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COMPARISON OF VARIABILITY GENERATED THROUGH BIPARENTAL MATING AND SELFING IN BARLEY (*HORDEUM VULGARE* L.)

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SUMMARY

The experiment was conducted to examine the extent of genetic variability generated through biparental mating and selfing for yield and related components in three inter-varietal crosses of barley, namely, IBON-W-61 x DWR 91(Cross I), BH 935 x BH 902 (Cross II) and BH 902/DWRUB 64 (Cross III). The BIPs and F_3 populations were grown in a compact family block design with three replications spaced at 30 and 15 cm between plots and plant, respectively. Data were recorded on 10 agronomic traits and subjected to different statistical analyses following their standard procedures. Considerable variation was observed among families for almost all the traits in both F_3 and BIPs of three crosses. When comparing the performance BIPs and selfed progenies for most of the traits, higher mean and wider range values were observed in BIPs than in F_3 except cross I, in which the range values were wider in F_3 for all the characters. The phenotypic and genotypic coefficients of variations were higher in BIPs for grains/spike, biomass yield/plant, grain yield/plant and days to heading in cross II; and for effective tiller number/plant, biomass yield/plant, grain yield/plant, harvest index and 1000-grain weight in cross III, while the PCV and GCV values were higher for all traits in F_3 in cross I. Similarly, higher broad sense heritability and genetic advance as per cent of means followed the same pattern as PCV and GCV in every cross.

Key words : Biparental, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance, barley

Barley (*Hordeum vulgare* L.), a member of the Poaceae family, is a fourth major cereal grain in the world next to rice, wheat and maize. In India, the annual production has been around 1.2 to 1.5 million tonnes in recent years from an area under cultivation of 0.7 to 0.8 m hectares with per hectare yield of 2131 kg (Anonymous, 2013). It is grown in the northern part of the country in states of Rajasthan, U. P., Haryana, M. P., Punjab, Bihar and Jharkhand in the plains and Himachal Pradesh, Uttarakhand and Jammu & Kashmir, among which Rajasthan is the largest barley growing state in recent years (Verma *et al*., 2011). Barley grain is used as animal feed, human food and malt. In all these three uses, there is a great range of diversity across the globe, which reflects the crop's wider variation and adaptability. Although barley is fed to a wide range of livestock in different ways on global basis, in the highlands of Tibet, Nepal, Ethiopia, Eritrea, in the Andean countries, and in North Africa, barley is important food stuff (Newton *et al*., 2011). In India, the major barley production has been for cattle feed and food, however, recently there is a considerable demand for malt barley due to an increase in consumption of beer and malt based products in India and other countries (Verma *et al*., 2008; Verma *et al*., 2011).

The barley genetic diversity, that is, the sum of genetic characteristics within its species (Rauf *et al*., 2010), is high both in cultivated and wild progenitor species. Among Asian barley landraces genetic diversity was highest in the Indian landraces followed by Pakistani while lowest for Turkmenistan and Uzbekistan landraces (Naeem *et al*., 2011). Genetic variability in the breeding gene pool is most important principle for further breeding and cultivar development. Lower genetic diversity in elite

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breeding material compared with progenitor accessions and mapping populations of barley was reported (Matus and Hayes, 2002), since barley has been intensively bred for improved performance and quality (Anonymous, 2008). It is argued that lack of the sufficient variability in the available genotypes hinders the breakthrough achievement of high productive cultivar in self-pollinated crop like barley.

Further efforts to increase yield in barley have become relatively difficult because of the fact that the ongoing breeding method such as pedigree is limited due to several drawbacks like limited parent participation, low genetic variability, reduced recombination, rapid fixation of genes, and/or due to association between genes for desirable and undesirable characters. In view of these observations, a fresh look on generating new genetic variability for yield and its component traits has become essential. Most of the agronomic traits are quantitative in nature and the expression of the desired combinations is hidden because of tight linkages among the interacting gene blocks. One of the designs recommended to break the linkage blocks is biparental mating in early segregating generation, particularly F_2, that forces recombination and breaking down of undesirable linkages among traits (Comstock and Robinson, 1952) than the selfing series. The biparental mating has been reported to effect forced recombination in rice (Manickavelu *et al*., 2006; Mahalingam *et al*., 2011a; Mahalingam *et al*., 2011b), in bread wheat (Yunus and Paroda, 1982; Verma, 1989) and in six-rowed barley (Prakash and Verma, 2006). Therefore, this experiment was undertaken in the three inter-varietal crosses of barley to examine the extent of genetic variability generated by biparental mating and selfing for yield and its component traits.

MATERIALS AND METHODS

The experiment was conducted at the Research Station of the Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, during 2013-14 **rabi** season. The experimental material consisted of 30 BIPs and 30 F_3s from every cross of IBON-W-61 x DWR 91 (Cross I), BH 935 x BH 902 (Cross II) and BH 902 x DWRUB 64 (Cross III). The two populations (BIPs and F_3s) in each cross were grown in a compact family block design with three replications and planted at space of 30 and 15 cm between plots and plants, respectively. Observations were recorded on 10 agronomic characters on five selected competitive plants (except for days to heading and days to maturity, which was on plot base) and data were subjected to analysis of variance following standard procedure for RBD for each population. The phenotypic and genotypic coefficients of variation were estimated according to Burton (1951). Heritability in broad sense (h^2_B) was calculated for all characters according to the method described by Johnson *et al.* (1955a), while genetic advance as per cent of mean was calculated to compare the extent of predicted genetic advance of different characters according to the method of Johnson *et al.* (1955b).

RESULTS AND DISCUSSION

The analysis of variance for family mean of 10 characters studied in biparental and selfed populations revealed significant variation for almost all traits, namely, plant height, spike length, grains/spike, effective tiller number/plant, biological yield/plant, grain yield/plant, harvest index, 1000-grain weight, days to heading and days to maturity in each population under three crosses (Table 1). This shows that both populations generated sufficient variation in three crosses which provided opportunity for selection of those traits for further improvement. The mean performance of BIPs was numerically higher than the corresponding F_3 progenies in three crosses for all the characters except harvest index in cross I and plant height, harvest index and 1000-grain weight in cross III (Table 2). Reduced plant height accompanied by increased grain yield/plant in biparental population in cross III compared to F_3 self indicated the chances for selecting shorter transgressive segregants barley lines with high yielding ability. Earlier research findings for short plant height and higher grain yield were reported in bread wheat (Nematualla and Jha,1993) and rice (Amudha *et al*., 2006).

In all crosses selection for early maturity type in BIPs was challenged since higher mean values were obtained in BIPs compared to F_3 which was against the selection direction for earliness. In bread wheat, Yunus and Paroda (1983) and Frederickson and Kronstad (1985) reported earliness in BIPs compared to selfed progenies, similarly, Amudha *et al.* (2006) and Mahalingam *et al.* (2011a) reported early heading and reduced plant height in BIPs compared to selfs in rice, which is in contrast with the present investigation. In this experiment intermating improved the mean

TABLE 1
Analysis of variance for 10 traits in each population of the three crosses of barley

Cross	Population	Source of	d. f.	Mean sum of squares									
				PH	SL	GPS	ETN	BM	GY	HI	TGW	DH	DM
I	F_3	Block	2	422.68	0.07	0.675	0.68	62.57	33.08	36.17	35.74	26.08	6.14
		Family	29	165.08**	1.62**	9.75**	5.52**	295.6**	53.0**	29.1**	39.1**	33.5**	12.3**
		Error	58	31.67	0.24	1.16	1.92	99.55	12.46	6.80	13.18	8.58	4.50
	BIP	Block	2	70.68	0.11	1.34	7.29	533.53	67.52	0.13	0.34	1.94	3.38
		Family	29	53.3*	0.5*	5.3**	5.8*	242.7**	45.2**	26.1**	15.1**	9.2**	2.96**
		Error	58	30.91	0.24	1.72	3.38	131.60	17.98	9.47	5.59	2.2	1.19
II	F_3	Block	2	295.35	4.09	62.18	32.17	1353.6	166.04	4.9	105.0	44.43	29.88
		Family	29	93.85**	1.23**	35.79**	5.35**	206.6**	29.3*	27.6**	84.1**	31.0**	21.1**
		Error	58	29.84	0.27	6.31	2.04	78.82	15.90	4.45	20.16	6.66	4.30
	BIP	Block	2	214.26	4.27	24.03	12.82	105.37	76.27	103.2	84.04	107.6	71.1
		Family	29	94.1**	0.71**	53.8**	8.24**	408.4**	67.7**	35.3*	82.9**	37.4**	7.5**
		Error	58	38.9	0.281	12.16	4.36	229.7	32.79	31.79	27.56	7.28	3.23
III	F_3	Block	2	77.07	1.26	0.06	2.25	248.66	48.58	5.78	13	5.91	14.48
		Family	29	64.9**	0.95**	43.7**	2.36**	178.1**	41.09**	17.93**	79.9**	5.4	2.71
		Error	58	24.8	0.31	13.17	0.59	70.69	14.13	3.81	17.1	3.7	3.09
	BIP	Block	2	241.33	0.22	86.82	5.19	302.3	48.8	3.18	6.68	31.14	3.7
		Family	29	32.95*	0.64	37.1**	6.01**	385.5**	66.8**	26.9**	125.2**	7.64	3.1**
		Error	58	18.38	0.4	17.94	2.04	85.97	16.01	2.77	12.61	6.33	1.01

PH–Plant height, SL–Spike length, GPS–Grains/spike, ETN–Effective tiller number, BM–Biomass, GY–Grain yield, HI–Harvest index, TGW–1000-grain weight, DH–Days to heading and DM–Days to maturity. *,**Significant at P=0.05 and P=0.01 levels, respectively.

performance of grain yield/plant compared to selfing by 18.81 and 18.61 per cent in crosses I and III, respectively. In rice, Amudha *et al*. (2006) reported that BIPs had yield advantage over the corresponding F_3 progenies by 57.59 per cent. Similar yield advantage results of biparental over F_3 were also reported in wheat (Yunus and Paroda, 1983; Verma, 1989; Nematualla and Jha, 1993), in barley (Prakash and Verma, 2006) and in rice (Mahalingam *et al*., 2011a; Mahalingam *et al*., 2011b).

Effective tillers per plant increased in BIPs for three crosses of barley which was in line with previous research report in rice (Mahalingam *et al*., 2011a; Mahalingam *et al*., 2011b), however, Nematualla and Jha (1993) indicated that there was no change in the mean performance for wheat effective tiller number/plant. Other yield component traits like spike length, grains/spike, biomass yield/plant and 1000-grain weight showed improved mean performance in BIPs in all crosses compared to selfs, which is in agreement with previous research findings reported on different crops (Yunus and Paroda, 1983; Verma, 1989; Nematualla and Jha, 1993; Amudha *et al*., 2006; Prakash and Verma, 2006; Mahalingam *et al*., 2011a; Mahalingam *et al*., 2011b).

In this experiment, harvest index was lower in BIPs compared to F_3 in crosses I and II which was due to much higher mean values of biomass yield/plant in those crosses compared to cross II. However, Prakash and Verma (2006) on six-row cross barley demonstrated high mean value of harvest index in BIP progenies than in F_3. The importance of harvest index as selection criteria in barley has been advocated (Riggs *et al*., 1981; Lalic *et al*., 2010); however, selection for higher harvest index affected grain yield, hence, selection for biological yield contributed more to yield.

A comparison of range values between biparental and selfed population mean values revealed wider for all traits in F_3 compared to BIP in cross I, however, in crosses II and III all the traits showed wider range values of means in BIP except plant height, spike length and harvest index in cross II and plant height, grains/spike and days to maturity in cross III. Reduced lower limits of mean's range values were observed in F_3 than in BIPs in all the three crosses except for the traits plant height (cross III), harvest index (crosses I and

TABLE 2
Mean performance and range of F_3 and BIP families of three crosses of barley

Character	Cross IBON-W-61 x DWR 91				Cross BH9 35 x BH 902				Cross BH 902 x DWRUB 64			
	F_3		BIP		F_3		BIP		F_3		BIP	
	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range
Plant height (cm)	127.8	110.9-138.2	133.5	125.6-139	116.2	102.7-126.7	119.5	111.6-133.4	110.5	101.1-121	108.8	100.7-116.4
Spike length (cm)	9.24	7.9-10. 7	9.98	9.33-11.0	7.091	5.98-8.23	7.974	6.83-8.83	7.933	7.0-8.93	8.42	7.27-9.4
Grains/spike	27.99	23.9-31.2	29.76	26.8-32.8	45.28	37.7-53.8	48.83	40.1-61.8	66.45	60.93-76	70.76	63.4-77.93
Effective tiller number	12.88	9.9-16.3	14.48	12.4-18.7	15.14	12.8-17.3	16.65	13.7-20.1	11.57	10.27-13.3	15.57	12.27-18.73
Biomass (g)	64.44	46.3-90.8	78.08	61.9-95.9	65.55	47.9-81.3	75.85	53.45-101.2	66.87	49.1-80.1	81.45	57.67-108.8
Grain yield (g)	21.58	15.7-31.27	25.64	19.3-34.3	25.53	18.83-31.2	26.76	18.44-38	25.96	17.4-34.3	30.79	20.53-40
Harvest index (%)	33.43	27.9-40.36	32.84	27.6-38.5	39.09	31.6-45.7	40.7	36.2-48.5	38.64	35.24-44.6	37.80	33.22-45.71
1000-grain weight (g)	64.26	57.7-76	68.21	63.7-72.3	59.81	45.33-69.4	59.62	46-70.7	45.37	38.33-58.3	43.64	34.67-58.67
Days to heading	89.19	81.7-94	93.01	90-96.3	84.97	80.33-92.3	88.5	82.3-95.3	91.59	89-94.3	94.26	91.33-98.33
Days to maturity	129.9	124.7-133.7	132.0	130-134	127.8	123-132.3	130.1	127.3-133	136.5	135-139.3	139.8	138.3-142

III) and 1000-grain weight (crosses II and III). On the other hand, the upper limits of the range values were higher in BIP than in F_3 for almost all the traits except plant height in cross III and harvest index and 1000-grain weight in cross I. This indicated that the upper and lower limits of range values in BIPs were shifted to the higher values compared to F_3, thereby shifting the overall mean for most of the traits towards higher values. As a result, lower limit of range was not foreshortened in BIPs for earliness and plant height (except in cross III), thus the variability created was in an undesired direction for these traits. However, for traits like spike length, grains/spike, grain yield/plant, biomass yield/ plant and number of tillers/plant and shift in upper limits to higher values indicated the increased variants in BIPs in the desired direction. Previous reports indicated the wider range of mean values for most of the assessed traits with reduced lower limits and increased upper limits in BIP compared to F_3 (Yunus and Paroda, 1983; Verma, 1989; Prakash and Verma, 2006; Mahalingam *et al*., 2011a); however, Nematualla and Jha (1993) reported higher values of both lower and upper limits for spike length, number of spikelets/spike, number of grains/spike, 1000-grain weight and grain yield/plant in bread wheat.

The phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV), as measure the magnitude of variability present within the population, were worked out and presented in Table 3. While a lower value of coefficient of variation (CV) generally depicts low variability among the samples of population; a higher proportion of GCV to PCV is desirable in breeding programme (Bello *et al*., 2012). The estimates of PCV values were higher than GCV values for all the traits in each population across three crosses. This is an indication of the environmental influence on the expression of quantitative characters measured. But for most of the traits, the PCV values were slightly higher than the corresponding GCV values in both populations across three crosses, suggesting that the influence of environment on the expression of those traits was slight. The PCV and GCV values were higher for all traits in F_3 than in BIPs in cross I, while they were higher in BIPs for grains/spike, biomass yield/plant, grain yield/plant and days to heading in cross II and for effective tiller number/plant, biomass yield/plant, grain yield/plant, harvest index and 1000-grain weight in cross III. Prakash and Verma (2006) reported higher PCV and GCV values in BIPs for grain filling period, peduncle length, spikelets/

TABLE 3

Estimates of genetic variability parameters for 10 quantitative traits in F_3 and BIP populations of three crosses of barley

Character	Pop.	IBON-W-61 x DWR 91 (Cross I)				BH 935 x BH 902 (Cross II)				BH 902 x DWRUB 64 (Cross III)			
		GCV	PCV	h^2	% GA	GCV	PCV	h^2	% GA	GCV	PCV	h^2	% GA
Plant height (cm)	F_3	5.22	5.80	81	9.64	3.98	4.83	68	6.81	3.31	4.21	62	5.35
	BIP	2.05	3.16	42	2.73	3.59	4.69	59	5.65	2.03	3.05	44	2.77
Spike length (cm)	F_3	7.34	7.96	86	13.93	7.98	8.99	78	14.52	5.78	7.06	67	9.72
	BIP	3.19	4.27	56	4.89	4.69	6.06	61	7.47	3.35	5.43	38	4.26
Grains/spike	F_3	6.05	6.45	88	11.68	7.89	8.69	82	12.92	4.83	5.77	71	8.32
	BIP	3.67	4.46	67.5	6.19	8.07	9.17	77	13.80	3.57	4.97	52	5.28
Effective tiller	F_3	8.52	10.50	66	14.25	6.70	8.53	62	11.20	6.63	7.67	75	11.78
number/plant	BIP	6.02	9.35	42	7.97	6.62	9.65	47	9.62	7.38	9.08	66	12.33
Biomass (g)	F_3	12.59	15.41	67	20.5	10.03	12.76	62	16.10	8.94	11.52	60	14.28
	BIP	7.79	11.5	46	10.84	10.19	15.23	45	14.16	12.27	13.92	78	22.24
Grain yield (g)	F_3	17.04	19.48	76	30.64	8.26	12.22	46	11.50	11.55	14.25	66	19.23
	BIP	11.8	15.1	60	18.74	11.12	15.47	52	18.87	13.38	15.35	76	23.97
Harvest index (%)	F_3	8.1	9.25	77	14.66	6.99	7.63	84	13.37	5.62	6.33	79	10.23
	BIP	7.16	8.97	64	11.78	2.65	8.42	10	1.71	9.215	9.73	90	14.60
1000-grain weight (g)	F_3	4.58	5.62	66	7.66	7.72	8.85	76	13.83	10.1	11.38	79	18.41
	BIP	2.63	3.3	63.3	4.30	7.12	8.74	66	11.92	14.05	14.81	90	27.42
Days to heading	F_3	3.23	3.75	74	5.73	3.35	3.78	79	6.11	0.82	1.467	32	0.95
	BIP	1.64	1.88	76	2.94	3.58	3.99	81	6.61	0.70	1.69	17	0.60
Days to maturity	F_3	1.24	1.56	63	2.03	1.85	2.08	80	3.40	4.04	4.06	99	8.15
	BIP	0.57	0.74	60	0.92	0.92	1.21	57	1.42	0.59	0.72	67	0.99

spike, harvest index and grain yield/plant in a cross of six-rowed barley populations, which is partly similar with cross III of this experiment. Similarly, Verma (1989) in bread wheat found that both GCV and PCV were higher in BIPs for effective tillers/plant, biological yield /plant and grain yield/plant, however, the GCV and PCV estimates were higher in F_3 for grains/ear and 1000-grain weight in two crosses. The higher estimate of GCV value in intermated populations in crosses II and III with more genetic variation for above mentioned traits could be due to presence of repulsion phase linkage in those selected parental plants as suggested by Meredith and Bridge (1971). The intermating might have broken such linkages thereby accumulating favourable genes in BIP population. On the other hand, the lower genotypic variance of BIPs for all traits in cross I and for some of the traits in crosses II and III might be due to coupling phase linkage in the parents. In this case, biparental mating might have broken such linkages and resulted in reduced genetic variability.

Regarding the relative magnitude of PCV and GCV, moderate values were noticed in BIPs and F_3 populations for biomass yield/plant, grain yield/plant and 1000-grain weight (cross I) and for biomass yield/plant and grain yield/plant (crosses II and III), indicating moderate variability among families in populations for these characters. Otherwise, for all rest of the traits in both the populations of the three crosses the PCV and GCV were low. The low estimate of PCV and GCV values for those traits revealed low variability among families within each population for those characters. In previous study, Manickavelu *et al*. (2006) reported high PCV and moderate to high GCV in both BIP and F_3 selfed populations for most of the traits of rice measured under drought condition. Similarly, Prakash and Verma (2006) and Verma (1989) demonstrated moderate to high genotypic and phenotypic coefficient of variations in biparental and selfed barley and wheat populations, respectively. In other study, Raju *et al*. (2010) noticed low to high PCV and GCV in BIPs and selfed progenies in okra.

The comparison of estimates of broad sense heritability between the BIPs and the F_3 revealed that heritability estimate improved in BIPs for heading days in cross I, grain yield/plant and days to heading in cross II, and biomass yield/plant, grain yield/plant, harvest index and 1000-grain weight in cross III. Higher heritability estimates for different traits in BIPs as compared to selfed progenies were also reported in bread wheat (Yunus and Paroda, 1983; Verma, 1989), in barley (Prakash and Verma, 2006) and in okra (Raju *et al*., 2010; Guddadamath *et al*., 2011). However, this difference in magnitude of heritability does not necessarily mean that the underlying difference is genetic since h^2 is a measure of variation in each population. Therefore, heritability alone does not provide clear picture about the nature of inheritance in traits, because high heritability does not necessarily imply an improvement in genetic advance. Hence, estimate of heritability should be accompanied with genetic advance as percentage of mean (% GA) to further determine the inheritance nature of characters.

The estimates of per cent GA in BIPs were lower for all traits compared to selfed in cross I; however, it was higher in BIPs for grains/spike, biomass yield/plant, grain yield/plant and days to heading in cross II, and for effective tiller number/plant, biomass yield/plant, grain yield/plant, harvest index and 1000-grain weight for cross III. Higher per cent GA in BIPs compared to F_3 for most of the characters was also reported from earlier research in barley (Prakash and Verma, 2006), in bread wheat (Verma, 1989) and in okra (Raju *et al*., 2010; Guddadamath *et al*., 2011); however, Manickavelu *et al*. (2006) demonstrated higher per cent GA in F_3 compared to BIPs for most of the measured traits in rice. In biparental progenies, biomass yield/plant, grain yield/plant and harvest index in cross I; grains/spike, biomass yield/plant, grain yield/plant and 1000-grain weight in cross II; and effective tiller number/plant, biomass yield/plant, grain yield/plant, harvest index and 1000-grain weight in cross III had high estimates of genetic advance as percentage of mean. For those traits with relatively higher per cent GA in BIPs under the respective cross, the estimate of broad sense heritability was also high which offered more opportunity for improvement through selection among the biparental families in the desired direction. For rest of the traits the per cent GA was low eventhough heritability estimate was moderate to high in most cases, hence, gave less chances for selection for the traits in BIPs for further improvement. This showed that the intermating of segregants in F_2 had only very little effect on recombination in those traits, which is in agreement with that of Yunus and Paroda (1983) in bread wheat. Therefore, more cycles of intermating of selected segregants may be suggested to release more variability for the improvement in such cases (Manickavelu *et al*., 2006).

In conclusion, the higher mean values in all crosses, wider range values in crosses II and III for most of the traits; higher PCV and GCV values for grains/ spike, biomass yield/plant, grain yield/plant and days to heading in cross II, and for effective tiller number/plant, biomass yield/plant, grain yield/plant, harvest index and 1000-grain weight in cross III for biparental progenies compared to selfed were observed. This might be due to additional variability released due to forced intermating by accumulating favourable genes (Nematualla and Jha, 1993; Prakash and Verma, 2006) and/or due to release of hidden genetic variability by breaking undesirable linkages (Sethi *et al*., 1995).

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