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# Genotype × environment interactions for grain yield in rice under no drought and drought conditions

**Ruth N. Musila[1,2]*, Julia Sibiya[1], John Derera[1], John M. Kimani[2] and Pangirayi Tongoona[1]**

[1]African Centre for Crop Improvement, School of Agricultural, Earth and Environmental Sciences, University of KwaZulu-Natal, Scottsville, Pietermaritzburg, Republic of South Africa.
[2]Kenya Agricultural and Livestock Research Organization (KALRO), Kaptagat Road, Loresho, P. O. Box 57811, City Square, Nairobi, 00200, Kenya.

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**Environments in sub-Saharan Africa fluctuate considerably across sites and seasons. This suggests the importance of assessing genotype x environment interaction (GEI) in cultivar development. The objective of this study was to estimate the magnitude of GEI for rice grain yield and identify high yielding and stable rice genotypes. Fifty six genotypes including 45 $F_3$ rice populations, their 10 parents and one check were evaluated in 7 x 8 alpha lattice design with two replications under three no drought and one random managed drought stress condition at reproductive growth stage at three sites in coast region of Kenya. The additive main effects and multiplicative interaction (AMMI) analysis and genotype plus genotype x environment interaction (GGE) biplot analysis were used to measure grain yield stability of the 45 $F_3$ populations and their 10 parents. Ranking of the genotypes changed in each environment and three mega environments were identified revealing a crossover type of GEI. The genotypes G39 (Luyin 46 x IR74371-54-1-1) and G40 (NERICA-L-25 x IR55423-01) were the most stable high yielding genotypes. These were identified as candidates with general adaption for advancement to homozygozity simultaneously selecting within each population good performing pure lines for release in the region.**

**Key words:** Additive main effects and multiplicative interaction (AMMI), genotype x environment interactions, genotype plus genotype x environment interaction (GGE) biplot, rice, yield stability.

## INTRODUCTION

Genotype x environment interaction (GEI) is the differential genotypic response to environmental changes (Fox et al., 1997). With significant GEI, differences between genotypes vary widely among environments. A significant GEI is manifested either as changes in the absolute differences between genotypes without affecting the rank order (non-crossover) or as rank order changes of the genotypes between environments (crossover GEI) (Crossa et al., 1995; Yan and Hunt, 2001). The crossover type of GEI is the most important to plant breeders (Fox

*Corresponding author. E-mail: ruthmusila@gmail.com. Tel: +251 911 395631. Fax: +251 116 814592.

et al., 1997). It reduces the association between phenotypic and genotypic values, complicating selection of superior cultivars and best testing sites for identifying superior and stable genotypes (Flores et al., 1998). Consequently, progress in providing farmers with high yielding cultivars is slowed down (Ceccarelli et al., 1994).

With occurrence of a large GEI, plant breeders tend to identify and recommend high yielding and stable genotypes that show little interaction with the environment or genotypes specifically adapted to certain environments (Fan et al., 2007). Several statistical methods which include regression (Finlay and Wilkison, 1963; Eberhart and Russell, 1966), principal component analysis (PCA) (Hill and Goodchild, 1981), additive main effects and multiplicative interaction (AMMI) (Gauch and Zobel, 1988) and genotype plus genotype by environment (GGE) analysis (Yan, 2001) have been developed to assess stability of a set of genotypes and patterns of GE. Of these, AMMI and GGE biplot are widely used. The AMMI model combines analysis of variance with PCA analysis generating a family of models (Yan and Hunt, 2001; Carlos et al., 2003). However, it is only the AMMI1 and AMMI2 models that may be used to visualise GEI patterns (Yan and Hunt, 2001). In AMMI1, a biplot of main effects with interaction PCA1 (IPCA1) facilitates visualisation of correlation among environments and the response patterns of the genotypes and their interactions with the environments by using sign and magnitude of IPCA1 values (Yan and Hunt, 2001). In AMMI2, a biplot of IPCA1 and IPCA2 is constructed which visualises magnitude of interaction for each genotype and environment (Yan and Hunt, 2001).

The GGE biplot analysis on the other hand puts together genotypic main effects (G) and genotype x environment interaction (GE) to facilitate graphical visualisation of cultivar evaluation and mega environment identification (Yan et al., 2000; Yan, 2002). The GGE biplot is constructed by the first two symmetrically scaled principal components (PC1 and PC2) derived from singular value decomposition (SVD) of environment centred data (Yan et al., 2000; Yan, 2002). This biplot is useful for visualisation and identification of the mega environments, specific and wide cultivar adaptations, high yielding and stable cultivars and interrelationship among environments (Yan and Tinker, 2006).

In sub-Saharan Africa, significant GEI for grain yield and other agronomic traits has clearly been demonstrated in studies involving evaluation of major field crops of economic importance (Badu-Apraku et al., 2011; 2012; Sanni et al., 2012; Nassir, 2013). For example, in a study involving rice germplasm evaluated in five environments in south West Africa, the AMMI analysis revealed significant GEI for grain yield and panicle attributes (Nassir, 2013). On grain yield, the first PCA axis of the interaction captured 52% of the interaction sum of squares while the GGE biplot captured 64% of the interaction component (Nassir, 2013). In another study evaluating 22 NERICA cultivars in three environments in two years again in West Africa, the AMMI analysis reported the existence of a significant GEI with the first four IPCA's contributing 98.5% of the total interaction sum of squares (Sanni et al., 2009). Significant GEI estimated using AMMI and GGE biplot statistical methods has also been reported in studies involving multi-location trials of maize germplasm across years in West Africa (Badu-Apraku et al., 2011, 2012) and in East Africa (Beyene et al., 2012). These studies clearly indicate that in sub-Saharan Africa, environmental conditions fluctuate considerably across years and locations and suggest the importance of considering GE effects in cultivar development and release.

At the beginning of this decade, a rice breeding programme was started at the Kenya Agricultural and Livestock Research Institute (KALRO) - Mtwapa to develop high yielding drought tolerant rice cultivars for the lowland and upland rice ecologies in the coastal lowlands of Kenya. Selected interspecific and *Oryza sativa* L. pure lines were hybridized and the breeding materials advanced to the third generation ($F_3$). At this stage, there is a need to identify and select promising populations so as to reduce the numbers to manageable levels. The objectives of this study were therefore to; a) estimate the magnitude of GEI for grain yield; b) identify high yielding and stable genotypes across the test environments and c) identify the most discriminating and representative environments as future multi-locational rice testing sites in the coastal lowlands of Kenya. This study is not meant for cultivar recommendation *per se* but to undertake early generation selections in $F_3$ rice populations.

## MATERIALS AND METHODS

### Germplasm

Forty five $F_3$ populations and their 10 parents were used in this study. The parents included five *O. sativa* L. and five interspecific rice pure lines drawn from the African Rice Centre (ARC), the International Centre for Tropical Agriculture (CIAT) and the International Rice Research Institute (IRRI). These parents were crossed in a 10 x 10 half diallel mating design and the resulting 45 $F_1$s advanced to $F_3$ populations using the bulk population method.

### Study sites

The study was conducted on-station at Kenya Agricultural and Livestock Research Organisation (KALRO)-Mtwapa and KALRO-Matuga and on farm at Msambweni sub-county of Kwale county. KALRO-Mtwapa is located 20 km north of Mombasa in Kilifi south county, along Mombasa-Malindi road. It lies on latitude 3°50'S and longitude 39°44'E at an elevation of 15 m above sea level (masl). Annual mean temperatures are between 22 and 26°C. The area receives bimodal mean rainfall of about 1200 mm with reliable long rains of 600 mm falling mid-March to August and the variable short rains of 250 mm falling in mid-October to December. The soils are dominated by orthicacrisols (80% sand) with low inherent fertility (Jaetzold and Schmidt, 1983). KALRO Matuga is situated 15 km

**Table 1.** Features of the four environments used in this study.

| Study site | Season | Ecology | Type of Environment | Code |
|---|---|---|---|---|
| Matuga | Short rain season (2014/15) | Upland | No drought stress | E1 |
| Mtwapa | Short rain season (2014/15) | Upland | No drought stress | E3 |
| Msambweni | Short rain season (2014/15) | Lowland | Random drought stress | E2 |
| Msambweni | Long rain season (2015) | Lowland | No drought stress | E4 |

south of Mombasa from the Likoni ferry in Kwale county. The site is at Latitude 4°9'S and longitude 39°34'E at an elevation of 132 masl. Annual mean temperatures are between 24 and 26°C. The area receives bimodal mean annual rainfall of about 1200 mm with the long rain season of 750 mm and short rain season of 350 mm. The soils are derived from Pliocene sandstones and are commonly referred to as Magarini sands (Jaetzold and Schmidt, 1983). They are low in C, N, P, K and are moderately acidic (Jaetzold and Schmidt, 1983). The typical agro-ecological zonation for KARLO-Mtwapa and Matuga is coastal lowland 3 (CL3-coconut cassava zone). The Msambweni on-farm site is 50 km south of Mombasa from Likoni ferry. The site is at latitude 4°28'S and longitude 39°29'E at an elevation of about 19 masl and lies in coastal lowlands 2, (CL2), classified as the coastal lowlands sugarcane zone and occurs as a pocket in Ramisi area in Kwale county and is the wettest zone. The annual average temperatures range from 19 to 24°C. Rainfall in this zone is bimodal ranging from 1200 to 1400 mm annually. The long rain season of 800 mm falls between March and August and short rain season of 400 mm falls between mid-October and December (Jaetzold and Schmidt, 1983).

**Experiments**

The experimental materials consisted of 56 treatments (entries) including 45 $F_3$ populations, their 10 parents and 1 check. These were evaluated in 7 x 8 alpha lattice design with two replications under four environments; one random managed drought stress and three no drought stress conditions. The random drought stress environment was planted on farm at Msambweni during the short rain season. It was planted in mid-October 2014 and the last rainfall of 44 mm was received 65 days after planting. Random drought stress occurred during the reproductive stage from the panicle initiation stage to harvesting. The no drought stress experiments included two experiments established on station at KALRO-Matuga and KALRO-Mtwapa during the short rain season and one established on farm at Msambweni during the long rain season. The KALRO-Matuga experiment was planted mid-October 2014 and received supplemental irrigation water since rainfall during the short rain season was not adequate. At Mtwapa, the experiment was established in December 2014 and was irrigated. The Msambweni site was planted in April 2015 and was purely rainfed since the rainfall was adequate. Features of the four environments are summarised in Table 1.

**Management of experiments**

At KALRO-Matuga and Msambweni, the fields were un-flooded and aerobic conditions. The experimental plot were 3.2 $m^2$ with inter- and intra-row spacing of 20 cm to give a total of 80 plants per plot. Seed for each entry was first planted in plastic containers and transplanted to the field on the 12$^{th}$ day. Two seedlings were transplanted and later thinned to one seedling per hill. At KALRO-Mtwapa, plants were planted in an open field in black polyethylene pots with 25 cm internal diameter and 30 cm height. Each pot was filled with 20 kg of upland soil. Pots were watered to field capacity before planting. Five seedlings per pot were transplanted and there were five plants per pot spaced at 10 cm each. Each entry was assigned eight pots to give a total of 40 plants per entry. From transplanting to dough stage, each pot received one and half liters of water each in the morning hours on daily basis and by the end of the day, there was no standing water in each pot. Thereafter, watering was done after every two days to allow the plants to dry up for harvesting. The overall management was application of basal inorganic fertilizers; calcium ammonium nitrate (CAN) as a source of N and diamonium phosphate (DAP) as a source of P. The P was applied during planting at recommended rate of 60kg P $ha^{-1}$. The N was top dressed at the rate of 120 kg N $ha^{-1}$ applied in three splits of 40 kg $ha^{-1}$ at 21 days after transplanting, tillering stage and at panicle initiation stage. Source of micro nutrients was foliar feed which was sprayed once during the tillering stage. Rice stem borer was effectively controlled using a synthetic pyrethroid. Weeds were controlled by hand picking. Harvesting was carried out manually.

**Data collection**

Grain yield data was taken as the weight of unhulled grains harvested from an area of 2 $m^2$ for the experiments planted under field conditions and from 40 plants for the experiment planted in pots. This was then converted to tons $ha^{-1}$ at 14% moisture content.

**Data analysis**

***Analysis of variance***

A combined analysis of variance (ANOVA) was performed to determine the effects of environment, genotype and GEI on grain yield of the 55 entries (45 $F_3$ populations and 10 parents) across four environments using PROC GLM in SAS (SAS Institute, 2012). The Genstat statistical package (14$^{th}$ Edition) (Payne et al., 2011) was used to estimate and graphically visualise grain yield stability of the entries using the AMMI (Additive Main Effects and Multiplicative Interaction) and the GGE (genotype and genotype x environment) biplot analyses.

***AMMI model***

The AMMI analyses were performed to clarify the presence of the GEI, summarize patterns and relationships of genotypes and environments and estimate the grain yield means that are adjusted for G x E using the model shown below (Crossa, 1990):

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{t} \lambda_k \xi_{ik} \eta_{jk} + \varepsilon_{ij}$$

Where, $Y_{ij}$ is the mean yield (t $ha^{-1}$) of the i$^{th}$ genotype in the j$^{th}$

**Table 2.** Analysis of variance of the grain yield (t ha$^{-1}$) of 45 $F_3$ rice populations and their 10 parents evaluated in four environments in coast region of Kenya.

| Source | df | Sum of squares | Mean squares | *F* test |
|---|---|---|---|---|
| Rep (Env) | 3 | 2.07 | 0.69 | 2.02$^{NS}$ |
| Environment (E) | 3 | 25.74 | 8.58 | 25.23*** |
| Genotype (G) | 54 | 112.15 | 2.08 | 6.11*** |
| Interactions (GxE) | 162 | 235.90 | 1.46 | 4.28*** |
| Error | 216 | 73.47 | 0.34 | |
| Total | 439 | 449.43 | | |

**Table 3.** AMMI analysis of variance of grain yield (t ha$^{-1}$) of 45 $F_3$ populations and their 10 parents evaluated in four environments in coast region of Kenya.

| Source of variation | df | Sum of squares | Mean squares | *F* test |
|---|---|---|---|---|
| Block | 4 | 2.20 | 0.54 | 1.60$^{NS}$ |
| Treatments | 219 | 374.20 | 1.71 | 5.02*** |
| Genotype | 54 | 112.30 | 2.08 | 6.11*** |
| Environments (E) | 3 | 25.80 | 8.60 | 15.81*** |
| Interactions (GxE) | 162 | 236.10 | 1.46 | 4.28*** |
| IPCA 1 | 56 | 114.10 | 2.04 | 5.99*** |
| IPCA 2 | 54 | 63.80 | 1.18 | 3.48*** |
| Residuals | 52 | 58.20 | 1.12 | 3.29*** |
| Error | 216 | 73.50 | 0.34 | |
| Total | 439 | 449.80 | 1.03 | |

environment, $\mu$ is the overall mean, $g_i$ and $e_j$ are the main effects of the genotype and environment, respectively, *t* is the number of PCA axes considered, k is the singular value of k$^{th}$ PCA axis, $\lambda_k$ Eigenvalues for k$^{th}$ PCA axis, $\xi_{ik}$ *and* $\eta_{jk}$ are scores for the i$^{th}$ genotype and j$^{th}$ environment on the k$^{th}$ PCA axis, and $\varepsilon_{ij}$ is the residual term which includes experimental error. The AMMI biplot showing the main effects (genotype and environment) and the first interaction principal components axis (IPCA 1) was also presented to assess the relationships among entries, test environments and GEI for grain yield.

### *GGE Biplot*

The GGE mathematical model based on PCA of environment-centred data (which contains G and GE as the main sources of variation) subjected to singular value decomposition (SVD) was used to visualize the relationship among genotypes and the environments. The basic model for a GGE biplot as described by Yan (2002) is:

$$Y_{ij} - \mu - \beta_j = \sum_{l=1}^{k} \lambda_l \xi_{il} \eta_{lj} + \varepsilon_{ij}$$

Where: $Y_{ij}$ = Mean grain yield (t ha$^{-1}$) of the i$^{th}$ genotype in the j$^{th}$ environment; $\mu$ = Overall mean; $\beta_j$ = main effect of the environment; $\lambda_l$= Eigen value associated with IPCA *l*; $\xi_{il}$= the Eigenvector of genotype *I* for PC *l*; $\eta_{lj}$= the eigenvector of environment *j* for PC *l*; $\varepsilon_{ij}$= error term associated with rice genotype *i* in environment *j*. The GGE biplot graphs were used to visualize interrelationships among the test environments, discriminating ability and representativeness of test environments, which-won-where-pattern polygon view and mean yield and stability among genotypes (Yan and Tinker, 2006; Yan et al., 2007).

## RESULTS

### Analysis of variance and AMMI analysis

The check was found to be late maturing and therefore was eliminated from the analysis. The combined analysis of variance for grain yield showed highly significant (*P*<0.001) genotype (G), environment (E) and genotype × environment (G×E) interaction explaining 25, 6 and 53% of the total sum of squares, respectively (Table 2). The G×E interaction effect was approximately nine times that of environmental effect and twice that of the genotype effect. The AMMI analysis of variance showed that grain yield of 55 genotypes at four environments was significantly (*P*<0.001) affected by the genotype, environment and genotype x environment interaction, explaining 30, 7 and 63% of the total treatment sum of squares, respectively (Table 3). The first and the second PCA axis (IPCA1 and IPCA2) of the interaction were highly significant (*P*<0.001). The IPCA1 explained 31% of the treatment sum of squares which is 48% of the G x E

**Table 4.** AMMI average grain yield (t ha-$^{1}$) of 45 $F_3$ rice populations and their 10 parents evaluated in four environments in coast region of Kenya.

| Code | Genotypes | Environment | | | | Mean |
|---|---|---|---|---|---|---|
| | | Matuga | Mtwapa | Msambweni | Msambweni | |
| | | No drought | | | Drought | |
| **$F_3$ Populations** | | | | | | |
| G1 | NERICA 1 x NERICA 2 | 4.43 | 4.19 | 3.94 | 4.05 | 4.15 |
| G2 | NERICA 1 x *Dourado* | 3.13 | 3.73 | 3.19 | 4.20 | 3.56 |
| G3 | NERICA 1 x CT16333(1)-CA-22-M | 4.17 | 3.49 | 3.10 | 3.11 | 3.47 |
| G4 | NERICA 1 x CT16323-CA-25-M | 3.82 | 3.31 | 2.60 | 3.12 | 3.22 |
| G5 | NERICA 1 x Luyin 46 | 2.84 | 2.31 | 3.19 | 1.73 | 2.52 |
| G6 | NERICA 1 x NERICA -L- 25 | 3.45 | 2.91 | 3.86 | 2.31 | 3.13 |
| G7 | NERICA 1 x IR55423-01 | 3.38 | 3.32 | 2.41 | 3.47 | 3.15 |
| G8 | NERICA 1 x Vandana | 3.77 | 2.99 | 4.84 | 2.02 | 3.40 |
| G9 | NERICA 1 x IR74371-54-1-1 | 2.28 | 3.10 | 4.00 | 3.36 | 3.18 |
| G10 | NERICA 2 x *Dourado* | 5.12 | 3.38 | 3.22 | 2.29 | 3.50 |
| G11 | NERICA 2 x CT16333(1)-CA-22-M | 3.47 | 3.94 | 4.09 | 4.15 | 3.91 |
| G12 | NERICA 2 x CT16323-CA-25-M | 3.19 | 2.63 | 3.57 | 2.02 | 2.85 |
| G13 | NERICA 2 x Luyin 46 | 3.07 | 3.07 | 4.84 | 2.60 | 3.39 |
| G14 | NERICA 2 x NERICA-L-25 | 2.15 | 3.31 | 4.47 | 3.72 | 3.41 |
| G15 | NERICA 2 x IR55423-01 | 3.56 | 3.38 | 3.66 | 3.16 | 3.44 |
| G16 | NERICA 2 x Vandana | 3.11 | 2.86 | 4.13 | 2.36 | 3.12 |
| G17 | NERICA 2 x IR74371-54-1-1 | 2.99 | 2.82 | 3.22 | 2.57 | 2.90 |
| G18 | *Duorado* x CT16333(1)-CA-22-M | 4.89 | 3.64 | 2.07 | 3.20 | 3.45 |
| G19 | *Duorado* x CT16323-CA-25-M | 3.82 | 3.59 | 2.39 | 3.69 | 3.37 |
| G20 | *Duorado* x Luyin 46 | 2.49 | 2.67 | 3.48 | 2.55 | 2.80 |
| G21 | *Duorado* x NERICA -L- 25 | 2.57 | 2.75 | 2.83 | 2.81 | 2.74 |
| G22 | *Duorado* x IR55423-01 | 3.06 | 2.23 | 2.53 | 1.60 | 2.35 |
| G23 | *Duorado* x Vandana | 3.12 | 2.72 | 2.81 | 2.40 | 2.76 |
| G24 | *Duorado* x IR74371-54-1-1 | 2.62 | 2.58 | 2.45 | 2.55 | 2.55 |
| G25 | CT16333(1)-CA-22-M x CT16323-CA-25-M | 3.85 | 3.08 | 2.64 | 2.66 | 3.06 |
| G26 | CT16333(1)-CA-22-M x Luyin 46 | 2.63 | 2.45 | 2.79 | 2.21 | 2.52 |
| G27 | CT16333(1)-CA-22-M x NERICA-L-25 | 2.55 | 3.14 | 2.30 | 3.68 | 2.92 |
| G28 | CT16333(1)-CA-22-M x IR55423-01 | 2.62 | 1.96 | 3.38 | 1.15 | 2.28 |
| G29 | CT16333(1)-CA-22-M x Vandana | 3.04 | 2.82 | 3.38 | 2.51 | 2.94 |
| G30 | CT16333(1)-CA-22-M x IR74371-54-1-1 | 3.81 | 3.03 | 3.30 | 2.44 | 3.14 |

interaction sum of squares in 35% of the interaction degrees of freedom. The IPCA2 explained 17% of the treatment sum of squares which is 27% of the G x E interaction sum of squares in the remaining 33% of the interaction degrees of freedom.

## Performance and ranking of the best four AMMI selections

Across environments, the AMMI average genotype grain yield ranged from 4.53 t ha$^{-1}$ in G37 to 2.28 t ha$^{-1}$ in G28 (Table 4). Grain yield for environments was highest at environment E1 (3.7 t ha$^{-1}$) and lowest at environment E2 (3.0 t ha$^{-1}$). Inconsistencies in genotype performance were observed across the four test environments (Table 5). The genotypes G37 (Luyin 46xIR55423-01) and G42 (NERICA-L-25 x IR74371-54-1-1), were ranked among the best four high yielding genotypes in more than one environment.

## AMMI and IPCA scores biplot

The complete AMMI (combined main effects and IPCA1) explained 67% of the total treatment variation, while AMMI2 (IPCA 1+ IPCA 2) explained 48% of the total treatment variation. AMMI2 was dropped in favour of AMMI1 because the noise in the treatment sum of squares in AMMI1 was less, 31% as compared to 48% in

**Table 4.** Contd.

| | | | | | | |
|---|---|---|---|---|---|---|
| G31 | CT16323-CA-25-M x Luyin 46 | 2.56 | 2.57 | 3.35 | 2.34 | 2.70 |
| G32 | CT16323-CA-25-M x NERICA-L-25 | 2.20 | 3.19 | 2.94 | 3.84 | 3.04 |
| G33 | CT16323-CA-25-M x IR55423-01 | 2.90 | 2.85 | 2.56 | 2.84 | 2.79 |
| G34 | CT16323-CA-25-M x Vandana | 4.24 | 3.96 | 4.12 | 3.71 | 4.01 |
| G35 | CT16323-CA-25-M x IR74371-54-1-1 | 3.03 | 2.86 | 3.01 | 2.68 | 2.90 |
| G36 | Luyin 46 x NERICA -L- 25 | 2.54 | 3.10 | 5.33 | 2.88 | 3.46 |
| G37 | Luyin 46 x IR55423-01 | 3.96 | 4.15 | 6.31 | 3.70 | 4.53 |
| G38 | Luyin 46 x Vandana | 4.35 | 3.56 | 6.75 | 2.24 | 4.23 |
| G39 | Luyin 46 x IR74371-54-1-1 | 2.05 | 3.77 | 4.65 | 4.61 | 3.77 |
| G40 | NERICA-L-25 x IR55423-01 | 3.90 | 3.89 | 4.27 | 3.75 | 3.95 |
| G41 | NERICA-L-25 x Vandana | 4.06 | 3.78 | 6.40 | 2.93 | 4.29 |
| G42 | NERICA-L-25 x IR74371-54-1-1 | 3.38 | 3.94 | 3.56 | 4.35 | 3.81 |
| G43 | IR55423-01 x Vandana | 3.43 | 3.83 | 3.87 | 4.03 | 3.79 |
| G44 | IR55423-01 x IR74371-54-1-1 | 3.21 | 3.73 | 3.43 | 4.10 | 3.62 |
| G45 | Vandana x IR74371-54-1-1 | 5.17 | 3.82 | 3.70 | 2.97 | 3.91 |
| **Parents** | | | | | | |
| P1 | NERICA 1 | 3.84 | 3.50 | 3.60 | 3.23 | 3.54 |
| P2 | NERICA 2 | 3.55 | 3.48 | 3.60 | 3.36 | 3.50 |
| P3 | *Dourado precoce* | 3.64 | 3.84 | 3.65 | 3.97 | 3.77 |
| P4 | CT16333(1)-CA-22-M | 3.94 | 3.14 | 3.10 | 2.60 | 3.20 |
| P5 | CT16323-CA-25-M | 3.80 | 3.38 | 2.25 | 3.35 | 3.20 |
| P6 | LUYIN 46 | 2.49 | 3.13 | 6.09 | 2.78 | 3.62 |
| P7 | NERICA-L-25 | 3.06 | 2.38 | 5.26 | 1.22 | 2.98 |
| P8 | IR55423-01 | 4.71 | 3.43 | 3.76 | 2.51 | 3.60 |
| P9 | Vandana | 4.31 | 3.62 | 4.74 | 2.86 | 3.88 |
| P10 | IR74371-54-1-1 | 2.89 | 3.62 | 2.60 | 4.30 | 3.35 |
| Mean | | 3.39 | 3.24 | 3.67 | 3.00 | 3.32 |

**Table 5.** The best $F_3$ populations from AMMI analysis at each environment.

| Environment | Mean GY (tha-1) | PCA Score | Rank | | | |
|---|---|---|---|---|---|---|
| | | | 1 | 2 | 3 | 4 |
| E2 | 3.00 | 1.28 | G39 | G42 | G55 | G2 |
| E3 | 3.24 | 0.55 | G1 | G37 | G34 | G42 |
| E1 | 3.39 | 0.48 | G45 | G10 | G18 | G53 |
| E4 | 3.67 | -2.32 | G38 | G41 | G37 | G51 |

See Table 1 for environment and Table 4 for genotype codes.

AMMI2. Thus, AMMI1 was more effective because it had less predictive errors. Therefore, a biplot of main effects against IPCA1 was used to graphically visualise average productivity of the genotypes and environments and GE interaction for all possible genotype x environment combinations (Figure 1). The four environments fell into three groups: Environment E1 had large positive IPCA1 score strongly interacting positively with genotypes that had positive IPCA scores and negatively with genotypes that had negative IPCA scores. Environment E2 had large negative IPCA1 score strongly interacting with genotypes but in the opposite direction to that of E1. Environments E3 and E4 formed the third group with small IPCA1 scores, suggesting that they had little interaction with the genotypes. The genotypes showed variability in mean yield and in interaction scores. Genotype G37 was the highest yielding followed by G41, G38, G1 and G34. The most stable high yielding genotypes were G41, G1 and G34 in that order. The most unstable but high yielding genotypes demonstrating

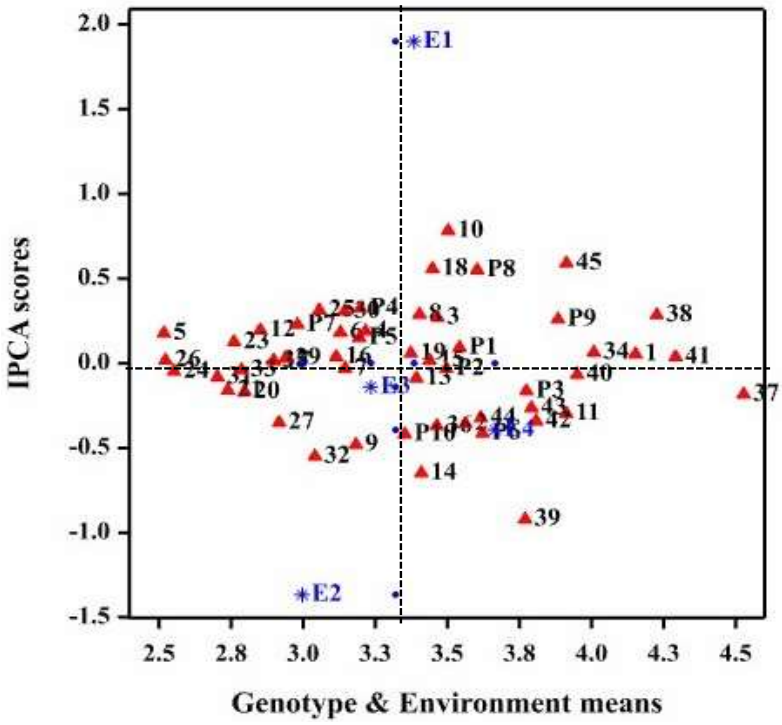


**Figure 1.** AMMI1 biplot on the grain yield of 45 $F_3$ rice populations and their 10 parents evaluated in four environments in coast region of Kenya. See Table 1 for environment and Table 4 for genotype codes.

a strong GEI were G10 and G39. G10 was specifically suitable for environment E1, while G39 was suitable for environment E4.

## GGE biplot analysis

The goodness of fit of the GGE biplot was 67.94%; PC1 contributed 39.01% while PC2 accounted for 28.93% of the total variation (Figure 2). The cosine of the angle between vectors of environments E4 and E2 was a right angle. The acute angle between vectors of E2 and E3 was the smallest and largest between vectors of E3 and E4. The distance between E2 and E3 was the shortest followed by the distance between E3 and E1. The distance between E3 and E1 from E2 was shorter than the distance between these two sites from E4. Environments were ranked based on discriminating ability and representativeness of the 'ideal" (average) environment (Figure 3). Environments E1 and E2 were found to be close to the average environment and therefore the most representative of the target region. However, E2 had a longer vector than E1 and therefore was both discriminating and representative of the whole region. Environments E4 and E3 were further away from the average environment and therefore the least representative of the whole region. Environment E4 had a long vector and therefore classified as discriminating and non-representative. Environment E3 was both non-discriminating and non-representative of the target region since it had a short vector and was farther away from the average environment.

The polygon view of the GGE biplot displayed which-won-where-pattern of genotype by environment dataset of the four environments (Figure 4). The radial lines originating from the centre of the biplot divided the polygon into eight sectors. The four environments fell into three sectors and there were three mega environments. The first mega environment consisted of E3 and E2 and the winning genotype was G2. The second mega environment was represented by E1 and the winning genotype was G37. The third was represented by E4 and here the winning genotype was G38. Among the $F_3$ populations, genotype G37 had the highest grain yield followed by G38 and G41 in that order (Figure 5). Genotype G28 was the lowest yielding genotype. Among the parents, P9 was the highest yielding parent followed by P3, P6 and P8. The lowest yielding parent was P7. Grain yield of seven $F_3$ populations namely G37, G38, G41, G1, G34, G11, G2 and G39, was higher than the highest yielding parent P9. The most stable $F_3$ population with above average mean performance was G39 as it was located almost on the AEC abscissa and had a near zero projection onto the AEC ordinate. This was followed by G40. In contrast, G38 although high yielding, was the least stable followed by G41. Parent P8 (close to G14)

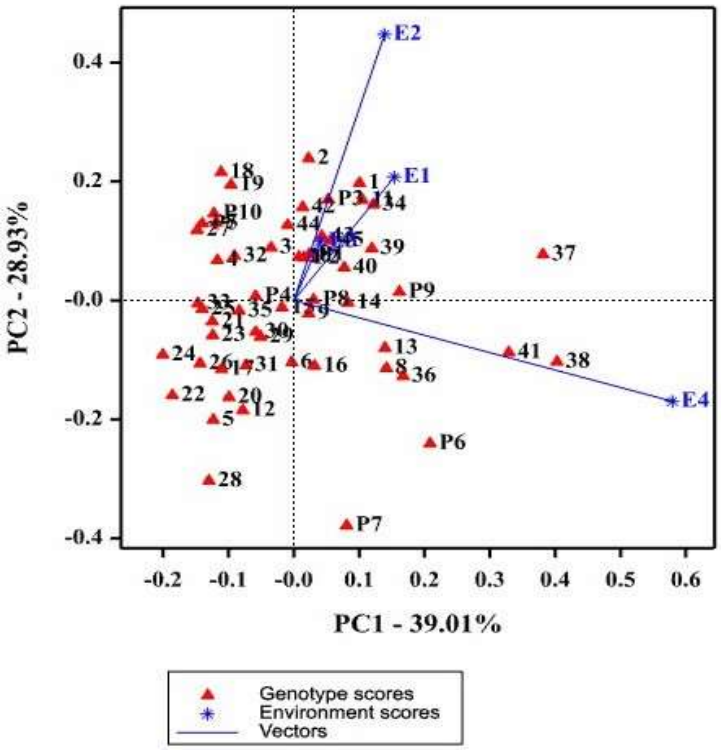


**Figure 2.** Relationship among test environments. See Table 1 for environment and Table 4 for genotype codes.

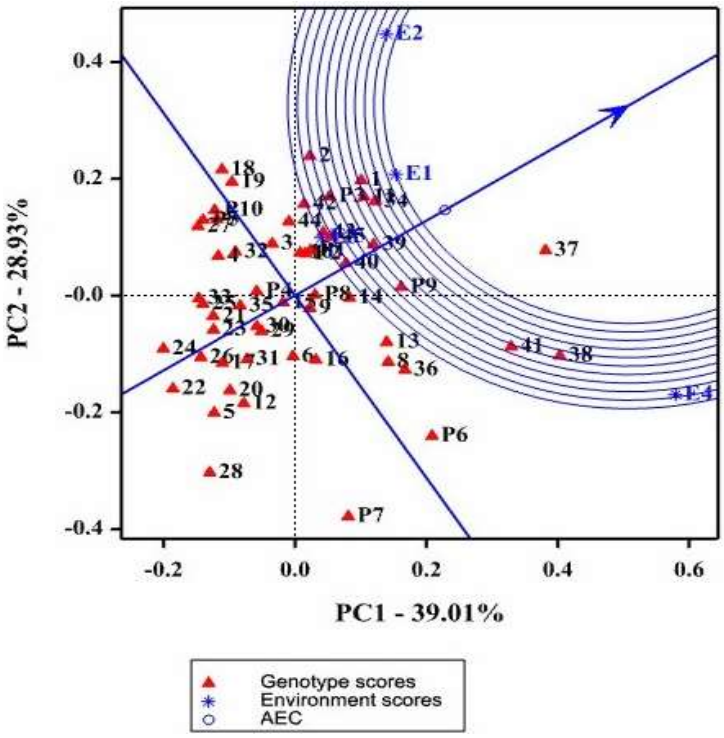


**Figure 3.** The discriminating and representative view showing the discriminating ability and representativeness of the test environments. See Table 1 for environment and Table 4 for genotype codes.

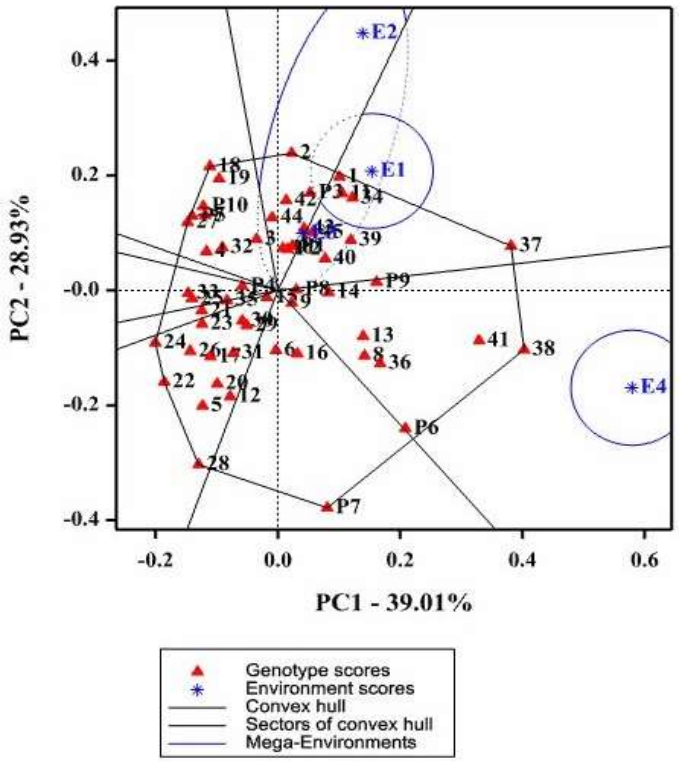


**Figure 4.** Polygon view of the GGE biplot based on symmetrical scaling. See Table 1 for environment and Table 4 for genotype codes.

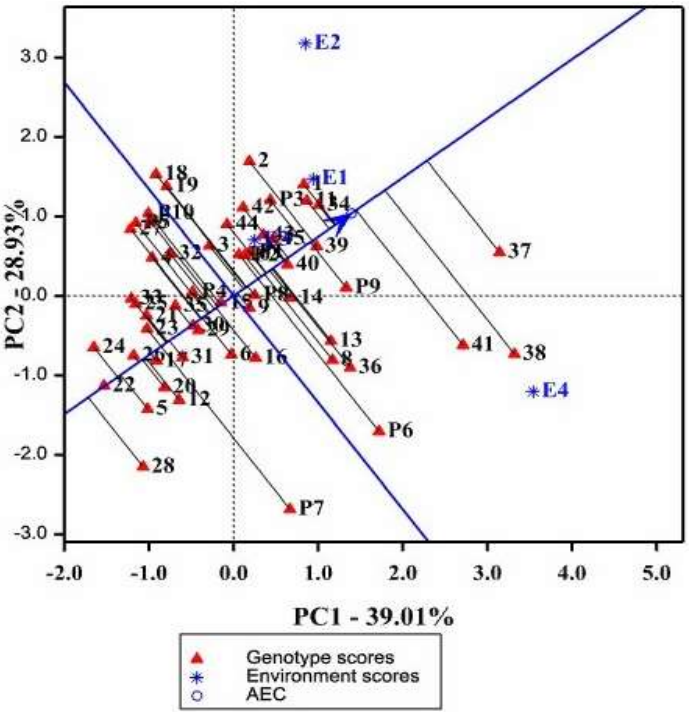


**Figure 5.** GGE-biplot based on genotype-focused singular value partitioning for comparison of the genotypes with the ideal genotype. See Table 1 for environment and Table 4 for genotype codes.

was found to be the most stable parent although it was located slightly away from the AEC abscissa. Parents P6 and P7 were found to be the most unstable among parents with almost similar level of poor stability with G41.

## DISCUSSION

### ANOVA and AMMI analysis

The ANOVA and AMMI analysis revealed that the environment and genotypic main effects and their interactions were highly variable. The genotype x environment interaction (GEI) for grain yield contributed approximately 50% of the total sum of squares. These effects were greater than what has been obtained in other studies (Sanni et al., 2009; Nassir, 2013). The high interaction effects observed could partly be explained by the wide variation among the genotypes and among the environments. The genotypes included in this study varied considerably since the parents were pure lines and their progenies were heterozygous in their third filial generation. In addition, the parents varied in species and maturity. Thus, the materials showed a wide genetic base in phenological, physio-morphological characters, grain yield and its contributing characters. Variability in environments could be attributed to differences in terms of levels of organic matter, soil nitrogen and other soil nutrients, water regimes and management conditions among others. The AMMI biplot classification of genotypes and environments revealed three mega environments: first, E1 (Matuga) with a large positive IPCA1 scores; second, E2 (Msambweni drought) with a large negative IPCA1 score and third, E3 (Mtwapa) and E4 (Msambweni no drought) with small IPCA scores. Environments E1 and E2 had the highest discriminating power and were therefore good for selecting genotypes with specific adaptation while E3 and E4 were good for selecting genotypes that perform well across the test environment. The most high yielding and stable genotypes across the test environments were G41 followed by G1 and G34. The most unstable but high yielding genotypes demonstrating a strong GEI were G10 and G39. G10 was specifically suitable for E1 while G39 was suitable for E2.

### GGE biplot analysis

Although, the environment main effect may contribute upto 80% or more of the total yield variation, it is usually the genotype main effect and the genotype x environment interaction (GEI) that are relevant to cultivar evaluation (Yan, 2002). The use of GGE biplots has been appreciated by many researchers in rice and other crops (Hagos and Abay, 2013; Kivuva et al., 2014; Lakew et al., 2014; Muthoni et al., 2015) as it graphically displays general pattern of genotype responses across environments in multi-environmental trials data usually concealed in the general ANOVA. In this study, the GGE biplot results revealed that there was no correlation between environments E2 and E4, indicating that these two environments discriminated the genotypes differently. This was expected because although the two environments were established on the same location, (Msambweni site), differences in water regimes and rainfall seasons contributed to lack of correlation. The random drought environment (E2) was set up during the short rain season and drought developed from flowering to harvesting. In contrast, no drought environment (E4) was set up during the long rain season and rainfall was adequate for growth and development of rainfed rice. This also implies that there is a need for separate breeding programmes for the short and long rain seasons. The distance between E3 and E1 from E2 was shorter than the distance between these two sites from E4. This indicated that E3 and E1 were more positively correlated to E2 than E4. Thus, environments E1, E2 and E3 may have discriminated the genotypes similarly but different from environment E4. Environments E3 and E1 were set up under upland aerobic conditions indicating that during growth and development of the rice genotypes under study, some level of stress similar to that observed in environment E2 may have developed. The environment E2 was close to the average environment and had the second longest vector after E4, indicating that it discriminated among the genotypes and was representative of the whole target region. Based on the observation that E2 was positively correlated to E3 and E1 upland ecologies, this environment may be a good site for selecting genotypes with general adaptation to the upland ecology and drought tolerant genotypes for the lowland ecology. On the other hand, E4 was discriminating but non-representative. This site is therefore good for selecting specifically adapted genotypes if the target environment can be divided into mega environments and/or for culling unstable genotypes if the target environment is a single mega environment.

The polygon view of GGE biplot is very useful for visualising the best genotypes in each environments and grouping environments for visualisation of possible crossover GEI and mega environments (Yan and Tinker, 2006). Different environments fall into different sectors, which imply that there are different high yielding cultivars for those sectors and it shows crossover GEI, suggesting that the test environments could be divided into mega-environments (Yan et al., 2007). In this study, the environments fell into three sectors revealing the possibility of three mega environments and the presence of crossover type of GEI. The environments E2 and E3 fell into one sector and genotype G2 as the best performing genotype in this sector. Environment E1 fell into the second sector and the winning genotype was G37, while E4 fell into the third sector with genotype G38

winning in this environment. Other researchers in sub-Saharan Africa have also appreciated the use of the polygon view of GGE biplot in identification of the best genotypes in different environments and revealing possible mega environments among the test environments (Kivuva et al., 2014; Lakew et al., 2014; Muthoni et al., 2015). The biplot view of mean yield and stability revealed that the average grain yield of G37, G41 and G38 was higher than that of the average (ideal) genotype across the test environments. However, they had poor stability and were therefore good for specific adaptation. Genotype G37 was specifically adapted to environment E1 while G38 and G41 were specifically adapted to environment E4. Advancing different $F_3$ populations for each mega environment would be more time and resource consuming than selection of the best one or a few populations for the whole target region. Therefore, genotype G39 followed by G40 combined high yield and stability across the test environments. These genotypes were therefore identified as candidates with general adaption.

## Conclusions

There were inconsistencies in the ranking of the genotypes in each environment while the four environments fell into three mega environments. This is a clear indication of crossover GEI. The environments E2 (Msambweni random drought) and E4 (Msambweni no drought) were shown to be two independent environments. The two environments were established on the same site but in different rain seasons and suggests the need for separate breeding programmes for the short and long rain seasons in the coast region of Kenya. For genotype evaluation, the GGE was more superior to the AMMI1 biplot since it explained more of the G + GE variation. Thus, based on GGE biplot, G37 was the highest yielding genotype followed by G38 and G41. However, these three genotypes were unstable across environments. The genotype G39 combined high yield and stability across the test environments. This was followed by G40. Therefore, these two genotypes were identified as candidates with general adaption for advancement to homozygozity simultaneously selecting within each population good performing pure lines for release in the region. The results of this study are based on a single year data, and therefore may not be decisive; more temporal and spatial environments will be needed to give meaningful recommendations.

## CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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