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Pattern Analysis of Multi-Environment Grain Yield Trial of Bread Wheat Genotypes in South Tigray, Ethiopia

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ABSTRACT

In multi location yielder trial selection of genotypes and determination testing site is important prerequisite for recommendation of genotypes for the production environment. Patten analysis was done up on 19 released bread wheat genotypes across 7 testing environments with objective of assessing the pattern response of genotypes across testing environment and identifying possible mega-environments. The trial was conducted in Randomized Completed Block Design (RCBD) having two replications. The pattern analysis showed that the environment captured large sum of square (78.3%) followed by the genotype by environment interaction (14.8%). The 19 bread wheat genotypes were classified into 9 genotypic cluster and 5 environmental clusters using the clustering analysis of the last cluster. The polygon view of the biplot analysis showed of the presence of two mega-environments. The testing environments were positively correlated except Atsella, 2013 and Adigolo, 2013 were negatively correlated.

Key words: Patten, clustering, biplot genotype

INTRODUCTION

In multi location yield trial the efficiency of selection mainly depends on the discriminating ability of the testing location and the magnitude of genotype by environment interaction. Genotype by environment interaction is the lack of corresponds between the genetic and non-genetic components.

Different models have been proposed for analysis of genotype by environment interaction such the regression approach of Eberhart and Russell (1966) by which genotypes are regressed on environmental index and it is being criticized that genotype mean is not independent of the site mean. Models that mainly depend on quantifying the magnitude of genotype by environment interaction and a stable genotype is with low genotype by environment interaction, also proposed by Wricke (1962) and Shukla (1972).

The multivariate methods such as the additive main effect and multiplicative interaction effect (AMMI) that was proposed by Gauch (1988) and this model combines conventional ANOVA with principal component analysis and provide reliable estimates of genotype performance by reduce background noise and it also use biplots help to visualize relationships among genotypes and environments; show both main and interaction effects. The GGE biplot is also effective tool for visual comparisons and important for detecting type of genotype by environment interaction and mega environment classification (Yan *et al.*, 2000).

The pattern analysis proposed (transformation) scale the data by removing main environmental effects and adjust scale dividing by the phenotypic standard deviation at each site use a classification procedure to identify environments which show similar discrimination among the genotypes and ordination procedure by singular value decomposition which is similar to the additive main effect and multiplicative interaction effect (AMMI). The only difference is pattern analysis use of transformed data (Cooper and DeLacy, 1994). Hence the objective of this study is to assess the pattern of bread wheat genotypes and clustering of the environment on the discriminating capacity and possible way of addressing the number of testing environment.

MATERIALS AND METHODS

Experimental design and data collection: The experiment was conducted at three locations during 2011, at two locations during 2012 and 2013 main cropping season (Table 1). Nineteen bread wheat genotypes (Table 2) were laid out in Randomized Complete Block Design (RCBD) with two replications. Each genotype was planted in a plot consisting of six rows of 2.5 m long with

Table 1: Description of the testing environments used in the study

Code	Environment	Year	Longitude	Latitude	Altitude (m.a.s.l.)	Mean grain yield	Cluster
E1	Adigolo	2011	39.33°E	120 31°N	2490	55.25	II
E2	Adigolo	2012	39.33°E	120 31°N	2490	43.57	I
E3	Adigolo	2013	39.33°E	120 31°N	2490	48.10	V
E4	Astella	2011	39.56°E	12.91°N	2580	38.40	III
E5	Astella	2012	39.56°E	12.91°N	2580	35.99	I
E6	Astella	2013	39.56°E	12.91°N	2580	29.71	IV
E7	Mekhan	2011	39.32°E	12.44°N	2430	34.86	IV

Table 2: List of 19 bread wheat genotypes which were evaluated in 7 environments

Genotypes	Year of release	Maturity (days)	Adaptation altitude (m.a.s.l.)	Source centre	Mean grain yield	Cluster
Danda'a	2010	110-145	2000-2600	KARC/EIAR	40.06	6
Kakaba	2010	90-1200	1500-2200	KARI/EIAR	41.33	3
Hawii	2000	105-125	1800-2200	KARI/EIAR	37.62	3
Tussie	1997	125-130	2000-2500	KARI/EIAR	38.74	3
Paven-76	1982	120-135	750-2500	KARI/EIAR	42.10	7
ET-13A2	1981	127-149	2200-2900	KARI/EIAR	31.56	8
K6295-4A	1980	128-131	1900-2400	KARI/EIAR	31.75	5
ETBW-5483	2011	-	1800-2400	KARI/EIAR	37.82	1
ETBW-5496	2011	-	2200-2600	KARI/EIAR	33.85	5
Digelu	2005	100-120	2000-2600	KARI/EIAR	41.65	7
Sofumar	2000	125-150	2300-2800	SARC/OARI	36.76	1
Mada-walabu	2000	100-125	2300-2800	SARI/OARI	41.07	2
Tay	2005	104-130	1900-2800	ADARC/ARARI	38.90	2
Senkegna	2005	105-125	1900-2800	ADARC/ARARI	34.75	4
Gasay	2007	118-127	1890-2800	ADARC/ARARI	40.99	6
Alidoro	2007	118-180	2800-3100	HARC/EIAR	38.16	3
Dinkinesh	2007	145	2400-3000	SRARC/ARARI	40.05	7
Tossa	2004	134-143	2400-3000	SRARC/ARARI	42.86	9
Kulkulu	-	-	-	Haramaya univ.	31.65	5
Grand mean					37.98	

spacing of 20 cm between rows. The distance between plots and replications were 0.5 and 1.5 m, respectively. A seed rate of 150 kg ha⁻¹ and fertilizer rates of 62 and 46 kg ha⁻¹ N and P₂O₅, respectively were applied. The data was collected on plot basis from the central four rows for grain yield.

Statistical analysis: In pattern analysis model the environment and genotype was classified based on the location standardized by which the column means subtracted and divided by column standard deviations using the classification method of incremental sum of square (ward) for both the genotype and environment. Using the fusion level criteria the number of genotype cluster and environmental clusters determined. To better view the relationship the genotypes and the environments biplot was visualized using the first interaction principal component and the second interaction principal component and to the pattern analysis and biplot was done by the crop stat 7.2 soft ware.

RESULTS AND DISCUSSION

The combined analysis of variance for the nine genotype clusters and five environmental clusters the environment explained the higher sum of square 78.3% followed by the genotype by environment interaction 14.8% and 1.5 times larger than genotype main effect.

The results of the classification (Fig. 1) for genotype and (Fig. 2) for environment implied nine genotype clusters and five environmental clusters. The clustering analysis indicated that among group the clusters explained 91.16% which was 10.36% greater than the within group sum of

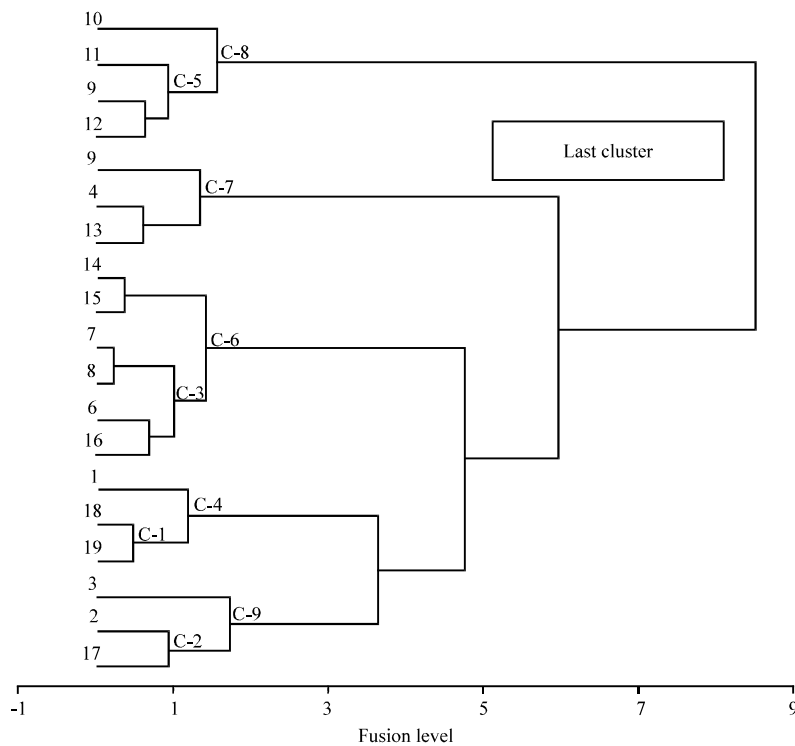


Fig. 1: Dendrogram for genotype clusters

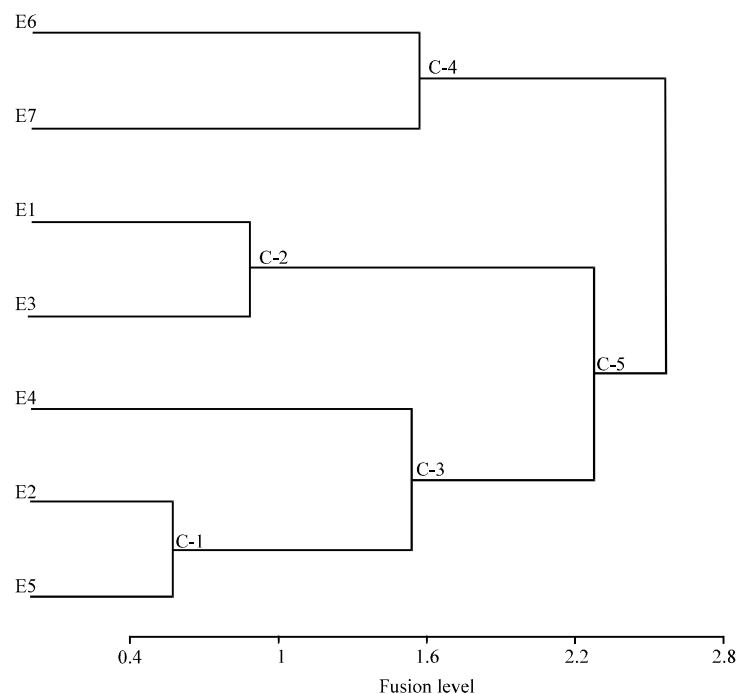


Fig. 2: Cluster dendrogram for environment, E1: Adigolo 2011, E2: Adigolo 2012, E3: Adigolo 2013, E4: Atsella, 2011, E5: Atsella, 2012, E6: Atsella, 2013 E7: Mekhan, 2011

square. Cluster 5 G11 (Kulkulu), G9 (ETBW-5496) and G12 (K6295-4A) were lower yielder genotypes lower than the grand mean. Cluster 3 G6 (Kakaba), G8 (Hawii) and G16 (Alidoro) were medium yielding genotypes nearly closed to the grand mean. The cluster 7 contained G13 (Dinkinesh) G4 (Digelu) G5 (Paven-76) were higher yielder genotypes. The last cluster showed the presence of two major grouping of the genotypes between cluster 5 lower yielder genotypes and the remaining cluster that was higher yielder and medium yielder genotypes. The lower smaller number of clusters could be associated with the similar pedigree of the wheat genotypes used in the study (Fig. 1).

The clustering analysis for the environment showed five clusters and the last cluster revealed two major mega environments between cluster four that confined E6 (Atsella, 2013) and E7 (Mekhan, 2011) and the second mega-environment continued E1 (Adigolo, 2011) E2 (Adigolo, 2012), E3 (Adigolo, 2013), E4 (Atsella, 2011) and E5 (Atsella, 2012). The result indicated the possible indication of minimizing the testing location and in most cause the year to year variation in yield performance of the bread wheat genotypes.

The genotypes is abbreviated as G1, G2...G19 and environments is abbreviated E1, E2...E7 G1 = Senkegna, G2 = Mada-Walabu, G3 = Tossa, G4 = Digelu, G5 = Paven-7, G6 = Kakaba, G7 = Tussie, G8 = Hawii, G9 = ETBW-5496, G10 = ET-13A2, G11 = Kulkulu, G12 = K6295-4A, G13 = Dinkinesh, G14 = Gasay, G15 = Danda, a, G16 = Alidoro, G17 = Tay, G18 = ETBW-5483, G19 = Sofumar.

Biplot analysis: The principal component analysis one explained 35.7% and the second principal component analysis explained 20.3% and the two principal components cumulatively 56% of the

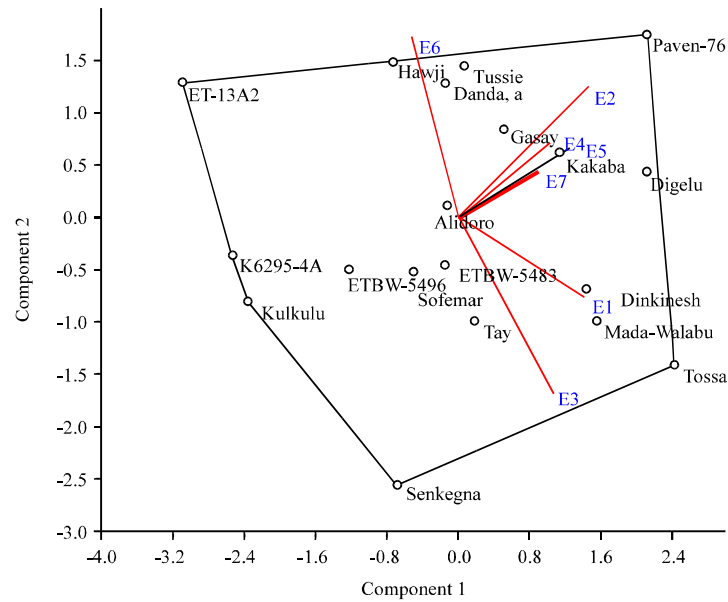


Fig. 3: Polygon view of the biplot analysis, E1: Adigolo 2011, E2: Adigolo 2012, E3: Adigolo 2013, E4: Atsella, 2011, E5: Atsella, 2012, E6: Atsella, 2013 E7: Mekhan, 2011

genotype by environment interaction. The polygon view of the biplot indicated that the genotype ET-A2, Senkegna, Tossa and Paven-76 were located in the vertex genotypes either perform well or bad in one or most of the environment, but generally such vertex genotypes are distant from origin and have unstable performance (Yan and Tinker, 2006).

The genotype Hawi performed best to the environment E6 (Atsella, 2013). The genotypes Tussie and Danda'a did moderately perform to the environment E6 (Atsella, 2013). Genotypes Gasay and Paven-76 were best adapted to the testing environment E2 (Adigolo, 2012). Genotype Kakaba was best adapted to the testing environments of E4 (Atsella, 2011), E5 (Atsella, 2012) and E7 (Mekhan, 2011). Genotypes: Dinkinesh, Mada-Walabu and Tossa performed well to the testing environment E1 (Adigolo 2011).

The length of the environmental vector indicates the discriminating capacity of the environment. The longer the vector, the more potential the environment is and the shorter the vector, the poor the environment to discriminate the genotypes. The cosine of the angle between the vectors of two environments approximates the correlation between them. The presence of wide obtuse angles indicates strong negative correlation whereas; an acute angle indicates positive correlation. When the association between the environments is 90°, they are independent (Yan and Tinker, 2006). The testing environments: E2 (Adigolo, 2012), E4 (Atsella, 2011), E5 (Atsella, 2012) and E7 (Mekhan, 2011) that have lower angle between each other indicates positive correlation. While, the testing environments E6 (Atsella, 2013) and E3 (Adigolo, 2013) were negatively correlated having wider obtuse angle (Fig. 3). The testing environments E6 (Atsella, 2013), E2 (Adigolo 2012) and E3 (Adigolo, 2013) with longest vector length from the origin were highly discriminating. The testing environment E7 (Mekhan, 2011) was non-discriminating with shortest vector length from the origin (Fig. 3).

CONCLUSION

The 19 bread wheat genotypes tested in 7 environments of Tigray and the Pattern analysis showed that the environment captured large sum of square 78.3% followed by the genotype by environment interaction 14.8%. The 19 bread wheat genotypes was classified in to 9 genotypic cluster and 5 environmental clusters and the last cluster for both genotype cluster and environmental cluster showed the two major genotype and environment clusters. The polygon view of the biplot analysis also showed that the testing environments were positively correlated except Atsella, 2013 and Adigolo, 2013 were negatively correlated.

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