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Research Article

Genetic analyses of malting quality attributes and SREG biplot study of high input-north western Indian environments in barley (*Hordeum vulgare* L.)

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Abstract

Fifteen advance barley genotypes were evaluated at 9 different agro-ecologies of north western India to assess the genotype by environment crossovers, identify discriminating and representative environments for malt barley and vis-a-vis study of variation, effectiveness and inter-relationship among malting quality traits. Average diastatic power and β-glucan were exhibited as 109.45°L and 4.51%, which ranged from 102.30-114.00°L and 3.10-6.30%, respectively. Hot water extract, Kolbach index and grain protein content ranged from 79.30-81.70%, 39.00-41.00 and 9.40-12.00%, respectively. Diastatic power, β-glucan, grain protein content, hot water extract, hectolitre weight and 1000 grain weight revealed effective in different principal components. The highest correlation coefficient was depicted r=0.85 (hectolitre weight and germinative energy) followed by r=0.83 (hectolitre weight and malt friability), r=0.70 (malt friability and germinative energy) etc. The pooled mean grain yield across the locations was exhibited as 45.38 q/ha., which ranged from 35.58 q/ha to 62.20 q/ha. The 9 locations were grouped into four mega environments and Durgapura location depicted the separate mega environment. The environments i.e. Navgaon and Modipuram were discriminating and representative, while the locations *viz.* Karnal, Bawal, Durgapura and Bhatinda were also informative under high input agro-ecologies of north western Indian plains.

Key words: Principal components, SREG-biplot, correlation, malt barley.

1. Introduction

Barley is one of the first domesticated cereals, which contributes 5.5-6% of the global cereals and 11.5-12% of the coarse cereals production (Pal *et al.*, 2012; Kumar *et al.*, 2013b; Kumar *et al.*, 2014). Barley is used as food crop in many countries of Africa, Middle-East, South America and in Asian countries including India. During 2013, globally the area under the crop was 49.14 million hectares with a production of 143 million metric tons (FAO Stat, 2015). In India, barley is an important coarse cereal crop, being grown in *rabi,* (winter) season in northern plains. Barley occupies area in the states of Rajasthan, Uttar Pradesh, Madhya Pradesh, Punjab, Haryana, and Bihar in plains and Himachal Pradesh, Uttarakhand and Jammu & Kashmir in the hills. During 2013-14, India contributed nearly 9-10% of the Asian barley production with estimates of 1.82 million metric tons (http://eands.dacnet.nic.in). Malt is the second largest use of barley and among cereals, barley is preferred for malting owing to presence of husk, firm texture of kernels and its enzymatic activity (α and β-amylases mainly). The utilization of barley for malting and brewing industry has picked up recently with an increase of consumption of beer, health drinks and other malt based products in India. Barley malting quality characters are the polygenic attributes and needs to be study for variation, effectiveness and interrelationship for directional selection in malt barley genetic enhancement.

Most of the plant breeding programmes are designed to culminate into superior genotypes, however the environment plays an important role in changing relative ranking of the breeding lines at different locations. Genotype x environment interaction affects the genetic analysis and give biased estimates of genetic parameters. The SREG (site regression) biplot is widely popular among agricultural researchers for genotype evaluation, mega environment delineation and representativeness (Yan *et al.*, 2007; Alwala *et al.*, 2010; Hagos and Abay, 2013; Rad *et al.*, 2013). The GGE-biplot exhibits the first two principal components derived from singular value decomposition (SVD) of environment-centered yield data (Yan *et al.*, 2000; Jalata, 2011; Mortazavian *et al.*, 2014). Therefore, the present study was undertaken to assess the genotype by environment crossovers, identifying discriminating environments, superior genotypes with delineation of component pattern and correlations studies for malting quality parameters.

2. Materials and methods

During *rabi*, 2011-12, experiments were conducted at 9 locations *viz.* Bawal, Bhatinda, Durgapura, Hisar, Modipuram, Mathura, Pantnagar, Karnal and Navgaon. The fifteen genotypes were grown in a randomized complete block design (RCBD) with 5.40 square m plot with 4 replications at each location. The processed grain samples (except Navgaon) were micro-malted as per standard cycle of 120-128 hrs. [steeping (4 steps), germination (3 steps) and kilning (8 steps)]. The data were recorded for two grain physical parameters *i.e.* 1000 grain weight (g), hectolitre weight (kg/hl) and eight quality parameters namely grain protein content (% dry wt. basis), malt yield (%), malt friability (%), hot water extract/ malt extract (%), germinative energy (%), β-glucan (%), diastatic power (^{o}Lintner) and Kolbach index (%). Grain protein content and Kolbach index were analyzed using Near Infrared Reflectance (FOSS NIR) system, while diastatic power was estimated by Institute of Brewing (IOB) method. The rest of the biochemical parameters were recorded as per European Breweries Convention (EBC) procedure (Analytica-EBC, 2003). Analysis of variance (ANOVA), locational pooling, correlations and principal component analyses were performed using SAS Institute, 9.3, 2013. The GGE biplot is based on Sites Regression (SREG) linear-bilinear multiplicative model and is environment centered (Yan *et al.*, 2000; Yan, 2001; Yan and Hunt, 2001; Gauch, 2006; Yan *et al.*, 2007; Gauch *et al.*, 2008). GGE biplots address two way data matrix (row x column) *i.e.* number of genotypes tested at multi-locations in replicated manner. Biplot was generated after analyzing G x L data using computing facility available at ICAR-Indian Agricultural Statistics Research Institute website (http://iasri.res.in/).

3. Results and discussion

Average diastatic power was exhibited as 109.45^{o}L and ranged from 102.30-114.00^{o}L. Malt friability, germinative energy, 1000 grain weight, hectolitre weight and malt yield had the general means of 67.00%, 94.86%, 47.36 g, 64.62 kg/hl and 84.79 %, respectively. β-glucan depicted the average value of 4.51%, which ranged from 3.10-6.30%. Hot water extract, Kolbach index and grain protein content were ranged from 79.30-81.70%, 39.00-41.00 and 9.40-12.00%, respectively.

The first five principal components (PCs) exhibited the eigen values >1 with 59.27, 78.43, 89.47, 95.60 and 97.50 per cents cumulative variation, respectively. The initial few PCs showed quite good amount of variation and could be used beneficially for grouping the malting attributes (Dehghani *et al.*, 2006). Diastatic power, β-glucan, grain protein content, hot water extract, hectolitre weight and 1000 grain weight were identified as effective traits in different PCs, respectively (Table 1).

Table 1. Principal components for different malting quality parameters

Characters	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9	PC 10
Diastatic power	0.28	0.92	0.17	-0.03	-0.01	-0.05	0.06	0.03	0.01	-0.18
Malt friability	0.81	-0.15	-0.42	-0.28	0.15	-0.06	-0.15	-0.01	-0.05	0.12
Germinative energy	0.32	-0.16	0.10	0.67	-0.23	0.15	-0.33	0.21	0.10	-0.43
Beta-glucan	0.04	0.12	0.07	0.30	0.17	0.23	-0.02	0.53	-0.29	0.66
1000 grain wt.	0.26	-0.25	0.83	-0.14	0.36	-0.13	0.04	-0.04	-0.11	-0.05
Hectolitre wt.	0.30	-0.11	0.12	0.12	-0.46	0.15	0.73	-0.13	0.21	0.22
Hot water extract	0.03	0.05	-0.05	0.13	0.24	0.68	0.03	-0.56	-0.37	-0.08
Kolbach index	-0.03	0.03	-0.14	0.21	0.66	0.10	0.23	0.05	0.66	-0.04
Malt yield	-0.04	-0.07	0.07	-0.52	-0.11	0.60	0.01	0.50	0.15	-0.27
Protein content	0.02	0.08	0.24	-0.10	-0.22	0.20	-0.53	-0.32	0.50	0.45

The highest significant positive correlation coefficient was depicted between hectolitre weight and germinative energy (r=0.85**) followed by r=0.83** (hectolitre weight and malt friability), r=0.70** (malt friability and germinative energy), r=0.62* (1000 grain weight and hectolitre weight) etc. (Table 2). β-glucan was positively associated with diastatic power, germinative energy and Kolbach index. The hot water extract was found positively correlated with Kolbach index, diastatic power, malt friability, germinative energy, hectolitre weight etc. Similar association among different malting quality traits have been also reported by Verma *et al.*, 2008.

Pooled mean grain yield across the locations was depicted as 45.38 q/ha., which ranged from 35.58 q/ha (Karnal) to 62.20 q/ha (Durgapura). The highest mean grain yield was

Table 2. Correlation coefficients between different malting quality parameters

Traits*	DP	Fb	GE	β-glu	1000 GW	Hl	HWE	KI	MY
Fb	0.33								
GE	0.17	0.70**							
β-glu	0.54*	0.09	0.48						
1000 GW	0.08	0.41	0.52*	0.10					
Hl	0.27	0.83**	0.85**	0.20	0.62*				
HWE	0.23	0.16	0.24	0.50	-0.09	0.13			
KI	-0.04	-0.11	-0.04	0.39	-0.35	-0.32	0.46		
MY	-0.20	-0.09	-0.46	-0.50	0.11	-0.13	-0.06	-0.41	
GPC	0.44	-0.013	0.07	0.12	0.50	0.19	0.03	-0.58*	0.30

**DP=diastatic power, Fb=friability, GE=germinative energy,*

β-glu=β –glucan, 1000 GW=1000 grain weight, Hl=hectolitre weight, HWE=hot water extract, KI=Kolbach index, MY=malt yield and GPC=grain protein content

Table 3. Grain yield *Per se* performances at 9 locations

Genotype	Bawal Yield Q/ha	Bhatinda Yield Q/ha	Durgapura Yield Q/ha	Hisar Yield Q/ha	Karnal Yield Q/ha	Mathura Yield Q/ha	Modipuram Yield Q/ha	Navgaon Yield Q/ha	Pantnagar Yield Q/ha
BH 902	54.35^{A}	56.04	56.76^{DEF}	51.99^{A}	37.81^{ABC}	62.80^{C}	44.57^{BCD}	47.13^{A}	42.27^{ABCD}
BH 963	40.91^{DEF}	54.77	64.01^{CDE}	42.45^{DE}	28.30^{CD}	46.50^{E}	34.93^{EF}	41.16^{ABC}	35.63^{DE}
BH 966	41.97^{CDEF}	54.11	70.05^{ABC}	26.14^{F}	39.62^{ABC}	71.26^{AB}	45.98^{BC}	40.27^{BC}	44.38^{ABC}
DWRUB 52	42.63^{CDEF}	57.00	64.61^{CD}	50.00^{ABCD}	39.04^{ABC}	24.76^{F}	43.78^{BCD}	42.10^{ABC}	42.87^{ABCD}
DWRB 101	44.08^{CD}	51.51	64.61^{CD}	51.03^{AB}	36.17^{ABC}	54.35^{D}	47.37^{AB}	42.10^{ABC}	49.82^{A}
DWRB 102	47.41^{BC}	54.41	56.76^{DEF}	42.42^{DE}	31.91^{BCD}	42.27^{E}	43.06^{BCD}	37.80^{BCD}	35.63^{DE}
DWRB 103	51.45^{AB}	52.78	79.11^{A}	50.52^{ABC}	30.07^{BCD}	28.38^{F}	33.48^{F}	42.59^{ABC}	39.86^{BCD}
DWRB 104	40.82^{DEF}	52.84	53.74^{EF}	40.31^{E}	44.20^{A}	30.80^{F}	40.91^{CD}	42.88^{ABC}	36.84^{CDE}
DWRB 105	37.32^{EFG}	53.50	59.18^{DEF}	42.90^{CDE}	31.74^{BCD}	64.61^{BC}	39.61^{DE}	43.61^{ABC}	37.14^{CDE}
K 551	43.48^{CDE}	49.64	48.91^{F}	39.01^{E}	39.31^{ABC}	60.99^{CD}	42.81^{BCD}	44.08^{AB}	27.17^{F}
PL 867	33.37^{G}	58.39	57.97^{DEF}	45.44^{ABCDE}	41.20^{AB}	42.27^{E}	51.96^{A}	40.97^{ABC}	41.06^{BCD}
PL 870	36.69^{FG}	57.00	57.97^{DEF}	45.89^{ABCDE}	38.09^{ABC}	55.56^{D}	47.77^{AB}	40.40^{ABC}	47.10^{AB}
RD 2850	42.87^{CDEF}	50.85	58.57^{DEF}	43.36^{BCDE}	34.12^{ABCD}	41.06^{E}	44.78^{BCD}	38.08^{BCD}	38.35^{CDE}
RD 2851	33.12^{G}	53.14	65.22^{BCD}	30.65^{F}	24.28^{D}	74.28^{A}	41.76^{CD}	33.37^{D}	38.65^{CDE}
RD 2668	42.88^{CDEF}	56.46	75.48^{AB}	41.52^{E}	37.80^{ABC}	30.80^{F}	34.96^{EF}	37.30^{CD}	31.70^{EF}
G. Mean	42.22	54.16	62.20	42.91	35.58	48.71	42.52	40.92	39.23
p-Value	<.0001	0.2736	<.0001	<.0001	0.0022	<.0001	<.0001	0.0008	<.0001
CV (%)	7.75	8.21	9.06	9.52	17.14	7.60	6.69	8.63	10.16
SE(d)	2.32	3.14	3.99	2.89	4.31	2.62	2.01	2.50	2.82
LSD at 1%	6.24	8.48	10.75	7.79	11.63	7.06	5.42	6.73	7.60

exhibited at Durgapura (62.20 q/ha.) followed by Bhatinda (54.16 q/ha.), Mathura (48.71 q/ha.), Hisar (42.91 q/ha.) locations etc. (Table 3). The genotype BH 902 (50.41 q/ha.) was the highest yielder followed by DWRB 101 (49.00 q/ha.), BH 966 (48.20 q/ha.), PL 870 (47.39 q/ha.), PL 867 (45.85 q/ha.) etc. across the locations (Table 3).

Analysis of variance revealed significant treatment mean squares ($p<.0001$) for all the locations, except Bhatinda. Similarly, combined analysis of variance also depicted highly significant differences for variety x locations ($p<.0001$), which exhibited the presence of genotype and environmental crossovers and bi-plot model would be good to identify niches and to draw further inferences.

In biplot analysis first two principal components altogether captured 71.45 per cent cumulative variation. The vertex genotypes in this investigation identified were RD 2850, PL 867, BH 902, DWRB 103, PL 870, RD 2668 and DWRB 102 (Figure1). The polygon view of GGE-biplot is very common and unique feature and easy to visualize the interaction patterns between genotypes and environments (Dehghani *et al.*, 2006; Yan and Kang, 2003). Nine locations were grouped into four sectors and exhibited the four different mega environments. The first mega-environment comprised of the locations Hisar and Navgaon, while the second mega-environment contained locations Karnal, Pantnagar, Mathura and Bawal (Figure 1).

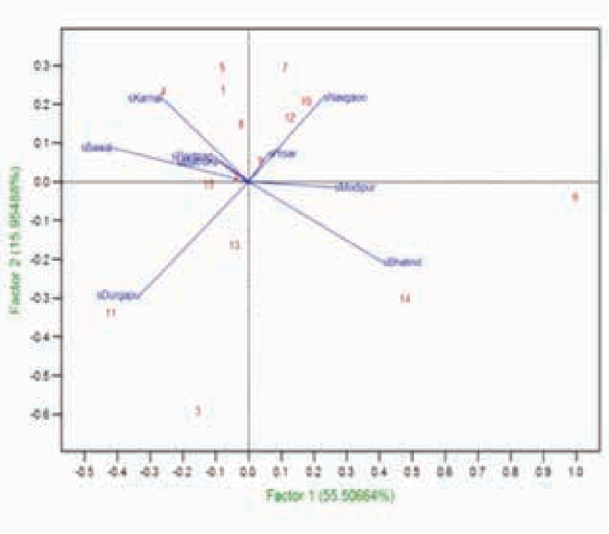

Fig. 1. SREG biplot for 9 locations and genotypes

Genotypes 1-15:DWRUB 52, K 551, RD 2850, PL 867, BH 902, DWRB 103, PL 870, BH 963, RD 2851, BH 966, RD 2668, DWRB 101, DWRB 104, DWRB 102 and DWRB 105

The locations Modipuram and Bhatinda formed third mega environment, whereas the Durgapura location depicted the separate mega environment. The genotypes BH 902, BH 966, DWRB 101, PL 870 etc. were high yielders across the locations. The ideal genotypes had the high *per se* and consistent performance in different environments (Yan *et al.*, 2000).

Discriminating ability and representativeness of the environments are two important features of the GGE-biplot technique, which enhances the efficiency of the programme (Yan, 2001). The locations Navgaon and Modipuram were the discriminating, while the environments viz. Pantnagar and Mathura were found non-discriminating and similar to each other (Figure 1).

The cosines between environments viz. Bhatinda, Hisar, Navgaon etc. were depicted acute and these were positively correlated environments, while the cosines between environments Durgapura, Modipuram, Hisar etc. were obtuse and negative correlations were observed. The highest negative correlations coefficients were depicted between Mathura and Hisar (-0.44**) followed by Modipuram and Bawal (-0.26*) and Navgaon and Durgapura (-0.23) etc. Similarly, the cosines between these environments were also obtuse and depicted negative correlations (Figure 1). The positive correlations were estimated between Bawal and Hisar (0.37**), Navgaon and Hisar (0.31*) and Navgaon and Bawal locations (0.30*).

The locations Navgaon and Modipuram were found more discriminating and representative under high input conditions. Yan *et al.*, 2000; Dehghani *et al.*, 2006; Yan and Tinker, 2006 also emphasized that the environments with long vectors and less cosines are more discriminating and representative and can be used as potential environments in future studies. The location Navgaon was also emphasized as representative and discriminating by Kumar *et al.,* 2014. Hence, these locations are best representatives for multi-locational evaluation under resource limitations. Out of considered 9 locations, the environments i.e. Durgapura, Bhatinda, Bawal and Karnal would also be discriminating in future varietal evaluation.

Malting quality traits are polygenic parameters and in addition to genetic effects, directly or indirectly affected by environment, agronomic practices and malting regimes. In different principal components the traits viz. diastatic power, β-glucan, grain protein content, hectolitre weight, 1000 grain weight and hot water extract were identified as effective traits and needs further emphasis for malt barley genetic enhancement. These above mentioned malting quality characters are important traits and have been also supported by Kumar *et al.,* (2013a). The estimates of correlation coefficients were also revealed variable association among different malting quality traits. Hectolitre weight was found positively associated with malt extract and revealed that the genotypes with bold grains, plump kernels and high starch are more desirable for better malt recovery. The malt friability is the measurement of conversion of starch into sugars and was found associated with hectolitre weight and malt extract. The grain protein content and malt extract were correlated minutely, which is desirable for beer stability and avoidance of chill haze formation.

In malt barley breeding programme for the improvement in hot water extract the quality characters namely hectolitre weight, malt friability, diastatic power, germinative energy coupled with low grain protein content can be regarded as efficient selection parameters. Whereas, high β-glucan coupled with high protein content would be desirable for food barley, energy drinks and multi grain blends. The genotypes BH 902, BH 966, DWRB 101 and PL 870 were high yielding across the locations. The environments Navgaon, Modipuram, Bawal, Karnal, Durgapura and Bhatinda were representative for genotypic evaluation under high productive conditions of north western Indian plains.

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