World Journal of Agricultural Sciences 10 (5): 210-215, 2014
ISSN 1817-3047

DOI: 10.5829/idosi.wjas.2014.10.5.1822

Parametric Stability Analysis of Malt Barley Genotypes for Grain Yield in Tigray, Ethiopia

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Abstract: An experiment was conducted using eight malt barley genotypes across eight environments with the objective of determining grain yield stability using parametric stability models. The trial was laid down in a randomized complete block design (RCBD) with three replications in the production year 2012-2013. The combined analysis of variance (ANOVA) revealed significant differences ($P \leq 0.01$) for genotype, environment and their genotype by environment interactions. The environment captured 72.71% of the variation. Strong rank correlation was observed between deviation from regression, Wricke's ecovalence, Lin and Binns's cultivar performance measure and additive main effect and multiplicative interaction effect stability value. The coefficient of variability and environmental variance were also strongly correlated. The interaction principal component one and two showed weak correlation with most of the parametric stability models. Mean grain yield was negatively correlated with environmental variance, Francis and Kannenberg's coefficient of variability, Wricke's Ecovalence, Lin and Binns's cultivar performance measure and additive main effect and multiplicative interaction stability value. Grain yield was positively correlated with deviation from the regression. Generally using the parametric stability models the genotype Bekoji was ranked first with regard to the stability and mean grain yield followed by the genotype Frie Gebs. Using parametric stability model the environmental variance, Francis and Kannenberg's coefficient of variability, Wricke's Ecovalence, Lin and Binns's cultivar performance measure, deviation from the regression and additive main effect and multiplicative interaction stability value the genotype Sabini was unstable coupled with low yield.

Key words: ASV · Genotype by Environment Interaction · Stability

INTRODUCTION

Crop failure is a usual phenomenon in developing countries where farmers are small-scale and characterized by fragile and marginal environments. Hence, yield stability plays a major role in reducing crop failure. The term stability of genotypes is central to all types of analysis of genotype by environment interactions, especially with reference to plant breeding stability has been described in many different ways over the years and there have also been different concepts of stability [1]. Generally stability is consistency in performance that would mean minimum variation among environments for a particular genotype [2].

The stability with which a plant breeder is concerned implies stability in those aspects of phenotype which are important economically, such as grain yield and quality. The desirable varieties that show low genotype by environment interaction for agriculturally important traits, especially grain yield, but not necessarily for other characteristics [3].Two different approaches commonly used to assessing stability are the static and the dynamic concepts [3].The static (biological) concept refers to the constant performance of a genotype over a wide range of environments implying that its variance among environments is zero. This type is seldom a desired feature of crop cultivars, since no response to improved growing conditions. The dynamic (agronomical) concept

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of stability implies that a stable genotype should always give high yield expected at the level of productivity of the respective environments. The performance of the genotype that has as lower genotype by environment interaction as small as possible is stable. Usually researchers [3] stated that all stability procedures based on quantifying genotype by environment interaction effects belong to the dynamic stability concept.

Different parametric stability models are available such as the environmental variance, coefficient of variation, Superiority index, Wricke's ecovalence, regression approach and additive main effect and multiplicative interaction effect stability value (ASV) is also comparable with the other stability parameters of AMMI model in the study of genotype by environment interaction and yield stability.

To recommend genotypes to the target environment, assessment of stability and using adequate stability measure is paramount important. Hence, the objective of this study is to assess the stability of released malt barley genotypes across diversified environments of Tigray using different parametric stability models.

MATERIALS AND METHODS

Experimental Design and Methods: The experiment was conducted in two locations during 2012 and six locations during 2013 cropping season. The detailed description of eight environments given (Table 1). The eight nationally released malt barley genotypes were: (Bekoji, Frie-Gebs, Sabini, IBONI174/03, Holker, Bahati, EH-1847 and HB-1533. The trial laid out in a randomized complete block design (RCBD) with three replications each. A total of 6 rows with row spacing of 0.2 meter and row length of 2.5 meter. Seed rate 80 kg ha^{-1} was used and drilling to the six rows. Fertilizer was applied 41 kg ha^{-1} N and 46 kg ha^{-1} P_2O_5 at planting and 23kg ha^{-1} N fertilizer urea was applied in split application in the vegetative stage of the crop and data for yield was collected from the four middle rows.

Statistical Analysis: A combined analysis of variance (ANOVA) was undertaken and the significant genotype by environment interaction was further substantiated by using different stability analysis. The environmental variance Coefficient of variation and Wricke's ecovalence were analyzed using (SAS, 2009) software. Superiority index of was analyzed using Genestat 13 software. The regression coefficient and deviation from regression was done using Crop stat 7.2 software. The additive main effect and multiplicative interaction effect stability value (ASV) was done by the formula suggested by [4] and ASV was calculated using Microsoft excel (2007).

$$ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA1score)^2 + \left\lceil IPCA2sccore \right\rceil^2}$$

Where

ASV = AMMI stability value
IPCA1 = interaction principal component analysis 1.
IPCA2 = interaction principal component analysis 2.
SSIPCA1 = sum of square of the interaction principal component one.
SSIPCA2 = sum of square of the interaction principal component two.

RESULTS AND DISCUSSION

Combined analysis of variance revealed that genotypes, environment and genotype by environment interaction were found significant ($P<0.01$). The environment captured 72.71% of the total sum of square followed by the genotype by environment interaction captured 23.31%. However, the genotype contributed 3.98% (Table 2). The large sum square of the environment implying that the environment was with higher differential in discriminating the performance of the genotype and caused most of the variation in grain yield.

Table 1: description of the testing environments

Code	Environment	Year	Longitude	Latitude	Altitude(m.a.s.l.)	Soil type
E1	Adigola	2013	39.33	120 31	2490	Clay
E2	Adigola	2014	39.33	120 31	2490	Clay
E3	Mekhan	2013	39.32°E	12.44°N	2423	Clay Loam
E4	Mekhan	2014	39.32°E	12.44°N	2423	Clay Loam
E5	Hashange	2014	39.52°E	12.58°N	2400	loam
E6	Emba-Hazti	2014	39.34°E	12.52°N	3000	Clay loam
E7	Atsella	2014	39.56°E	12.91°N	2800	Clay loam
E8	Hagere-selam	2014	39015' E	13061' N	2225	Clay loam

Source: Tigray regional Bureau of Agriculture (2013)

Table 2: Combined analysis of variance for eight malt barley genotypes across eight environments.

Source	df	SS	MS	% explained
Environments	7	20439	2919.9**	72.71
Replication/E	16	4721	295.1	
Genotypes	7	1119	159.8**	3.98
Genotype by Environment	49	6553	133.7**	23.31
Error	112	5292	47.2	

Table 3: Mean grain yield and environmental variance for eight malt barley genotypes across eight environments.

Genotypes	Environmental mean	Rank	Environmental Variance	Rank
Bekoji	38.33	1	170.860	4
Frie Gebs	36.07	3	112.680	2
Sabini	31.94	7	182.137	6
IBONI174/03	35.45	4	136.057	3
Holker	34.97	5	198.799	8
Bahati	32.38	6	173.055	5
HB-1533	31.21	8	98.495	1
EH-1847	37.16	2	191.540	7

The magnitude of the environment was 18.26% and 5.85% times greater than the genotype and genotype by environment interaction respectively.

In multi location yield trials the variation captured by the environment is 80% and genotype and genotype by environment interaction explained 10% [5]. Large environmental sum square was reported [6], [7] in food barely and [8] in malt barley had found large environmental variance. From the combined analysis of variance (Table 2), genotype by environment interaction is highly significant and hence superiority of genotypes across environments cannot be identified by considering only their mean grain yield. Thus, partitioning the genotype by environment interaction using different stability models is paramount important in selection and recommendation of genotypes in specified location.

Stability Analysis

The Environmental Variance: The smaller environmental variance, the more stable is the genotype and where the environmental variance is larger the unstable the genotype performance across testing environments. Genotype HB-1533 was stable followed by the genotype Frie Geb while, the genotype Holker was unstable genotype with higher environmental variance (Table 3). When grain yield and stability were simultaneously considered the genotype Frie Gebs was better genotype with grain yield greater than the grand mean and second rank with stability analysis.

Francis and Kannenberg's Coefficient of Variability (CVi): Stability and mean yield of the genotypes were being simultaneously considered and genotypes with lower coefficient variability are considered as stable while, genotypes with higher coefficient variability unstable but the gain yield for selection should be simultaneously considered. When the coefficient variability only considering the G2 (Fire-Gebs) was with lower coefficient variability and stable genotype and the genotype G3 (Sabini) was interactive genotype with higher coefficient variability. When the mean grain yield and stability considered the G1 (Bekoji), G2 (Fire-Gebs) and G4 (Holker) were best genotypes respectively (Fig. 1).

Lin and Binns's Cultivar Performance Measure (Pi): Genotype with the lowest (Pi) value is considered the stable [1].The genotype Bekoji was with lower Lin and Binns's cultivar performance measure and as a result it was stable genotype. Sabini was with higher Lin and Binns's cultivar performance measure and was the most unstable genotype coupled with the lower yield less the grand mean (Table 4)

Wricke's Ecovalence Analysis: A genotype with lower ecovalence W = 0 is regarded as stable in all environments. The genotype Bekoji was with lower Wricke's Ecovalence value. Hence, it was stable genotype followed by the genotype Fire-Gebs. The genotype sabini was with higher Wricke's Ecovalence value and as a result the genotype was unstable genotype (Table 5)

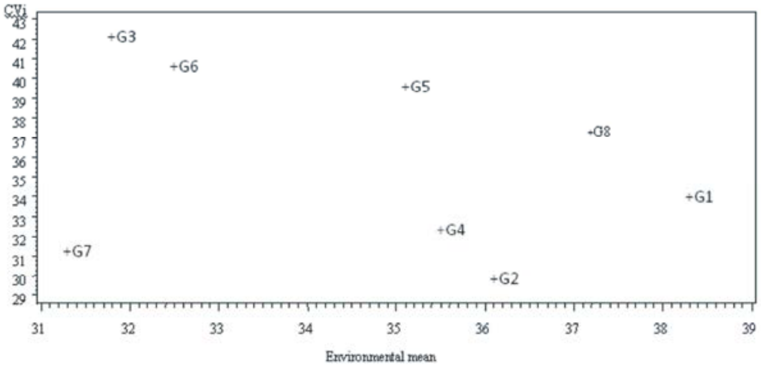

Fig 1: Mean yield (qt/ha) plotted against CV (%) from eight malt barley genotypes over eight environments.

Table 4: Lin and Binns's cultivar performance measure for eight malt barley genotypes over eight environments.

Genotype	Pi	Rank	Mean Yield	Rank
Bahati	73.93	6	32.38	6
Bekoji	15.57	1	38.33	1
EH-1847	32.03	3	37.16	2
Frie Gebs	29.93	2	36.07	3
HB-1533	103.84	8	31.21	7
Holker	39.82	4	34.97	5
IBONI174/03	50.09	5	35.45	4
Sabini	89.87	7	31.94	8

Table 5: Wricke's Ecovalence value for eight malt barley genotypes over eight nvironments.

Genotype	Environmental mean	Rank	Wi	Rank
Bekoji	38.33	1	98.5	1
Frie Gebs	36.07	3	106.1	2
Sabini	31.94	7	646.8	8
IBONI174/03	35.45	4	344.3	6
Holker	34.97	5	153.1	3
Bahati	32.38	6	220.8	5
HB-1533	31.21	8	345.9	7
EH-1847	37.16	2	215.1	4

using this stability [8] recommend two malt barley genotypes with lower contribution to genotype by environment interaction.

Eberhart and Russell's joint regression analysis: genotypes performance is generally expressed in terms of three parameters, mean yield, regression coefficient (bi) and deviation from the regression (S^2di). According to this model a stable genotype should have a high mean yield, b = 1 and $S^2di = 0$. Considering the three evolution of joint regression the genotype Bekoji was stable with outstanding yield performance, having the regression slope b=1 and the minimum standard deviation. Generally according to the regression coefficient (bi) all the malt barley genotypes had similar response to the varying environmental condition.However, all the malt barley genotypes had large environmental variance (Table 6). The Stability of barley genotypes measured by regression was not significantly different from 1.0 for most genotypes indicating a good potential for higher yields under improved environmental conditions.

AMMI Stability Value (ASV): The additive main effect and multiplicative interaction effect stability analysis (ASV) is used to decompose the interaction effect. Considering mean grain yield as first criteria for evaluating the malt barley genotypes Bekoji was with higher mean grain yield of 38.33 Qt/ha followed by the genotype EH-1847 with 37.16 and the genotype HB-1533 was with low mean grain yields (Table 8). The interaction principal component one (IPCA1) scores and the interaction principal component two in the AMMI model are indicators of stability [12]. Considering the first interaction principal component (IPCA1) the genotype Fire-Gebs was stable (0.02) was followed by Holker (0.05).When the second interaction principal component (IPCA2) was considered Fire-Gebs and Bekoji was the most stable genotypes (Table 7).

The two principal components have their own extremis, but calculating the AMMI stability value (ASV) is a balanced measure of stability [4]. The Genotype with lower ASV value is considered stable and genotype with higher ASV is unstable. According to the ASV ranking,

Table 6: Joint regression analysis for eight malt barely genotypes over eight environments.

Genotype	Mean	Rank	b_i	S^2d
Bekoji	38.33	1	1.154	13.11
Frie Gebs	36.07	3	0.907	16.46
Sabini	31.94	7	0.874	105.58
IBONI174/03	35.45	4	0.862	54.73
Holker	34.97	5	1.238	17.61
Bahati	32.38	6	1.090	35.68
HB-1533	31.21	8	0.705	45.45
EH-1847	37.16	2	1.171	31.78

Table 7: AMMI stability value of eight malt barley genotypes across eight environments.

Genotype	Mean yield	IPCA1	IPCA2	ASV	Rank
Bahati	32.38	-1.13	1.64	2.73	4
Bekoji	38.33	-0.54	-0.53	1.17	2
EH-1847	37.16	1.96	1.89	4.23	6
Frie Gebs	36.07	0.02	0.12	0.12	1
HB-1533	31.21	1.75	-2.30	4.08	5
Holker	34.97	0.05	2.38	2.38	3
IBONI174/03	35.45	2.19	-1.86	4.62	7
Sabini	31.94	-4.30	-1.35	8.43	8

Table 8: Spearman rank correlation of stability models.

	Si2	Cvi	Pi	WI	bi	s2di	ASV	Yield	IPCA1	IPCA2
Si2										
Cvi	0.78*	0								
Pi	-0.14	0.285	0							
WI	-0.09	0.30	0.92**	0						
bi	0.78*	0.38	-0.61	-0.66	0					
s2di	-0.047	0.33	0.85**	0.97**	-0.64	0				
ASV	0.190	0.42	0.64	0.85*	-0.40	0.90*	0			
Yield	0.14	-0.26	-0.95**	-0.8*	0.54	-0.714*	-0.42	0		
IPCA 1	-0.57	-0.35	0.26	0.30	-0.59	0.38	0.19	-0.142	0	
IPCA 2	-0.14	-0.21	0.38	0.11	-0.11	0.047	-0.26	-0.57	0.071	0

the genotype Frie-Gebs was the most stable with an ASV value of 0.12 followed by the genotype Bekoji with ASV value of 1.17.The genotype Sabini was the most unstable with ASV value of 8.43 (Table 7).

Comparison of the Parametric Stability Models: Spearman rank correlation was computed among stability parameters and mean grain yield (Table 9). Significant and positive ($P<0.01$) rank correlation was obtained between Wricke's ecovalence and Lin and Binns's cultivar performance measure ($r=0.92$). The regression coefficient was positively and significantly ($P<0.05$) correlated ($r=0.78$) with the environment variance. The stability model deviation from the regression was significantly and strongly correlated with Wricke's ecovalence, Lin and Binns's cultivar performance measure and ASV value implying that the stability models were similar in arrangement of the malt barley genotypes with regard to their stability (Table 8). The coefficient of variability and environmental variance were strongly correlated and gives similar pattern in ranking of the genotypes and this implying that they can be used interchangeably in the study of genotype by environment of malt barley and the result was in agreement with [9].Yield was negatively correlated with most of the stability models implying that Compatibility of high yield and stability of grain yield performance is an important but difficult to achieve at the same time [10] similar result was reported by [8] in malt barley.

ACKNOWLEDGEMENTS

The first author would like to thank to Alamata agricultural research center and Meklle agricultural research center for the support provided during the stud. My especial thanks also goes to meklle university CASCAPE project and Tigray agricultural research institute for funding of the research.

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