

Maize Grain Yield Stability Analysis in Full Season Lowland Maize in Ghana

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ABSTRACT

The objectives of this study were to, (i) Determine the importance of genotype by environment interaction (GE) in late maturing lowland maize varieties, (ii) Determine yield stability of the genotypes and (iii) Use the information to exploit GE for the development of high and stable yielding varieties. GE was attributed to climatic factors. Seven out of the nine genotypes were stable, when b-values alone were considered. When the b-values and the deviations from regression (s^2d) were considered, (GH24 x 1368) x 5012 and (GH22 x 1368) x 5012, were the most stable, but when the coefficient of determination was added to the b-value and s^2d , GH132 - 28 was the most stable genotype. Kpeve consistently produced above average grain yields and was the most stable location. A good level of precision was obtained with two replications, when genotypes were evaluated for 4 years at 8 locations.

Key Word: Genotype by environment interaction; Yield stability; Deviations; Coefficient of determination

INTRODUCTION

Crop varieties are grown under a wide range of conditions such as different soil types, soil fertility levels, moisture levels, temperatures and cultural practices. All these variables encountered during the production of the crop variety are collectively referred to as the environment. The objective in many plant breeding programs is to select genotypes that are consistently high yielding over the range of environments that occur in the target region. However, selection is often inefficient due to genotype by environment interactions (GE) i.e., when genotypes fail to have the same relative performance in different environments (Knight, 1970). Since the relative rankings usually differ across environments, demonstrating the superiority of any single variety becomes difficult if not impossible.

The basic causes of GE are believed to be due to biochemical pathways of certain physiological processes taking place in plants. Even though genotypes may be similar phenotypically, they still differ by a few nucleotide sequences. This results in differential expression of genes in different environments as reported by Langridge and Griffing (1959) for hybrid *Arabidopsis thaliana* plants.

In West and Central Africa, GE have been reported in maize (Fakorede & Opeke, 1986; Badu-Apraku *et al.*, 1997 & 2003) and cassava (Asante & Dixon, 2002). GE continues to challenge plant breeders by complicating the selection of genotypes evaluated in diverse environments by reducing the correlation between phenotypic and genotypic values (Comstock & Moll, 1963; Kang & Gorman, 1989). When GE are present, one of the options open to the breeder is to use stability analyses to identify the most high yielding and stable

genotype. Therefore, several statistical methods have been proposed and used to study the adaptation and stability of varieties to varying environments as summarized by Lin *et al.* (1986). The variance of a genotype evaluated across environment has been used as a measure of stability and a genotype with a low variance is considered stable. The mean of the estimated variance components of GE for all pairs of genotypes that include a specific genotype is the stability measure for that genotype (Plaisted, 1959 & 1960). This approach involved the deletion of a genotype from the entire set of data and the GE interaction for the variance for the subset is the stability index for the deleted genotype. Francis and Kannenberg (1978) on the other hand used the coefficient of variation (CV) of each genotype as a measure of stability. A high yielding genotype with a low CV was considered stable. Other stability indices include Wricke's (1962) ecovalence, Shukla's (1972) stability variance, Perkins and Jinks' (1968) regression coefficient, Finlay and Wilkinson's (1963) and Eberhart and Russel's (1966) coefficients.

In Finlay and Wilkinson (1963) model, the observed yields of the varieties were regressed on an environmental index defined as the difference between the marginal mean yield of the environments and the overall mean. The regression coefficient (b) for each genotype was considered a measure of stability. A b-value approximating to 1.0 indicated average stability, genotypes with b = 1.0 and above average yield were considered as having general adaptation, while a genotype with b = 1 and below average yield was associated with poor adaptation to all environments. In this model, stability was defined by the regression coefficient, while adaptability was defined by the relative mean yield of the variety. In addition to the regression coefficient, Eberhart and Russell (1966) estimated the mean square of deviation from the regression as

Table I. Characteristics of full season maize genotypes evaluated at 8 locations in Ghana from 1995 to 1998

Genotype	Type	Endosperm type
(GH24x1368)x5012	Three-way cross	normal maize
Okomasa	Open pollinated	normal maize
Dobidi	Open pollinated	normal maize
(GH22x1368)x5012	Three-way cross	normal maize
GH132-28	Three-way cross	Quality protein maize
GH110-5	Three-way cross	Quality protein maize
(GH31x1368)x9071	Three-way cross	Normal maize
8321-18	Single cross	Normal maize
Local check	Open-pollinated (farmers' variety)	Normal maize

another stability parameter. The regression coefficient and the deviations from regression were considered to describe the performance of a variety over a series of environments. The regression coefficient measured the increase of response of a variety per unit of environmental index, whereas the deviations from regression measured the agreement between predicted and observed responses. A high yielding genotype with a b-value of one or below one (< or = 1) indicated that the genotype had high stability over all environment. The most stable variety was therefore, one with low sum of squares deviation and a high coefficient of determination. In yet other cases the additive main effects and multiplicative interaction (AMMI) model has been used widely for yield stability analysis (Badu-Apraku *et al.*, 2003) to identify stable genotypes across environments.

The objectives of this study were to, (i) determine the importance of GE in late maturing lowland maize varieties, (ii) determine yield stability of the genotypes using various parameters and (iii) use the information to effectively exploit GE for the development of high and stable yielding varieties.

MATERIALS AND METHODS

The maize genotypes were late maturing (115 to 120 days from planting to harvest). They comprised four open pollinated varieties and eight experimental hybrids. The entries per trial (Table I) varied from year to year as less superior genotypes were replaced by superior ones. The evaluations were conducted at eight locations across Ghana (Lat. 4° 44' - 11° 11'N, Long. 1° 11'E - 3° 11' W.) for four years (1995 to 1998) using a randomized complete block design with four replications per location. Sowing was done after the experimental fields were ploughed and harrowed by the third week of May each year in Nyankpala, Damongo and Wa in the Guinea Savannah zone. No till was practiced in the Forest, transitional and Coastal Savannah zones (Fumesua, Ejura, Pokoase, Kwadaso & Kpeve).

The consisted of 4 rows of 5.0 m long and 0.75 m between rows. Three seeds were sown per hill at 0.5 m within the rows and the seedlings were thinned to two plants per hill at three weeks after planting to obtain the target populations of 53,000 plants ha⁻¹. Pre-emergence chemical weed control was

practised and consisted of an application of a combination of Pendimethalin [N - (1-ethylpropyl) - 3, 4 - dimethyl - 2, 6 - dinitrobenzenamine] and Gesaprim [2 - chloro - 4 - (ethylamino) - 6 - (isopropylamino) - s - triazine] at 1.5 l ha⁻¹ and 1.0 l ha⁻¹ a.i., respectively at planting. Where there was heavy weed growth prior to planting, Paraquat (1, 1'- dimethyl - 4, 4' - bipyridinium ion) was applied at 1.0 l ha⁻¹ a.i. in addition to Pendimethalin and Gesaprim.

Basal fertilizer was applied at 1 - 2 weeks after planting at the rate of 30 kg N ha⁻¹ and 60 kg P₂O₅ ha⁻¹ and top-dressed with additional N at 60 kg N ha⁻¹ at four weeks after planting.

Data were taken from the inner two rows of each plot on days to flowering, plant and ear height, root and stem lodging and grain yield. Grain yield was expressed in mega-grams ha⁻¹. An analysis of variance was conducted to estimate the significance of and magnitude of genotype x location, genotype x year and genotype x location x year effects using the random model. The variance components for the various interactions were estimated with Procedure Varcomp of statistical analysis system (SAS institute, 1996) with the REML method.

GE occurs in both short-term (3 to 4 years of testing at a location) and long-term (several years at several locations) crop yield trials (Kang, 1994). Since increasing number of years of testing is expensive (Saeed *et al.*, 1984), so the theoretical standard errors of a genotype mean were obtained for various combinations of number of locations in a year of testing and number of environments (locations by years) of testing. The expected standard error of genotype mean SE_g, was computed as follows:

$$SE_g = \sqrt{l \left[\frac{\sigma_{gl}^2}{l} + \frac{\sigma_{gy}^2}{y} + \frac{\sigma_{gyl}^2}{yl} + \frac{\sigma_e^2}{ryl} \right]}$$

Where

g is the number of genotypes, l is the number of locations, y is the number of years and r is the number of replications. By substituting the estimated values of various components of variance in the above equation, information to the number of tests needed to evaluate late maturing genotypes for a desired level of precision was obtained.

The stability of genotypes across environments was determined by; (i) Francis and Kannenberg (1978) grouping technique. This was achieved by plotting the genotype mean yields against their coefficient of variation across environment with the grand mean yield and grand mean coefficient of variation serving as base lines on x- and y-, respectively, (ii) regressing yield of each variety on the environment index to estimate the b-values and the squared deviations from regression using the model:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij} ,$$

Where

Y_{ij} is the variety mean of the ith variety at the jth environment (i = 1, 2, ..., v; j = 1, 2, ..., n), μ_i is the mean of the ith variety over all environments, β_i is the regression coefficient

that measures the response of the i^{th} variety to varying environments, δ_{ij} is the deviation from regression of the i^{th} variety at the j^{th} environment, I_j is the environment index obtained as the mean of all varieties at the j^{th} environment minus the grand mean and (iii) contribution of each genotype to the GE sum of squares proposed by Shukla (1972) and called stability variance.

RESULTS AND DISCUSSION

The expected standard errors of genotype mean for various combinations of replications for years and replications are presented in (Fig. 1 & 2). The precision as measured by the estimated standard error of genotype mean increased as the number of test environments was increased up to 12. Beyond 12 environments there was no benefit for further testing. For the number of locations at our disposal, there was no need designing experiments to have more than two replications per location if testing was to be done for four years. Further more, the curves showed that apart from number of environments below 12, there was no need to replicate the entries within each location if the number of years was more than four. When the number of years was increased to four (Fig. 1) the precision also increased. However, there was no effect on the level of precision for any number of years, when the number of environments was increased beyond eight. Therefore, to achieve a good level of precision, designing experiments with less than three replications per location and testing in 12 environments will suffice. The analyzes of variance combined over locations and years for mid-silk, plant height, ear height and grain yield are presented in (Table II). There were significant differences ($p < 0.01$) among locations, years and genotypes for all the traits evaluated. The location x year, genotype x location, genotype x year and genotype x location x year interactions were all highly significant for all the traits. GE was due largely to climatic factors rather than edaphic factors. The 1998 growing season was the most productive year. It was followed by 1995, then by 1996 (Fig. 3). The total rainfall for 1997 was below average especially for Damongo in the Guinea Savanna Zone. Genotype x location interaction, genotype x year interaction and genotype x location x year interaction were significant ($p < 0.01$). That indicated that there were rank changes for the genotypes from location to location within a year and from year to year across locations. This could be attributed to genotypic differences. Some genotypes were more adapted to humid regions, whereas others were more adapted to semi-arid zones and were photoperiod sensitive. Therefore, when these genotypes were grown in areas they were not adapted to they did not perform as expected. For maize genotypes with photoperiod sensitivity, genotype x location and genotype x location x year interaction are more important than genotype x year interaction. Therefore, genotype x environment (location x year) interactions obtained could be explained by the concept of adaptation of the genotypes to the different environments.

Fig. 1. Expected standard error of a genotype mean yield for various assumed number of replications and environments for four years of testing

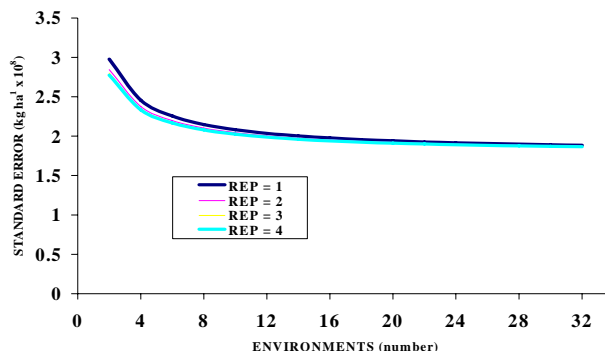


Fig. 2. Expected standard error of genotype mean yield for various assumed numbers of years and environments within years when replications = 4

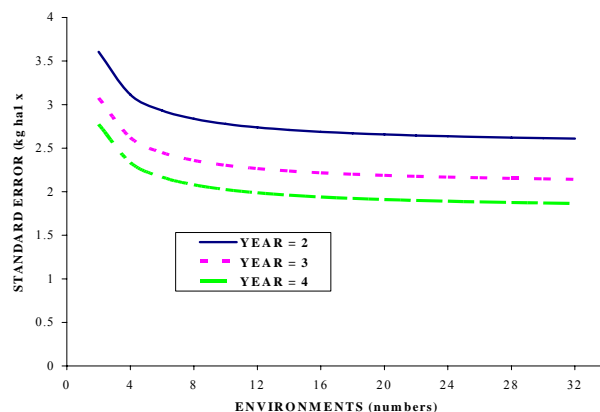
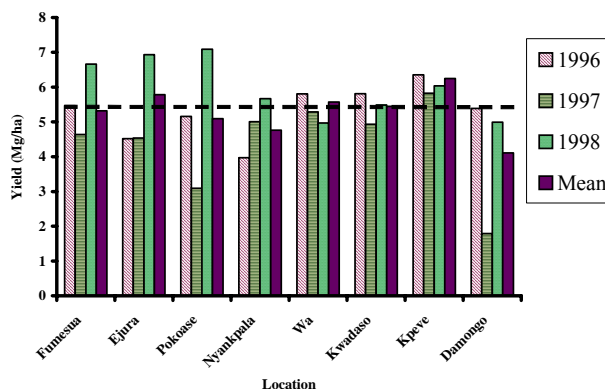


Fig. 3. Histogram of location mean yields for four years of evaluation of 9 maize genotypes. The dotted line denotes the overall mean grain yield (5.23 Mg/ha) across locations and years



Mean grain yields for the environment (year-location) revealed that Kpeve (transitional zone) consistently produced above average yields over the period, while Damongo, Nyankpala and Kwadaso consistently produced below average yields. Significant differences among the years for the mean

Table II. Mean squares from the analyzes of variance for four traits in nine genotypes evaluated at 8 locations from 1995 to 1998

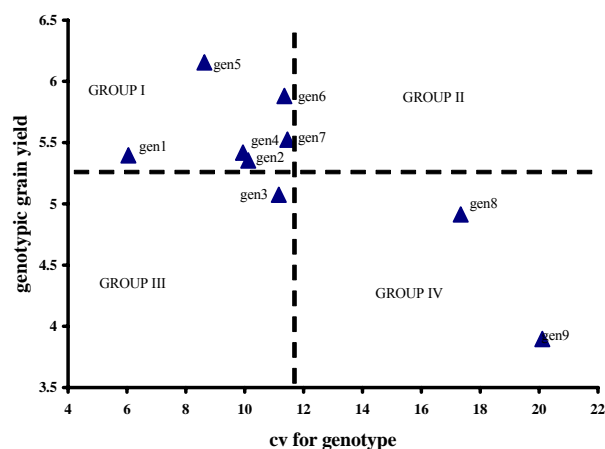
Source	df	Mid-silk (days)	Plant height (cm)	Ear height (cm)	Grain yield (Mg/ha)
Year	3	353.96***	22211.52***	5234.08***	133.86***
Location	7	643.76***	49103.91***	18397.73***	64.12***
Location*year	21	84.79***	15203.87***	6593.48***	33.81***
Rep(location*year)	96	3.32***	1938.36***	285.18*	1.92***
Genotype	8	493.92***	19370.44***	23930.27***	53.03***
Genotype*year	24	21.96***	729.00*	469.75**	2.40***
Genotype*location	56	11.56***	909.68***	569.85***	2.92***
Genotype*location*year	168	5.88***	649.07***	375.04***	1.31***
Error	768	1.80	462.89	216.53	0.70
CV		2.42	11.12	14.94	15.69
Mean		55.44	193.42	98.46	5.29

*, **, *** = significant at 5%, 10% and 1%, respectively

Table III. Mean grain yields of nine genotypes evaluated across locations and years, their stability parameters and ranks

Genotypen	Mean grain yield		Reg. Coefficient b	rank	s ² d	Deviation rank	Rank sum	Shukla	Coefficient of determination
	Mg/ha	Rank							
(GH24x1368)x5012	5.397	(5)	1.035	(3)	0.326	(1)	(9)	0.290	0.936
Okomasa	5.355	(6)	1.074	(9)	0.542	(4)	(19)	1.244	0.850
Dobidi	5.075	(7)	1.214*	(7)	0.566	(5)	(19)	1.677	0.869
(GH22x1368)x5012	5.419	(4)	1.014	(2)	0.510	(2)	(8)	1.048	0.851
GH132-28	6.155	(1)	0.924	(5)	0.531	(3)	(9)	1.210	0.814
GH110-5	5.881	(2)	1.104	(6)	0.667	(7)	(15)	2.021	0.798
(GH31x1368)x9071	5.524	(3)	1.010	(1)	0.633	(6)	(10)	1.745	0.787
8321-18	4.914	(8)	0.925	(4)	0.852	(9)	(21)	3.390	0.630
Local check	3.897	(9)	0.700*	(8)	0.784	(8)	(25)	3.435	0.535

Fig. 4. The relationship between genotypic grain yield and genotypic coefficient of variation across environments (gen* = genotype 1 - 9)



grain produced were observed. Mean grain yields for 1995, 1996, 1997 and 1998, were 5.492, 5.309, 4.389 and 5.98 Mg ha⁻¹, respectively. The yields were low for all the locations in 1997 due to low and poorly distributed rainfall during.

Peterson and Pfeiffer (1989) and Peterson (1992) have suggested the formation of variety testing regions or zones of adaptation in view of large genotype x environment interactions, because when testing zones are created, the stable genotypes may be suitable for growing in the test location only. However, when broadly adapted cultivars are desired, a more

reliable evaluation of genotypes over environments cannot be avoided. Genotype coefficient of variation across environments (Francis & Kannenberg, 1978) was used to discriminate against stable and un-stable genotypes. The mean genotypic grain yield was plotted against the coefficient of variation (CV) associated with each genotype (Fig. 3). The procedure divided the genotypes into four groups. In this study, the genotypes were distributed in only three groups. A genotype having a low CV and high grain yield was considered stable. Based on these criteria, the genotypes in group I [(GH24 x 1368) x 5012, Okomasa, (GH22 x 1368) x 5012, GH132 - 28, GH110 - 5 and (GH31 x 1368) x 9071] were the most stable genotypes. Genotypes, which did not perform consistently across environments gave high CVs. Eberhart and Russell's regression coefficients (b-values) for each genotype and deviations from regression (s²d) are presented in Table III. The b-values did not differ significantly from one for seven genotypes. The deviations from regression ranged between 0.33 and 0.85 and R-square values from 0.52 to 0.94. Based on these, Dobidi and the local check variety had low stability, whereas GH132 - 28 was the most stable genotype.

Ranking based on grain yield, regression coefficient, deviation from regression and R-squared values (Table III), genotype with the least rank sum was (GH22 x 1368) x 5012 and the one with the highest was the local variety. Owing to the lowest s²d and the highest R-squared value, genotype (GH24 x 1368) x 5012 was the most. The rank sum combined the power of high production potential, the b-value and the deviation from regression (s²d) of the genotypes in the same way as selection

indices do. With the approach (GH22 x 1368) x 5012, (GH24 x 1368) x 5012 and GH132 - 28 were judged the most stable genotypes. This was confirmed by Shukla's stability variance for each genotype.

From this study, evaluating genotypes for 4 years at 8 locations was adequate in identifying stable genotypes. No single approach was able to identify all the stable genotypes. However, GH132 - 28 was always included among the stable genotypes. Therefore, to select stable genotypes it will be useful to use an approach most convenient to the researcher but should cross check the results with other methods.

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