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Short Communication

Assessment of barley genotypes for malting quality: Genotype x environment interactions

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Abstract

Investigating and improving malting quality in barley is long-standing objective worldwide. Genotype by environment interactions (G x E) result inconsistent genotypic performance and obstruct realization of quality traits under varying environments. The present investigation delineated implications of G x E on malting quality parameters studied for 45 genotypes over three years. The combined analysis showed significant G x E interactions (P<0.01) for 1000 grain wt., malt friability and hot water extract (malt extract). The year source of variation highly affected malt extract (82.57 %) followed by malt friability (51.82 %). Average malt extract was observed higher (81.06 %) during the year 2013, which received higher precipitation. The significant G x E were further portrayed into GGE biplots and initial two principal components depicted higher variation of 93.07, 92.00 and 92.45 % for 1000 grain wt., malt friability and hot water extract, respectively. Grain protein content revealed negative correlations with malt extract (-0.60) and malt friability (-0.53**). The exotic genotypes Sloop-VIC-VB9953, Henley and Xanadu exhibited marginal high malting quality but suffered with low grain yield and prolonged maturity.**

Key words: G x E, malting quality, barley, GGE and GT biplot

Barley is an ancient and one of the first domesticated sacred grains principally utilized for feed, food and malting and brewing purposes worldwide (Baik and Ullrich 2008; Kumar et al. 2018). Malting quality is a complex phenomenon and majorly defined by grain physical and biochemical traits (Arends et al. 1995; Fox et al. 2003). The grain physical parameters define the grain plumpness, boldness and uniformity and are indicators of higher starch content, consistent germination and processing for better malt recovery (Fox et al. 2003; Gupta et al. 2010). Grain protein content is a crucial factor during malting, modification and mashing and required in optimal range (10-12% dwtb) for yeast amino acid nutrition, shelf life of beer, foam stability, avoidance of chill haze formation and has negative association with carbohydrates and hot water extract (Molina-Cano et al. 1997; Fox et al. 2003; Kumar et al. 2015a). Hordeins are major storage proteins in barley, soluble in aqueous alcohol and comprised of sulphur poor B and C and sulphur rich D and A fractions (Shewry et al. 2001; Fox et al. 2003). Arends et al. 1995 and Kumar et al. 2017 reported that the key enzymes *i.e.* α-amylase, β-amylase, limit dextrinase and α-glucosidase play significant role during malting and mashing and collective activity of these starch hydrolysing enzymes known as diastatic power (DP) and indicates apparent attenuation limit (AAL). Hot water extract is an ultimate trait of interest for consideration by researchers and industries and highly influenced by genetic constitution, environment, agronomic package, malting recipes, mashing process etc. (Fox et al. 2003). Genotype by environment interaction influences genotypic ranks, impair selection efficiency, cultivar development under varying environments and impedes the real genetic expression and realization (Rakshit et al. 2012; Kumar et al. 2016b). Site regression linear-bilinear based GGE biplot method has provided quick and graphical visual tool for cultivar evaluation and to comprehend genotype by environment interaction in an easy manner (Yan et al. 2000; Yan and Tinker 2006). The concrete research

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efforts are imperative as beer industry growth has been forecasted as 7.5% during 2017-2021 and the number of craft micro-breweries has risen tremendously to 80 during 2017 from 02 in 2008 in India. Therefore, we studied the malting quality of 45 barley genotypes over three years to delineate genotype by environment interactions and to identify promising genotypes using GGE biplot method.

To study malting quality characters the experiments were conducted consecutively over three years during 2011-12, 2012-13 and 2013-14 at ICAR-IIWBR, Karnal (earlier DWR) with 45 indigenous and exotic barley genotypes, where the genotypes G1 (DWRUB52), G2 (DWRUB64) and G3 (DWRB73) were the commercial cultivars. After harvesting the processed grain samples were micro-malted in *Joe White micro malting system* as per standard cycle of 120-128 hrs. Data were recorded for two grain physical characters i.e., 1000 grain weight (g), hectolitre weight or test wt. (kg/hl) and three quality parameters viz., grain protein content (% db), malt friability (%) and malt extract (%). The malting quality was analyzes as per European Breweries Convention (EBC) procedures (Analytica-EBC 2003) and GGE biplots were constructed using R version 3.3.2 and delineated as reported by Yan et al. (2007).

The pooled analysis of variance revealed significant genotype and year mean squares and year source of variation explained 82.57 % for hot water extract, 51.82 % for malt friability and 48.50 % for 1000 grain wt. of total variation, respectively. G × E interaction mean squares were found significant for 1000 grain wt., malt friability and hot water extract and necessitated to further study genotype and malting quality traits by any robust stability method. Genotypes by environment interactions were found non-significant for hectolitre wt. and grain protein content. These non-significant effects could be explained as the experiments were conducted under similar timely sown, irrigated conditions and maximum temperature during grain filling did not much differ over three years and ranged between 34-37^{0}C. However, the high temperature during grain filling may lead to overall high grain protein content with more accumulation of sulphur poor C hordeins (Shewry et al. 2001; Kumar et al. 2015b). On the basis of pooled *per se* performances the control variety DWRB73 showed the highest 1000 grain wt. of 56.78 g followed by the genotypes, BK306 (56.70 g), DWR45 (56.69 g), DWR46 (54.54 g) and BCU1 (52.20 g) etc. The pooled hectolitre wt., grain protein content and malt friability were ranged from 56.36-70.86 kg/hl, 8.00-12.49% and 44.45-85.33 %, respectively. The pooled average hot water extract was observed to be 80.16 %, which ranged from 76.14-84.25 per cent. The highest best linear unbiased estimates (BLUEs) for 1000 grain wt. (45.58g) and grain protein content (10.37%) were observed during 2011-2012, which varied from 31.36-62.14g and 7.51-13.44%, respectively. The hectolitre weight (64.24 kg/hl) was recorded higher during 2012-2013, whereas the malt friability (72.81%) was exhibited higher during 2013-2014.

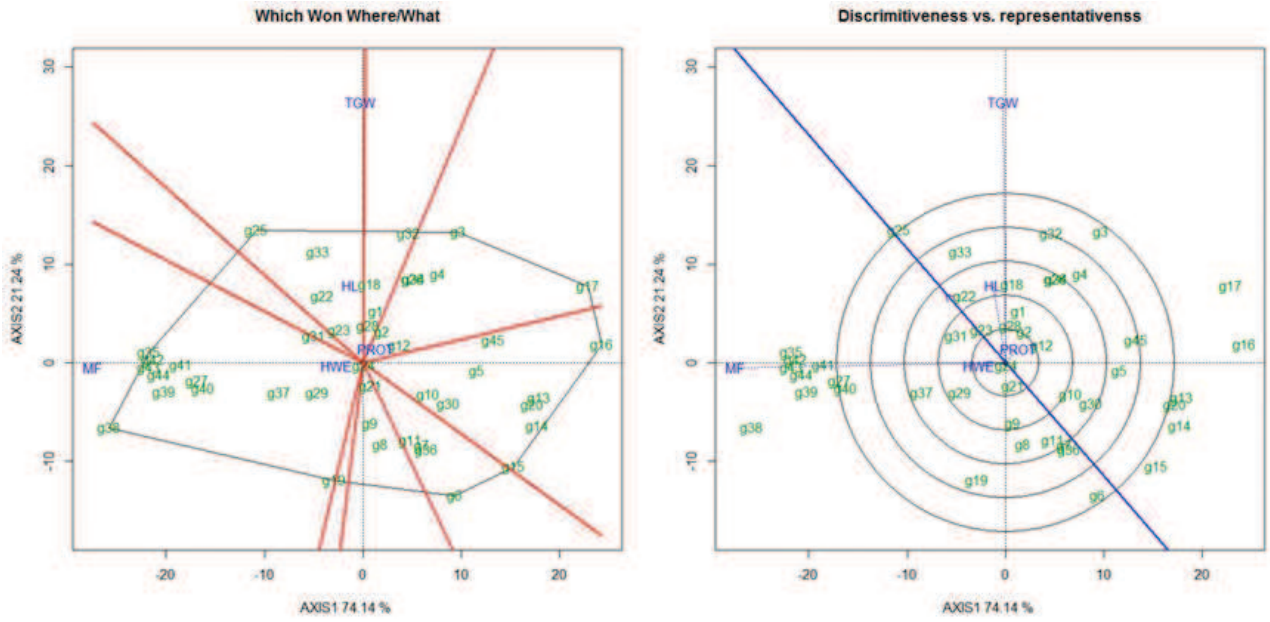

Fig. 1. Polygon view and genotype by trait biplot for quality characters in barley

In general, barley grains, which are bold, plump and uniform with moderate 1000 grain wt. are preferred for malting purposes and two-row barley grains are bold with high starch content and uniform due to the fertile central spikelets. Barley starch comprises linear polymer amylose (25%) with α-(1-4) glucosidic bonds and branched polymer amylopectin (75%) with α-(1-4) glucosidic and α-(1-6) glucosidic bonds (Fox et al. 2003; Gupta et al. 2010). During malting process of steeping, germination and kilning the starch breakdowns in to fermentable sugars i.e., maltose, maltotriose, maltotetrose etc. with raised enzymatic activity. Starch further disintegrates during mashing by the enzymatic activity of α-amylase, β-amylase, α-glucosidase and limit dextrinase (Arends et al. 1995). The malt friability is an important trait to determine the friable and homogenous part of the malt, which is accessible by the enzymes during mashing. Hot water extract is the most important quality trait, polygenic in inheritance and also called as malt extract of wort (Gupta et al. 2010; Kumar et al. 2017). Hot water extract is highly influenced by the environment, malting regimes, agronomic packages and used further for fermentation for brewing and distillation (Fox et al. 2003). The estimates for hot water extract revealed that the average performance (81.06 %) was higher during 2012-13, which ranged from 73.73-85.73 %, respectively. The highest significant positive correlations were obtained between malt friability and hot water extract (0.63**) followed by 1000 grain wt. and hectolitre wt. (0.49**). Grain protein content revealed significant negative correlations with hot water extract (–0.60**) and malt friability (–0.53**).

In genotype by trait biplot, the first two principal components PC1 and PC2 explained 74.14 % and 21.24 % variations and the vertex genotypes were exhibited as G3 (DWRB73), G6 (BCU131), G15 (BCU551), G16 (BCU553), G17 (BCU554), G19 (BCU729), G25 (BK306) and G38 (Marnie), respectively. The malting quality parameters were grouped into the three different sectors. The grain physical characters viz., 1000 grain wt. and hectolitre wt. were grouped in to single sector, while grain protein content was plotted near the biplot origin and represented the different sector. The biplot also corroborated the correlations observed for different traits based on acute angles between 1000 grain wt. and hectolitre wt. and malt friability and hot water extract. The genotypes namely, G3, 25, 32, 33 were again confirmed for 1000 grain wt. and G35, 42, 43, 44, 38 showed higher malt friability.

The two initial PCs altogether captured high variation of 93.07, 92.00 and 92.45 per cents for 1000 grain wt. malt friability and hot water extract, respectively. For 1000 grain wt. the years 2012-13 and 2013-14 were grouped together and the genotypes namely, G3, 32, 33, 4, 26, 17 and 1 showed consistent performance with high AEC abscissa scores over the years with high 1000 grain wt. The biplots obtained for malt friability showed that the years 2011-12 and 2012-13 fell together in the same sector and the genotypes namely, G38, 42, 43, 35, 39, 41, 44, 27 and 40 were stable with high malt friability per cent. In the polygon view for hot water extract it was observed that the years 2011-12 and 2013-14 were grouped in the same sector and the genotypes viz., G38, 40, followed by 35, 26, 44, 39 and 43 were consistent over the years. The positive correlations obtained between 1000 grain wt. and hectolitre wt. (0.49**), malt friability and hot water extract (0.63**) and negative correlations of grain protein content with malt friability (–0.53**) and hot water extract (–0.60**) were also corroborated by discriminative and representative biplot (Molina-Cano et al. 1997; Kumar et al. 2015a).

On the basis of high AEC absicca and low ordinate scores the genotypes namely, DWRB73, BCU1, DWR45, DWR46, CARUSO and BCU554 showed consistent performance for 1000 grain wt. The genotypes namely, Marnie, Sloop SA WI 3167, Sloop-VIC-VB9953, Henley, Prestige, Shebac, Xanadu, CDC Bold and Schooner were found stable with high malt friability and the genotypes *viz*., Marnie, Schooner, Henley, CARUSO, Xanadu, Prestige and Sloop-VIC-VB9953 were consistent for hot water extract over the years. Here, the Indian check varieties namely, DWRUB52, DWRUB64 and DWRB73 showed moderate to high 1000 grain wt., medium friability with satisfactory hot water extract. However, the exotic genotypes viz., Henley, Marnie, Prestige, Schooner, Sloop-VIC-VB9953, Sloop-SA-WI3167, CARUSO, CDC bold, Shebac and Xanadu revealed slighlty high malt friability and hot water extract above 80 %. On the other side, these exotic genotypes were low yielding and late maturing than all the Indian checks under sub-tropical climatic conditions. The grain yield and quality traits have negative associations and apparently Indian varieties showed comparable quality while having higher grain yield levels due to the climatic adaptations. Moreover, the prolonged season due to the western disturbances led to the bio-synthesis of more starch content in late maturing genotypes by the heterotetramer enzyme ADP Glucose

pyrophosphorylase, which is favourable during conversion of starch during malting and mashing (Kumar et al. 2015b). This data trend warranted to enhance quality of Indian barley by incorporating some of the promising exotic genotypes in hybridization with good quality characters.

In conclusion, grain protein content exhibited significant negative correlations with malt friability and hot water extract, whereas, malt friability and malt extract were found highly correlated. The genotypes namely Henley, Marnie, Prestige, Schooner, Xanadu and Sloop VIC VB9953 exhibited marginally high *per se* for malt friability and hot water extract but showed low grain yield with prolonged heading and crop maturity. These selected genotypes are low yielding and susceptible to biotic stress and should be included in hybridization for improving malting quality with high yielding and disease resistant genotypes.

Author's contribution

Conceptualization of research (VK, RPSV, DK); Designing of experiments (VK, RPSV); Contribution of materials (VK, RPSV); Execution and coordination (VK, DK, RPSV), analysis of data, quality analysis, compilation, proof reading and interpretation (VK, DK, ASK, GPS); Preparation of manuscript (VK, ASK, GPS).

Declaration

The authors declare no conflict of interest.

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