production environments are found in Southern Africa and elsewhere.

There are various factors that call for G x E analysis of experimental hybrids in the region. Currently maize is

exposed to changing environmental conditions. These include biotic and abiotic stresses due to global climatic changes that influence behaviour of maize hybrids in space and time. Additionally, maize growing areas are changing because of its displacement from its traditional production belts by higher-value crops such as vegetables. It is increasingly being grown in more difficult and marginal production environments that are characterised by declining soil organic matter, reduced soil fertility, and soils with low water-holding capacity among other challenges in tropical areas and developing countries. These dynamic environmental conditions are particularly evident in sub-Saharan Africa and more pronounced in Rwanda where limited resources do not allow additional inputs and irrigation to be supplied [9-11]. In Rwanda, Production of maize grain is also dominated by smallholder farmers (less than 1 ha)

who lack the means to condition the environment [12]. This therefore reveals the need for development of high yielding stable genotypes. However, high yielding and stable maize hybrids not only in Rwanda but also in East and Central Africa region are scarce [2, 8].

The consequences of environment and genotype interaction in the selection and release of improved genotypes cannot be ignored. For this reason, plant breeders have been striving to develop genotypes with superior and stable grain yield, quality and other desirable characteristics over a wide range of environmental conditions. However, genotype x environment (G x E) interaction is one of the main complications in the selection of broadly adapted varieties in many breeding programmes [13, 14, 8]. Various studies [14, 15] have shown that a proper understanding of the environmental and genetic factors causing the interaction as well as an assessment of their importance in the relevant G x E system could have a large impact on plant breeding. It is for this reason that in many countries including Rwanda, research programmes are regularly testing many varieties in various locations and for several years before giving recommendations to farmers of which varieties to grow in a given environment [14, 16, 15]. In this regard, newly developed single cross maize hybrids, generated from a diallel cross mating design were evaluated in multi

environment trials across all representative agro-ecologies of Rwanda. The objectives were to determine G x E interaction and yield stability and identify suitable hybrids for medium and highland ecologies.

## 2. Materials and Methods

### 2.1. Germplasm, Field Evaluation and Measurements

Forty-five Single Cross Hybrids (SCHs) (Table 1) from a 10 x 10 diallel cross and three commercial hybrid checks were evaluated in twelve environments. The environments were defined by site and season combination. Three consecutive seasons (2015A, 2015B and 2016A) and four locations were treated as twelve environments. Seasons were defined as; 2015 season A (season A=from September to February), 2015 season B (season B=from March to July) and 2016 season A. Evaluation environments comprised: Bugarama site; located in the semi-arid mid-altitude (2°28'S, 29°00'E, 900 m asl) ranging from 900-1200 metres above sea level (m asl), Nyagatare(1° 20'S, 30° 20'E, 1450 masl) and Rubona(2° 29'S, 29° 46'E, 1650 mas) located in the moist mid-altitude ranging from 1200-1700 m asl and Rwerere(1° 29'S, 29° 52'E; 2,100 m asl) located in the highlands which are above 1700 m asl.

**Table 1.** Maize hybrids and mean grain yield (tha<sup>-1</sup>) from 12 environments across tropical medium and highland ecologies of Rwanda.

Code	Hybrid	Mean	Code	Cross	Mean	Code	Cross	Mean
1	S1/S2	5.90	17	S2/S10	5.94	33	S5/S8	7.93
2	S1/S3	7.81	18	S3/S4	8.67	34	S5/S9	8.33
3	S1/S4	9.46	19	S3/S5	7.83	35	S5/S10	7.86
4	S1/S5	8.71	20	S3/S6	7.22	36	S6/S7	3.12
5	S1/S6	7.57	21	S3/S7	7.24	37	S6/S8	6.76
6	S1/S7	7.68	22	S3/S8	6.66	38	S6/S9	7.61
7	S1/S8	7.76	23	S3/S9	7.26	39	S6/S10	7.48
8	S1/S9	7.29	24	S3/S10	7.65	40	S7/S8	7.19
9	S1/S10	6.37	25	S4/S5	9.70	41	S7/S9	6.94
10	S2/S3	6.25	26	S4/S6	9.03	42	S7/S10	7.09
11	S2/S4	7.72	27	S4/S7	8.26	43	S8/S9	6.03
12	S2/S5	8.45	28	S4/S8	7.41	44	S8/S10	6.59
13	S2/S6	6.37	29	S4/S9	8.59	45	S9/S10	6.46
14	S2/S7	6.16	30	S4/S10	8.40	46	Check1	8.54
15	S2/S8	5.53	31	S5/S6	8.38	47	Check2	9.71
16	S2/S9	6.59	32	S5/S7	8.68	48	Check3	8.53

The 45 F1 hybrids and three checks were evaluated in a 6 x 8 alpha-lattice design with two replications. Plot sizes were one row, 4.0 - 5.0 m long, with 0.75 m inter-row spacing and 0.25 m intra-row spacing. Two seeds were planted per hill and later thinned to one plant giving a population density of approximately 53,333 plants ha<sup>-1</sup>. All agronomic practices like fertilisation and weeding were followed according to recommendations for maize cropping at each site. In all environments, maize genotypes of similar vigour were used as borders.

Though several traits were assessed, the study focused on

grain yield (GY). Grain yield (t/ha), was calculated as grain mass per plot adjusted to 12.5% moisture content. Field weight (FW) (weight of the harvested ears) per plot was multiplied by 0.80 shelling percentage to obtain grain yield (t/ha), adjusted to 12.5% grain moisture.

### 2.2. Statistical Analysis

Prior detailed analyses, to determine the existence of G x E interaction on grain yield, data from individual sites was first submitted to ANOVA (data not shown) using Genstat 17<sup>th</sup> edition computer software [17]. Genotypes were treated as

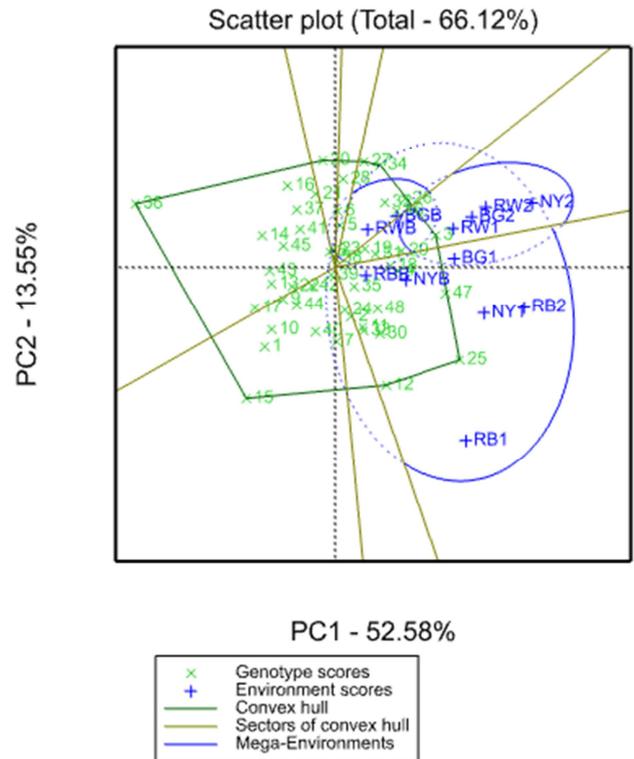
fixed effects and environments (both temporal and spatial), replications within environments and blocks within replications were considered as random effects. This analysis was complemented by genotype main effect (G) and genotype-by-environment (G x E) interaction (GGE) biplot analysis [18]. The GGE biplot model was applied based on singular value decomposition (SVD) of principal components as follows:  $\bar{Y}_{ij} - \mu_i - \beta_j = \sum_{k=1}^t \lambda_k \alpha_{ik} \gamma_{jk} + \epsilon_{ij}$  Where:  $\bar{Y}_{ij}$  =the performance of genotype i in the environment j,  $\mu$  = the grand mean,  $\beta_j$  = the main effect of environment j, k is the number of principal components (PC);  $\lambda_k$  is singular value of the k<sup>th</sup> PC; and  $\alpha_{ik}$  and  $\gamma_{jk}$  are the scores of i<sup>th</sup> genotype and j<sup>th</sup> environment, respectively for PC<sub>k</sub>; while  $\epsilon_{ij}$  is the residual associated with genotype i in environment j.

The analysis was interpreted based on studies by Yan and Yan et al. [19, 7, 18, 20]. To assess visual relationships among genotypes, ranking them on the basis of yield and stability and their testing environments, the GGE biplot based on principal component analysis (PCA) of environment-centred data was applied [13, 19]. Ideal genotypes were the ones showing high PC1 values (related to high mean grain yield) and PC2 values close to zero. On the other hand, the best testing environments were those providing better discrimination of the genotypes (show a high PC1 value and PC2 values close to zero) [19, 20].

### 3. Results

#### 3.1. Polygon View of the GGE Biplot Analysis of Diallel Cross Maize Hybrids

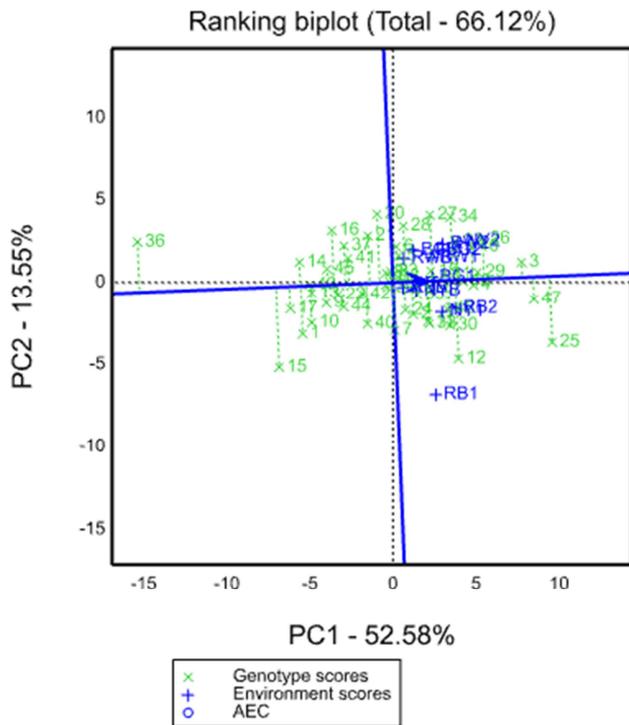
Figure 1 presents the schematic view of mega-environment classification and the winning genotypes. Based on the GGE biplot, the first two PCs explained 66.12% (PC1=52.58 and PC2=13.55%) of the total GGE variation for grain yield. Consequently, eight sectors were drawn from the polygon, where environments fell into three sectors representing mega-environments. The environments were grouped as follows: six environments BG1, BG2, BG2, RW1, RW2 and NY2 in one sector, five environments RB1, RBB, RB2, NY1 and NYB in another sector and one environment RWB appeared in its own sector. The vertex genotype for the mega-environments composed by the 6 environments was genotype 25 (S4/S5), whereas vertex genotype for the mega-environment of five environments was genotype 3 (S1/S4) and the sector with one environment was genotype 34 (S5/S9). Though vertex genotypes 15 (S2/S8), and 36 (S6/S7) were observed, none of these fitted in any of the mega-environments as they were displayed out of all the mega-environments. Genotype 39 (S6/S10) and others were also located very close to the origin while others were located far from the origin. Both checks (genotype 47 and 48) were located in the same mega-environment with genotype 47 closer to the origin.



**Figure 1.** Polygon view of the GGE biplot based on grain yield for 48 maize single cross hybrids across twelve environments (location x season). Environments are: NY1=Nyagatare first season; NYB=Nyagatare second season; NY2=Nyagatare third season; RB1=Rubona first season; RBB=Rubona second season; RB2=Rubona third season; BG1=Bugarama first season; BGB=Bugarama second season; BG2=Bugarama third season; RW1=Rwerere first season; RWB=Rwerere second season and RW2=Rwerere third season.

#### 3.2. Ranking of Diallel Cross Hybrids Based on Mean Performance and Stability

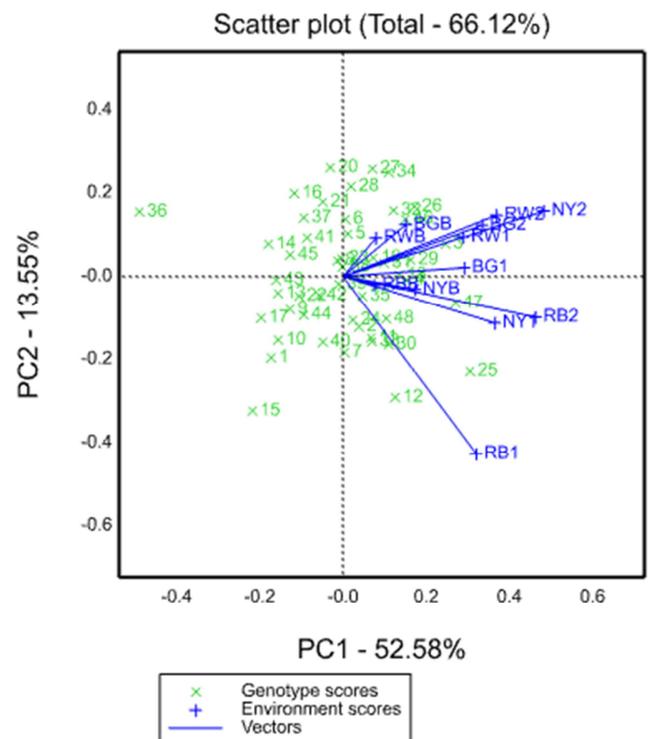
Figure 2 displays the average environment coordination (AEC) view of the GGE biplot showing stability and performance ranking of the hybrids across twelve environments. High performance as well as the stability of the tested genotypes were revealed. This was achieved by drawing an AEC on the genotype-focused biplot. The arrow headed line points to higher performing genotypes across environments while the crossing lines point to greater variability (poor stability) in either direction. It was revealed that high yielding hybrids were 3, 25, and 29. On the contrary, hybrids 1, 15, 17 and 36 exhibited the poorest yields. Regarding hybrids stability across the testing environments, hybrids 3, 13, 29, and 42 demonstrated high stability. On the other hand, the worst stable hybrids were 12, 15, 25, 27 and 34. Both high yield as well as high stability were displayed by hybrids 3, and 29. This trend was also exhibited by one of the checks (47) while the other check did not display a clear pattern.



**Figure 2.** Biplot of the average environment coordination (AEC) view showing mean performance and stability of 48 maize single cross hybrids across twelve environments (location  $\times$  season). Environments are: NY1=Nyagatare first season; NY2=Nyagatare second season; NY3=Nyagatare third season; RB1=Rubona first season; RB2=Rubona second season; RB3=Rubona third season; BG1=Bugarama first season; BG2=Bugarama second season; BG3=Bugarama third season; RW1=Rwerere first season; RW2=Rwerere second season and RW3=Rwerere third season.

### 3.3. Discriminating Power and Representativeness of the Test Environments for Diallel Cross Hybrids

Environment patterns to display different behavior of diallel cross hybrids were revealed in Figure 3. Environmental vectors were drawn from the biplot origin to join the environments for genotypes evaluation based on environment focused scaling. Except environment RB1 displaying obtuse angles (greater than 90) with environments BGB and RWB, the rest of the eleven environments exhibited among them an acute angle (less than 90), however, with variable angle size among environments. The smallest acute angle was observed in three groups of environments; group: NY2, RW1, RW2 and BG2, followed by group RBB, NYB and RB2, also followed by group: BGB and RWB. Regarding the length of vectors from the biplot origin to discriminate the genotypes. The twelve testing environments aligned into three groups. Environments RB1, RB2, and NY2 clustered in their own group with the longest vectors from the biplot origin followed by the cluster of NY1, BG1, RW1, RW2, and BG2 and finally the cluster of RWB, BGB, RBB and NYB.



**Figure 3.** GGE biplot based on grain yield for twelve environments (location  $\times$  season) showing the relationship among environments for maize single cross hybrids evaluation. Environments are: NY1=Nyagatare first season; NY2=Nyagatare second season; NY3=Nyagatare third season; RB1=Rubona first season; RB2=Rubona second season; RB3=Rubona third season; BG1=Bugarama first season; BG2=Bugarama second season; BG3=Bugarama third season; RW1=Rwerere first season; RW2=Rwerere second season and RW3=Rwerere third season.

## 4. Discussion

### 4.1. Polygon View of GGE Biplot Analysis of Diallel Cross Maize Hybrids

Polygon view of GGE biplot analysis was required to present the schematic view of mega-environment classification and point out genotypes possibly suitable to specific mega-environments [18, 1]. It was earlier reported that a mega-environment denotes a group of fairly homogeneous environments steadily sharing the best genotypes [18, 13]. With regards to the hybrids, variation explained by the two PCs was high (66.12%). This revealed that the GGE biplot was efficient in representing variation due to G and G  $\times$  E. Regarding hybrids response in different environments, two mega-environments were identified, these mega-environments displayed different high yielding genotypes thus indicating presence of cross-over G  $\times$  E interaction and inconsistent performance for these genotypes across environments. It was reported that dividing the target environments into different mega-environments and deploying different hybrids in these mega-environments is helpful to make use of GEI [21]. Hybrids such as G3, G25 and others were located on the vertices of the polygon and then identified as winning genotypes in different mega-environments. These winning hybrids are environment specific and can be recommended for

production in their respective mega-environments as more responsive to environments, while the remaining hybrids were less responsive to environments. It was earlier [6] pointed out that cultivar evaluation within a mega-environment should be based on both mean performance and stability to avoid the random GEI rather than trying to exploit it. Although the hybrids were specific to certain mega-environments, they were more fitting in environments where they were closer within these mega-environments. Some hybrids were located on the vertices of the polygon however not fitting in any of the mega-environments, suggesting that such hybrids were among the superior hybrids but in lower yielding environments.

#### 4.2. Hybrids Rank Based on Mean Yield and Stability

According to Yan and Tinker [7], genotypes exhibiting both high mean performance and high stability across environments are qualified as ideal genotypes. Consequently, under this study, hybrids 3 and 29 and 47 (check) displayed both high mean yield and high stability. High yield was defined using the single-arrowed line which is the AEC abscissa pointing to higher mean yield across environments. On the other hand, high stability was defined using the crossing lines in either direction, the shorter was the crossing line for a genotype, the higher was the stability of that genotype. It implies that these stable hybrids were broadly adapted and had high consistent ranking across environments under the current study. Similar cases where broad adaptation is important than narrow adaptation have been reported [1, 4].

#### 4.3. GGE Biplot Showing the Discriminating Power and Representativeness of the Test Environments for Hybrids

Environment patterns were revealed based on the length of vectors drawn from the biplot origin based on environment focused scaling and the cosine of the angle between the vectors of two environments [22, 23, 1]. Consequently, eleven testing environments were positively correlated. They had an acute angle between them (less than 90). However, the strength of correlation among them varied following the size of their acute angle among them. Hence environments NY2, RW2, BG2 and RW1 were revealed as redundant testing environments and the similar applied to environments BGB and RWB. These environments displayed very small angles showing strong positive associations among them across the two seasons of evaluation. Therefore, the presence of close associations among test environments suggests that a single environment could have sufficed to obtain information on the hybrid genotypes to reduce the cost and increase breeding efficiency. If two test environments are closely correlated consistently across years, one of them can be dropped without loss of much information about the genotypes [6, 7]. With regards to discriminating the hybrids, all environments clustered into three groups based on the length of vectors from the biplot origin. Hence environments RB1, RB2 and NY2 were identified as the most discriminating. This is because they had longer vectors than

other environments for the genotypes. The vector length of an environment measures the discriminating power of its ability to differentiate the cultivars [7, 14], signifying that these three environments were the best for genetic differentiation of the genotypes. On the contrary, environments RWB, BGB, RBB and NYB appeared the least discriminating. This was justified by their very short vectors and qualified as non-discriminating test environments hence considered as less useful because they provided little discriminating information about the genotypes. According to Yan and Tinker [7], test environments that are consistently non-discriminating (non-informative) provide little information on the genotypes and, therefore, should not be used as test environments.

## 5. Conclusions

Applying GGE biplot analysis under the current study enabled the visual comparison and identification of superior genotypes and environments for breeding purposes in variety selection and making assured recommendation in tropical medium and highland ecologies of Rwanda. Different mega-environments were revealed among the genotypes studied justifying presence of variation in Rwandan environments regarding genotype separation. Hybrids such as 3, 25 and 34 were identified as winning genotypes in mega-environments and could be recommended for production in their respective mega-environments. Hybrids 3, 29 and 47(check) were qualified as high yielding and highly stable genotypes and can be used as a reference genotype for evaluation and used for broad selection. Some of the testing environments displayed strong positive association among each other suggesting that a single testing environment could have been recommended to obtain sufficient information on the genotypes for rational resource management.

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