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Research Article

Yield Stability and Genotype by Environment Interaction of Bread Wheat Genotypes in Northern Ethiopia

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ABSTRACT

Nineteen bread wheat genotypes were growing in six environments to quantify the magnitude of genotype by environment interaction and phenotypic stability by imposing the Eberhart and Russell (1966) model. The experiment was laid out in randomized complete block design with three replicates. The combined analysis of variance showed significant genotype, environment and genotype by environment interaction. The total sum of square explained by the environment was eleven times greater than the genotypic main effect and five times greater than the genotype by environment interaction effect implying the higher variability of the testing environments. The genotype ETBW7867, ETBW7881 and Mekelle-4 was significant at the 1% against the Pooled deviation. The genotypes ETBW6969, ETBW7862, ETBW7867, ETBW-7879, ETBW7881and ETBW7888 were with mean grain yield greater than the grand mean which is 4.07ton/ha. Using the Stability analysis by Eberhart and Russel ETBW7888, ETBW7879, ETBW7082 and ETBW7042 was stable and adaptable genotypes with higher mean grain yield, a regression coefficient near to 1 and minimum deviation from the regression coefficient near to zero. The standard check Meklle-4, ETBW-7867 and ETBW-7881 was unstable genotypes with relatively higher deviation from the regression coefficient.

Key words: Bread wheat, Stability, Grain yield

INTRODUCTION

Bread Wheat (*Triticum*spp) in Ethiopia, one of the major crops that are central to achieving development in agriculture and the fourth most important cereal crop after tef (*Eragrostistef*), maize (*Zea mays L.*) and sorghum (*Sorghum bicolor* L.) in area coverage and production wheat occupies an area of about 1.69 million ha with total production of more than 4.53 million tons per year (CSA, 2016). The crop is not only critical to smallholder incomes but the food and nutrition security of tens of millions of Ethiopians.

Regardless of the importance of wheat, the national average yield of wheat is (2.3 t ha^{-1}) is far below the average yield level obtained in experimental plots in the same area (>5t ha^{-1}). The low association between research plot yield and farmer's field yield could be associated with the occurrence rust disease, use of low yielder genotypes and use of genotypes with wider adaptation nature that failed to perform in pocket areas that lead to crop failer. Response of genotypes across the testing environment is considered as a hindrance in selecting and recommending of crops and cause yield fluctuation. The yield loss due to variability of growing condition is severed in a marginal environment with poor soil fertility and fragile economy that cause failure in the case of staple crops, contributes to food insecurity at national and household level (Kang, 1998).

A number of stability studies have been carried out on different crop plants as well as on bread wheat in Tigray and Large magnitude of genotype by environment interaction reported in the region in barley (Abay *et al.*, 2009). Hence, study on the yield stability and mega environment classification for specific adaptation is mandatory. Different stability measurement have been imposed in plant breeding for quantifying the magnitude of genotype by environment interaction and phenotypic stability and the Eberhart and Russell (1966) stability model has been exploited by breeders widely. Their model assumes that the genotypes have a linear response to change with environments. According to this model, a genotype is said to be stable having high mean yield, with coefficient of regression (bi) equal to one and deviation from linear regression(Sdi2) equal to zero.

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MATERIALS AND METHODS

Plant material and Field condition

Dandaa, ETBW6965, ETBW6969, ETBW6993, ETBW7038, ETBW7042, ETBW7082, ETBW7107, ETBW7862, ETBW7864, ETBW7866, ETBW7867, ETBW7870, ETBW7879, ETBW7881, ETBW7888 and three standard check (Hidase, Mekelle-3 and Mekelle-4) was incorporated as a planting material.

Table 1: site description and agronomic descriptions.

Environment	location	year
E1	A/gara	2014
E2	Aiba	2014
E3	Mekhan	2014
E4	A/gara	2015
E5	Aiba	2015
E6	Mekhan	2015

Statistical analysis

An analysis of variance (ANOVA) was done for each location separately as randomized complete block design using R software. Before combining the data, assumption of (ANOVA) normality test and test of equal variance was done using R software for grain yield. There was no series ANOVA assumption violation. The combined analysis was done using the R software edition 4.2.1 Mean comparison was done using LSD at 5 and 1% level of significance. phenotypic stability using the commonly used regression model Eberhart and Russell .

Was done using R software using the plant breeding package (Umesh and Rosyara (2014) According to the Eberhart and Russell (1966), bi approximating to1 and S^2d near zero indicate average stability when, this is associated with high mean yield, genotypes have general adaptability and when associated with low mean yield, genotypes are poorly adapted to all environments.

$$S^2{}_{di}=\frac{1}{E-2}\left[E_j(Y_{ij}-\bar{Y}_i-\bar{Y}_j+\bar{Y}_{..})^2-(b_i-1)^2E_j(\bar{Y}_j-\bar{Y}_{..})^2\right](9)$$

RESULTS AND DISCUSSION

Mean grain yield varied among testing environments ranging 1.69 ton /ha for environment 2 to 7.76 ton /ha in environment 5. The testing environment E1 and E3 was low yielding environments by which all the genotypes scored below the average productivity 4 tone /ha. While, the testing environment E4 and E5 was better yielder environment by which most of the genotypes scored above the grand mean.

A combined analysis of variance for the six environments(Table 3) revealed that there were significant differences among environments, genotypes and GEI for yield (ton/ha) indicating the presence of variability in genotypes as well as diversity of growing conditions at different environments. The GEI was highly significant, reflecting the differential response of genotypes across environments (Rodrigues *et al*., 2008). The partitioning of the total sum of square of the combined analysis of variance 60% of the total sum of square was attributed due to environmental variance. While, the genotype by environment interaction and genotypic effect was 11.25 % and 5.42%, respectively.

Table 2: mean grain yield of nineteen bread wheat genotypes tested across six environments

	E1	E2	E3	E4	E5	E6
Dandaa	3.63	1.97	2.83	5.11	5.33	2.65
ETBW6965	4.18	2.83	1.78	4.15	5.48	3.18
ETBW6969	5.53	2.25	4.15	4.89	7.66	4.55
ETBW6993	4.35	3.10	3.25	4.01	4.62	3.11
ETBW7038	4.56	1.69	1.97	4.90	5.99	3.04
ETBW7042	5.33	1.99	2.80	4.33	6.03	2.87
ETBW7082	4.55	2.80	3.15	4.84	5.98	2.52
ETBW7107	3.77	2.07	3.21	5.00	5.43	2.94
ETBW7862	4.43	2.88	4.26	4.30	7.12	3.52
ETBW7864	2.94	2.24	3.20	4.41	6.55	3.24
ETBW7866	4.88	2.57	3.12	4.93	6.02	2.74
ETBW7867	3.98	2.11	5.12	4.62	6.76	3.92
ETBW7870	4.16	2.42	2.44	4.22	6.63	2.91
ETBW7879	4.71	3.07	3.42	5.41	5.98	2.98
ETBW7881	6.03	3.13	2.35	4.32	7.24	3.20
ETBW7888	6.22	3.88	3.82	4.82	6.81	4.15
Hidase	3.80	2.05	2.27	4.05	6.04	3.67
Mekelle-3	4.73	2.42	3.15	5.00	5.97	2.86
Mekelle-4	3.39	2.66	2.04	5.34	7.76	1.87

Table 3: Combined ANOVA for yield (ton/ha) and the percentage sum of squares of the 19 bread wheat genotypes tested at six environments over a period of two years.

	Degree of freedom	Sum of square	Mean square	F value	Pr(>F)	% explained
Gen	18	48.15	2.675	4.4458	4.837e-08***	5.42
env	5	534.76	106.951	177.7653	2.2e-16 ***	60
env:rep	11	86.40	7.855	13.0557	2.2e-16 ***	
gen:env	90	99.91	1.110	1.8451	0.0002059***	11.25
Residuals	198	119.13	0.602			

Where: Gen =genotype, env=environment rep = replication.

Table 4: Eberhart and Russell stability regression, estimates of mean population mean, regression coefficient (bij) and deviation from regression (sdij) for grain yield ton/ha

	Degree of freedom	Sum of square	Mean square	F value	Pr(>F)	Grain yield ton/a	bij	sdij
Total	113	237.321	2.1					
Genotypes	18	18.114	1.006	2.7783	0.0010295**			
Env + (Gen x Env)	95	219.207	2.307					
Env (linear)	1	183.48	183.489					
Gen x Env(linear)	18	8.19	0.455	1.2561	0.24145			
Pooled deviation	76	27.528	0.362					
Dandaa	4	1.222	0.306	1.7546	0.1389	3.6	0.921958	0.104669
ETBW6965	4	1.272	0.318	1.8255	0.1248	3.7	0.871314	0.117724
ETBW6969	4	2.001	0.5	2.8728	0.0238	4.9	1.191922	0.300161
ETBW6993	4	0.241	0.06	0.346	0.8467	3.8	0.459627	-0.14029
ETBW7038	4	1.008	0.252	1.4468	0.2194	3.8	1.199352	0.051207
ETBW7042	4	1.139	0.285	1.6348	0.1664	4	1.092523	0.084294
ETBW7082	4	0.546	0.136	0.7833	0.5371	4	0.95161	-0.06424
ETBW7107	4	0.937	0.234	1.3449	0.2541	3.8	0.865025	0.033419
ETBW7862	4	1.59	0.397	2.2819	0.0614	4.4	0.961473	0.197192
ETBW7864	4	2.209	0.552	3.1704	0.0146	3.8	0.995969	0.351615
ETBW7866	4	0.462	0.116	0.6632	0.6182	4	1.001254	-0.08515
ETBW7867	4	4.425	1.106	6.352	0.0001***	4.4	0.873681	0.905895
ETBW7870	4	0.378	0.095	0.5427	0.7046	3.9	1.138539	-0.10589
ETBW7879	4	0.687	0.172	0.9858	0.416	4.3	0.884119	-0.02908
ETBW7881	4	2.986	0.746	4.2859	0.0023**	4.5	1.246862	0.546371
ETBW7888	4	1.383	0.346	1.985	0.0977	5	0.837799	0.145411
Hidase	4	1.184	0.296	1.6991	0.1511	3.7	0.973964	0.095473
Mekelle-3	4	0.366	0.091	0.5248	0.7176	4	0.994837	-0.1093
Mekelle-4	4	3.492	0.873	5.0131	0.0007***	3.9	1.538172	0.672224
Pooled error	Error	228	39.71	0.174				

Signif. Codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘’ 1.

Stability analysis by Eberhart and Russel (1966)

Following the significant effect of the GEI in the combined analysis of variance for grain yield, Further partitioning in to E + G x E effects was done using Eberhart and Russell’s model(1966).Hence, the genotype showed significant difference ($P<0.01$) implying wider genetic diversity among genotypes. The Env + (Gen x Env), Env (linear), Gen x Env (linear) and Pooled deviation was non significant difference. On examining the significance of deviation from linear regression for the 19 bread wheat genotypes in Table 3, The genotypes ETBW7867, ETBW7881 and Mekelle-4 was significant at 1% level of significant.

According to the Eberhart and Russell (1966), a stable genotype is one with a high mean, a regression coefficient ($\beta i = 1$), and a minimum deviation from the regression coefficient ($S2di$) = 0). Where, $\beta i > 1$* the genotype is responsive to favorable environment. If $\beta i < 1$*, the genotype performs well in an unfavorable environment. When this is associated with high mean yield, genotypes have general adaptability and when associated with low mean yield, genotypes are poorly adapted to all environments. The genotypes ETBW7888, ETBW6969and ETBW7881 were with higher mean grain yield of 5, 4.9 and 4.5ton/ha respectively. However, the genotypes Dandaa and ETBW6965 was low yielder with 3.6 and 3.7 ton/ha respectively.

The genotypes ETBW7888, ETBW7879, ETBW7082 and ETBW7042 was stable and adaptable with higher mean grain yield, a regression coefficient near to 1 and minimum deviation from the regression coefficient near to zero. The standard check Meklle-4, ETBW7867 and ETBW7881 was unstable genotypes with relatively higher deviation from the regression coefficient. The genotypes Meklle4, ETBW881, ETBW7038, ETBW6969 and ETBW7870 were adapted to favorable environments having regression coefficient greater than one. While, the only genotype ETBW6963 was adapted to unfavorable environment., Generally all the tested genotypes was well adapted in good growing environment and this could be associated with the availability of good rainfall distribution in the growing season.

Conclusion

The combined analysis of variance for mean grain yield showed significant effect for genotype, environment and genotype by environment interaction and the total sum of square explained by the environment was eleven times greater than the genotypic main effect and five times greater than the genotype by environment interaction effect.

The genotypes ETBW6969, ETBW7862, ETBW7867, ETBW7879, ETBW7881and ETBW7888 were with mean grain yield greater than the grand which is 4.07ton/ha. The genotypes ETBW-7866, ETBW-7864 and Meklle-3 was with regression coefficient $\beta i = 1$ implying this genotypes are adaptable to all environments. The genotypes Meklle-4, ETBW-881, ETBW7038, ETBW-6969 and ETBW7870 were adapted to favorable environments having regression coefficient greater than one.

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