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Evaluation of pearl millet (Pennisetum glaucum L.) Genotypes for Yield and Yield Stability in South Omo and West Hararghe

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Abstract

Sixteen pearl millet genotypes were evaluated in randomized complete block design with four replications during 2011 at four locations to study the magnitude of genotype by environment interaction for yield and yield related traits and identify the most stable high yielding genotypes. ANOVA of data at individual location revealed significant differences among genotypes at Jinka ,Konso,Meiso and Weioto for days to flowering, at Jinka, Konso and Meiso for days to maturity, productive tillers per plant, grain weight per head and biomass, and for panicle length at Konso, Weioto and Meiso where as harvest index and stalk weight showed significance at two Weioto and Konso, for plant height at Jinka and Konso and number of tillers per plant and thousand seed weight showed significant only at Jinka. Combined analysis of variance showed that the Genotype and location main effects and the genotype by environment interaction interaction were highly significant ($P \leq 0.01$) for grain yield and other traits, indicating differential response of genotypes across testing locations and the need for stability analysis. Weioto was the most suitable environment and gave highest mean grain yield of 3307.5231 kg/ha. The lowest yield 1491.23 Kg/ha was observed at Jinka. Genotypes SOSATC88 (8), ICMP97774 (6), MCSRC (5) and ICMV95490 (13) produced high mean yield of 2844.10, 2840.17, 2835.42 and 2725.00 kg/ha respectively. The lowest grain 2056.60kg/ha was obtained from genotype ICMV91450 (1). Five stability parameters were used to identify stable pearl millet genotypes for wide growing conditions. Based on the parameters of stability, three stable (widely adapted) and high yielding genotypes (ICMP97774 **(**6**)** MCSRC (5)**,** and ICMV92901 (12) were identified. They also out yield the standard check and have the mean yield above grand mean . These stable high yielding genotypes can be used for yield and verification trial with standard check to be released as widely adapted varieties. GGE biplot techniques was used identify specifically adapted genotypes. ICMV155white (4) was specifically adapted to Jinka, ICMV221 (Br) (11) to Konsso, SRCLLC4 (7) to Meisso and ICMV95490 (13) to Weioto.

Keywords: Genotype by environment interaction, Stability, Pearl millet, Yield

1. Introduction

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is a staple diet for the vast majority of poor farmers and also form an important fodder crop for livestock population in arid and semi arid regions of world. It is a widely grown rainfed cereal crop in the arid and semiarid regions of Africa and southern Asia. Pearl millet is a crop of hot and dry climates, and can be grown in areas where rainfall is not sufficient (250-600 mm) for maize and sorghum. Pearl millet is often referred to as the “Camel”, because of its exceptional ability to tolerate drought. Even with minimal rainfall pearl millet can typically produce a reasonable yield. In many areas where millet is the staple food, nothing else will grow. Besides providing food for human, pearl millet stems are used for a wide range of purposes, including: the construction of hut walls, fences and thatches, and the production of brooms, mats, baskets, sunshades, etc (IFAD, 1999).

Crop performance, the observed phenotype, is a function of genotype, environment and genotype by environment interaction. Genotype by environment interaction is commonly observed as differential ranking of cultivar performances among locations or years. Genotype by environment interaction is said to occur when different cultivars or genotypes respond differently to diverse environments. Researchers have long been aware of the various implications of Genotype by environment interaction in breeding program. Genotype by environment interaction is important only when it is significant and causes significant change in genotypes` ranks in different environments (Crossa, 1997). Genotype by environment interaction has a negative impact on heritability. A significant genotype by environment interaction can seriously impair efforts to selecting superior genotypes for crop introductions and cultivar development programs (Yan and Racjan, 2002). Knowing the effect of genotype by environment interaction, as well as the estimate of its magnitude relative to the magnitude of genotype and environment effects is very important for efficient breeding program. Therefo the structure and nature of genotype by environment interaction is particularly useful to breed determine whether to develop cultivars for all environments or to develop specific cultivars for specific target environments (Bridges, 1989). Gauch and Zobel (1996) explained the importance of Genotype by environment interaction as where there is no interaction, a single cultivar would yield the same and serve all over the world.

Hence, the variety trial can be conducted at any one location to provide universal results. In such cases, the best variety can be identified without error, and one replication at one location would identify one best variety that flourishes worldwide. The importance of evaluating many potential genotypes in different environments (location and years) before selecting desirable ones for release and commercial cultivation has been recognized by breeders (Gupta and Ndoye, 1991). A desirable cultivar is one that does not only yield well in its area of initial selection, but also maintains the high yielding ability over a wide range of environments within its intended area of production (Yahaya *et al.*, 2006).

In Ethiopia formal research to improve pearl millet has started decade ago. Only one variety have been identified for cultivation (Kola-1) and its production has expanded to dry low land areas of the country. But appropriate management practices and food processing mechanisms are also still lacking. Encouraged by the expanded adoption, the Ethiopian national sorghum research program increased its effort to identify additional high yielding varieties that can fit in to a wide range of environments but it does not much progressed because of funding limitation as well as the crop is not among the priority commodities.. At present the production of this variety has expanded to dry low altitude areas, such as Konso, Alamata, Meiso (West Hararghe), and across South Omo.

Pearl millet was introduced to southern region by Jinka and Awassa Agricultural Research Centers. Adaptation trial was conducted during 2008 and 2009 at South omo zone, Benatesmay woreda and at Konso special woreda. Variety (Kola-1) showed very good performance and gave on average 50 quintal per hectare during the adaptation trial (Jinka Agri., 2009). During year 2010 Jinka Agricultural Research Center conducted demonstration in three woreda, two kebles, six farmers' fields in each woreda and 300 agro-pastoralists participated on the field day and high demand of participant was seen. Its earliness and drought tolerance, good oppoutinty for animal feed and reasonable yield, creates high demand at the farming community. Therefore studying different genotypes across different locations will provide a good opportunity to identifying high yielding genotypes that can adapt to a wide range of environments and specifically adapted genotypes. So this investigation was conducted in four locations three in South Omo and one at Mieso in west Hararage zone based on following objectives.

- To study the magnitude of genotype by environment interaction for yield and yield attributing traits.
- To identify high yielding widely adapted (stable) and specifically adapted (narrow adaptation) pearl millet genotypes.

2. Materials and Metods

2.1. Experimental Sites

The study area (South Omo, Konso and West Hararage) are characterized as hot to warm semi-arid lowlands which is almost habited by an Agro pastoral community, in which major crops are Pigeon pea, finger millet, Sesame, lowland maize and sorghum. Pearl millet was introduced to these areas around 2008/2009 and its productions is at expanding rate.

The experiment was conducted at four locations, three locations (Jinka, Konso and Weioto) in the southern region and one location (Meiso) in western Hararege, during 2011 cropping season (July to December). These locations are found within altitudinal ranges of 566 to 1587 m.a.s.l and are in the range of environments suitable for pearl millet growth. Since these locations are different in soil type, altitude, mean annual temperature and rainfall, they were considered as an individual environment. Description of the study locations is given in Table1

Table1: Description of the experimental locations and their overall agro-climatic conditions.

Location	Altitude	*Mean annual rainfall(mm)	*Mean annual temperature (^{0}C)	Position/Coordinate	Soil Type	Zone
Jinka	1373	1326.00	21.92	05°46'46.9"N,036°33'34.7"E	Nitosol	South Omo
Woito	566	513.70	No data	05°21'47.8"N,036°59'58.6"E	Fluvisols	South Omo
Konso	1587	915.30	No data	05°25'25.6"N,037°19'06.0"E	Fluvisols	Segan people's
Mieso	1400	688.53	22.46	9.14°N,40.5°E	Vertisol	West Hararghe

*=Mean of 10 years from 2002 to 2011 for all locations.

Source: National Meteorological Agency (Awassa and Adama Branch Directorate)

2.2. Experimental Materials (genotypes)

Sixteen genotypes of pearl millet obtained from Melkassa Agricultural Research Center were used in this study. The description of the genotypes included in the experiment is given in table 2.

Table2. List and descriptions of pearl millet genotypes studied at four locations in 2011

No.	*Genotype*	*Seed source*	*Status*	*Seed color*
1	*ICMV91450*	*MARC*	*Under NVT*	Brown
2	*ICMV93191*	»	Under NVT	Brown
3	*ICMV155*	»	Under NVT	Brown
4	*ICMV155*	»	Under NVT	white
5	*MCSRC*	»	Under NVT	Brown
6	*ICMP97774*	»	Under NVT	Brown
7	*SRCLLC4*	»	Under NVT	Brown
8	*SOSATC88*	»	Under NVT	White
9	*HiTiP89*	»	Under NVT	Brown
10	*ICMV155*	»	Under NVT	Brown
11	*ICMV221 (Br)*	»	Under NVT	Brown
12	*ICMV92901*	»	Under NVT	Brown
13	*ICMV95490*	»	Under NVT	Brown
14	*ICMV84400*	»	Under NVT	White
15	*ICMV91773*	»	Under NVT	Brown
16	*Kolla-1(check)*	»	Under production	Brown

NVT=National variety trial

2.3. Experimental Design and Trial Management

The Randomized Complete Block Design (RCBD) with four replications was used to conduct the experiments. The experiments were planted at different times due to difference in the planting time for the test locations; Jinka, and Konso were planted in August while Weioto, and Mieso were planted in September and July respectively.

Seeds of each genotype were drilled at a rate of 10 kg /ha in a plot consisting of three rows each 4.95m long with 0.75m inter-row spacing resulting a plot size of 11.14m^2. Thinning was done two weeks after planting, when seedlings attained height of 0.12-0.15m to provide spacing of 0.15m between plants to obtain a uniform plant density of 33 plants per raw i.e. 99 plants per plot. Fertilizer rates of 50/50 kg/ha DAP/urea was used at all locations. Urea splited at planting with DAP and at tillering stage. At Weioto supplementary furrow irrigation was given twice, at planting and after two weeks later planting. Field managements such as weed control, insect-pest control were carried out uniformly for all plots.

2.4. Data Collection

The middle row (3.7125 m^2) was used for data collection and harvested at maturity. Individual plant data as well as plot data were collected on different traits of pearl millet genotypes. Data recorded on individual plant basis were plant height (cm), total number of tillers per plant, number of productive tillers per plant, head length (cm) and weight of grain per head (g). Eight plants' average was used for statistical analysis. Data collected on plot bases included days to flowering (days from planting up to the time when 50% of plants have flowered), days to maturity (days from planting up to the time when 95 % of plants matured(seed texture become hard)), stand count at harvest, bird damage (using 1-5 scale with 1 =least damaged and 5= sever damaged), grain yield(g), total biomass (total above ground part in kilo gram), harvest index (ratio of grain yield to biomass), 1000 seed weight (weight of 1000 seeds in gram drawn randomly from the bulk seeds of each plot).

2.5 Statistical Analysis

2.5.1. Analysis of Variance (ANOVA)

Randomized Complete Block Design Analysis of variance was done for all data of each location separately after checking for homogeneity of experimental error. The following model was used for ANOVA of data of individual location.

$$Y_{ij} = \mu + G_i + B_j + e_{ij}$$

Where;

Y_{ij} = observed value of genotype i in block j,
μ = Grand mean of the experiment,
G_i = the effect of genotype i,
B_j = the effect of block j,
e_{ij} =the error of genotype i in block j.

A combined analysis of variance was performed for yield and other traits after checking for homogeneity of experimental error. In the combined analysis of variance, genotypes were assumed to be fixed while locations were considered as random variables (Gomez and Gomez, 1984). Combined analysis of variance over locations was carried out using the following statistical model.

$Y_{ijk}=\mu + G_i +E_j +GE_{ij}+ B_{k(j)+} e_{ijk}$

Where; Y_{ijk} = observed value of genotype i in block k of environment (location) j,
μ = Grand mean of the experiment,
G_i = the effect of genotype i,
E_j =the effect of the j^{th} environment
GE_j = the interaction effect of genotype i with environment j,
$B_{k(j)}$ =the effect of block k in location (environment) j,
e_{ijk} =the error effect of genotype i in block k of environment j.

Mean separation was done using Duncan's multiple range test. To compute the proportion of the total variance, estimation of variance components was performed by equating mean square to their expectations as shown in Table 3.

Table 3. Estimates of variance components and methods of determining variance component

Source of variation	SS	DF	MS	F-test			
				Obtained	Required 5%	1%	Variance components
Total	SST	255	MS_T	-	-	-	
Environment	SSL	3	MS_L	$MS_L/MSB_{(L)}$	3.49	5.95	$\sigma^2E+g\sigma^2_{B(l)}+gr\sigma^2 l$
Block(L)	$SS_{B(L)}$	12	$MSB_{(L)}$	$MSB_{(L)}/MS_E$	1.75	2.18	$\sigma^2E+g\sigma^2_{B(L)}$
Genotypes	SS_G	15	MS_G	MS_G/MS_{GxL}	1.83	2.35	$\sigma^2E+r\sigma^2_{GxL}+rl\sigma^2 g$
GxL	SS_{GxL}	45	MS_{GxL}	MS_{GxL}/MS_E	1.39	1.59	$\sigma^2_E+r\,r\sigma^2_{GxL}$
Error	SS_E	180	MSE				σ^2_E

Where; L, G and B are the number of locations, genotypes and blocks, respectively. The σ^2_L, $\sigma^2_{B(L)}$, σ^2_G, σ^2_{GxL}, and σ^2_E, are variance components of environment blocks within environment, genotypes, genotype by environment interaction and error respectively.

GxL= Genotype by environment interaction

σ^2_E= variance component due to experimental error $=MS_E$

σ^2_{GxL} = the variance component due to genotype by environment interaction $=MS_{GxL}-MS_E/r$

σ^2_G = the variance component due to genotypes= $MS_G -MS_{GxE}/rl$

$\sigma^2_{B(L)}$ = variance component due to blocks with in environments $=MS_B-MSE/g$

σ^2_L = variance component due to location = $MS_L-MS_{B(E)}/rg$

σ^2T =total variance $=\sigma^2_l+\sigma^2_{B(l)}+\sigma^2_G+\sigma^2_{GxE}+\sigma^2E$

σ^2_k =variance due to one components (L, G.etc)

The proportion of variance accounted for each component was determined by dividing the variance component by the total variance component (σ^2_k/σ^2_T).

2.5.2. Stability Analysis

ANOVA only detects the existence of genotype by environment interaction (effects). Therefore, significance of genotype by environment interaction mean square was further elaborated using various stability parameters. For this the means of genotypes over the replications were subjected to stability analysis using SAS (Hussien et al., 2000). Eberhart and Russell's joint regression analysis (Eberhart and Russell's, 1966); Wricke's ecovalence (Wrcke, 1962); Shukla's Stability Variance (σ^2i); AMMI model and biplot technique proposed by kempton (1984); and AMMI stability value (ASV) as described by Purchase (1997) were used for stability analysis .

2.5.2.1. Joint Linear Regression Analysis

The breeder proceeds to this regression analysis only if the genotype by environment interaction is significant. In Joint linear regression analysis, genotypic means are regressed on environmental indices. In this study, the stability of grain yield for each genotype was calculated by regressing mean grain yield of individual genotype on environmental indices as per Eberthart and Russel (1966).

The Eberthart and Russel's model is:

$Y_{ij}=\mu +\beta_iI_j+ \quad_{ij}+e_{ij}$

Where;

Y_{ij} = Observation of the i^{th} (i=1, 2,…n) genotype in the j^{th} (j=1, 2,..n) environment, μ = grand mean of the experiment, β_i = regression coefficient, ${}_{ij}$ = the deviation from the fitted regression line of the i^{th} genotype in the j^{th} environment, I_j = environmental index obtained by the difference among the mean of each environment and the general mean ($I_j = \square_{.j} - \square_{..}$), e_{ij} = effect of the mean experimental error.
This linear regression model is used for genotype by environment interaction study and in this model a stable genotype should have low deviation from regression (${}_{ij}$). The regression coefficient (β_i) and the deviations from regression (${}_{ij}$) were considered to describe the performance of a variety over a series of environments. The regression Coefficient measures the average increase of response of a variety per unit increase of an environmental index. The deviations from regression measure the agreement between predicted and observed responses. A stable variety is a variety with $\beta_i = 1$ and deviations from regression as sma1l as possible. Regression coefficient less than 1.00 indicates a variety lacking the ability to respond well to favorable conditions (does better in unfavorable conditions). Regression coefficient greater than 1.00 and significant deviation from regression indicates a variety with the ability to respond to favorable conditions (not stable). The linear regression model does not provide for critical analysis of interaction of genotypes in specific environments and does not help in identifying promising genotypes to take advantage of their high positive interaction with the agro ecological conditions of specific locations or specific agro-management conditions like early or late sowing, high or low fertility, rained or irrigated etc (Misra et al., 2009).
The regression coefficient (β_i) and deviation from regression ${}_{ij}$ were determined from the regression of each cultivar's mean on environment means on an environmental index and these estimates were defined from the model:

$$x\square_{ij} = \beta_i I_j + {}_{ij}$$

Where: $x\square_{ij}$ = the observed mean of the i^{th} genotype in the j^{th} environment,
β_i = a linear regression coefficient for the i^{th} cultivar's response to varying environments
I_j= Environmental index calculated as the overall cultivar mean within an environment minus the garnd mean
${}_{ij}$ = the deviation from regression of the i^{th} cultivar in the j^{th} environment

The estimate of stability parameters, namely, β_i (regression coefficient) and S^2di (the deviation from regression) were calculated as:

$$\beta_i = \sum_j(Y_{ij} I_j)/ \sum j(I_j)^2$$

$$S^2_{di} = [\sum_j(\quad {}_{ij})^2/l\text{-}2] - S^2_e/r$$

Where : l= number of location, r = number of replications, S^2_e/r = combined (pooled) error mean square on mean bases, S^2_e=estimate of pooled error mean square.
The regression coefficients (β_i) were tested for their significant differences from unity using t-test, while the significances of the S^2di from zero were tested by the F-test by comparing deviation from regression with pooled error estimate (S^2_e/r).

2.5.2.2. Wricke's Ecovalence

Wrike's (1962) ecovalence (W^2i) evaluates stability on the basis of the contribution of each genotype to the total genotype by environment interaction sum of squares. Accordingly, genotypes with higher ecovalene value (Wi) have much contribution to genotype by environment interaction and are therefore unstable while genotypes with lower ecovalene (Wi) value have lower contribution to genotype by environment interaction sum of squares and are stable across environments.
Wricke's Ecovalene (Wi) or the stability of i^{th} genotype is its interaction with the environments, squared and summed across environments and expressed as:

$$Wi = \sum_j (x\square_{ij} - x\square_{.j} - x\square_{i.} + \mu)^2$$

Where: $x\square_{.j}$ =mean of environment j, $x\square_{i.}$ = mean yield of genotype i across environments, μ and $x\square_{ij}$ where explained in the above model.

2.5.2.3. Shukla's Stability Variance (σ^2i)

The stability variance of Shukla (1972) is an unbiased estimate of the variance of a genotype across environments. It is based on the partioning of the genotype by environment interaction sum squares in to its components attributable to individual genotypes. The genotype is said to be stable when its contribution to genotype environment interaction is minimum. Is estimated as follows:

$$\sigma^2i = \frac{g}{(g\text{-}2)(l\text{-}1)(l\text{-}1)}\left[\sum_j\left(\bar{x}_{ij} - x\square_{.j} - x\square_{i.} + \mu\right)^2 - \frac{\sum_j\left(\bar{x}_{ij} - x\square_{.j} - x\square_{i.} + \mu \right)^2}{(g\text{-}1)(g\text{-}2)(l\text{-}1)}\right]$$

Where $x\square_{ij}$, $x\square_{.j,}$ $x\square_{i}$, and μ where explained in the previous section.

2.5.2.4. Additive Main Effects and Multiplicative Interaction (AMMI) Model

Additive main effects and multiplicative interaction analysis (Zobel et al., 1988; Crossa, 1990) was also performed for grain yield using SAS (Hussien et al., 2000) software. It first fits additive effects for genotypes (G) and environment (E) by the usual additive analysis of variance (ANOVA) procedure to separate the additive effects of genotypes and environments, and then fits multiplicative effects for genotype by environment interaction by principal component analysis (PCA) to extract the pattern from the remaining genotype-environment interaction portion of the ANOVA. Essentially this means stripping out the additive effects of genotypes and environments from the two-way genotype – environment table, and then conducting a principal components analysis on the residuals. The resulting statistical model is therefore a hybrid of this two models, estimates (Zobel, 1990).

The AMMI model for the observed performance (Yij) of the ith genotype in the jth environment is: $Yij = \mu + gi + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij,}$ Where μ+g_i + e_j and e_{ij} are as described in the above equations, n is the number of principal component axes considered, λ_k is the singular value of the kth axis in the principal component analysis, α_{ik} is the eigenvector of the ith genotype for the kth axis, γ_{jk} is the eigenvector of the jth environment for the kth axis, *eij* is the corresponding random error.

The first axis represents that environmental variable which accounts for the largest amount of interaction, and which therefore discriminates most effectively between genotypes, and so on. The significance of the analysis was measured by appropriate F-test at various probability levels by comparing each principal components mean squares with the pooled within environment mean square. Those PCA axes, which were not significant, were pooled into residual term (eij).

Biplot presentation was employed to show similarities both between genotypes and between environments. The biplot technique proposed by Kempton (1984) provides a graphical presentation of interaction patterns which allows the response of each variety in each environment and to indentify. The bioplt shows the relative performance of the varieties over environment to be predicted, though the accuracy of these predictions will depend on how much of the genotype by environment interaction sum of squares is explained by the heterogeneity of regressions (Hill et al., 1998). Integrating biplot display and genotypic stability statistics enable genotypes to be grouped based on similarity of performance across diverse environments.

Genotypes with IPCA scores near zero had little interaction across and those far along the axis had high interaction. Genotypes and environments with the same sign on the IPCA axis had positive interaction and vice verse (Zobel et al.,1988).The closer the ICPA scores to zero, the more stable the genotypes are across their testing environments (Purechase, 1997).

Success in evaluating germplasm, breeding lines, and cultivars in multiple environments and for complex traits to identify superior genotypes with specific or wide adaptation can be achieved if the genotypic and environment effects and their interaction are estimated (Yan et al ., 2000).The use of genotype main effect plus genotype-by-environment interaction biplot analysis by plant breeders and other agricultural researchers has increased dramatically during the past five years for analyzing multi-environmental trial (MET) data (Yan et al., 2007). Genotype main effect plus genotype-by-environment interaction biplot (Yan and Hunt, 2002) is used to visually identify the highest yielding genotypes for each of the environments, by connecting genotypes far away from the biplot origin with straight lines so that polygon is formed with all other genotypes included in the polygon.

Perpendicular lines to the sides of the polygon are drawn, starting from the biplot origin, to divide the biplot into quadrants each having a vertex genotype. The vertex genotype for each quadrant is the one that gave the highest yield for the environments that fall within that quadrant, so it is specifically adapted to that environment (Hunt, 2002).

2.5.2.5. AMMI Stability Value /ASV/

The AMMI model does not provide measure for quantitative stability. But quantitative stability measure is crucial in order to quantify and rank genotypes according to yield stability. For this reason AMMI stability value (ASV) was proposed by Purchase (1997). ASV was calculated as:

$$ASV = \sqrt{} \; [(\text{IPCA1 sum of square/IPCA2 sum of square})(\text{IPCA1 score})^2] + [\text{IPCA2 score}]^2$$

Actually ASV is the distance from zero in two dimensional scatter diagrams of IPCA1 score against IPCA2 scores. Since the IPCA1 score contributes more to GEI sum of squares, it has been weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 total GEI sum squares. The distance from zero was determined by using the Pythagoras theorem (Purchase, 1997).

2.5.3 Correlation between Traits

The association between grain yield and yield related traits and among yield (related) traits themselves were estimated using Pearson's product moment correlation coefficients, as per the standard procedure given by Gomez and Gomez (1984). Using the r-table at appropriate degrees of freedom and probability level, significance of the correlation coefficients were tested.

3. Results and Discussion

3.1. Seasonal Rainfall of the Four Locations

Mean monthly temperature and rainfall data of the experimental sites during the 2011 cropping season is presented in Appendix -I. At Weioto and Konso high rainfall was observed during October and continued through increasing up to maturity, while at Weioto high rainfall occurred in November. At Meiso high rain fall was observed in an increasing trend from planting up to maturity (July to September). High fluctuation in rainfall pattern was observed across locations during the study season. Due to variation in rainfall, temperature and other factors (soil and elevation above sea level), difference in the performance of the test genotypes were observed over locations.

3.2. Analysis of Variance (ANOVA)

Analysis of variance for data of individual environment and combined over environments was conducted for days to flowering (DTF), days to maturity (DTM), total number of tiller (Ntill), number of productive tillers (NPT), grain yield(GY) , total biomass (BMY), harvest index (HI), plant height(PH), panicle length (PL) and grain per head (GH). ANOVA data for both individual as well as combined analysis for grain yield, biomass and other ten traits were discussed separately below.

3.2.1. ANOVA of Data of Each Location

Analysis of variance of data of individual environments for all traits is presented in appendix-II. Significant difference between genotypes was observed at all location for day to flowering (DTF) and grain yield (GY), at three locations for DTM, Ptill, Pl, GWH and BM, where as HI, PH and Stlkwt showed significance at two locations and Ntill and TSW showed significance only at one location. Jinka, Konso and Weioto discriminated between the genotypes most effectively (9 and 10 traits out of the 12, respectively) and Mieso was discriminated less between genotypes (only 3traits out of 12 traits). Because they all genotypes to express their potential fully.

The mean grain yields at individual locations (Table 4) ranged from1122.2 kg/ha ICMV91450 (1) at Jinka to 4594.4 kg/ha for ICMV95490 (13) at Weioto. Weioto and Meiso gave highest grain yield of 3307.52 kg/ha and 3275.1 kg/ha, respectively. Because these two locations have similar mean annual rainfall which is the range suited for pearl millet production (Table 1). Despite the high rainfall, Jinka gave lowest yield of 1491.23 kg/ha. These may due to high monthly total rainfall during growing season (Appendix I). Genotypes ICMV155white (4), MCSRC (5), ICMV95490 (13) and SRCLLC4 (7) gave highest yield at Jinka, Konso, Weioto, respectively. These genotypes are specifically recommendable.

Table 4.Mean grain yield (kg/ha) of sixteen pearl millet genotypes in each four locations

		Locations				
No	Genotypes	Jinka	Konso/Arf	Weioto	Mieso	Genotype mean
1	ICMV91450	1122.2d	1877.8d	2870.8d	2355.6cd	2056.60
2	ICMV93191	1375.00cd	2236.1c	2618.1d	2666.7c	2223.97
3	ICMV155Br	1462.50c	1723.6d	2391.7e	2777.8c	2088.89
4	ICMV155white	1901.3a	2025.0cd	3177.8c	3066.7b	2542.70
5	MCSRC	1644.4b	3004.2a	3715.3b	2977.8bc	2835.42
6	ICMP97774	1693.1b	2416. 7bc	3939.8b	3311.1a	2840.17
7	SRCLLC4	1448.6c	1986.1d	3797.2b	3466.7a	2674.65
8	SOSATC88	1456.9c	2866.7a	4052.8ab	3000.0b	2844.10
9	HiTiP89	1375.00cd	2425.00bc	2237.5e	2844.4bc	2220.49
10	ICMV155	1833.3a	2313.9bc	2744.4d	3355.6a	2561.81
11	ICMV221(Br)	1250.00d	2973.6a	3559.7b	2977.8bc	2690.28
12	ICMV92901	1411.1c	2644.4b	3647.2b	3066.7b	2692.35
13	ICMV95490	1272.2d	2188.9c	4594.4a	2844.4bc	2725.00
14	ICMV84400white	1351.4cd	2412.5bc	3266.7c	2822.2bc	2463.20
15	ICMV91773	1768.1b	2376.4bc	3102.8c	2222.2cd	2367.36
16	Kolla-1(check)	1494.4c	2501.4b	3204.2c	2600.0c	2500.00
Environment mean		1491.22	2373.26	3307.52	3275.1	2537.3
Least sign. difference(LSD)		23.14	21.39	22.34	19.32	21.55
Coefficient of variation (%)		18.86	17.21	13.51	16.21	16.45

a=highest, b=medium, c=poor, d=poorest, e=bad mean grain yield, genotype having same letters are same in mean performance.

3.2.2. Combined Analysis of Variance

The Combined analysis of variance showed that the effects of locations and genotypes were significant ($p\leq 0.01$) for all 12 traits (Table 5).

The significant effect of locations is due to their variation in rainfall amount and seasonal distribution, temperature and soil type (Table 1.and Appendix-I).Therefore environments played a significant role in the expression of these traits. Genotypes were significantly different in days to flowering, maturity, tillering, total number of tiller (Ntill), number of productive tillers (NPT), grain yield(GY) , total biomass (BMY), stalk weight (stlkwt), harvest index (HI), plant height(PH), panicle length (PL) and grain per head (GH). This result is in agreement with the findings of Yahaya (2005), Gupta and Ndoy (1991), Echekwu and Mohammed (2005) in pearl millet in which effects due to environment and genotypes were very highly significant for all traits.

Mean performance over locations for genotypes for grain yield, stalk weight, biomass and other traits is presented in Table 4 and 6 respectively. The poorest genotypes across location were ICMV91450 (1), ICMV155Br (3), HiTiP89 (9), ICMV93191 (2) and ICMV91773 (15) respectively. Genotypes ICMV155wh (4) best adapted to Jinka, ICMV221 (Br) (11) best adapted to Konso, ICMV95490 (13) best adapted Weioto and genotype SRCLLC4 (7) best adapted to Meiso respectively in grain yield. Genotypes MCSRC (5), ICMP97774 (6) and ICMV92901 (12) gave high yield across locations. They showed wide adaption across locations in grain yield.

In general, Days to flower ranged from 45 (Kolla-1) up to 54 days (SOSATC88). Genotypes ICMV91450 (1), ICMV155Br (3), HiTiP89 (9), ICMV93191 (2) and ICMV91773 (15) were medium for yield attributing traits such as tillering, panicle length, stalk weight, biomass, harvest index and thousand seed weight. The tallest genotype with highest biomass (10100.3kg/ha), lowest productive tiller and thousand seed weight, and late maturing genotype was SOSATC88 (8) while the shortest genotype was ICMV92901 (12). The specifically adapted genotypes ICMV155white (4), SRCLLC4 (7), ICMV221 (Br) (11) and ICMV95490 (13) showed medium performance for tillering, panicle length, stalk weight, biomass, harvest index and thousand seed weight. The high yielding genotypes MCSRC (5), ICMP97774 (6) and ICMV92901 (12) gave high grain per head, stalk weight ,biomass and showed medium in for tillering, panicle length, harvest index and thousand seed weight across locations.

Environmental means for grain yield and other traits is indicated in Appendix-IV. Among the test sites, genotypes showed best performance at Weioto for grain yield, grain per head, biomass, stalk yield, number of tillers and panicle length this may due to difference in agro-climatic conditions and relatively medium seasonal rainfall pattern (Table1 and Appendix-I). The genotypes also showed earliness in flowering and maturity at Weioto. The poorest location for the performance of genotypes was Jinka where low grain yield, Short plant height, low grain per head, low biomass, long days to emerge and maturity.

Genotype by environment interaction was statistically highly significant ($p \leq 0.01$) for DTF, Ptill, DTM, PH, GWH, GY (Table 5). This indicates genotypes performed differently across location for these characters. And non-significant for DTE, Ntill, Stlkwt, BM and HI, implies genotypes were similar across location for these traits.

Table 5. Mean square results of the combined analysis of variance for yield and other traits of 16 genotypes

Source of variation	DF	DTE	DTF	Ntill	Prtill	DTM	PH	Pl	GWH	Stlkwt	GY	BM	HI
Location(L)	3	23.92**	5302.32**	7.36**	5.62**	3192.21*	73312.77*	2226.20*	5375.95*	367123285**	39303621.5*	1892307**	0.06**
Genotype(G)	15	0.99^{NS}	58**	0.52**	0.75**	62.55**	2059.27**	70.43**	146.51**	9483698*	1112737.7**	9733951**	0.013*
G*L	45	0.67^{NS}	21.37**	0.26^{NS}	0.51**	15.87**	343.13***	20.26**	79.70**	3424664^{NS}	585105.8**	3387012^{Ns}	0.007^{NS}
Rep (E)	12	0.69	20.17**	0.42^{NS}	0.18^{NS}	21.01**	621.64**	3.75^{NS}	27.70^{NS}	5719140*	204540.5^{NS}	5055561^{Ns}	0.005^{NS}
Error	180	0.61	4.56	0.22	0.25	5.73	156.15	6.16	26.77	2752429	229253.9	2572743	0.005
Mean		5	48.25	2.73	1.35	83.55	155.68	30.72	27.35	7140.67	2517.309	8847.90	0.29
CV (%)		15.67	4.42	16.93	36.90	2.86	8.02	8.08	18.92	23.23	19.02	18.12	25.30
R-square		0.53	0.95	0.55	0.54	0.91	0.90	0.88	0.82	0.74	0.79	0.80	0.45

**=highly significant, *=significant, NS= non-significant at 1 and 5% probability level, G*L =genotype by location interaction, DTF=days to flower, DTM=days to maturity, Ntill=number of tillers, Ptill=productive tillers, DTM= days to maturity, PH=plant height, Pl=panicle length, GWH=grain per head, Stlkwt= stalk weight ,GY =grain yield per hectare BM =biomass/ha ,HI= harvest index.

Table 6. Mean performance of 16 genotypes for different traits over location

Entry	Name	DTF	Ntill	Prtill	DTM	PH	Pl	GWH	Stlkwt	BM	HI	TSW
1	ICMV91450	46.25c	2.75b	1.43b	83.75b	155.76bc	29.50b	23.20d	7556.3b	8648.3b	0.24c	16.45c
2	ICMV93191	47.44bc	3.12a	1.75a	82.18b	150.21bc	31.94b	23.63cd	6482.1c	7925.5c	0.29b	16.66b
3	ICMV155Br	47.56b	2.87b	1.62ab	83.37b	148.15bc	31.55b	22.11d	6307.7c	7710.9c	0.28b	16.66b
4	ICMV155wh	49.06b	2.69bc	1.25c	83.50b	163.38b	31.39b	27.95bc	7176.8b	8984.5b	0.29b	16.58b
5	MCSRC	49.75b	2.87b	1.12d	84.87b	157.117bc	32.51b	30.88a	7418.5b	9429.7ab	0.31ab	16.91b
6	ICMP97774	48.44b	2.69bc	1.25c	84.94b	165.71b	35.10a	31.44a	7907.2ab	9783.5ab	0.29b	16.56b
7	SRCLLC4	48.19b	2.50d	1.37b	84.37b	154.08bc	31.86b	28.32bc	6828.9bc	8744.8b	0.31ab	17.70a
8	SOSATC88	54.19a	2.75b	1.37b	89.31a	191.00a	28.16c	30.08ab	8163.2a	10100.3a	0.28b	15.62b
9	HiTiP89	48.56b	2.94a	1.62ab	84.68b	160.25b	30.97b	23.92cd	8283.5a	9583.6ab	0.23c	17.25a
10	ICMV155	48.93b	2.68c	1.37b	83.81b	154.35bc	32.94b	28.54b	8412.0a	10039.1a	0.25c	16.25c
11	ICMV221(Br)	47.68b	2.50d	1.43b	82.25b	153.42bc	28.66bc	29.39b	6671.9c	8620.9b	0.31ab	16.70b
12	ICMV92901	47.68b	2.93a	1.37b	81.50c	142.33d	27.80c	29.34b	6693.3c	8716.9b	0.30b	15.95d
13	ICMV95490	48.06b	2.81b	1.37b	82.56c	147.00bc	28.88bc	30.60a	6017.5d	8182.2b	0.32a	16.75b
14	ICMV84400wh	48.00b	2.50d	1.37b	83.37b	150.21bc	30.46b	26.20c	7323.8b	8973.3b	0.28b	15.87d
15	ICMV91773	46.56bc	2.56c	1.25c	81.31c	152.89bc	31.98b	24.59cd	6912.8bc	8512.0 b	0.29b	17.29a
16	Kolla-1(check)	45.62c	2.62c	1.25c	81.12c	145.04c	27.75c	27.41c	6095.3d	7611.0c	0.35a	16.29c

Critical Range (334.0, 409.3),

a=highest=medium=poor, d=poorest mean performance, genotype having same letters are same in mean performance for that trait

Genotype by location interaction effects were plotted for each location-genotype combination as shown (Fig 1.and Fig 2.). As indicated at figure 1 below, genotype 1, 4, 6, and 15 had very short genotype by location interaction bars and they contribute little to the genotype by location interaction and are therefore stable. Genotype, 9, 12 and 13 had relatively short interaction bars and they contribute medium to the genotype by locationt interaction than the check and therefore relatively stable than the rest. Genotype, 2, 5, 10 and 16 were highly interacted with Weioto while 3, 7 and 14 were highly interacted with Jnka, Konso and Meiso respectively (Fig1.). Jinka and Meiso had short interaction bars and contribute little to the overall genotype by location interaction and therefore they were discriminated less between the genotypes and the genotype by environment interaction interactio while Konso had relatively medium interaction bars and contributed more to overall genotype by environment interaction and it discriminated more between the genotype by environment interaction than Jinka and Meiso. Weioto had longest interaction bars and contributed high to overall genotype by environment interaction and it was the most discriminated between the genotype by environment interaction (Fig2.). Genotype 5 had long positive bar at Weioto, so it has great probability to provide high yield at this location.

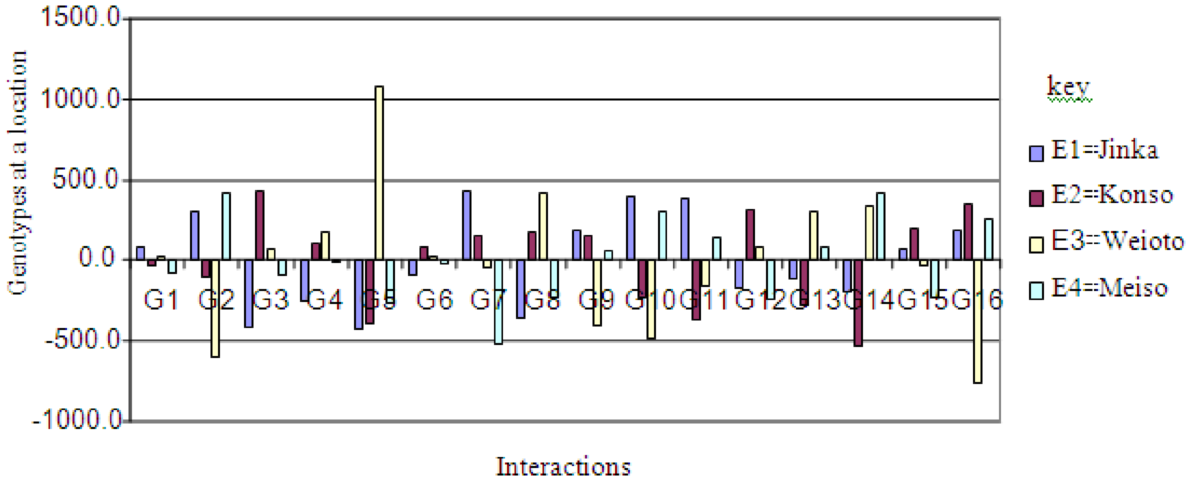


Figure 1. Genotype by environment interaction effects against genotypes at each location

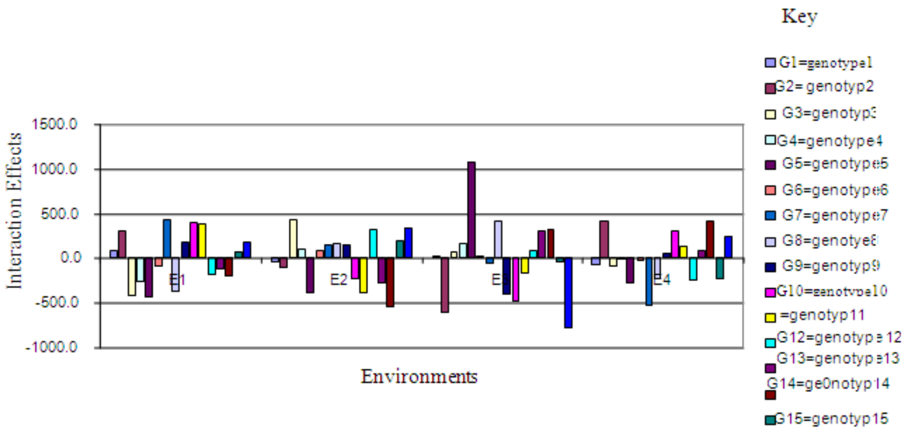


Figure 2. Genotype by environment interaction effects against environments

3.2.3. Proportion of Variance Accounted for G, E and GxL interaction

The result of partitioning of sum squares for grain yield is shown in table 7. The sum of squares due to environment has taken the largest portion (57.61 %) of the total variance. Error portion also shared a large portion (20.16%) of the remaining sum of squares followed by genotype by environment interaction and genotype sum of squares that took 12.86% and 8.15 % respectively. Replication was non-significant in most of the traits examined and that is why it has taken a very small portion (1.2%) of the total sum of squares. The largest portion of the total sum of squares accounted for by environment reveals the significant influence of locations in evaluation of pearl millet genotypes for yield performance in test sites. Also large portion of the total sum of squares taken by error and genotype by environment interaction, which were equal/ more than two-fold of the sum of squares , which shows the vulnerability of grain yield to the influence of this components and the importance of determining genotype by environment interaction effects and stability.

Table 7. Percent contribution of sum of squares of each component to total sums of squares for grain

	Source of variation				
	Enviroment(E)	Genotype(G)	GxE	Rep(E)	Error
DF	3	15	45	12	180
Yield	57.615	8.155	12.86	1.199	20.16

The proportions of different components to total sum squares were also determined for 11 agronomic traits of pearl millet genotypes (Table 8). Variation due to environments, genotypes and their interaction was highly significant (p≤0.01) for most of these agronomic traits. In most of the traits, environment has taken the largest portion of the total sum squares followed by error and genotype by environment interaction. The largest portion of the total sum of squares taken by environment signifies the influence of location in determining difference in agronomic traits among genotypes.

The magnitude of the components of variance gives information about the importance of the different interactions. The estimate of the components of variance for grain yield is given in Table 10. The variance component due to environment was 63.50%, 0% was due to block within environment, 3.43% was due to genotype, 9.24% was due to genotype by environment interaction and 23.82% was due to error term. The large proportion of variance due to environment implies greater influence environment on yield performance in the study area. Also grain performance is sensitive to random variation as variance component due to error shown (23.82). The large proportion of genotype by environment interaction variance component was also observed by Mira et al., (2010) and Asfaw et al.,(2011), in grain yield of finger millet during stability and adaptability analysis. For the majority of multi-environmental trials, environment accounts for the maximum variation (Delacy et al., 1990; Cooper et al., 1996; Haussmann et al. 2001; Zhang et al. 2006; Mohammadi et al., 2009)

Table 8. Estimation of variance components of genotypes and their interactions for grain yield.

Variance component	Yield	% accounted
σ^2E	229253.9	23.82
σ^2_{GxL}	88962.97	9.24
σ^2_{G}	32976.99	3.43
$\sigma^2_{B(L)}$	0	0
σ^2L	610923.14	63.50

3.3. Stability Analysis for Grain Yield

Genotype by environment interaction continues to be challenging issue among plant breeders, geneticists, and agronomist who conduct crop performance trials across different environments. For release of a variety for wider and variable environments, stability of performance had considerable importance for yield trials, especially when significant genotype x environment is detected. Therefore, four different stability parameters with different techniques were used to measure stability of pearl millet genotypes for grain yield as shown below.

3.3.1. Joint Linear Regression

The analysis of variance for the regression model is presented in Table 9. Eberhart and Russell's (1966) analysis of variance revealed highly significant ($p \leq 0.019$) difference between genotypes for yield, implying that considerable differential performance of the genotypes and they are genetically diverse for yield. The genotype by environment (linear) interaction was not significant; it indicated that variation for this trait was not influenced by non-linear component of variation and the stability parameter "b_i" estimated by linear response to change in environment was the same for all genotypes which in agreement with the findings by Abdullah(2009) and Amadou Fofana (1984). However, several finding by different authors (Abdul shakoor., 1999 and Hanif Munawwar., 2007) shows genotype by environment interaction linear was significant for pearl millet. The mean square due to pooled deviation from regression was significant showing that the performances of some of the genotypes were not stable over environments (Table 9).

The genotype performance is expressed in terms of three parameters, mean yield (X□), regression coefficient (bi) and deviation from regression (S^2di). And a stable genotype is the one with high mean yield, bi=1 and $S^2di=0$. However, deviation from regression is specially used as a measure of stability of a genotype across locations. Regression coefficients (bi) and the deviation from regression (S^2_{di}) were calculated for grain yield (Table 10) for the 16 pearl millet genotypes

According to these stability parameters, significant difference were noted for regression coefficients (bi) and deviation from regression (S^2_{di}). The stable genotype with the highest mean grain yield value were ICMP97774 (6), MCSRC (5) and ICMV92901 (12) with rank of 2nd, 3rd and 5th in mean yield respectively. The most stable genotypes with the lowest grain yield were ICMV91450 (1) and ICMV93191 (2). When we consider the mean grain yield (X□), regression coefficient value (bi) and the deviation from the regression S^2_{di}, the most stable genotypes were MCSRC (5) and ICMP97774 (6) with mean yield, X□= 2835.42kg/ha, 2840.17 kg/ha, bi=1.05685, 1.24075; which is not significantly differ from unity and the S^2_{di}=34459.57, -12312.43 which is not deviate from zero. Also genotype ICMV84400white (14) had mean yield above average of check, regression coefficient (bi) not significantly of different from unity and deviation from regression closer to zero; it was more stable relative to others.

Table 9. Eberhart and Russell's analysis of variance for grain yield of 16 pearl millet genotypes tested at each locations in 2011.

Source	DF	SS	MS	F-value	Pr>F
Total	255	40232969.65			
Genotypes(G)	15	4172758.63	278183.91	2.38	0.019*
Env.+ (GxE)	48	36060211.02	32318272.26		
Environment (linear)	1	29477769.57	29477769.57	252.08	
Gen.Env.(linear)	15	2840502.69	189366.85	1.62	0.1
Pooled deviation	32	3741938.76	116935.58	2.04	0.0007**
Residual	192	4172758.63	21733.12		

Grand mean=2532.09 R-squared= 0.89 CV =17.18%

Table 10. Mean grain yield, regression coefficient (bi) and deviation from regression (S^2_{di}) for the 16 pearl millet genotypes tested at four locations.

Entry	Name	Beta(bi)	Deviation(S^2_{di})	R	Mean gain yield(x□)	R
1	ICMV91450	0.94526	-51699.83	1	2056.60	16
2	ICMV93191	0.73219	-15069.90	5	2223.97	13
3	ICMV155Br	0.64934	100294.71*	7	2088.89	15
4	ICMV155white	0.77812	63556.64	10	2542.70	9
5	MCSRC	1.05685	34459.57	8	2835.42	3
6	ICMP97774	1.24075	-12312.43	6	2840.17	2
7	SRCLLC4	1.38147	117014.24*	12	2674.65	7
8	SOSATC88	1.32136	39269.42	16	2844.10	1
9	HiTiP89	0.59086	194231.67*	14	2220.49	14
10	ICMV155	0.66711	160493.94**	13	2561.81	8
11	ICMV221(Br)	1.21219	85722.13	11	2690.28	6
12	ICMV92901	1.20404	-44927.18	3	2692.35	5
13	ICMV95490	1.67748	304067.02**	15	2725.00	4
14	ICMV84400white	1.04183	-50587.60	2	2463.20	10
15	ICMV91773	0.61857	50792.87	9	2367.36	12
16	Kolla-1(check)	0.8826	-21351.90	4	2450.00	11

Grand mean=2532.09, R= Rank

3.3.2. Wricke's Ecovalence

Wricke's ecovalene was estimated for the 16 pearl millet genotypes for their grain yield across the four locations (Table 11). Accordingly, ICMV84400white (14) was the most stable genotype for grain yield but it ranked 10th in its mean yield, followed by ICMV91450 (1) and ICMV92901 (12) they ranked 16th and 5th respectively for their mean grain yield. The most unstable genotypes according to Wricke's Ecovalene were ICMV155Br (3), SRCLLC4 (7), HiTiP89 (9), ICMV155 (10), ICMV95490 (13) and ICMV91773(15) with mean yield ranking of 15th , 7th , 8th, 14th ,4th, and 12th, respectively. Relatively the high yielding genotypes MCSRC (5) and ICMP97774 (6) were found stable for grain yield and ranked 5th and 6th respectively in Wricke's ecovalence, therefore can be recommended for wide adaptation. The highest yielding genotype SOSATC88 (16) was found unstable and ranked 10th in its stability.

Table 11. Wricke's ecovalence value of grain yield for 16 pearl millet genotypes tested at four locations in 2011.

Entery	Name	Wricke's ecovalence	R^{Wi}	Mean gain yield	R^y
1	ICMV91450	16748.89	2	2056.60	16
2	ICMV93191	216622.66	7	2223.97	13
3	ICMV155Br	541754.73*	12	2088.89	15
4	ICMV155wh	332439.84	8	2542.70	9
5	MCSRC	189500.10	5	2835.42	3
6	ICMP97774	196787.67	6	2840.17	2
7	SRCLLC4	616753.15*	13	2674.65	7
8	SOSATC88	383435.74	10	2844.10	1
9	HiTiP89	811497.75**	15	2220.49	14
10	ICMV155	639772.96*	14	2561.81	8
11	ICMV221(Br)	369026.32	9	2690.28	6
12	ICMV92901	101474.81	4	2692.35	5
13	ICMV95490	1568367.69***	16	2725.00	4
14	ICMV84400wh	16674.80	1	2463.20	10
15	ICMV91773	484257.40*	11	2367.36	12
16	Kolla-1(check)	97326.95	3	2450.00	11

*, **, ***=significantly unstable at P<=0.05, 0.01 and p<=0.001probability level respectively; R^{Wi} =rank by Wricke's ecovalence, R^y=rank by grain yield

3.3.3. Shukla's Stability Variance ($\sigma^2 i$)

Shukla's(1972) stability variance values and the stability ranking as well as the mean yield with its ranking are given in table 12. The most stable genotypes for grain yield according to this stability variance were ICMV84400white (14), ICMV91450 (1), ICMV92901 (12) and MCSRC (5). According to this parameter genotypes with poor stability were ICMV95490 (13), HiTiP89 (9), ICMV155 (10), and ICMV155Br (3). The high yielding genotypes ICMP97774 (6) and MCSRC (5) have low contribution to genotype by location interaction so they were relatively more stable than others. Accordingly genotypes stable with above mean of the standard check and grand mean such as ICMV92901 (12), MCSRC (5), ICMP97774 (6) were widely adapted and high yielding genotype SOSATC88 (8) was less stable was specifically adapted.

Table 12. Shukla's stability variance for 16 genotypes tested at four locations.

	Genotype	σ 2 i	Rank	Mean	Rank
1	ICMV91450	-4067.79	2	2056.60	16
2	ICMV93191	72074.60	7	2223.97	13
3	ICMV155Br	195934.43*	12	2088.89	15
4	ICMV155white	116195.43	8	2542.70	9
5	MCSRC	61742.19	5	2835.42	3
6	ICMP97774	64518.41	6	2840.17	2
7	SRCLLC4	224505.26*	13	2674.65	7
8	SOSATC88	135622.44	10	2844.10	1
9	HiTiP89	298693.68**	15	2220.49	14
10	ICMV155	233274.71*	14	2561.81	8
11	ICMV221(Br)	130133.14	9	2690.28	6
12	ICMV92901	28208.75	4	2692.35	5
13	ICMV95490	587025.09***	16	2725.00	4
14	ICMV84400white	-4096.01	1	2463.20	10
15	ICMV91773	174030.69*	11	2367.36	12
16	Kolla-1(check)	26628.61	3	2450.00	11

3.3.4. Additive Main Effects and Multiplicative Interaction

Results from AMMI analysis (Table 13) showed that the first and second interaction principal component axis (IPCA 1 and IPCA 2), were significant and explained 62.8 % and 25.9% of the total genotype by environment interaction sum of squares using 17 and 15 degree of freedom respectively (Table 16). This showed that the two IPCAs accounted for 88.7% of the genotype by environment interaction.

Distribution of genotype points in the AMMI biplot at figure 3 revealed that the genotypes, ICMV84400white (14), and ICMV92901 (12) were scattered close to the origin, indicating minimal interaction of these genotypes with locations. Genotypes ICMV93191 (2), ICMV155white (4), MCSRC (5), ICMP97774 (6), ICMV92901 (12), and ICMV91773 (15) were relatively closer to origin; they had intermediate interaction with environments. The remaining 7 genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental interactive forces. Interaction of genotypes with specific environmental conditions was judged by projection of genotype points on to environment spokes. Accordingly, SOSATC88 (8) and ICMV91773 (15) had high interaction with Konso (B), genotype ICMV155 (10) had high interaction with Jinka (A)), while genotype ICMV155white (4), and ICMV95490 (13) had high interaction with Mieso (D)and Weioto(C) respectively.

The polygon view of the GGE biplot (Figure 4) indicates the best genotype(s) in each environment and groups of environments (Hunt, 2002). The highest yielding genotype in location Jinka (A) was ICMV155white (4), in Konso(B) the highest yielding genotypes were MCSRC (5) and ICMV221(Br)(11), in Weioto (C) the highest yielding genotype was ICMV95490 (13), and in Meiso (D) the highest yielding genotype were ICMP97774 (6) and SRCLLC4 (7) respectively. The vertex genotypes ICMV155Br (3) and HiTiP89 (9) were poorest across all environments.

High variability among environments on the interaction effects for grain yield was observed in the figure 4. High correlation between Jinka and Meiso was observed because they have small angle relative to others and therefore they were discriminated genotypes in similar way. Environments Weioto (C) and Konso (B) have large angle between them at origin implies great variation among them discriminated between the genotypes in different way. With respect to the test sites, Weioto(C) was the most discriminating between the genotype by environment interaction as indicated by the longest distance between its marker and the origin, Konso(B) was the next most discriminating as shown at figure 3. Jinka(A) and Meiso (4) were poorly discriminated between the genotype. This result is coincident with the geographic pattern which belongs to different environment type. Similarity between Jinka(A) and Meiso(D) in discriminating between the genotype by environment interaction was observed, this mainly due to their similarity in elevation and mean annual temperature as shown in table 1.

GGE biplot of 16 pearl millet genotypes for grain yield across four locations was shown in figure 4.The line which passes through the origin and is perpendicular to the average environment axis with arrows represents the stability of genotypes. Either direction away from the biplot origin, on this axis, indicates greater genotype by environment interaction and reduced stability (Yan, 2002). Accordingly genotypes ICMV155Br (3), ICMV155white (4), SRCLLC4 (7), HiTiP89 (9), ICMV221 (Br)(11) and ICMV95490 (13) had great genotype by environment interaction and therefore they had very low stability across environments. Genotypes ICMV92901 (12) and ICMV84400white (14) are closer to the origin, so they had little genotype by environment interaction and they are stable across locations (figure 4).

Genotype ICMV84400white (14) was stable with low yield so it could not recommendable for wide verification while ICMV92901 (12) was stable with high yield so it could be recommendable for verification trial. Genotype 6 had also high mean yield and relatively closer to average environment axis so it could be recommendable for yield and verification trail. On the other hand, for specific selection, the ideal genotypes are that have high mean yield but low stability and respond best to particular environments. Therefore, for Weioto the ideal genotype was ICMV95490 (13), while for Meiso genotypes ICMP97774 (6) and SRCLLC4 (7) were ideal. For these two environments the worst genotypes were ICMV155Br (3) and HiTiP89 (9)

Table 13.The analysis of variance table for AMMI of grain yield for the 16 pearl millet genotypes tested at four locations

Source of variation	DF	SS	MS	% of total Explained	% of G×E Interaction SS
Total	255	204651881.2			
Environments	3	117910864.4	39303621.5**	57.61	
RepswithinEnv.	12	2454486.4	204540.5^{NS}	1.2	
Genotype	15	16691064.9	1112737.7**	8.15	
Genotype xEnv.	45	26329759.8	585105.8**	12.86	
IPCA 1	17	4135554.75	243267.92**	2.57	62.8
IPCA2	15	1703655.90	113577.06*	1.04	25.9
IPCA3	13	743230.80	57171.6	0.004	11.3
IPCA4	11	0.00			
Residual	180	61013024.05	338961.24		

***,NS =significant and non-significant at P≤0.01 level, respectively.
Grand mean=2532.09 R-squared= 0.79 CV= 22.99%

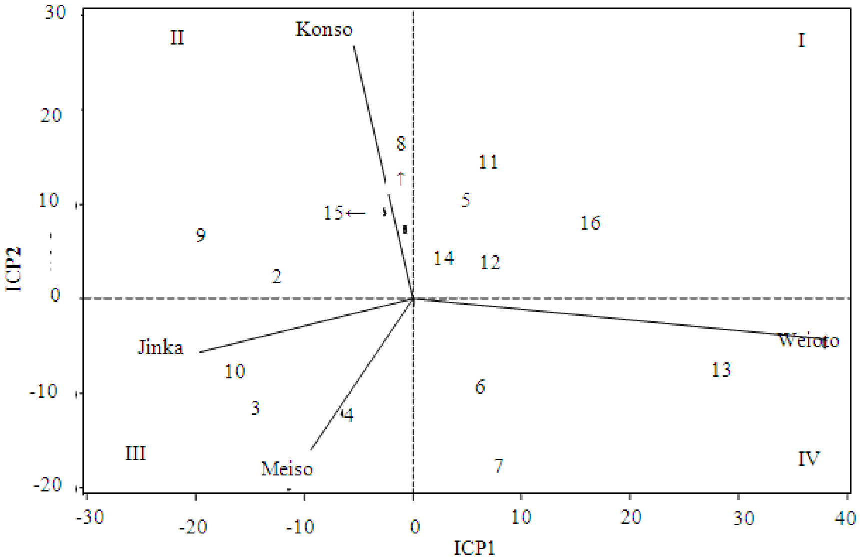


Figure 3. Biplot for PCA 1 vs. PCA 2 scores (AMMI biplot) obtained from yield data of 16 pearl millet genotypes. The 4 locations are indicated as vectors drawn from origin. Genotypes are denoted by numbers.

Weioto

-10

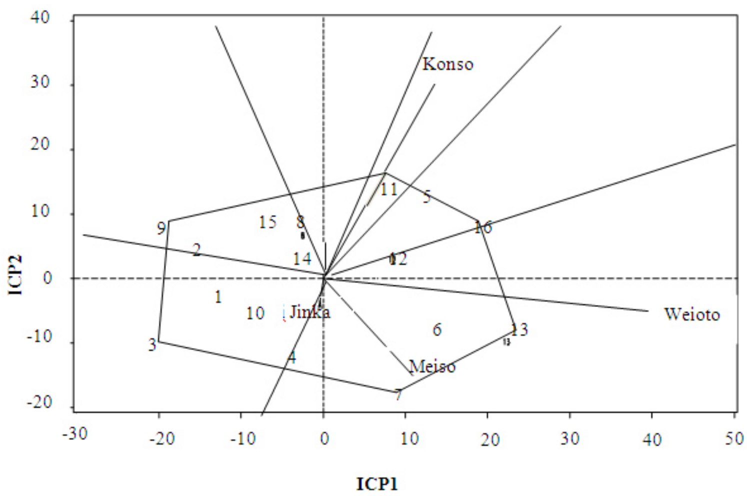


Figure 4. GGE biplot of 16 pearl millet genotypes for grain yield across four locations.
The 4 environments are indicated as vectors drawn from origin. Genotypes are denoted by numbers.

Environments Weioto and Mieso gave above average mean grain yield, while environments Konso and Jinka gave below average (Table 14). Also Weioto and Konso have large EIPCA1 and EIPC2 scores; they had high interactions with genotypes, so the genotypic differences observed at these locations may not exactly reflect the genotypes in average yield over all sites. Jinka and Meiso have relatively small EIPC1 and EIPC 2 so they had weak interaction with genotypes.

Table14. Environment mean of grain yield of four locations for the 16 pearl millet genotypes

Enviroments	Graph ID	EIPC1	EIPC2	Yield
Jinka	A	-20.6435**	-5.9232**	1491.23
Konso	B	-6.0107*	29.6043*	2373.27
Weioto	C	37.9858	-4.3124	3307.52
Mieso	D	-11.3316	-19.3687	2897.22

*=Significant, **= highly significant

3.3.5 AMMI Stability Value (ASV)

ASV and AMMI model IPCA1 and IPCA2 scores of grain yield are shown in table 15. According to this parameter, ICMV91450 (1), ICMV84400white (14), and ICMV91773 (15) were found stable for their grain yield with mean grain yield rank of 16th, 10th and 12th respectively. The best high yielding genotypes MCSRC (5), ICMP97774 (6), ICMV221 (Br) (11) and ICMV92901 (12) were also found stable. The highest yielding genotype SOSATC88 (8) was ranked 12th in stability according to ASV. The three most unstable genotypes grain yield were ICMV95490 (13), HiTiP89 (9) and ICMV155 (10). Genotype ICMV91450 (1) and ICMV84400white (14) had little IPCA1 implies they had no interaction with locations, i.e. were stable. While genotype ICMV93191 (2), ICMV155Br (3), ICMV155white, HiTiP89 (9) and ICMV155 (10) had large IPCA1 implies they had large interaction i.e. were less stable. Genotype MCSRC (5), ICMP97774 (6) and ICMV92901 (12) have relatively small IPCA1 implies they had small interaction with locations i.e. they were relatively stable.

Table15. AMMI stability value (ASV) ranking with the IPCA1 and 2 scores of yield for the 16 genotypes tested at four locations.

Entry	name	IPCA1	IPCA2	ASV	R^a	Yield	R^y
1	ICMV91450	-0.0716	-0.0830	0.1927	1	2056.60	16
2	ICMV93191	10.0086	3.1162	24.4945	10	2223.97	10
3	ICMV155Br	14.2298	-9.8062	35.9073	13	2088.89	15
4	ICMV155white	6.5013	-11.8459	19.7328	9	2542.70	9
5	MCSRC	-3.7476	11.0717	14.3298	6	2835.42	3
6	ICMP97774	-7.3275	-8.1623	19.5707	8	2840.17	2
7	SRCLLC4	-7.5510	-18.6558	26.1537	11	2674.65	7
8	SOSATC88	-12.2377	7.3591	30.6045	12	2844.10	1
9	HiTiP89	18.6659	6.0194	45.7088	15	2220.49	14
10	ICMV155	16.3690	-7.8401	40.5011	14	2561.81	8
11	ICMV221(Br)	-4.9363	12.6825	17.4479	7	2690.28	6
12	ICMV92901	-5.4119	2.8775	13.4486	5	2692.35	5
13	ICMV95490	-27.1006	-6.6566	66.1216	16	2725.00	4
14	ICMV84400white	-0.9584	2.7724	3.6193	2	2463.20	10
15	ICMV91773	2.8825	9.5075	11.8049	4	2367.36	12
16	Kolla-1(check)	-12.2377	7.6434	7.8225	3	2450.00	11

R^a =Rank by ASV, R^y =Rank by grain yield

3.3.6 Correlation between Traits

Simple Pearson's product moment correlation coefficients were calculated among ten characters to see if there was any interrelationship between any two traits. The results are indicated in Table 16. Grain yield was positively and significantly correlated with number of tillers per plant(r=0.396*, p<0.01), plant height (r=0.572*, p<0.001), grain weight per head(r=0.969*, P<0.001), biomass yield (r=0.745*, P<0.001), harvest index (r=0.365*, P<0.001), and thousand seed weight (r =0.319*, P<0.001). There was a negative and significant correlation of grain yield with days to flowering (r = -0.229*, P<0.001) and days to maturity (r = -0.429* .p<0.001). The correlation of grain with other traits was not significant.

The significant correlation of grain with Ntill, DTM, PH, GWH, Stlkwt, BM, GY, HI,and TSW; indicates they can be used for direct selection to identify genotypes with high grain yield. Therefore, any improvement of these characters would result in a substantial increment on grain yield of finger millet. And negative correlation between grain yield and DTF and DTM implies these traits can be selected independently.

Table 16. Correlation of grain and other traits of 16 pearl millet genotypes tested at four locations.

DTF	Ntill	Prtill	DTM	PH	Pl	GWH		Stlkwt	BM	GY	HI	TSW
DTF	-0.067	0.180*	0.795*	0.249*	-0.672*	-0.215*	-	-0.263*	-0.275*	-0.229*	0.047	0.495*
Ntill	0.346*		0.228*	0.390*	-0.127*	0.40*		0.360*	0.090	0.396*	0.405*	0.048
Ptill			0.046	0.237*	-0.334			0.195*	0.182*	0.051	-0.132*	0.095
DTM			0.066					-0.405*	-0.429*	-0.429*	- 0.02	-0.507*
PH				-0.023	-0.392*	-0.428*		0.582*	0.631*	0.572*	-0.028*	0.283*
Pl					-0.411*	0.601*		0.024	0.212*	0.022	-0.012	0.212*
GWH						-0.028*		0.596*	0.757*	0.969*		0.314*
Stlkwt								0.328*				
BM									0.962*	0.570*	-0.426*	0.390*
GY										0.745*	-0.277*	0.404*
HI											0.365*	0.319*
TSW												-0.075

DTF=Days to flowering; Ntill= Number of tillers; Ptill=productive tillers; DTM= days to maturity; PH=plant height (cm); Pl=panicle length (cm); GWH= grain weight per head (g); stlkwt= stalk weight (g); BM= biomass yield (g); HI= harvest index;TSW=thousand seed weight(g)

4. Summary and Conclusion

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is an important cereal of traditional farming system in hot and semi-arid tropical areas of the Indian sub-continent and Africa. The major production constrains of these regions include highly variable and unpredictable drought, low soil fertility and poor stand establishment as pearl millet is grown as a rain fed crop on marginal lands without the application of fertilizer. Pearl millet is adapted well to growing areas characterized by drought and high temperature, performs well in soils with high salinity or low pH. In Ethiopia there are no other alternative crops except early maturing sorghum varieties in most drought prone areas. Even though pearl millet is new in both production and utilization; the crop can be importantly used as substitute in poor rainfall distribution areas of Ethiopia. Under these circumstances genotypes with a stable performance across changing environments, even with modest yield, are considered more relevant than high yielding cultivars with inconsistent performance across unpredictable crop seasons in order to provide food security in fragile environments. Presence of significant genotype by environment interaction due to the differential response of genotypes in different environments represents a major challenge to plant breeders and hence stability analysis is very important under such conditions to obtain information on yield performance and stability over variable environments.

Sixteen pearl millet genotypes (out of which one was released and fifteen were elite genotypes under national variety trial) were evaluated at four locations in randomized complete block design with three replications during 2011 cropping season. The experiment was carried out to identify high yielding widely adapted (stable) and specifically adapted (narrow adaptation) pearl millet genotypes and study the nature and magnitude of genotype by environment interaction for yield and yield attributing traits.

Significant differences between genotypes were observed at all locations for days to flowering and grain yield (kg/ha); at three locations for days to emergence, productive tillers per plant, days to maturity, biomass yield and grain weight per head; at two locations for plant height, panicle length, stalk weight and harvest index; at one location for thousand seed weight and non-significant for total number of tillers per plant.

The mean grain yields at individual locations ranged from 1122.2 kg/ha for ICMV91450 (16) at Jinka to 4594.4 kg/ha for ICMV95490 (13) at Weioto. Jinka was lowest yielding (1491.22 kg/ha) environment while Weioto was the highest yielding (3307.52 kg/ha) environment. Based on mean grain yield, genotypes ICMV155white (4), MCSRC (5), ICMV95490 (13) and SRCLLC4 (7) gave highest yield at Jinka, Konso, and Weioto, respectively (Table 4).

Combined ANOVA showed significant variation among locations for all traits. Significant variations among genotypes were also observed for all traits except for days to emergence. The significant difference among environments implies that they have great variation in soil, rainfall, temperature and elevation above sea level as shown in Table 1 and therefore, environments played a significant role in the expression of traits being significant. Genotype also responded differently and had great genetic variation for traits such as days to flowering and maturity and grain yield.

Partitioning of the variance components indicated that 57.6% was due to environmental, 8.2% due to genotype, 12.9% due to genotype by environment interaction, 1.2% due to replication and 20.2 % due to experimental error. The large proportion of variance was due to environments and the high GEI contributions to the total sums of squares as compared to the genotypes denotes the significant influence of environment on genotypes for yield performance in southern and western part of Ethiopia.

Genotype by environment interaction was statistically significant for days to flowering, productive tillers per plant, days to maturity, plant height, panicle length, grain yield per head and grain yield (kg/ha). The significance of genotype by environment interaction for these traits indicates the differential response of genotypes across locations and that genotype by environment interaction is very influential component of variation in pearl millet; care should be taken when selecting genotype for these traits and the need to assess the stability of genotypes across locations. As shown in figures 1 and 2 the type of interaction was cross over type because the performance of genotypes across location was inconsistent. High yielder genotype at Weioto was not high yielder at Konso (Table 4).

Among the test locations Weioto was found to be the most suitable environment for grain yield and gave highest overall mean grain yield 3307.52 kg/ha. It was also found best for most yield related traits such as number of tillers per plant, panicle length, grain weight per head, stalk weight and biomass yield and for days to flowering and maturity. Konso and Meiso showed better performance of test genotypes in grain yield and yield attributed traits. The highest mean grain yield was obtained from genotype ICMV95490 (2925 kg/ha) and the lowest mean grain yield was obtained from ICMV155Br (2026.39kg/ha).The poorest location for the performance of genotypes was Jinka for yield and yield attributed traits.

Five stability parameters were used to identify genotypes for wide adaptation. The GGE biplot was used to identify genotypes with narrow adaptation. For identification of best high yielding and stable genotypes across locations, the top ten high yielding as well as stable genotypes were used for each stability procedures. Among the top yielding genotypes for grain yield across locations, genotypes ICMV84400white (14), ICMV92901 (12), MCSRC (5) and ICMP97774 (6) exhibited general stability according to regression coefficient(β_i), deviations from regression ($_{ij}$), Wricke's Ecovalene (Wi), Shukla's Stability Variance (σ^2i), AMMI model and AMMI stability value /ASV/ stability parameters and bipolt techniques. So they can be included in verification trials to be released for wider adaptation. The result of GGE biplot also indicated that genotype ICMV155white (4) was specifically adapted to Jinka while genotype ICMV221 (Br) (11) was specifically adapted to Konso, genotype SRCLLC4 (7) was specifically adapted to Meiso and genotype ICMV95490 (13) was narrowly adapted Weioto. Therefore, the national breeding program should also focus on recommending genotypes for specific environments besides recommending widely adapted genotypes.

Grain yield was positively and significantly correlated with number of tillers (r=0.396*), plant height (r=0.572*), grain weight per head (r=0.969*), stalk weight (0.57*), biomass (r=0.74*), thousand seed weight (0.36) and harvest index (0.32). It showed negative and significant correlation with days to flower and maturity. The correlation with productive tiller per plant and panicle length was positive and non-significant.

The strong and positive correlation between grain yield and plant height, grain per head, saltk wieght and biomass provides opportunity to improve grain yield with these traits simultaneously. On the other hand, those traits (productive tiller per plant and panicle length) that did not show significant correlation with grain yield indicate that selection for increased levels of these traits may not bring significant change in grain yield.

In general, three stable (wide adapted) and high yielding genotypes (ICMP97774 (6), MCSRC (5), ICMV92901 (12)) and two widely adapted genotypes but with low yield (ICMV91450 (1) and ICMV93191 (2)) as compared average yield and check (Kolla-1) were identified. The remaining genotypes showed inconsistent performance across location in this study. The stable high yielding genotype can be used for further yield and verification trial with standard check for release but with great care because the magnitude of genotype environment interaction was significant for yield and yield attributed traits.

5. References

Abdullah, J.D., S Ghuam.,Q.Al. Adel. 2009. Stability of pearl millet genotypes under irrigation with different salinity levels, European Journal of Scientific Research.

Abdul,S.,Muhammad,N. and M. Hanif.1999. Evaluation of pearl millet genotypes for stability and yield performance. National Agricultural research center, Islamabad park Road Pakistan, Pp.1401.

Aebebe mankir, kebede and B. Gebrekidan .1984.Genotype by enviroment interaction and yield stability in sorghum of intermediate maturity. Ethiopian journal of Agricultural sciences:1-11

Acquaah, George.2007.Principles of plant genetics and breeding. Blackwell. United Kingdom.

Ahmad J., M. Chaudhary, S. Salah-ud-Din and M.A. Ali. 1996. Stability for grain yield in wheat. Pakistan. J. Bot. 28: 61-65.

Allard,R.W and A.D. Bradshaw, 1964. Implications of genotype-environment interactions. Crop Science, 4:503-507.

Amadou,F. 1984. Genotype by environment interaction and stability of grain yield and some other characteristics in pearl millet Lincoln.M.S.C. Thesise presented to the school of graduate studies of Nebraska university. studies of Nebraska university, Vol.2.

Asfaw,D.,Tessfaye,T.,Erenso.D, Taye,T., Feyera,M., Wasihun,L., Alemu,T., H/selassie,K., Andualem,W., Chemeda,D. 2011.Genotype by environment interaction and yield stability analysis in finger millet(*Eleusine corancana*) in Ethiopia, American Journal of Plant Sciences,Pp.412-414.

Becker,H.C.1981. Correlation among some stastical measures of phenotypic stability. Euphytica 30:835-840.

Becker,H.C and J.Leon, 1988. Stability analysis in plant breeding: plant breeding, 101:1-23.

Benti,Tolessa, Gezahen Bogale and Assefa Afeta.1996.Genotype by environment interaction and yield stability of maize cultivar. Ethiopian journal of Agricultural Sciences: 15:1-7.

Bridge WC Jr. 1989. Analysis of plant breeding experiment with heterogeneous variance using mixed model equation. *In:* Applications of Mixed Models in Agriculture and Related Dicipline. So. Coop. Ser. Bull. No. 343. Baton Rouge, LA: Lousiana Agricultural Experiment Station: 145–151.

Burton, G.W. 1983. Breeding pearl millet. Plant Breed. Rev. 1:162–182.

Cannon, W.B. 1932. The wisdom of the body. Norton, New York.pp.164-172.

Cooper M, Brennan PS, Sheppard JA (1996) A strategy for yield improvement of wheat which accommodates largegenotype-by-environment interactions. In: Plant Adaptation and Crop Improvement (Eds. M Cooper, GL Hammer).CAB International, Wallingford, UK, Pp. 487

Cross,J., 1990. Statistical analysis of multilocation trials. Advance in agronomy, 44:55-85.

Crossa, J., H. G. Gauch and R. W. Zobel, 1990. “Additive Main Effects and Multiplicative Interaction Analysis of Two International Maize Cultivar Trials,” *Crop Science*, Vol. 30, No. 3, Pp. 493-500.

Comstock R.F.,R.H.,Mof.,1963. Genotype by environment interaction,In:Statistical genetics and plant breeding,Nat.Acad.Sci.Res. Council.Pp.164-196.

Chaturvedi, A. and G. Sarojini, 1996. Malting of pearl millet (Penniseturn typhoidium). Its effects. on starch and protein digestibilities. J. Food Sci. Tech. 33 (4): 343-344.

Davis, A.J., N.M. Dale, and F.J. Ferreira. 2003. Pearl millet as an alternative feed ingredient in broiler diets. J. Appl. Poult. Res. 12:137–144.

Das,S., R.C. Misra and M. C. Patnaik,2009.AMMI Model analysis of stability and adaptability of late duration finger millet (*Eleusine corancana*) genotypes,Department of plant breeding and genetics, College of Agriculture, Orissa university of Agriculture and Technology,Bhubaneswar-751003,Orissa,India

DeLacy IH, Eisemann RL, Cooper M (1990) Th e importance of genotype-by-environment interaction in regional variety trials. In: Genotype-by-Environment Interaction and Plant Breeding (Ed. MS Kang). Louisiana StateUniversity, Baton Rouge, Louisiana, USA, Pp. 287-300.

Dinesh kumar, S. P., 1986, Variation for protein content, its stability and association with yield and. other characters in white and brown finger millet (*Eleusine coracana* Gaertn.). *M. Sc. (Agri.) Thesis,* University of Agricultural Sciences, Bangalore.

Dudley, J.W. and R.H. Moll, 1969. Interpretation and use of estimates of heritability and genetic variances in plant breeding. Crop Science 9:257-262.

Eagles,H.A.,P.N.Hisz.,K.J.prfy.1977.selecation of superior cultivars of oats (Avena Sativa L.) by. using regression coefficients, crop sci.17:101-105

Eberhart, S.A. and W.A. Russel.1966.Stability parameters for comparing varieties.Crop science 6:36-40.

FAO (Food and Agriculture Organization of the United Nations). 2000. Bulletin of statistics. Vol. 1, FAO, Rome. Pp. 16–36.

Finlay,w., andG.N.Wilkinson.1963.The analysis of adaptation in a plant breeding program,Aust.J.Aric.Res.14:742-754.

Gauch, G.H. and R.W.Zobel, 1996. AMMI of yield trials.In: Genotype by environment interaction. Kang, M.S. and Gauch, H.G. (Eds), 85-122pp.Boca Raton: New York, USA, CRC.

Gomez,K.A. and A.A. Gomez. 1984. Statistical procedures for agricultural research,2nd edition.New york :Wiley.

Gupta SC, Ndoye AT (1991). Yield stability analysis of promising pearl millet genotypes in Senegal. Maydica. 36:83-86.

Gulia, S.K., C.T. Hash, R.P. Thakur, W.A. Breese, and R.S. Sangwan. 2007. Mapping new QTLs for downy mildew [*Sclerospora graminicola* (Sacc.) J. Schroet.] resistance in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. p. 373–386. In: D.P. Singh, V.S. Tomar, R.K. Behl, S.D. Upadhyaya, N.S. Bhale, and D. Khare (eds.), Crop production in stress environments: Genetic and management options. Agrobios Publ., Jodhpur, India.

Hussien, Mohammed Ali., Asmund Bjornstand, A.H. Aastveit, and Trygve Berg.2000. SASGxESTAB-A SAS program for computing genotype by environment stability statistics. Awassa, Ethiopia.84p.

Hill, J., C.Becker andP.M.Tigersted.1998.Quantitative and ecological aspects of Plant breeding. Chapman and hall.

IFAD. 1999. Farmer participatory testing of technologies to increase sorghum and pearl millet production in the Sahel. www.ifad.org/grants.

Jinka Agricutural Research Center .2009. Demonsteration of pearl millet, Crop science; Unpublished.

Kempton, R.A.1984. The use of biplots in interpreting variety by variety interactions.J, of Agric.Sci.103:123-135.

Kenga, R.S. Alabi and S.C. Gupta, 2003. Yield stability of sorghum hybrids and parental lines. Aferican crop science Journal, 11 (2):65-73.

Khairwal, I.S., K.N., Rai, D.J. Andrews, and G. Harinarayana, (Eds), 1999. Pearl Millet Breeding Sci. Publishers Inc. USA.

Kumar, P., Kapoor, R. L., Chandra, S. And Das, S., 1982, Stability and its genetic basis with regard to grain size in pearl millet. *Haryana Agricultural University Journal of Research*, 12(1) : 107-111.

Kumar, K.A. 1989. Pearl millet: Current status and future potential. Outlook on Agriculture 18:46–53.

Lerner, I.M.1954.Genetic homeostasis. Oliver and Boyd,London.

Lewonting R.C.1957.The adaptation of populations to varying environments. Cold spring Harb.Symp.Quant.Biol.22:395-408.

Liang, G.H.L., and T.L. Walter. 1966. Estimates of variety x environment interactions in yield tests of three small grains and their significance in the breeding programs. Crop Sci. 6: 135-139.

Lin, C.S.,MR.Binns, and L.P.Leffkovitch,1986. Stability analysis :where do we stand? Cro sci.26:894-900.

Lin,C.S. and Binns,,M.R. 1988. A method for analyzing cultivar-location-year experiments: a new Stability parameter. Theoretical and Applied Genetics,76,425-30.

Luthra,O.P. and R.K.Singh.1974.Acompersion of different stability models in wheat. Theor.Appl.Genet. 45:143-149.

National Research Council. 1996. Lost crops of Africa. Volume I : Grains. National Academy Press. Washington DC.

Mahgoub, E.O. Salah and S.A. Elhag. 1998. Effect of milling, soaking, malting, heat treatment and fermentation on phytate level of flour Sudanese sorghum cultivars. Food Chem. 61 (1): 77-80.

Mailana, K.N., R. Millikarjunaradhya, M.V. Channabyze Gowda, and R.V. Shanker. 1982. Phenotypic stability for yield in finger millet.Ind. J. Agric. Sci. 52: 151-153.

Manawwar,H.M.,Javed,F.Javed,H.I.,Malik N.H., and Hussain,M.2008. stability of millet varieties across diverse environments in pakistain. Sarhad J. Agric. Vol. 23, No. 3, 2007.

Manga, V. K., 2001, Phenotypic stability for grain yield in open pollinated varieties of pearl millet genotypes. *Indian Journal of Agricultural Sciences*, 71(11) : 719-720.

Ministry of Agriculture and Rural Development (MoARD), Crop Development Department. 2007. Crop Variety Register. Issue No 10. Addis Ababa, Ethiopia.

Mohammadi R, Amri A, Haghparast R, Sadeghzadeh D, Armion MM, Ahmadi M (2009) Pattern analysis of genotype-by-environment interaction for grain yield in durum wheat. J Agric Sci 147:537-545.

Petersen, R.R., 1994.Agricultural field experiments: Design and analysis. marcel Dekker, New York.

Pethani K.V., Kapoor.1985. Phenotypic stability in pearl millet, Indian journal.Genet.45:362-367.

Purchase, J.L.,1997. Parametric analysis to describe GxE interaction and yield stability in winter wheat .PhD dissertation.Derpartment of Agronomy, Faculty of Agriculture, university of the free state, Bloemfonten, South Aferica.

Ram, C., H. Singh, D.S. Jatasra, and D.V.S. Panwar. 1978. Stability analysis for grain yield in rice. Cereal Research Communications 6: 275-283.

SAS Institute.2004.SAS/STAT Guide for Personal Com[uters,Version 9.0 Edition.Cary,NC: SAS Institute Inc.

Shukal, G.K.,1972. Some statistical aspects of partitioning genotype-environmental components of variability. Heredity,29:237-245.

Shakoor, A, M. Naeem and H. Munawwar.1999. Evaluation of different pearl millet genotypes for stability and yield performance. Pak. J. Biol. Sci. 2(4):1401-1404.

Singh S.,P.K. Gupta,1978.Phenotypic stability in pearl millet, Indian journal.Genet.38:440-450.

Suryavanshi, Y. B., Ugale, S. D. and Patil, R. B., 1991, Phenotypic stability of yield and yield components in pearl millet. Journal of Maharashtra Agricultural Universities, 16(2) : 218-222.

The Syngenta Foundation for Sustainable Agriculture.2002.Millet: pearl Millet. http://syngentafoundation.org/what is pearl millet.htm.

Virk, D.S, N.B. Singh, M. Srivasta and G. Harinaryana 1984. Regression analysis for general adaptation in pearl Millet using different environmental indices. Theoret.Applied Genet. 68 (6): 509-513.

Virk, D.s., S.S.Chahai., H.S.Poont,1985 repeatability of stability estimators for down mildew incidence in pearl millet.Theor.Appl.Genet.70:102-106.

Wrike, G., 19 62. Uber eine Methode Zur Erfussung der okologischen streubreite in Feldversuchen.Z.*Planzenzuecht*.47:92-96.

Witcombe J.R.,1988. Estimates of stability for comparing varieties,*Euphytica* 39:11-18.

Yadav, O.P. 1996. Pearl millet breeding: achievements and challenges, Plant Breed. Abst.,66:157-163.

Yan W.,L.A. Hint,Q.sheng and Z.szlavnics,2000.Cultivar evaluation and Mega-environment investigation based on the GGE biplot .crop science,40:597-605.

Yan, W., and Racjan, I. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. *Crop Sci.Vol.* 42 .Pp.11-20.

Yan, W. and L.A. Hunt.2002.Biplot Analysis of multi-environment trial data. In: kang, M.S.(ed) Quantitative Genetics, Genomics and Plant breeding. CAB International.Pp.289-303.

Yan, W., M.S.Kang,B.Ma,S. Woods and P.L. Cornelius.2007.GGE biplot vs. AMMI analysis of genotype-by-environment data.crop seci.Vol.47,Pp.643-653.

Ykbyahaya,Y., C.A. Echekwu and S.G. Mohammed .2005. Yield stability analysis of pearl millet hybrids in Nigeria.African Journal of Biotechnology. Pp.250-251.

Yates, F and W.G. Cochran, 1938. The analysis of groups of experiments. *Jouranal of Agricultural science.Vol.28 Pp.556-580.*

Zhang Y, He Z, Zhang A, van Ginkel M, Ye G (2006) Pattern analysis on grain yield performance of Chinese and CIMMYT spring wheat cultivars sown in China and CIMMYT. Euphytica 147: 409-420.

Zobel, R.W.,M.J.Wright and J.H.G.Gauch,1988. Statistical analysis of a yield trial. *Agronomy Journal.Vol.80,Pp.388-393*

6. Appendix tables

Appendix I. Monthly total rain fall and Mean monthly temperature distribution of the test sites during 2011.

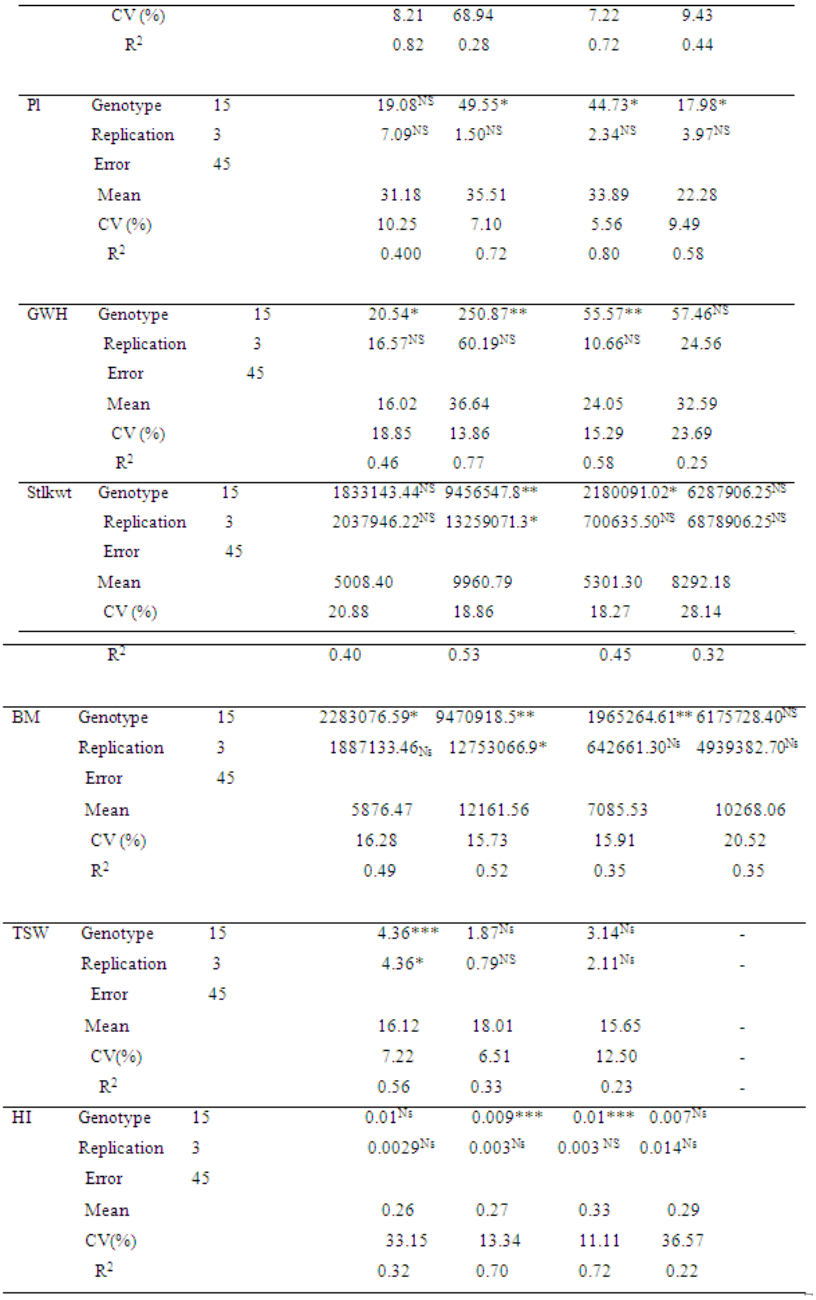
Location		Month						RF-Total
		July	August	September	October	November	December	
Jinka	RF	97.3	143.5	177.4	157.4	205.2	NA	780.8
	T^{0}Min	16.8	16.9	16.8	16.7	16.4	NA	
	T^{0}Max	26.6	26.0	25.9	26.3	25.1	NA	
	T^{0}Mean	21.7	21.45	21.35	21.5	20.75	NA	
Konso	RF	44.9	75.6	NA	155.6	220.1	NA	496.2
	T^{0}Min	NA	NA	NA	NA	NA	NA	
	T^{0}Max	NA	NA	NA	NA	NA	NA	
Weioto	RF	20.3	36.7	53.4	113.7	299.6	22.1	545.8
	T^{0}Min	NA	NA	NA	NA	NA	NA	
	T^{0}Max	NA	NA	NA	NA	NA	NA	
Meiso	RF	99.6	130.1	201.5	0	19.8	0	451.0
	T^{0}Min	18.59	18.4	16.9	11.6	12.4	8.6	
	T^{0}Max	32.4	36.8	30	31.3	29.6	27.9	
	T^{0}Mean	25.49	27.6	23.45	21.45	21.00	18.25	

NA=Data not available, RF=rainfall (mm), T^0=Temperature (^{0}C)
Source: National Meteorological Agency (Awassa and Adama Branch Directorate)

Appendix II. Analysis of variance at individual environments for all traits

			Locations			
Trait	Sources of variations	DF	Jinka	Weioto	Konso	Mieso
GY	Genotype	15	193387.76**	1662503.55**	558138.96**	659844.08**
	Replication	3	346109.00**	156454.73^{Ns}	121524.33^{Ns}	659844.08^{Ns}
	Error	45				
	Mean		1491.23	3307.52	2373.26	2956.52
	CV (%)		18.86	13.51	17.21	16.20
	R^2		0.53	0.73	0.54	0.49
DTF	Genotype	15	63.99***	6.94**	7.95**	43.24***
	Replication	3	14.06^{Ns}	0.30^{Ns}	37.20***	29.14***
	Error	45				
	Mean		50.65	36.29	47.81	58.23
	CV (%)		6.11	3.72	3.75	3.25
	R^2		0.69	0.56	0.61	0.82
Ntill	Genotype	15	0.28^{NS}	0.53^{NS}	0.39^{NS}	0.09^{NS}
	Replication	3	0.26^{NS}	1.08*	0.22^{NS}	0.10^{NS}
	Error	45				
	Mean		2.26	3.0	2.72	2.96
	CV (%)		20.22	17.74	19.24	10.27
	R^2		0.34	0.46	0.34	0.29
Ptill	Genotype	15	0.762*	0.61*	0.58*	0.34^{NS}
	Replication	3	0.39^{NS}	0.05^{NS}	0.05	0.22^{NS}
	Error	45				
	Mean		1.15	1.23	1.23	1.79
	CV (%)		51.27	41.97	35.37	24.29
	R^2		0.44	0.43	0.50	0.40

Trait	Source	DF	Jinka	Weioto	Konso	Mieso
DTM	Genotype	15	28.0***	42.80***	18.61***	20.76^{Ns}
	Replication	3	2.79^{Ns}	7.29^{Ns}	41.43***	32.54^{NS}
	Error	45				
	Mean		88.5	73.25	84.73	87.76
	CV (%)		2.47	1.65	1.76	4.31
	R^2		0.66	0.90	0.79	0.38
PH	Genotype	15	1301.85**	15158.39^{NS}	740.06*	514.97^{NS}
	Replication	3	385.50*	16124.16^{NS}	83.37^{NS}	1652.47*
	Error	45				
	Mean		121.69	182.15	136.62	198.04



	CV (%)		8.21	68.94	7.22	9.43
	R^2		0.82	0.28	0.72	0.44
Pl	Genotype	15	19.08^{NS}	49.55*	44.73*	17.98*
	Replication	3	7.09^{NS}	1.50^{NS}	2.34^{NS}	3.97^{NS}
	Error	45				
	Mean		31.18	35.51	33.89	22.28
	CV (%)		10.25	7.10	5.56	9.49
	R^2		0.400	0.72	0.80	0.58
GWH	Genotype	15	20.54*	250.87**	55.57**	57.46^{NS}
	Replication	3	16.57^{NS}	60.19^{NS}	10.66^{NS}	24.56
	Error	45				
	Mean		16.02	36.64	24.05	32.59
	CV (%)		18.85	13.86	15.29	23.69
	R^2		0.46	0.77	0.58	0.25
Stlkwt	Genotype	15	1833143.44^{NS}	9456547.8**	2180091.02*	6287906.25^{NS}
	Replication	3	2037946.22^{NS}	13259071.3*	700635.50^{NS}	6878906.25^{NS}
	Error	45				
	Mean		5008.40	9960.79	5301.30	8292.18
	CV (%)		20.88	18.86	18.27	28.14
	R^2		0.40	0.53	0.45	0.32
BM	Genotype	15	2283076.59*	9470918.5**	1965264.61**	6175728.40^{NS}
	Replication	3	1887133.46_{Ns}	12753066.9*	642661.30^{Ns}	4939382.70^{Ns}
	Error	45				
	Mean		5876.47	12161.56	7085.53	10268.06
	CV (%)		16.28	15.73	15.91	20.52
	R^2		0.49	0.52	0.35	0.35
TSW	Genotype	15	4.36***	1.87^{Ns}	3.14^{Ns}	-
	Replication	3	4.36*	0.79^{NS}	2.11^{Ns}	-
	Error	45				
	Mean		16.12	18.01	15.65	-
	CV(%)		7.22	6.51	12.50	-
	R^2		0.56	0.33	0.23	-
HI	Genotype	15	0.01^{Ns}	0.009***	0.01***	0.007^{Ns}
	Replication	3	0.0029^{Ns}	0.003^{Ns}	0.003^{NS}	0.014^{Ns}
	Error	45				
	Mean		0.26	0.27	0.33	0.29
	CV(%)		33.15	13.34	11.11	36.57
	R^2		0.32	0.70	0.72	0.22

**=highly significant, *=significant, NS= non-significant at, 1 and 5% probability level. GY= grain yield (g), DTF=Days to flowering; Ntill= Number of tillers; Ptill=productive tillers; DTM= days to maturity; PH=plant height (cm); Pl=panicle length (cm); GWH= grain weight per head (g); stlkwt= stalk weight (g); BM= biomass yield (g); HI= harvest index, TSW=thousand seed weight(g)

Appendix III. Percent contribution of sum of squares of each component to the total SS for different agronomic traits of pearl millet genotypes.

	Source of variation				
	Enviroment(E)	Genotype(G)	GEI	Rep(E)	Error
DF	3	15	45	12	180
DTF	84.60	4.63	5.12	1.29	4.37
Ntill	25.86	9.25	13.70	5.91	45.29
Ptill	17.12	11.49	23.49	2.23	45.66
DTM	76.53	7.50	5.71	2.02	8.24
PH	72.87	10.23	5.12	2.47	9.31
Pl	68.14	10.78	9.30	0.46	11.32
GWH	59.59	8.12	13.25	1.23	17.81
Stlkwt	56.14	7.25	7.86	3.50	25.25
BM	66.00	6.04	6.30	2.51	19.15
HI	11.12	11.54	19.25	3.72	54.37
TSW	30.38	8.02	13.37	3.32	44.91

DF=degree of freedom; GEI=Genotype by environment interaction; Rep(E)= Replication within environment; DTF=Days to flowering; Ntill= Number of tillers; Ptill=productive tillers; DTM= days to maturity; PH=plant height (cm); Pl=panicle length (cm); GWH= grain weight per head (g); stlkwt= stalk weight(g); BM= biomass yield(g); HI= harvest index;TSW=thousand seed weight(g)

Appendix IV. Environment means for grain yield and other agronomic traits.

Location	DTE	DTF	Ntill	Ptill	DTM	PH	Pl	GWH	Stlkwt	BM	HI
Jinka	5.86_{A}	50.65_{B}	2.26_{C}	1.15B	88.50_{A}	121.68_{D}	31.18_{C}	16.01_{D}	5008.4_{C}	5876.5_{D}	0.26C
Konso/Arf/	4.84_{B}	48.71_{C}	2.71_{B}	1.23_{B}	84.73_{B}	136.48_{C}	33.89_{B}	24.18_{C}	5301_{C}	7085.5_{C}	0.33A
Weioto	4.46_{C}	36.29_{D}	3.00_{A}	1.23_{B}	73.25_{C}	166.52_{B}	35.51_{A}	36.62_{A}	9960.8_{A}	12161.6_{A}	0.3_{BC}
Meiso	4.72_{BC}	58.23_{A}	2.96_{A}	1.79_{A}	87.75_{A}	198.04_{A}	22.28_{D}	32.59_{B}	8292.2_{B}	10268.1_{B}	0.29_{B}

DTE =days to emergence, DTF=Days to flowering; Ntill= Number of tillers; Ptill=productive tillers; DTM= days to maturity; PH=plant height; Pl=panicle length; GWH= grain weight per head; stlkwt= stalk weight; BM= biomass yield; HI= harvest index; TSW=thousand seed weight,
Means followed by the same latter are not significantly different.