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Genetic architecture, inter–relationship and selection indices in F_4 generation of barley *(Hordeum vnlgare)*

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ABSTRACT

The experimental material consisting of 24 F_4 segregating populations obtained by crossing of 32 parents of barley *(Hordeum vulgare* L.*)* were grown in randomized block design with four replications during *rabi* 2013–14 at JNKVV, Instructional farm, College of Agriculture, Rewa (MP). Thirty randomly competitive plants were selected to record the observation on days to 50% heading, days to maturity, plant height, number of tillers/plant, spike length, grains/spike, 1 000 grain weight, biological yield/plant, harvest index and grain yield/plant. Significant differences were found for all the traits. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield/plant and tillers/plant. High heritability coupled with high genetic advance as percent of mean was registered for grains /spike, biological yield/plant, 1 000 grain weight and grain yield/plant indicated predominance of additive gene action. Significant and positive association exhibited by grain yield/plant with spike length, grains/spike, biological yield/plant and 1 000 grain weight. Based on linear combination of traits, sequential and simultaneous selection indices revealed that out of 24 genotypes, 14 genotypes were sorted for higher yield and its components. Crosses, viz. K 792 × BH 674, JB 284 × PL 751, JB 1 × NDB 1276, K 792 × NDB 1276, RD 2668 × K 792, RD 2581 × JB 1 and RD 2503 × JB 58 were identified as superior genotypes having high genetic potential for grain yield.

Key words*:* Barley, Genetic architecture, Heritability, Selection indices

Barley *(Hordeum vulgare* L.) is a self–pollinated annual cereal crop of Poaceae family having basic chromosome number n=7. It has high potential to produce satisfactory grain yield under stressed soils (Kumar *et al.* 2013). Barley is a major cereal for large number of people in the cooler and semi–arid areas of the world where other cereals are poorly adapted. Though, the barley has been neglected even in our country due to priority on wheat, rice and other cash crops (Singh *et al.* 2014). Hence, efforts are being made here to develop the desirable genotypes. Genetic architecture of grain yield, in barley, is based on the balance or overall net effect produced by various yield components directly with one another. Therefore, identification of important yield components and information about their association with yield and also with each other is very useful for selecting efficient genotypes for evolving high yielding varieties or cultivars for a particular trait (Sharma *et al.* 2001, Choudhary and Suri 2014). Hence, selection of desirable segregant depends on variability and heritable portion of desirable components. Since, genetic variability is the pre–requisite for any crop improvement programme, heritability and genetic advance are other important selection parameters which provide information on transmission of characters from parents to the progeny (Falconer and MacKay 1996). In this respect, the correlation coefficient which provides symmetrical measurement of degree of association between characters, help us in understanding the nature and magnitude of association among yield and yield components and it provides the basic criteria for selection (Binod *et al.* 2013). Therefore, selection based on combined information on all the characters associated with dependent variable is the better way of exploiting genetic correlation. The retention of desired genotypes and elimination of undesirable ones are major and important process in improvement of one or more plant attributes.

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MATERIALS AND METHODS

The experimental material consisted of 24 F_4 segregating populations obtained by crossing of 32 parents of barley, grown in a randomized block design with four replications during *rabi* 2013–14 at JNKVV, Instructional farm, College of Agriculture, Rewa (MP). The genetic material grown in three rows of 4 meter row length with row spacing of 23 cm .Thirty randomly competitive plants were selected from each replication for recording the observations *viz.,* days to 50% heading, days to maturity, plant height, number of tillers/plant, flag leaf area, upper leaf area, spike length, grains/spike, 1000 grain weight, biological yield/plant, grain yield/plant and harvest index. The genetic parameter of variability, estimation of heritability and genetic advance were computed as per methods suggested by Johnson *et al.* (1955) for understanding the transmissibility of characters. The genetic association was estimated from variance and co– variance components (Fisher 1954, Al-Jibouri *et al.* 1958).

Whereas, the selection indices were computed as proposed by Smith (1936) for all the traits. Phenotypic and genotypic variances and covariances were computed as described by Singh and Chaudhary (1979). The Smith' selection index was calculated as follows:

$I = b1X1 + b2X2 + \ldots + bnXn$

where Xi = Observed phenotypic value of the ith trait, bi = weight assigned to that trait in the selection index, b = P–1 G a, Where b= vector of index coefficients, P^{-1}= inverse of the phenotypic variance–covariance matrix, G= genotypic variance covariance matrix, and a= Economic values or weights.

Expected genetic gain was calculated using the following formula given by Singh and Chaudhary (1979).

Expected genetic gain: $\Delta G = (Z/V) + W + V_P$

where $W = \sum\sum a_i\, b_i\, G_{ij}$ and $V_p = \sum\sum a_i\, b_i\, P_{ij}$. Here, Z/v is the standardized selection differential (s), indicating intensity of selection (*i*), ai= Economic weightage, bi= Regression coefficient, Gij= Genotypic variance–Covariance matrix, Pij= Phenotypic variance–Covariance matrix.

RESULTS AND DISCUSSION

The analysis of variance revealed that mean sum of squares of all the 12 characters presented in Table 1 were highly significant, thereby, indicated considerable range of variation among the segregating population under study. Besides, there is very less differences in magnitudes of PCV and GCV for the characters, days to 50% heading, days to maturity, plant height, spike length, grains/spike, biological yield/plant, 1 000 grain weight, grain yield/plant and harvest index, indicating that these characters are less influenced by the environment. While, numbers of tillers/ plant, flag leaf area and upper leaf area were highly influenced by the environment. Similar kind of results were also reported by Jalata *et al.* (2011), and Al–Tabbal (2012). Heritability in broad sense ranged from 40 to 99% and maximum heritability was recorded for days to 50% heading (99), days to maturity (60), plant height (69), grains/spike (98), biological yield/plant (96), 1000 grain weight (89), grain yield/plant (86) and harvest index (60). High estimates of heritability for component traits were also reported by Jalata *et al.* (2011), Singh (2012), and Vir and Sultan (2013). The expected genetic advance over mean was ranged from 1.97% to 47.7% and the highest expected genetic advance to the extent of 47.7% was observed for the grain yield/ plant followed by grains/spike, biological yield/plant and 1000 grain weight. Present findings are in confirmation with Jalata *et al.* (2011), and Verma and Verma (2011).

The association between yield and yield components was found positive and significant for biological yield/plant (0.630), harvest index (0.427), grains/spike (0.285), plant height (0.270), 1000 grain weight (0.262), upper leaf area (0.246) and spike length 0.209 (Table 2). It indicates that selection of such characters can directly be followed for immediate yield improvement of barley crop. Days to 50% heading also exhibited positive association with yield however, magnitude of correlation coefficient was less indicating that during selection these characters cannot be neglected. While, characters like days to maturity and flag leaf area exhibited negative association with grain yield, indicating that the direct selection for these character may not be helpful for improving the yield and for these indirect selection will have to be followed by via grains/spike and

Table 1 Estimates of genetic parameters for different quantitative characters barley

Character	Mean	Range		GCV	PCV	h^2 (bs) (%)	GA as % of mean
		Min.	Max.				
Days to 50 % heading	74.8	64.0	85.5	8.51	8.55	99	17.47
Days to maturity	120.7	117.8	124	1.25	1.62	60	1.97
Plant height(cm)	91.5	78.5	103.2	7.44	8.95	69	12.75
Tillers/plant	8.2	5.3	10.4	13.73	21.52	41	18.06
Flag leaf area (cm^2)	15.5	11.8	18.9	10.45	16.43	40	13.68
Upper leaf area (cm^2)	22.4	18.3	28.5	10.36	16.29	40	13.58
Spike length (cm)	17.6	15.4	19.8	5.41	8.34	42	7.24
Grains/spike	41.8	25.5	48.3	18.45	18.61	98	37.68
Biological yield/plant (g)	36.1	26.6	49.6	19.54	19.89	96	39.54
1 000 grain weight (g)	42.7	34.5	50.5	11.10	11.79	89	21.53
Grain yield/plant (g)	13.5	9.1	20.8	24.97	26.93	86	47.70
Harvest index (%)	36.9	32.8	42.6	6.71	8.75	60	10.61

Table 2 Phenotypic correlation between seed yield and its component characters in barley

Character	Days to 50% heading	Days to maturity	Plant height (cm)	Tillers/ plant	Flag leaf area (cm^2)	Upper leaf area (cm^2)	Spike length (cm)	Grains/ spike	Biological yield/ plant (g)	1000 grain weight (g)	Harvest index (%)	Grain yield/ plant (g)
Days to 50% heading	1	–0.121	0.109	–0.138	–0.027	0.103	0.229**	0.268**	0.167	–0.250**	0.061	0.150
Days to maturity		1	0.012	0.042	0.111	0.069	–0.055	0.303**	– 0.277**	0.056	–0.073	–0.214*
Plant height (cm)			1	0.365**	0.169	0.362**	0.403**	–0.073	0.289**	0.184	0.170	0.270**
Tillers/ plant				1	0.015	0.053	0.311**	–0.160	0.204*	0.165	0.038	0.127
Flag leaf area (cm^2)					1	0.341**	0.032	0.261**	–0.056	0.066	0.051	–0.007
Upper leaf area (cm^2)						1	0.266**	0.135	0.257**	0.142	0.154	0.246**
Spike length (cm)							1	–0.114	0.293**	0.164	0.036	0.209*
Grains/spike								1	–0.041	0.419**	0.343**	0.285**
Biological yield/plant (g)									1	0.264**	0.337**	0.630**
1 000 grain weight (g)										1	–0.111	0.262**
Harvest index (%)											1	0.427**

**Significant at 1% level of significance,* Significant at 5% level of significance

upper leaf area. Similar findings are also observed by Najeeb *et al.* (2004) and Pal *et al.* (2010).

Among the association of yield attributing characters themselves days to 50% heading has exhibited positive and significant association with character spike length (0.229) and grains/spike (0.268); indicating that the improvement in days to 50% heading (for earliness), if selection imparted may hamper the *per se* performance of these characters. While, it exhibited significant and negative association with 1 000 grain weight (–0.250) followed by negative non-significant association with days to maturity (–0.121), tillers/plant (–0.138) and flag leaf area (–0.027) indicating that selection for earliness may boost the *per se* performance of these characters. Tillers/plant has exhibited significant and positive association with spike length (0.311) and biological yield/plant (0.204) indicating that improvement in tillers/plant, if selection imparted may boost up the *per se* performance of these characters. Similarly, flag leaf area has exhibited positive and significant association with upper leaf area (0.341) and grains/spike (0.261) while, grains/spike with 1 000 grain weight (0.419) and harvest index (0.343).Similar finding also reported by Najeeb and Wani (2004), and Ataei (2006). Days to maturity had the significant positive correlation with grains/spike, however significant but negative correlation was found with biological yield/plant. Carpc (2012) and Kishor (2000) found significant positive correlation of plant height with tillers/ plant, upper leaf area, spike length and biological yield/ plant. Bhatta *et al.* (2005) and IrfanulHaq *et al.* (1997) reported that tillers/plant had significant positive correlation with spike length and biological yield/plant.

Selection indices built on single traits, were inefficient over straight selection for grain yield/plant alone because of dependent variables and polygenic in nature. The multi–traits' selection considerably important and effectively enhanced the yield potential. The direct and indirect selection and by constructing the indices using, Smith–Hazel index was the most efficient in improving the aggregate genotype for grain yield/plant (Asghar and Mehdi 2010). Plant height taken as 1st independent variable (assumed 100%) and simultaneous inclusions of other independent variables remarkably enhance the genetic advancement and relative improvement over the 1st variable (Table 3). Selection was performed within the treatments only for economic weights, i.e. considering all the components characters equally important. The expected genetic advance (5.7%) and percentage gain (100%) over 1st variable (plant height) was observed. The highest genetic advancement (21.1%) and relative gain (372.5%) were observed when, ten characters, i.e. plant height, days to 50% heading, spike length, grains/ spike, 1 000 grain weight, flag leaf area, upper leaf area, biological yield/plant, grain yield/plant and harvest index together formed an efficient selection indices (1256789ABC), followed by a selection index (1245789ABC) of another ten characters combination, i.e. plant height, days to 50 % heading, spike length, tillers per plant, 1000 grain weight, flag leaf area, upper leaf area, biological yield/plant, grain yield/plant and harvest index had recorded high genetic advancement (21.1%) with high relative gain (372.1 %) over the 1st variable and these traits may be useful for simultaneous improvement in the respective groups. It was observed that inclusion of characters one by one in the function gave fluctuating changes in the value of genetic advance and genetic gain over 1st variable. The data pertaining to genetic correlation also revealed that these traits were significantly and positively associated with grain yield/plant except flag leaf area. Thus, it indicates that the observed variables could effectively be utilized in yield improvement programme of barley.

Based on βi value and phenotypic variance, a score has been drawn out 24 crosses of barley, among 7 were sorted out for their suitability (Table 4) for higher grain yield, viz. K 792 × BH 674, JB 284 × PL 751, JB 1 × NDB 1276, K 792 × NDB 1276, RD 2668× K 792, RD 2581× JB 1 and RD 2503 × JB 58 had the high genetic potential for grain yield.

Overall, it is concluded that the substantial genetic variability was observed for yield and its components. Traits

Table 3 Selection indices

Trait combination	Plant height (cm)	Days to 50% heading	Days to maturity	Tillers/ plant	Spike length (cm)	Grains/ spike	1000 grain weight (g)	Flag leaf area (cm²)	Upper leaf area (cm²)	Biological yield/ plant (g)	Grain yield/ plant (g)	Harvest index (%)	Genetic adv.	S.I. 5%	% gain
Code	1.0	2.0	3.0	4.0	5.0	6.0	7.0	8.0	9.0	A	B	C			
1.0	0.7												5.7	11.7	100.0
2.0		1.0											6.3	13.1	111.9
6.0						1.0							7.6	15.8	135.0
12.0	0.7	1.0											9.2	19.0	162.6
1A	0.7									1.1			10.7	22.0	188.3
12A	0.7	1.0								1.1			13.5	27.8	238.5
1AB	0.7									1.5	0.0		13.6	28.0	239.9
124A	0.7	1.0		0.3						1.1			13.8	28.4	243.5
125A	0.7	1.0			0.6					1.1			14.2	29.2	249.8
127A	0.7	1.0					0.9			1.1			14.7	30.2	258.8
129A	0.7	1.1							0.6	1.1			14.9	30.7	263.3
12AB	0.7	1.0								1.6	–0.1		16.1	33.2	284.9
124AB	0.7	1.0		0.3						1.6	–0.1		16.4	33.9	290.4
125AB	0.7	1.0			0.6					1.5	0.0		16.8	34.5	295.9
127AB	0.7	1.0					0.8			1.7	–0.3		17.3	35.5	304.6
129AB	0.7	1.1							0.6	1.7	–0.2		17.5	36.1	309.1
12ABC	0.6	1.0								2.8	–3.0	1.8	17.7	36.4	311.9
1249AB	0.8	1.0		0.2					0.6	1.7	–0.2		17.8	36.7	314.6
124ABC	0.7	1.0		0.1						2.7	–2.7	1.6	18.0	37.0	317.1
1259AB	0.7	1.1			0.9				0.6	1.6	–0.1		18.2	37.4	320.8
125ABC	0.7	1.0			0.6					2.6	–2.6	1.7	18.3	37.6	322.3
126ABC	0.6	1.1				1.1				2.8	–3.0	1.7	18.6	38.3	328.0
1279AB	0.7	1.0					0.8		0.6	1.8	–0.4		18.7	38.4	329.4
129ABC	0.7	1.1							0.6	2.7	–2.8	1.6	19.0	39.1	335.0
12479AB	0.8	1.0		0.2			0.8		0.6	1.8	–0.4		19.0	39.2	335.7
1249ABC	0.7	1.0							0.5	2.7	–2.5	1.5	19.3	39.7	340.3
12579AB	0.7	1.0			1.1		0.8		0.6	1.7	–0.2		19.4	39.9	342.0
1259ABC	0.7	1.1			0.8				0.6	2.6	–2.3	1.5	19.6	40.4	346.2
1269ABC	0.7	1.1				1.1			0.5	2.7	–2.6	1.4	20.0	41.3	353.8
12469ABC	0.7	1.0				1.1			0.5	2.7	–2.4	1.4	20.2	41.6	356.4
12479ABC	0.8	0.9		0.1			0.7		0.5	2.6	–2.2	1.2	20.3	41.8	358.5
12569ABC	0.7	1.1			0.8	1.1			0.6	2.5	–2.1	1.2	20.6	42.4	363.2
12579ABC	0.7	1.0			1.1		0.7		0.6	2.5	–2.0	1.2	20.6	42.5	364.4
124569ABC	0.7	1.0		0.0	1.0	1.1			0.5	2.5	–2.1	1.2	20.7	42.7	366.1
124579ABC	0.7	0.9		–0.1	1.3		0.7		0.6	2.4	–1.7	1.0	21.0	43.3	370.9
1245679ABC	0.7	0.9		–0.2	1.3	1.0	0.7		0.6	2.5	–2.0	1.2	21.0	43.3	371.0
1245689ABC	0.7	1.0		0.1	1.1	1.1		0.4	0.7	2.6	–2.3	1.4	21.1	43.4	371.6
1245789ABC	0.7	0.9			1.4		0.8	0.4	0.7	2.5	–2.2	1.4	21.1	43.4	372.1
1256789ABC	0.7	1.1			1.2	1.1	0.9	0.3	0.7	2.6	–2.4	1.4	21.1	43.5	372.5
Eco. weights	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0			

Table 4 Selection criterion//index values for the crosses in selection indices

Variables	Eco. weight	βi	Vp	Crosses	Scores	Crosses	Scores
Days to 50% heading	1.0	1.0	38.8	K792 × BH674	575.7	JB58 × BH264	528.3
Days to maturity	1.0	0.9	0.0	JB284 × PL751	564.4	PL751 × HUB208	526.4
Plant height	1.0	0.7	80.5	JB1 × NDB1276	561.3	NDB1173× RD2552	521.4
Tillers/plant	1.0	–0.1	4.7	K792 × NDB1276	558.4	JB1 × HUB208	521.0
Flag leaf area (cm^2)	1.0	0.4	8.6	RD2668 × K792	556.8	K603 × AZAD	520.7
Upper leaf area (cm^2)	1.0	0.7	35.7	RD2581 × JB1	550.9	RD2668 × BH393	518.5
Spike length (cm)	1.0	1.3	12.2	RD2503 × JB58	547.9	NDB1475 × JB1	517.3
Grains/spike	1.0	1.0	41.9	PL172 × K478	537.5	RD2787 × RD2715	516.3
Biological yield/ plant (g)	1.0	2.8	117.2	NDB1020 × RD2634	535.0	NDB1173 × JB58	513.1
1 000 grain weight (g)	1.0	0.8	16.5	RD2552 × JB14	532.2	RD2035 × JB26	512.2
Grain yield/plant (g)	1.0	–3.0	58.0	BH393 × RD2715	532.2	K560 × LAKHAN	499.8
Harvest index (%)	1.0	1.7	36.6	BH393 × RD2618	529.9	JB14 × BH393	499.2

like plant height, days to 50% heading, spike length, grains/spike, 1 000 grain weight, flag leaf area, upper leaf area, biological yield/plant, grain yield/plant and harvest index were found most outstanding to inbuilt the genetic architecture. Hence, direct selection for these characters in barley may prove highly effective to enhance the yield potential of barley crop.

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