Genetic analysis of forage yield and other traits in barley (*Hordeum vulgare* L.)

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Abstract
Twenty one genotypes of six – parent half diallel were analyzed for estimating gene effects of variance, combining ability and standard heterosis for forage yield and other traits in barley. The estimates of gene effects revealed the significant role of additive genetic component (D) for the inheritance of days to 50% heading, plant height and spikelets per ear. The non-additive component (H_1) was found to be important for the genetic control of all the traits except for days to 50% heading and tillers per plant. However, the relative magnitude of dominant component (H_1) was higher as compared to additive component (D) in all the traits, indicating the preponderance of dominant gene effects in controlling the inheritance of these traits. The genetic component (H_2) was recorded with low magnitude than (H_1) for all the traits, except days to 50% heading and tillers per plant, indicating that beneficial positive alleles are not proportional to that of deleterious negative alleles at all loci among parents.The ratio of *gca* and *sca* effects was less than unity for all traits except spikelet per ear, indicating the predominant role of non-additive genetic components in the inheritance of all the traits. Among parents, BHS 352 and HBL 276 were identified as good general combiners for forage yield, days to 50% heading and spikelets per ear, whereas parent, HBL 113 was found to be good general combiner for tillers per plant, ear length and biological yield. The predominance of non–additive components of genetic variance (H_1, H_2) along with positive values of additive component (D), high *per se* performance, significant *sca* effects and significant standard heterosis in top ranking hybrid, HBL 276 X HBL 113, suggested the scope of improvement for forage yield per plant, tillers per plant, ear length, biological yield per plant and grain yield per plant through bi-parental mating.
Key words: Barley (*Hordeum vulgare*), diallel analysis, genetic components, forage yield, grain yield, heterosis.

Introduction
Archaeological evidence has revealed that barley (*Hordeum vulgare*) is one of the oldest crop used by ancient farmers (Pourkheirandish and Komatsuda, 2007). In India, the area brought under barley cultivation is 0.77m ha with production estimated to 1.33m tons (Anonymous, 2008). It is a traditional crop of hill people due to their dietary needs for human consumption in the form of a variety of foods like "Sattu", Puk / Moori besides brandy and "Chhang" the local beverages, and for fodder requirements of live stock. Fodder scarcity and availability of limited feed during the winter season is a serious problem for livestock production in high altitude of northern hills of India (Sharma *et al*., 1999) probably due to cultivation of local land races which are low yielding and susceptible to diseases. Farmers' preference for barley cultivation in hills lies in the varieties which would give high fodder yield for their live stocks and food grain for human consumption. Cultivation of newly released variety "Himadri" having yield potential of 3.86 t/ha with resistance to blotch and stripe rust would stabilize the barley productivity in the hills of northern India (Kumar and Pal, 2004). Breeding efforts are very much needed for

developing dual purpose barley varieties capable of giving high grain yield even after harvesting the crop for green fodder. The information on genetic components of variance, *per se* performance, *gca* and *sca* effects of parents coupled with high heterotic effects for fodder yield, grain yield and associated traits are useful for selecting parents for developing dual purpose varieties of barley. Moreover, among all the mating designs, diallel mating, especially half diallel provided a simple and convenient method for estimating genetic parameters (Kearsey, 1965; Ghannadha *et al*., 1995). The present study therefore, was aimed at estimating genetic components of variance, *gca* and *sca* effects along with heterotic response of hybrids which might be useful to breed dual purpose barley varieties having increased potential of giving forage and grain yield.

Materials and methods
Four commercial varieties (BHS 169, BHS 352, HBL 113, HBL 276) and two elite lines (BHS 365, BHS 369) of barley were crossed in a half diallel fashion to produce a set of 15 crosses. The experimental materials consisting of 6 parents and 15 F_1's were planted in a randomized block design with three replications during *rabi*, 2007-08 at Research Farm of IARI Regional Station, Shimla, India located at 1900m above mean sea level. The plot size was 2 x 1.25m with spacing 23 x 10 cm between row to row and plant to plant, respectively. The crop was harvested for green fodder after 70 days of sowing by adopting common practice of farmers. The recommended dose of fertilizers an additional 25% dose of nitrogen was applied after cutting the crop for green fodder. Data were recorded on 30 randomly selected plants for FY-forage yield per plant (g), DH- days to 50% heading, TP- tillers per plant, PH- plant height (cm), EL – ear length (cm), SE – spikelets per ear, BY- biological yield per plant (g), and GY – grain yield per plant (g). The mean values of parents and their F_1's were subjected to estimate components of genetic variance and allied genetic parameters *viz*., D (additive), H_1 (dominance), F (mean co – variance of D and H_1), H_2 (proportion of +/- genes), $\sqrt{H1/D}$ (mean degree of dominance), $H_2/4H_1$ (proportion of genes with $\pm$ effects), $(\sqrt{4DH_1}) + F/ (\sqrt{4DH_1}) – F$ (proportion of dominant and recessive genes) and h² ns (narrow sense heritability) following numerical approach of diallel analysis (Hayman, 1954). Combining ability analyses were carried out as per the method of (Griffing, 1956).

Results and discussion
The analysis of variance revealed significant differences among 21 genotypes (6 parents + 15 F_1's) for all the traits, indicating the presence of considerable amount of genetic diversity in the material (Table1).

Components of genetic variance: The diallel analysis revealed significant role of additive genetic component (D) for the inheritance of DH, PH and SE. The non-additive component (H_1) was found to be important for the genetic control of all the traits except DH, BY and TP. Additive and non-additive genetic components were significant for PH and SE. However, the relative magnitude of dominant component (H_2) was higher as compared to additive component (D) in all the traits, indicating the preponderance of dominant gene effects in controlling the inheritance of these traits. The genetic component (H_2) was recorded with low magnitude than (H_1) for all the traits, except DH and TP indicating that beneficial positive alleles are not proportional to that of deleterious negative alleles at all loci among parents (Table2). The bi–parental mating approach suggested by (Joshi and Dhawan, 1966) and/or the diallel selective mating scheme

suggested by (Jensen, 1970) could be the best option to exploit both of these components for improvement of these traits. Moreover, intermating of superior segregants followed by cyclic selection would enhance the frequency of desirable alleles in later generations (Hallauer, 1968). The estimates of F component were positive for FY, PH, EL, BY and GY, indicating unequal distribution of dominant and recessive gene frequencies in the parents. The proportion of dominant genes with positive or negative effects in the parents can be judged from the ratio of $H_2/4H_1$ with maximum 0.25 value as arises when p=q=0.5 at all the loci. Any deviation suggests the presence of asymmetrical distribution of positive and negative genes in the parents. Kuczynska *et al*., 2007 reported that the frequency of transgression and symmetry / asymmetry in number of +/- segregants in a given population of homozygous lines depends on both traits and cross combinations. In our study, a general asymmetrical distribution of genes in the parents was observed for all the traits. Similar results were reported by (Bouzerzour and Djakoune, 1998) in barley. However, the gene frequency seemed to be nearly symmetrical for GY, DH and TP as the range of this component ($H_2/4H_1$) as was observed between 0.23 – 0.24 for these traits. The component ($\sqrt{4DH_1}$) + F/ ($\sqrt{4DH_1}$) – F measures the proportion of dominant and recessive genes among the parents. The characters *viz*., FY, PH, EL, BY and GY have shown the values for this component above unity, indicating the role of dominant genes in the expression of these traits. The proportion of $\sqrt{H_1/D}$ (degree of dominance) was greater than unity for all the traits, indicating ample scope for heterosis breeding in barley. This finding is in agreement with earlier reports of (Ciulca *et al*., 2000 ; Bhatnagar *et al*., 2001). The narrow sense heritability was high for SE and moderate for DH and TP, indicating that selection for improvement of these traits would be effective.

Combining ability effects and heterosis: The analysis of variance for combining ability revealed significant mean sum of squares due to *gca*, except GY and *sca* for all the traits, indicating importance of both additive and non–additive gene effects in the expression of these traits. However, the ratio of additive genetic variance to total genetic variance was less than unity, indicating the predominant role of non additive genetic components in the inheritance of all the traits except SE (Table 3). Previous findings of (Budak, 2000; Soylu, 2002 ; Sharma *et al*., 2003) also indicated the role of additive and non–additive gene effects in the expression of various traits in barley. The estimates of *gca* effects indicated that the parents, BHS 352 and HBL 276 were good general combiners for FY, DH and SE, whereas parent HBL 113 was found to be good general combiner for TP, EL and BY. Among all the parents, HBL113 and BHS 352 have shown positive values of *gca* effects for GY (Table 4). These parents could be used in crossing programme for enhancing favorable genes in later generations. Among 15 hybrids, HBL 276 X HBL 113 was found to be the best combination as it had shown high *per se* performance, significant *sca* effects along with significant standard heterosis for FY, TP, EL, BY and GY. High *sca* effects and heterosis as observed in this combination could be due to divergence and high and low *gca* values of the parents. It is suggested that high *sca* effects for plant height, ear length, number of grains per ear, grain yield and 1000-grain weight were the result of cross having high x low general combining abilities (Chaudhary *et al*., 1974) . The hybrid BHS 352 X HBL 113 possessed significant *sca* effects for all the traits along with significant standard heterosis for EL, BY and GY (Table 4). Similarly, the cross combination HBL 276 X BHS 169 exhibited significant *sca* effects for all the traits, except EL along with conspicuous heterosis for SE and GY. Another hybrid BHS 352 X HBL 276 has shown high *per se* performance, significant *gca* effects in its parents, significant *sca* effects along with conspicuous heterosis for

improvement of FY through hybrid breeding programme. The predominance of non–additive components of genetic variance (H_1, H_2) along with positive values of additive component (D), high *per se* performance, significant *sca* effects and significant standard heterosis in top ranking hybrid, HBL 276 X HBL 113, suggested the scope of improvement for FY, TP, EL, BY and GY through bi – parental mating approach as suggested by (Joshi, 1974) and /or diallel selective mating scheme suggested by (Jensen, 1970 ; Frey, 1975). Moreover, intermating of superior segregants of this hybrid followed by cyclic selection would enhance the frequency of desirable alleles in the later generations for improvement of green fodder yield, grain yield and its associated traits in barley.

Table 1. Mean sum of squares for forage yield and other traits in barley.

Source of variation	df	FY	DH	TP	PH	EL	S/E	BY	GY
Replication	2	19.7	2.7	0.7	60.7*	0.3	32.7	1.9	1.9
Genotypes	20	54.5*	70.9*	29.7*	116.1*	3.1*	1038.2*	283.3*	52.2*
Error	40	6.5	3.9	5.0	6.0	0.7	6.6	29.4	5.0
CV (%)		20.3	4.4	14.1	2.7	8.8	4.5	12.6	13.8

@ explained in the text. * Significant at $P < 0.05$., CV- Coefficient of variation.

Table 2. Gene effects and heritability estimates for forage yield and other traits in barley.

Gene effect #	Trait @							
	FY	DH	TP	PH	EL	SE	BY	GY
D	6.6 ±6.3	25.7* ±9.6	7.6 ±4.1	40.2* ±14.6	0.48 ±0.45	274.1* ±14.1	6.6 ±74.6	1.5 ±11.9
F	3.4 ±15.5	-6.6 ±23.5	-3.1 ±9.9	47.0 ±35.7	0.2 ±1.09	-347.2* ±34.5	36.3 ±182.4	5.6 ±29.0
H_1	63.7* ±16.1	37.2 ±24.4	19.0 ±10.4	141.2* ±37.1	2.7* ±1.1	279.2* ±35.9	418.3* ±189.5	82.2* ±30.1
H_2	50.7* ±14.4	34.3* ±21.8	17.4* ±9.3	121.3* ±33.2	2.2* ±1.0	149.3* ±32.0	364.8* ±169.3	77.6* ±26.9
$H_2/4H_1$	0.20	0.23	0.23	0.21	0.20	0.13	0.22	0.24
$\sqrt{H_1/D}$	3.10	1.20	1.58	1.87	2.37	1.01	7.96	7.40
$(\sqrt{4DH_1})+F/$ $(\sqrt{4DH_1})-F$	1.18	0.81	0.77	1.90	1.14	0.23	2.05	1.66
h^2 (ns)	0.35	0.64	0.51	0.16	0.35	0.90	0.10	0.01

@ , # explained in the text. * Significant at P< 0.05

Table 3. Analysis of variance for combining ability effects for forage yield and other traits in barley.

Source of Variation	df	Mean sum of squares							
		Character @							
		FY	DH	TP	PH	EL	SE	BY	GY
gca	5	24.6*	65.4*	22.9*	34.3*	1.5*	1217.0*	25.9*	1.2
sca	15	16.0*	9.7*	5.5*	40.1*	0.9*	55.7*	117.3*	22.8*
Error	40	2.1	1.3	1.7	2.0	0.2	2.2	9.8	1.6
gca : sca		0.20	0.95	0.69	0.10	0.24	2.83	0.01	-0.01

@ explained in the text, * Significant at P< 0.05, *df*- degree of freedom.

Table 4. Combining ability and heterotic effects for forage yield and other traits in barley.

Genotype	Trait@							
	FY	DH	TP	PH	EL	S/E	BY	GY
***gca effects* (P)**								
BHS 352	1.78**	-2.53**	-1.54**	0.92*	-0.15	7.34**	-0.83	0.27
HBL 276	2.24**	-.178**	-0.01	-1.63**	-0.21	6.14**	-2.04*	-0.05
BHS 369	0.39	-0.94*	-2.30**	2.73**	0.15	2.32**	-1.59	-0.58
BHS 365	-1.78**	-1.17**	0.22	1.07*	0.21	7.14**	0.51	-0.11
HBL 113	-0.88	5.27**	2.00**	-3.05**	0.47**	-24.7**	2.58*	0.54
BHS 169	-1.75**	1.14**	1.63**	-0.05	-0.76**	1.75	1.37	-0.08
SE (gi)	0.47	0.37	0.42	0.46	0.15	0.47	1.01	0.41
***sca effects* (F$_1$'s)**								
BHS352/HBL 276	7.31**	0.58	0.48	-0.55	-0.05	0.15	-1.11	-0.74
	60.3**	**-0.5**	**-21.9***	**-7.7****	**-1.4**	**21.3****	**-2.3**	**1.7**
BHS352/BHS369	-1.47*	0.27	0.43	-2.01**	0.58**	6.93**	4.23**	0.92
	-10.9	**-0.2**	**-34.1****	**-4.7***	**9.1**	**26.4****	**12.1**	**9.0**
BHS352/BHS365	-1.12	0.56	-2.12**	6.38**	-0.42**	2.42**	-4.29**	-1.45*
	-23.1	**-0.1**	**-34.3****	**2.1**	**-0.9**	**26.9****	**-3.9**	**-3.2**
BHS352/HBL 113	2.07**	-4.04**	2.03**	7.84**	0.91**	-8.12**	10.1**	2.93**
	4.2	**1.13**	**-3.1**	**-0.6**	**15.9***	**-45.3****	**37.1****	**29.3***
BHS352/BHS169	-2.85**	-1.54**	0.22	5.61**	0.16	5.38**	2.84*	0.99
	-34.5*	**0.1**	**-14.6**	**0.2**	**-4.9**	**22.7****	**16.0**	**12.7**
HBL276/BHS369	-2.23**	1.09*	-1.52**	-6.46**	-1.24**	-1.66*	-14.3**	-6.32**
	-12.9	**0.9**	**-36.4****	**-11.9****	**-14.1**	**9.7****	**-37.0****	**-39.8****
HBL276/BHS365	-1.45*	1.38**	1.19*	4.16**	-0.11	2.33**	1.98	0.90
	-22.2	**0.9**	**-8.9**	**-2.7**	**-1.4**	**24.7****	**8.7**	**9.9**
HBL276/HBL113	5.68**	-4.52**	6.07**	10.6**	2.03**	-5.98**	25.6**	10.2**
	31.5*	**1.31**	**26.1****	**-0.3**	**24.1****	**-43.7****	**72.6****	**74.6****
HBL276/BHS169	3.27**	-1.79**	-1.99**	4.79**	0.10	3.71**	4.98*	6.08**
	9.6	**0.4**	**-18.2**	**-3.3**	**-9.4**	**17.8****	**18.3**	**43.5****
BHS369/BHS365	1.59*	-0.03	-0.86	4.17**	0.35	6.90**	11.7**	6.97**
	-14.3	**0.6**	**-31.7****	**1.7**	**7.2**	**25.9****	**33.9****	45.7**
BHS369/HBL113	-4.59**	1.43**	-1.21*	1.13	0.11	-6.77**	-3.41*	-3.88**
	-49.6**	**5.9****	**-24.2***	**-5.6****	**7.4**	**-51.6****	**1.6**	**-20.3**
BHS369/BHS169	3.62**	-1.70**	0.77	1.49*	0.72**	1.63*	1.56	3.58**
	-0.4	**1.0**	**-15.8**	**-2.2**	**0.9**	**7.8***	**10.9**	**23.9***
BHS365/HBL113	-1.49*	-1.87**	-2.60**	-0.42	0.68**	-9.38**	-2.54	-1.85**
	-43.4**	**3.5****	**-18.2**	**-8.9****	**14.2**	**-47.8****	**8.9**	**-4.1**
BHS365/BHS169	3.56**	-017	-2.94**	-0.88	0.30	0.01	3.90**	-0.03
	-15.4	**1.9**	**8.9**	**-6.3****	**-2.8**	**13.2****	**22.0**	**3.7**
HBL113/BHS169	-4.40**	8.96**	-1.61**	-6.36**	0.08	-7.66**	5.16**	-1.18*
	-62.7**	**12.4****	**-5.6**	**-16.1****	**-2.5**	**-54.1****	**30.3****	**0.4**
SE (sij)	0.62	0.48	0.54	0.59	0.20	0.62	1.32	0.54
SE (Heterosis)	2.1	1.6	1.8	2.0	0.6	2.1	4.4	1.8

@ explained in the text.*, ** Significant at P< 0.05 & 0.01, respectively. Bold numeral – Heterosis

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