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RESEARCH ARTICLE

Identification of superior bread wheat variety under multi-environment evaluation trial in North Shewa, Ethiopia using AMMI analysis

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Abstract

Bread wheat is important food crop in Ethiopia. Multi-environment bread wheat regional variety trial comprised of 18 genotypes along with two standard checks, HAR2501 and HAR2562 and the respective local check of Inewary, Keyit and Mehalmeda was carried out in 2007-2008 main seasons. The objective of this study was to identify stable and better yielding bread wheat variety under North Shewa areas of Ethiopia. The experiment was arranged in randomized complete block design replicated three times within an experiment. Based on AMMI analysis genotypes FH-934, HAR3816, HAR1911 and ETBWCO89MAMBA/ HAR1384 were superior to both the standard and local checks. In addition, these promising genotypes were also resistant to yellow rust, and hence these genotypes have been verified, and the genotype HAR3816 has been registered by the Ethiopian national variety releasing committee by the given name 'Bollo' for commercial production under North Shewa wheat growing areas. However, the highest yielding and stable variety, FH-934 was found to be susceptible to yellow rust and was not selected for on-farm verification.

Key words: Bread wheat, mixed model, AMMI, Grain yield

Introduction

The major wheat producing countries in the world are China, United States of America, Russian Federation and Canada and these 5 countries together contribute more than half of the global wheat production (Singh *et. al.*, 2010; Ahmad *et. al.*, 2017). Bread wheat is important food crop in Ethiopia and particularly in North Shewa highlands, where Vertisol is abundant. It accounts about 31.5% of the total cereal production in the Zone (CSA, 2008/09). Notwithstanding the immense potential uses of bread wheat in Ethiopian in general, and in North Shewa in particular, several biotic and abiotic factors inescapably induce an absolute reduction of grain yield of wheat, and consequently the gap between demand and supply is still wide.

Development of improved bread wheat varieties, which are adaptive and that can give better grain yield under these prevailing environment is therefore not a matter of choice to Ethiopia known to suffer heavily from wheat importing. Sharing the national and regional wheat production constraints, a regional bread wheat variety trial was started with the objective of identifying high yielding, yellow rust resistant and relatively stable bread wheat variety under North Shewa highlands conditions.

Materials and methods

Experimental design

Eighteen bread wheat cultivars were used along with two standard checks, HAR2562 and HAR2501,local checks of the respective locations were added in randomized block design with three replications. The experiment was conducted at Inewary, Mehalmeda and Keyit for two years (2007-2008). Inewari and Mehalmeda were characterised as Vertisol areas while Keyit had Cambisol soil. Seeds were drilled at the rate of 150kg/ha in 20cm spaced six rows, each being 2.5m long. All agronomic practices were applied uniformly to all experimental plots as per the recommendation. Data on days to heading, days to maturity, plant height (cm), yellow rust, grain yield (kg) and thousand-grain weight (g) were recorded on plot basis.

Statistical analysis

SAS and Agrobase99 softwares were used to analyse the data. Though blocks, years and locations are sampled giving due consideration of their representativeness, accessibility and other costs, their respective and possible interaction effects were considered as random effects. And hence, the findings of this experiment can be inferred to similar locations and years. On the other hand, the tested genotypes were considered as fixed effect. Thus, the mixed model was used for the analysis of variance. The first order interaction component of genotypes, locations and years were tested against the second order interaction, found that genotype by year interaction was not significant, and hence was removed from the ANOVA model (Bridges, 1989; Nachit *et. al.*,1992; Annicchiarico, 2002).

$Y_{ijkm} = \mu + b_i + l_j + y_k + (ly)_{jk} + b(ly)_{jk} + t_m + (tl)_{jm} + (ty)_{km} + (lyt)_{jkm} + e_{ijk}$,

where;

Y_{ijkm} $= is\ the\ yield\ observation\ from\ the\ i^{th}\ block, the\ j^{th}\ location, k^{th}\ year\ of\ m^{th}\ genotype$

μ is the experimental grand mean; b_i is the random block effect; l_j is the random location effect; y_k is the random year effect; t_m is the fixed genotype effect; $(ly)_{jk}$= is the random location by year interaction; $(tl)_{jm}$ = is random genotypes by location interaction; $(ty)_{km}$ is random genotypes by year interaction effect; $(lyt)_{jkm}$ is the random location, year and genotype interaction effect, and e_{ijk} is the random experimental error. Because the location by genotype interaction is not significant, the model is reduced, and hence the new model would be:

Y(ijkm)= μ + bi +lj +yk + 〖(yg) mk +b(ly)jk + g〗 m+ (gl)jm+ (lyg)jkm+ eijk, and the analysis of variance table would contain the following:

Sources	Df	Mean square	Expected MS = E (MS)
Genotype (g)	g-1	MS_g	$\delta e^2 + b(\delta^2)_{lyg} + bl(\delta^2)_{gy} + bly\,(\delta^2 gm)$
y*g	(y-1)(g-1)	MS_{gy}	$\delta e^2 + b(\delta^2)_{lyg} + bl(\delta^2)_{gy}$
l*g	(l-1)(g-1)	MS_{gl}	$\delta e^2 + b(\delta^2)_{lyg} + bl(\delta^2)_{gl}$
l*y*g	(y-1)(l-1)(g-1)	MS_{lyg}	$\delta e^2 + b(\delta^2)_{lyg}$
Error	yl(b-1)(g-1)	MS_e	δe^2

The genotype by environment interaction sum square was exploited using the Additive Main and multiplicative interaction/ AMMI/ model as described in Nachit *et. al.*, (1992). The AMMI model takes the following equation

y_ge=μ+α_g+β_e+∑λ_n γ_gn δ_en+θ_ge+ε_ger

Where,

Y (ge)= is the yield of variety g in environment e;

μ = is the grand mean; α_g=are the variety mean deviations (the variety means minus the grand mean); β_e= are the environment mean deviations (the environment mean minus the grand mean);

λ_n=is the eigenvalue of nth principal components analysis (PCA) axis n;

γ_gn=is the variety eigenvector value for IPC axis n

δ_en=is the environment eigenvector value for IPC axis n

ε_ger=is the random error

Results and discussion

Analysis of variance

Analysis of variance was done assuming that not only all the effects are random except that of genotype but also the random effects are normally distributed with a mean of zero and the respective variances. Using the mean square of error as error term, analysis of variance for grain yield revealed that the tested bread wheat genotypes were significantly different at P ≤0.01%. But, this analysis is valid only if genotypes, year locations and block assumed to have fixed effect. However, because both locations, years and block are sampled out of the unlimited number of locations, years and block, the correct error term is either the location x genotype interaction, year x genotype or interaction component between year x location, genotype was tested against the error mean square. And this test was found to be significant, and hence the first order interaction components genotypes x locations or genotypes x years were tested against the second order interaction. genotype x location x year interaction components. Thus, to do valid analysis of variance, the second order interaction that is

This test also indicated that genotype x location interaction was not significant, and was removed from the model. The expected values of the mean squares, E (MS) in the combined analysis of variance as shown in Table 1 indicated that none of the other mean squares have an expectation that contains all of the components of the variance of genotypes except the component involving $\delta^2_{gm.}$

In general, there is no ratio of mean square to use as an F- statistic for testing genotypes. If either year x genotype or location x genotype interaction is not significant when tested against the mean square of error, the other interaction may be used for testing the significance of genotypes. In this particular experiment, the year x genotype interaction was not significant, and hence the location x genotype interaction component was used as an F-statistic for testing the significance of mean square of genotypes. Therefore, testing the genotype mean square against the mean square of error, i.e. using equation (1), would inevitably brought about confounding of variance components of genotype x year x location interaction and genotype x location interaction with the genotypic variance, and consequently inflated F value of genotypes. And hence the researcher may commit a type I error by rejecting the true null hypothesis, which states that the genotypes means are equal.

On the other hand, if the researcher uses equation (2) in testing the significance of genotypic variance, nothing would be confounded with the genotypic variance. And thus when genotypes mean square are tested using equation (2), analysis of variance proved

that the tested bread wheat genotypes are not statistically different in terms of grain yield (Table 1). From this analysis one can say that the use of improper use analyses model and test statistics can lead to wrong conclusion and recommendation. When both two fact interactions, for example year x genotype and location x genotypes are significant, it is possible to construct a test ratio by combining mean squares of both the numerator and denominator of the ratio. Considering Table 1, it can be seen easily that the $E\left(MS_{gly}+MS_{g}\right)$ contain the genotypic variance component while $E\left(MS_{gy}+MS_{gl}\right)$ contains all of the variance components of the preceding sum squares except the genotypic variance. This suggests that the researcher can form a test statistics for genotype mean square using the ratio $\frac{(MS_{gly}+MS_{g})}{MS_{gy}+MS_{gl}}$. In this particular data, no matter how effort is made to conduct valid analysis of variance, there is no possibility to know which bread wheat genotype is consistently yielded above the experimental average. Because most of the interaction components are significant, no need of worrying about the main effects and hence exploiting the interaction component is essential. This necessitated the use of other statistical tool, in such AMMI is imperative to determine the relative stability of genotypes.

$$F_g = \frac{MS_g}{MS_e} = \frac{\delta^2{}_e + b\delta^2{}_{gly} + by\delta^2{}_{gy} + bly\delta^2{}_g}{\delta^2{}_e} - -(1)$$

$$F_g = \frac{MS_g}{MS_{gy}} = \frac{\delta^2{}_e + b\delta^2{}_{gly} + by\delta^2{}_{gl} + bly\delta^2{}_g}{\delta^2{}_e + b\delta^2{}_{gly} + by\delta^2{}_{gy}} - -(2)$$

Table 1: Analysis of variance based on three locations and two years

Sources of variations	Degree of freedom	Mean squares	Used error term for F-test of genotypes	
			Year*genotype	MSE
Total	377			
Block (b)	2	90960.4	0.470	0.47
Location (l)	2	13459859.0	69.97	69.97
Year (y)	1	12479592.1	64.87	64.87
Loc*year	2	13531511.5	70.34	70.34
Bloc(loc*year)	12	171531.9	0.890	0.89
Genotypes (g)	17	12171221.0	1.00NS	6.33**
l * g	40	756245.8	1.61NS€	3.93**
y * g	20	1212274.0	2.58**€	6.30**
l * y * g	40	469441.6	2.44**	2.44**
Error	238	192367.222		

€ tested using l*y*g as error term

AMMI analysis

AMMI analysis identified that three of the interaction principal components axis were significant at P≤0.01% (Table 2), and could explain 89% of the genotype by environment interaction sum square. In table 3 AMMI adjusted and re-ranked grain yield of each genotypes by their respective IPCA axis score and environmental IPCA axis scores, and thereby brought about a significant change in the ranks of genotypes. Relative contribution of each environment and genotypes to the GXE interaction were measured from the magnitude of respective IPCA 1 score, which is measured as their perpendicular distance from the IPCA 1 = 0.

Generally, the more genotypes or environments deviate from the IPCA1 = axis, the more they would contribute to the G x E interaction variances and the more unstable it they would be (Yan *et. al.*, 2000; Muhe and Assefa, 2011). Varieties and environments at the extreme top or bottom edge of the bi-plot are known to contribute more than their counterparts located closer to the IPCA1axis = 0(Fig.1). Accordingly, genotype, FH-934 contributed very low to the total genotype x environment interaction sum square whereas its counterpart HAR2575 highly contributed to genotype x environment interaction sum square. The standard checks HAR2562 and HAR2501 had the IPCA score of 11.22 and 3.8753, suggesting that they are highly interactive with growing environments. Each environment and variety main effects were plotted along the abscissa against their respective IPCA1 score as ordinate.

The dotted vertical line passing through the center of the bi-plot is represented by the experimental grand mean derived from all varieties and environments, and the dotted horizontal line showed the point where IPCA1 score = 0 (Fig 1). In the bi-plot, genotypes and environments are represented by small and capital letters, respectively. Those genotypes found at the right side of the grand mean are considered to be high yielding genotypes and environments while their counterparts located to the left side of the grand mean are lower yielding genotypes and environments (Crossa *et.al*., 1990; Muhe and Assefa, 2011). Genotypes and environments located at same side of the IPCA axis are interacting positively and produced desirable effects. As one can see in figure 1, the top yielding genotypes, FH-934, HAR2025, HAR3816, HAR1911 and ETBWC089MAMBA / HAR1384 were represented by 'c', 'f', 'k', 'i' and 'b', respectively.

All of these genotypes were selected and multiplied in 2008, a season characterized by yellow rust epidemics, genotypes FH-934 and HAR2025 were severely affected by yellow rust, and hence were not advanced to verification trial. Thus, bread wheat genotypes, HAR3816, HAR1911 and ETBWC089MAMBA/HAR1384 were verified, and only HAR3816 was officially released by the National Variety Releasing Committee and registered by the given name '*Bollo'* in 2009 for large scale production of wheat among the farmers.

Table 2: Additive main effects and multiplicative interaction based on grain yield kg/ha from bread wheat genotypes and 6 environments

Source	DF	SS	MS	F-value	Pr>F
Total	305	175279034.3			0.0000
Environments	5	55538082.4	11107616.5	64.76	0.0307
Reps within Environment	12	2058383.1	171531.9	13.24	0.0000
Genotype	16	21609634.2	1350602.1	1.82	0.0000
Genotype x Env.	80	59300678.9	741258.5	3.87	0.0000
IPCA 1	20	30236055.3	1511802.8	7.89	0.0001
IPCA 2	18	13332797.0	740710.9	3.87	0.0615
IPCA 3	16	9725319.7	607832.5	3.17	0.7985
Residual	192	36772255.680	191522.165		
Grand mean = 2945.822		R-squared = 0.7902		C.V. = 14.86%	

Genetic variance for entries = 33852.425, with a std. error of 25824.804; and Genetic variance for entries x genotype is 183245.441 with a std. error of 39129.012

Table 3: AMMI adjusted grain yield (kg/ha) of bread wheat genotypes across three locations and over two years

Genotype	Inewary		Keyit		Mehalmeda		
	2007	2008	2007	2008	2007	2008	Mean
F6-99,22-5	3866.33	2894.08	3174.02	2595.05	3829.52	2553.75	3152.13
ETBWC089MAMBA/HAR 1384	3140.32	2305.39	2446.39	3491.62	3856.97	3693.65	3155.72
FH 934	3690.32	2794.14	2997.11	3317.86	4070.88	3411.35	3380.28
HAR 2656	2951.73	2064.70	2258.41	2687.41	3382.51	2797.12	2690.31
HAR 2575	3709.73	2644.81	3018.52	1343.56	3164.50	1138.08	2503.20
HAR 2025	3392.31	2515.38	2698.87	3247.30	3878.49	3374.90	3184.54
HAR 2317	3011.29	2111.59	2318.13	2597.23	3372.54	2684.48	2682.54
HAR 2746	3393.03	2438.79	2700.51	2334.60	3455.05	2325.22	2774.53
HAR 1911	3325.67	2457.05	2632.14	3278.85	3857.45	3421.18	3162.06
HAR 2657	2912.96	2014.83	2219.78	2517.39	3282.79	2607.42	2592.53
HAR 3816	3285.84	2417.92	2592.30	3247.27	3821.45	3390.84	3125.94
HAR 3925	3010.92	2155.09	2317.24	3115.16	3612.84	3280.14	2915.23
HAR 1381	3349.13	2449.03	2655.97	2930.36	3708.19	3016.90	3018.26
HAR 2501 (c)	3215.12	2336.33	2521.71	3048.14	3691.10	3172.45	2997.48
HAR 3740	3138.78	2301.21	2444.89	3458.79	3840.90	3656.13	3140.12
F6-99,22-1	3143.99	2303.71	2450.12	3432.08	3831.28	3624.63	3130.97
HAR 2562 (c)	2519.67	1673.09	1825.88	2733.23	3172.36	2914.61	2473.14

Conclusion

Notwithstanding the immense potential uses of bread wheat in Ethiopia in general, and in North Shewa in particular, several biotic and abiotic factors inescapably induce an absolute reduction of grain yield of wheat. Sharing the national and regional wheat production constraints, a regional bread wheat variety trial was implemented with the objective of identifying high yielding, yellow rust resistant and relatively stable bread wheat variety under North Shewa highlands conditions. AMMI analysis identified that three of the interaction principal components axis were significant at P≤0.01%, and explained 89% of the genotype by environment interaction of sum square. The top yielding genotypes, FH-934, HAR2025, HAR3816, HAR1911and ETBWC089MAMBA / HAR1384 were represented by 'c', 'f', 'k' 'i' and 'b', respectively. Thus, bread wheat genotypes, HAR 3816,HAR1911andETBWC089MAMBA/HAR1384 were verified, and HAR3816 was officially released by the National Variety Releasing Committee and registered by the given name '*Bollo'* in 2009 for large scale production.

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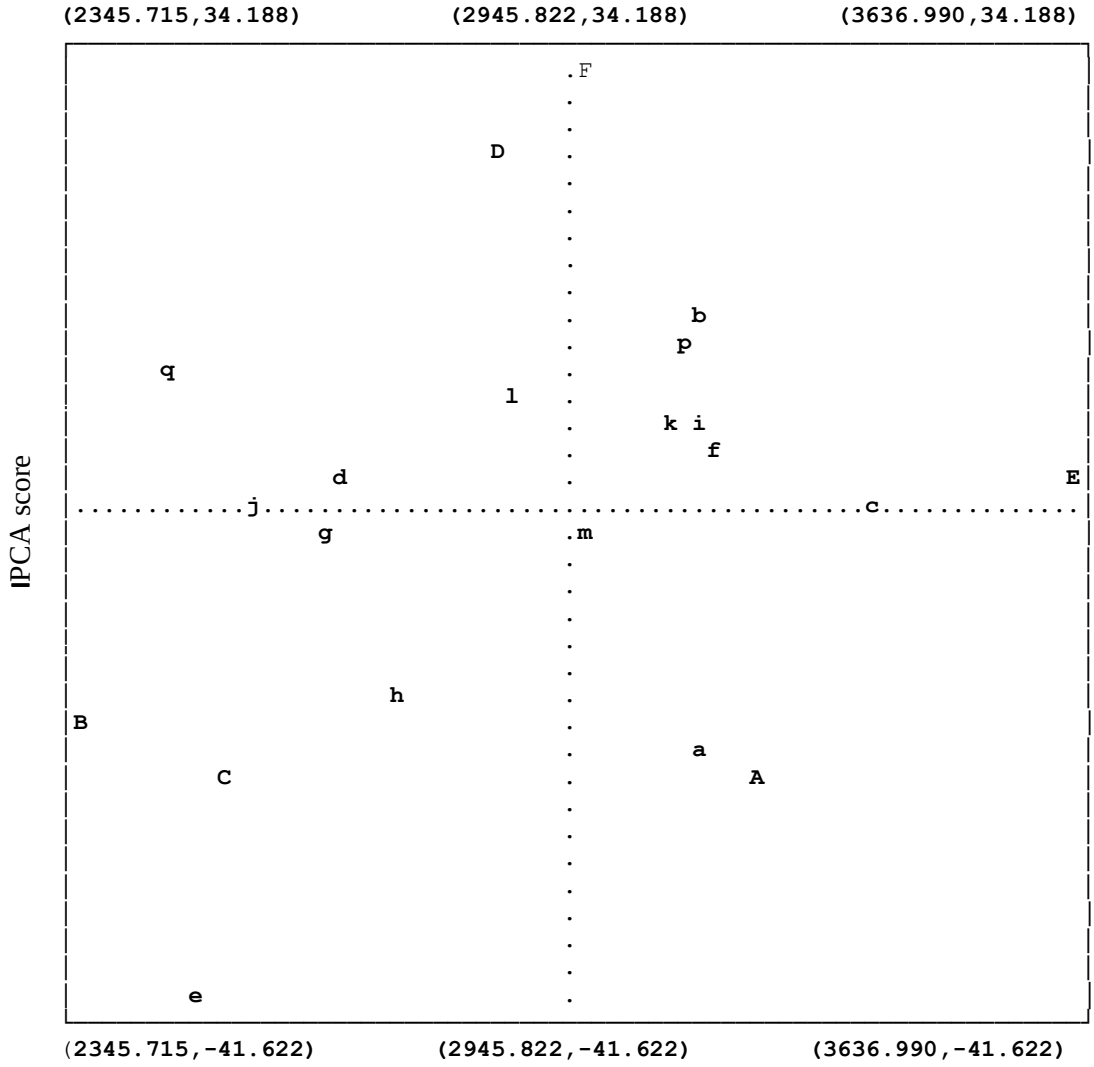
Fig 1: Bi-plot with abscissa (X-axis) plotting means from 2345.715 to 3636.990 and with ordinate (Y-axis) plotting IPCA1 from -41.622 to 34.188. Genotypes plotted as a,b,c, ... ; and environments as A,B,C,..., Note:1 genotypes in place of others with similar means and not shown.



Genotype and environment main effect

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