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Short communication

Genetic analyses of malting quality characters in barley (*Hordeum vulgare* L.)

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Abstract

The present study was undertaken to delineate the nature of gene effects, epistasis type and estimation of genetic parameters in barley. Mean hectolitre weight, grain protein content and malt friability were exhibited as 58.45 kg/hl, 10.27 and 59.25 per cents, respectively. Additive x additive effects were predominant for all the quality traits, while dominance x dominance epistasis was also observed for grain protein content and Kolbach index. Duplicate type epistasis was observed for malting parameters, except hectolitre weight and 1000 grain weight in the cross PL 426/RD 2592. The highest significant positive correlation coefficient (r=0.62) was exhibited between hectolitre weight and 1000 grain weight followed by malt extract and filtration rate (r=0.55**) etc.**

Key words: C and D scaling test, five parameter model, malting quality, barley

The knowledge of gene effects and epistasis are helpful for the enhancement of genetic potentialities and to set the favourable gene constellations. Barley is an ancient cereal being used as feed, food and malt purposes (Baik and Ullrich 2008). The utilization of barley for malting and brewing has picked up recently with an increase consumption of beer and other malt based products in India (Kumar et al. 2013). Therefore, the present study was undertaken to delineate the nature of gene effects, epistasis type and to identify the grain physical parameters having association with malt parameters.

Two cross combinations i.e. PL 426/RD 2592 and RD 2552/IND 183 along with their F_1, F_2 and F_3 generations were evaluated during *rabi*, 2012-13 in randomized block design with three replications. The processed grain samples were micro-malted as per standard cycle of 120-128 hrs. Data were recorded for two grain physical characters i.e. 1000 grain weight (g), hectolitre weight (kg/hl) and seven malting quality parameters *viz*., grain protein content (% db), malt yield (%), malt friability (%), malt extract (%), filtration rate (ml/hr), diastatic power (^{0}L) and Kolbach index (%). Grain protein content and Kolbach index were analysed using FOSS NIR system. Other biochemical parameters were recorded as per European Breweries Convention (EBC) procedure (Analytica-EBC 2003). C and D scaling tests were used to check the adequacy of the additive-dominance model and five parameter model was applied (Hayman 1958) to compute different parameters. Phenotypic and genotypic coefficient of variation (PCV and GCV), heritability (broad sense) and genetic advance (5 per cent, K = 2.06) were computed as per standard procedure (Singh and Chaudhary 1985).

Analysis of variance revealed significant differences (p>0.01) for all the characters, except diastatic power. Malt extract had the mean value of 77.41 %, while mean filtration rate and Kolbach index were exhibited as 232.52 (ml/hr) and 38.63, respectively. The high estimates of PCV than GCV revealed the environmental influence for all the traits. The highest PCV per cents were observed for filtration rate (18.17) followed by grain protein content (14.09),

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Table 1. C and D scaling tests and five parameters in barley

Cross	C	D	m	d	h	i	l
Hectolitre wt							
PL 426/RD 2592	1.76	–115.56**	57.46**	–1.01	1.15	0.43	0.88
RD 2552/IND 183	2.50	–116.43**	57.53**	2.81**	3.04	1.56	–0.62
1000 grain wt							
PL 426/RD 2592	0.33	–82.53**	42.23**	–2.93**	3.97	–0.05	0.44
RD 2552/IND 183	4.70	–84.30**	38.70**	2.45**	5.93**	6.48**	–8.26
Grain protein content							
PL 426/RD 2592	2.76	–23.63**	9.63**	0.01	1.35	3.20**	–3.64
RD 2552/IND 183	5.30**	–24.50**	9.93**	–1.85**	3.44**	3.49**	–1.68
Malt yield (%)							
PL 426/RD 2592	–4.50	–154.76**	83.53**	–3.28**	–10.62**	–12.73**	20.97
RD 2552/IND 183	–0.50	–163.23**	80.40**	–3.18**	8.46**	5.48	–11.46
Malt friability							
PL 426/RD 2592	–1.36	–116.23**	55.40**	0.50	8.06*	7.98*	–17.33*
RD 2552/IND 183	–1.30	–81.36**	60.16**	2.08*	–55.11**	–52.82**	104.35**
Malt extract							
PL 426/RD 2592	–1.70	–154.56**	78.30**	–2.75**	–4.55	–2.93	4.17
RD 2552/IND 183	–3.43	–141.43**	76.73**	–0.05	–3.46	–9.98**	16.53**
Filtration rate							
PL 426/RD 2592	197.00	–417.66**	182.33**	–2.16	–158.66*	–80.16	357.33
RD 2552/IND 183	–94.00	–340.66**	236.00**	22.66**	–95.33	–115.00*	136.00
Kolbach Index							
PL 426/RD 2592	–2.00	-76.26**	38.73**	0.26	1.06	0.06	–2.13
RD 2552/IND 183	–8.50*	-83.50**	41.10**	–1.25**	5.62*	5.83*	–20.17*

* Significant at 5 % level, and ** Significant at 1 % level

malt friability (13.07) etc. The medium to high values of heritability coupled with high genetic advance were depicted for malt friability, malt yield and 1000 grain weight.

D scaling test was highly significant for all the traits and indicated the presence of additive x additive epistasis. The C scaling test was also significant for grain protein content and Kolbach index and revealed the complicated inheritance in presence of the dominance x dominance interactions (Table 1). Additive effects (d) were significant for all the traits, while the dominance effects were also found significant for 1000 grain weight, protein content, malt yield, friability, filtration rate and Kolbach index. Hectolitre weight was controlled by additive effects, while 1000 grain weight, protein content, malt yield and filtration rate were controlled by additive and dominance effects with preponderance of additive x additive effects. The friability and Kolbach index were under control of additive and dominance effects with prevalent additive x additive and dominance x dominance interactions.

The negative sign of additive x additive interactions was recorded for 1000 grain weight, malt yield, friability, malt extract and filtration rate, which revealed the dispersive nature of the genes in the parental lines. Opposite sign of dominance component (h) and dominance x dominance (l) interactions were observed for all the quality characters, except for hectolitre weight and 1000 grain weight in the cross PL 426/RD 2592. These opposite signs of h and l indicated the presence of duplicate type epistasis (Kearsey and Pooni 1996).

The highest significant positive correlation coefficient was depicted between hectolitre weight and 1000 grain weight (r=0.62**) followed by r=0.55** (malt extract and filtration rate), r=0.50** (malt yield and 1000 grain weight), r=0.49** (malt extract and malt yield) etc. Hectolitre weight was found significantly associated with malt extract and revealed that the genotypes with bold grains and plump kernels are more desirable for better malt recovery. The protein content was negatively correlated with malt extract, which is desirable for beer stability and avoidance of chill haze formation (Molina-Cano *et al*. 1997). Malt friability is a measurement of conversion of starch into sugars and was found associated with hectolitre weight, malt extract and filtration rate.

The prevalent additive gene effects, presence of additive x additive (i) interactions and duplicate epistasis indicated employment of directional selection with high hectolitre weight and 1000 grain weight would be quite effective for malt barley breeding. The prevalent dominance x dominance interactions suggested bi-parental mating or diallel selective mating would be more realistic for further improvement in malt friability and Kolbach index.

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