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Research Article

Genetic architecture of barley (*Hordeum vulgare* L.) genotypes for grain yield and yield attributing traits

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Abstract

Combining ability for yield and its related traits was studied in 13 barley genotypes and their F_1 progenies obtained through line x tester mating design. Significant differences for most of the traits in both *gca* and *sca* components revealed the importance of both additive and non-additive gene actions with the predominant effect of non-additive gene action. Among parents, lines DWRB 134, BH 902 and RD2919 emerged as good general combiner for yield and important component traits whereas DWRUB 52 was identified as the best tester. Hence, these are considered as good general combiners for deriving desirable transgressive segregants for specific characters. However, line BH 902 emerged as good general combiner for maximum number of yield contributing traits i.e., peduncle length, spike length, awn length, productive tillers per plant, flag leaf area, number of grains per spike, weight of spike, 1000 grain weight, biological yield per plant and grain yield per plant. Among thirty crosses, seven displayed significant and positive *specific combining ability (sca)* effects for grain yield. Out of these seven crosses, four hybrids viz., BH 976 × RD 2849, DWRB 134 × DWRUB 52, BH 965 × DWRUB 52, BH 902 ×DWRB 101, were identified as the best promising combinations having good specific combining ability effects along with high per se performance for grain yield as well as other attributing characters in desired direction. The estimates of general combining ability (*gca*) effects as a whole suggested that if most of the characters are to be improved, inclusion of F1 hybrids showing high *sca* in crop improvement program and parents with good *gca*, into multiple crosses, bi-parental mating, and diallel selective mating could prove a worthwhile approach for tangible advancement of grain yield in barley..

Keywords: Barley, combining ability, grain yield, line x tester

1. Introduction

Barley is most cosmopolitan crop and considered as "Poor Man's Crop" due to low input requirement, better adaptability to drought, salinity, alkalinity, and marginal lands. It is primary feed crop in semi-arid parts of Asia, Africa, and South America. Barley has 7% share among world cereal crop production. It ranks fourth in area and production after wheat, rice and maize. Barley grows particularly well where the ripening season is long and cool, where the rainfall is moderate rather than excessive and where the soil is well drained but not sandy. It can stand high temperature if the humidity is low but it does not do so well where both are high. In India it occupies around 0.68 mha area that produces 1.79 mt with the productivity of 26.41 q/ha (Singh, 2018). Rajasthan ranks first in barley production (0.86 mt) followed by Uttar Pradesh (0.43 mt) and Madhya Pradesh (0.30 mt) with the productivity level of 30.46 q/ha, 27.74 q/ha and 22.89 q/ha, respectively however highest productivity is in the state of Punjab (35.96 q/ha). In the state of Uttarakhand area under barley is 20 thousand ha, production 26 thousand tons with the productivity of 13 q/ha which is rather low as compared to the national average of 26.41 q/ha (Singh, 2018). Usage pattern shows that in India, 75% barley is used for feed, 20% for malt and the remaining 5% for food purpose. Its utilization as food crop (mainly hull less type) is restricted to the tribal areas of hills. Barley is very rich in essential nutrients like manganese (63% Daily Value, DV), phosphorus (32% DV), including protein, dietary fibres, the vitamins Niacin (31% DV) and vitamin B6 (20% DV). In hilly states like Uttarakhand, sloppy region, water scarcity and leaching of nutrients is the main problem so yield mainly depends on the genetic worth of variety. Hence, effective breeding strategies need to be developed for improvement in the genetic yield potential of barley. In order to achieve the goal, one should be aware of certain information regarding the relative significance of additive and non additive gene action and the nature of combining ability of available parents. Combining ability effects are very important in constructing the next phase of a systematic crop improvement programme by selecting suitable parents for hybridization, their best promising combinations and understanding the genetic behavior of the trait under study. Hence, the present investigation was undertaken to study combing ability effects for yield and its components traits through line x tester analysis in barley.

2. Material and methods

Ten lines of barley *viz*, BH 965, DWRUB 64, DWRB 73, BH 976, DWRB 134, RD 2918, RD 2919, BH 902, BH 946, DWRB 140 (female parent) were crossed with three testers i.e., DWRUB 52, DWRB 101, RD 2849 (male parents) in *rabi* crop season, 2015-16. Necessary precautions were taken to avoid contamination of genetic material at the time of crossing. The F_1 seeds of the thirty crosses (10 X 3) along with their parents (female and male) were planted in a randomized complete block design with three replications at Norman E. Borlaug Crop Research Centre of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar during rabi 2016- 17. Each replication consisted of 43 treatments consisting of 10 lines, 3 testers and 30 crosses. Each treatment was planted in two rowed plot of two meter length with inter-row and inter-plant distances of 23 and 10 cm, respectively. The experimental plot was kept under normal agronomic care from sowing to maturity. Observations were recorded at specific stage on five randomly taken plants for the sixteen traits *viz.*, days to 75% heading, days to physiological maturity, plant height (cm), peduncle length (cm), spike length (cm), awn length (cm), tillers per plant, flag leaf area (cm^2), grains /spike, spike weight, 1000 grain weight, hectolitre weight (kg/hl), biological yield per plant (g), grain yield per plant(g), harvest index % and protein content. The mean data recorded were subjected to the analysis of variance to determine significant differences among genotypes and combining ability analysis through line x tester analysis as described by Kempthorne (1957) and detailed by Singh and Chaudhary (1985).

3. Result and discussion

The analysis of variance for combining ability (Table 1) revealed that the mean square due to females were highly significant for peduncle length, plant height, spike length, awn length, productive tillers per plant, flag leaf area, spike weight and significant for 1000 grain weight and biological yield per plant. Male accounted highly significant differences for only one trait i.e., days to 75% heading and significant for flag leaf area and 1000 grain weight. The significant differences from female and male suggested

Table 1: Analysis of variance for combining ability in line x tester crosses for different yield and its attributes in barley

Source of variation	d.f	Mean sum of squares															
		DH	DM	PH	PL	SL	AL	TP	FLA	GS	SW	TGW	HW	BY	GY	HI	PC
Replication	2	0.28	4.55	5.88	6.98	0.59	0.24	43.15	0.58	1.02	0.003	3.53	22.69	22.2	9.87	22.91	0.65
Treatment	42	94.66**	68.58**	134.71**	34.68**	1.68**	3.89**	71.49**	28.47**	390.61**	.85**	95.15**	48.81**	742.96**	103.79**	84.12**	2.38**
Females (Lines)	9	38.05	21.77	434.46**	49.41**	3.87**	5.31**	161.18**	42.19**	10.24	0.81**	85.51*	44.84	1458.19*	206.14	66.1	1.96
Males (Testers)	2	260.33**	34.23	4.95	13.8	0.65	0.23	15.26	46.81*	0.23	0.41	152.36*	102.81	141.59	23.28	72.68	2.41
Line x tester	18	29.10**	38.77**	43.18**	11.94**	0.64**	1.00**	51.50**	13.64**	7.79**	0.28**	34.58**	53.62**	686.91**	104.84**	66.42**	1.61**
Error	84	1.85	1.87	12.3	2.41	0.27	0.35	3.98	0.37	0.37	0.02	3.56	3.07	11.65	6.44	15.09	0.34
σ^2gca		0.35	-0.1	2.22	0.21	0.01	0.02	0.58	0.2	0.005	0.003	0.44	0.01	3.77	0.48	0.006	0.003
σ^2sca		9.01	12.29	10.04	3.27	0.11	0.2	15.86	4.4	2.51	0.08	10.48	16.95	225.52	32.51	17.01	0.42
σ^2gca/σ^2sca		0.03	-0.09	0.22	0.64	0.09	0.1	0.37	0.45	0.01	0.04	0.04	0.005	0.017	0.014	0.000	0.007

DH- Days to 75% heading, DM- Days to physiological maturity, PH- Plant height (cm), PL- Peduncle length (cm), SL- Spike length (cm), AL- Awn length (cm), TP- Productive tillers per plant, FLA- Flag leaf area (cm2), GS- Grains /spike, SW- Spike weight, TGW-1000 grain weight, BY- Biological yield per plant (g), GY- Grain yield per plant (g), HI- Harvest index; *, ** significant at 5% and 1% levels, respectively that the female and male possess good amount of genetic variability among them for various traits. Significant variation among genotypes for grain yield and related traits were also reported by Joshi *et al.* (2004) and Saeed *et al.* (2010). Further, mean sum of squares due to female were higher than due to male for all the characters except days to 75% heading, days to physiological maturity, flag leaf area, 1000-grain weight, hectoliter weight, harvest index and protein content, indicating the larger contribution of female toward the general combining ability (*gca*) variance components. Female x male (line x tester) interaction mean square manifested high significant differences for all the studied traits. This revealed the significant contribution of hybrids for specific combining ability (*sca*) variance components for all the studied characters. Moreover, the ratio of variance of general combining ability (*gca*) and specific combining ability (*sca*) was less than unity for all the characters studied (Table-1), indicating the predominance of non additive gene action in the expression of all the characters. The result is in consent with the results presented earlier by Dholariya *et al.* (2014) for days to flowering, days to maturity, peduncle length, Ali *et al.* (2014) for plant height, flag leaf area; Singh *et al.* (2012) for productive tillers per plant, spikelets per spike, grains per spike, biological yield per plant, 1000 grain weight and grain yield per plant, Desale and Mehta (2013) for harvest index. Kumar et al. (2013) and Amer *et al.* (2012) also indicated preponderance of non-additive gene effects in the expression of various quantitative traits whereas, additive gene action for spike length were reported by Singh *et al.* (2012) and Dholariya *et al.* (2014). Since non additive type of gene action was present for the traits, it is, therefore, suggested that the selection of the desirable plants should be followed in the later generations. Estimates of *gca* effects were partitioned for both female (line) and male (tester) for all the characters (Table-2) to search out the potential parents for further breeding. The results revealed that none of the parents were good general combiner for all the studied characters. Results thereby suggest use of multiple parent participation through multiple crossing for substantial improvement in yield and its components. The results obtained are in accordance with Potla *et al.* (2013), Amer *et al.* (2012) and Patial *et al.* (2016). Among lines, BH 902 was identified as good general combiner for maximum number of traits (ten) *viz.* peduncle length, spike length, awn length, productive tillers per plant, flag leaf area, number of grains per spike, weight of spike, 1000 grain weight, biological yield per plant and grain yield per plant. Line RD 2918 showed highly significant *gca* for nine traits *viz.* plant height, peduncle length, spike length, awn length, flag leaf area, number of grains per spike, weight of spike, 1000 grain weight and biological yield per plant. Line DWRB 134 also, turned to be a good general combiner for seven traits like, earliness, number of productive tillers per plant, weight of spike, hectolitre weight, biological yield per plant, grain yield per plant and harvest index while DWRUB64 was good for days to physiological maturity, peduncle length, awn length, grains per spike, spike weight, 1000 grain weight and BH 976 for days to heading, productive tillers, hectolitre weight, biological yield and protein content. Among testers, *gca* effects indicated towards DWRB 101 as a good combiner for five characters *viz.* days to heading, flag leaf area, hectoliter weight, spike weight and biological yield per plant. Tester DWRUB 52 found to be good general combiner for days to heading,

Table 2: General Combining Ability (GCA) effect of lines and testers with respect to different yield and its attributes in barley

Material	DH	DM	PH	PL	SL	AL	TP	FLA	GS	SW	TGW	HW	BY	GY	HI	PC
BH 965	1.60**	-0.87	-3.77**	0.41	-0.14	0.34	-2.82**	-0.56*	-0.91**	-0.27**	0.99	-2.03**	0.68	-1.08	-2.42	0.39*
DWRUB64	-0.07	2.13**	5.05**	1.89**	0.16	0.68**	-7.33**	0.05	0.45**	0.43**	3.54**	0.3	-13.79**	-5.46**	0.08	0.37
DWRB 73	-3.18**	-1.64**	-4.64**	-1.20*	-0.87**	-0.46*	-2.45**	-1.46**	-0.40*	0.28**	-4.67**	-1.37*	-23.46**	-9.10**	0.65	-0.57**
BH 976	1.93**	0.91	-7.31**	-1.28**	-0.85**	-0.69**	1.88**	0.28	-1.60**	-0.45**	-5.06**	3.97**	3.37**	-0.15	1.05	0.48*
DWRB134	1.71**	-2.64**	-3.19**	-3.00**	0.36	-0.43*	6.94**	-0.70**	0.03	0.20**	1.09	2.63**	5.82**	4.87**	3.24*	-0.09
RD 2918	1.38**	2.13**	-6.07**	3.94**	1.16**	1.15**	0.88	3.31**	1.10**	0.10*	4.04**	0.52	5.68**	-0.37	-3.05*	-0.19
RD 2919	-1.40**	0.47	1.43	-0.31	-0.37*	-0.3	1.03	-2.65**	0.29	-0.1	-1.20*	0.3	6.52**	4.05**	1.95	-0.95**
BH 902	1.27**	0.47	11.94**	2.93**	0.67**	0.65**	5.29**	4.02**	1.83**	0.21**	2.00**	0.86	24.16**	6.92**	-3.32*	0
BH 946	0.38	-0.98*	4.71**	-0.32	0.31	0.42*	0.02	-2.24**	0.48**	0.01	0.44	-1.70**	-3.46**	1.58	4.32**	0.35
DWRB140	-3.62**	0.02	-10.29**	-3.05**	-0.44*	-1.36**	-3.45**	-0.06	-1.27**	-0.42**	-1.18*	-3.48**	1.23	-1.26	-2.34	0.2
SE(gi)	0.47	0.46	1.2	0.48	0.18	0.2	0.65	0.21	0.16	0.05	0.59	0.55	1.07	0.9	1.3	0.19
SE (gi-gj)	0.67	0.65	1.7	0.68	0.26	0.29	0.93	0.3	0.22	0.07	0.83	0.78	1.51	1.27	1.84	0.27
DWRUB52	2.47**	1.03**	0.06	0.53*	0.11	0.09	-0.82*	-0.35**	-0.1	-0.13**	-0.04	-0.08	1.34**	0.81	0.22	-0.21
DWRB101	0.80**	0.07	-0.43	-0.77**	-0.17	-0.09	0.4	1.39**	0.06	0.11**	-2.23**	1.89**	1.17*	-0.94	-1.66*	-0.12
RD 2849	-3.27**	-1.10**	0.37	0.24	0.06	-0.01	0.42	-1.04**	0.04	0.02	2.27	-1.81**	-2.51**	0.13	1.43*	0.32**
SE(gi)	0.26	0.25	2.08	0.26	0.1	0.11	0.36	0.11	0.08	0.02	0.32	0.96	0.58	0.49	0.71	0.1
SE (gi-gj)	0.36	0.35	0.93	0.37	0.14	0.15	0.51	0.16	0.12	0.03	0.45	0.42	0.83	0.69	1.01	0.15

DH- Days to 75% heading, DM- Days to physiological maturity, PH- Plant height (cm), PL- Peduncle length (cm), SL- Spike length (cm), AL- Awn length (cm), TP- Productive tillers per plant, FLA- Flag leaf area (cm2), GS- Grains /spike, SW- Spike weight, TGW- 1000 grain weight, BY- Biological yield per plant (g), GY- Grain yield per plant (g), HI- Harvest index; *, ** significant at 5% and 1% levels, respectively days to physiological maturity, peduncle length and biological yield. A similar approach of multi-parental crosses has been suggested by Sharma *et al.* (2002) and Eshghi and Akhundova (2009). High *gca* effect for a particular character of a parent indicated the presence of additive gene effects for that character which is, in turn, fixable component of genetic variation. Lines with good per se performance and highly significant *gca* effects are considered as good general combiners for deriving desirable transgressive segregants in self- pollinated crops. A perusal of *sca* effects estimates revealed that no specific cross was superior for all the parameters under study (Table-3). Character-wise estimation of *sca* effects showed that out of 30 hybrids, seven hybrids *viz*, BH 976 × RD 2849 (11.02), DWRB 134 × DWRUB 52 (8.79), BH 965 × DWRUB 52 (7.02), RD 2918 × DWRB 101 (5.52), DWRB 140 × DWRUB 52 (5.19), DWRUB 64 × DWRB 101 (4.27), BH 902 × DWRB 101 (3.70) exhibited significant and desirable *sca* effects for grain yield per plant. Out of these seven significant crosses, five crosses exhibited highly significant and highest positive *sca* effects along with high per se performance for grain yield per plant. All the seven hybrids also exhibited significant and desirable *sca* effects for more than one yield attributing characters. Similar results regarding high *sca* effects for grain yield and other yield contributing traits in several crosses were also reported by earlier workers *viz*, Potla *et al.* (2013) and Patial *et al.* (2016). The highest positive sca effects for grain yield was depicted by the cross BH 976 × RD 2849 (11.02) followed by DWRB 134 × DWRUB 52 (8.79) and BH 965 × DWRUB 52 (7.02). In this study, there was some degree of correspondence between sca effects and mean performance. But there was no linearity found between the same, i.e., a cross showing highest *sca* effect may not exhibit the highest mean performance for the character. Although mean performance and *sca* effects expressed an association to some extent, and suggested that both criteria must be considered for selecting the promising cross combination. The highest positive *sca* effects was observed in the cross BH 976 × RD 2849 that involved average x average general combining parents and had fourth position in per se performance for grain yield. This combination also registered highest significant *sca* effects in desirable direction for component traits *viz*, days to 75% heading (3.93), days to physiological maturity (3.99), flag leaf area (0.86), grains per spike (1.62), spike weight (0.36) and biological yield per plant (25.30). The cross, DWRB 134 × DWRUB 52 which involved good x average general combining parents occupied seventh rank in per se performance, second position in *sca* effect for grain yield. It also recorded significant and highest *sca* effects for peduncle length (2.31), grains per spike (0.89), 1000 grain weight (3.08) and biological yield per plant (23.14). The cross combination BH 965 × DWRUB 52 involving average x average general combiner parents had third ranking in *sca* effect and fourth position in mean performance for grain yield. It also recorded significant and highest *sca* effects for productive tillers per plant (6.31), spike weight (0.49), 1000 grain weight (2.39), biological yield per plant (5.59) and harvest index (6.80). Similarly, the cross combination BH 902 X DWRB 101 attained seventh position in *sca* effect, third rank in per se performance and it involved good x average general combiner parents for grain yield. This cross combination exhibited significant and desired highest *sca* effects for two more yield attributing characters *viz*, flag leag area (1.91), grains per spike (2.25), 1000 grain weight (3.08) and biological yield per plant (11.04). These four crosses

Table 3: Superior cross combinations with specific combining ability (SCA) effects with respect to grain

Cross combinations	Grain yield/ plant	*sca* effects	*gca* effects				Significant *sca* effects for other characters
			Female		Male		
BH976 × RD2849	38.93	11.02**	-0.15	A	0.13	A	DH (3.93**), DM (3.99 **), FLA (0.86*), GS (1.62**), SW (0.36**), BY (25.30)
DWRB134 × DWRUB52	42.4	8.79**	4.87**	G	0.81	A	DM (3.74**), PL (2.31**), TP (-5.34**), GS (0.89**), TGW (3.08**), BY (23.14**)
BH965 × DWRUB52	34.66	7.02**	-1.08	A	0.81	A	DH (-2.47**), TP (6.31**), SW(0.49**), TGW (2.39*), BY (5.57**), HI (6.80**)
RD 2918 × DWRB101	32.13	5.52**	-0.37	A	-0.94	A	TP (2.82*), FLA (1.29**), GS (1.16**), SW (-0.18*), BY (21.12**)
DWRB140 × DWRUB52	32.66	5.19**	-1.26	P	0.81	A	DM (-4.59**), TP (2.60*), GS (-1.71**), SW (-0.33**), BY (16.59**)
DWRUB64 × DWRB101	25.8	4.27**		P	-0.94	A	DH (-3.47**), PL (2.30**), FLA (3.17**), GS (0.70*), TGW (2.20*), HI (6.74**)
BH902 × DWRB101	37.6	3.70*		G	-0.94	A	TP (-2.37*), FLA (1.91**), GS (2.25**), TGW (3.08**), BY (11.04**)

DH- Days to 75% heading, DM- Days to physiological maturity, PH- Plant height (cm), PL- Peduncle length (cm), SL- Spike length (cm), AL- Awn length (cm), TP- Productive tillers per plant, FLA- Flag leaf area (cm2), GS- Grains /spike, SW- Spike weight, TGW-1000 grain weight, BY- Biological yield per plant (g), GY- Grain yield per plant (g), HI- Harvest index; *, ** significant at 5% and 1% levels, respectively can be utilized for further breeding programme. Desirable *sca* effects of the crosses involving at least one good combiner or average combiner as parent, seems to be mainly due to complementation effects of the genes and these crosses could yield better genotypes in segregating generations. These results are supported by the findings of Aslam *et al.* (2007). Such genotypes/ crosses may be useful to develop desirable hybrids and transgressive segregants or in barley population improvement programme. The crosses showing high *sca* effects, involving good or average general combiner parents could be further exploited by selection and pedigree breeding, provided the additive x additive component of interaction was significant. However, cross combinations with poor (low *gca*) x good (high *gca*) and poor (low *gca*) x average (medium *gca*) combiners can be improved through bi-parental mating (Joshi and Dhawan, 1966) and/or diallel selective mating (Jensen, 1970) which allows intermating of selections in different cycles to exploit both additive and non-additive gene effect.

Table 4: Correspondence of per se performance and sca effects of best barley cross combinations

Character	Best parent (per se)	Best parent (*sca* effects)
Days to 75% heading	DWRB 73 X RD 2849	DWRB 73 X RD 2849
Days to physiological maturity	DWRB 73 X RD 2849	BH 976 X DWRUB 52
Plant height (cm)	DWRB 140 X RD 2849	BH 902 X RD 2849
Peduncle length (cm)	RD 2918 X DWRUB 52	DWRB 73 X RD 2849
Spike length (cm)	RD 2918 X DWRUB 52	DWRB 73 X RD 2849
Awn length (cm)	RD 2918 X DWRUB 52	BH 976 X DWRB 101
Productive tillers per plant	DWRB 134 x RD 2849	BH 965 X DWRUB 52
Flag leaf area (cm2)	BH 902 X DWRB 101	DWRUB 64 X DWRB 101
Grains /spike	BH 902 X DWRB 101	DWRB 73 X DWRUB 52
Spike weight	BH 965 X DWRUB 52	DWRUB 64 X RD 2849
1000 grain weight	DWRUB 64 X RD 2849	RD 2919 X DWRB 101
Hectolitre weight (kg/hl)	BH 902 X DWRUB 52, BH 976 X DWRUB 52	DWRB 140 X RD 2849
Biological yield per plant (g)	BH 902 X DWRB 101	BH 976 X RD 2849
Grain yield per plant(g)	DWRB 134 X DWRB 52	BH 976 X RD 2849
Harvest index %	DWRB 140 X RD 2849	DWRB 140 X RD 2849
Protein content	DWRUB 64X RD 2849	RD 2918 X DWRB 101

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