Research Article

www.ekinjournal.com

Ekin
Journal of Crop Breeding and Genetics

3(2):88-97, 2017

Ekin International biannual peer-reviewed journal

Change in Traits' Association with Intermating

Agdew BEKELE[1*] **Sada R. VERMA**[2] **Rishi K. Behl**[2]

[1] Southern Agricultural Research Institute (SARI), Hawasa Ethiopia
[2] CCS Haryana Agricultural University, India

[*] Corresponding author e-mail: agdew_bek@yahoo.com

Citation:
Bekele A., Verma S.R., Behl R.K., 2017. Change in Traits' Association with Intermating. Ekin J. 3(2):88-97.

Received: 12.03.2017 ***Accepted: 21.05.2017*** ***Published Online: 29.07.2017*** ***Printed: 31.07.2017***

ABSTRACT

The present investigation was conducted to examine the extent of phenotypic and genotypic correlation in bi-parental mating and selfing for yield and related components. Sixty plants from every cross of barley (IBON-W-61 x DWR91, BH935 x BH902 and BH902/DWRUB64) were randomly selected and crossed as well as selfed to generate 30 BIPs and 30 selfed progenies in 2012-13. In 2013-14 those slefed and intermated progenies were grown in a compact family block design with three replications. Data were recorded on days to heading, days to maturity, plant height, spike length, grain/spike, effective tiller number per plant, biomass yield per plant, grain yield per plant, harvest index and 1000-grain weight. The genotypic and phenotypic correlation coefficients were calculated between pair of characters. From the study it was concluded that intermating has improved mean performance and variance of characters by breaking linkages between genes and resulted in breakage of coupling phase and repulsion phase linkages that led to decreased and increased correlations, respectively.

Keywords: Intermating, selfing, biparental, coupling phase, repulsion phase.

Introduction

Archaeological evidence has suggested that barley is an oldest crop cultivated during ancient times at about 10,000 to 12,000 years ago. It is most likely originated in the Fertile Crescent area of the Near East (Anonymous, 2012), since the wild progenitor of barley, *Hordeum spontaneum*, is still found in this area. Barley grain is used as animal feed, human food and malt. The use of barley which brings the largest added value, however, is for the production of malt, which has contributed to the crop's expansion to the world. Developed countries use barley predominantly for animal feed and malt production. 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).

A six-row and two-row feature of barley is an important morphological architecture (Palmer *et al.,* 2009). Through selection and domestication process, the six-rowed barley was evolved from the two-row wild type (Pourkhiranandish and Komatsuda, 2007) as a result of spontaneous mutations. Following this mutation, six-row was favored more than the two-row during selection because of the three fold number of grains per spike.

Two-rowed barleys usually have a more number of tillers per plant and larger, heavier grain than six-rowed varieties. On the other hand, six-rowed types usually have more grains per inflorescence. Thus the compensatory effects of yield components lead to similar levels of yield potential (Hayes *et al*., 2003). In six-rowed barley all the florets are fertile and produce grains, while in the two-rowed plants the outer florets of each group are sterile. Two-row character is dominant over the six-row character in F_1 (Khan, 1985) and in the F_2 population this character is segregated into two row, six-row and intermediate types. Genetically, there are at least five independent loci controlling the six rowed spike phenotype in barley (Pourkhiranandish and Komatsuda, 2007). Six-rowed spike *1* (*vrs1*), a recessive gene located on chromosome 2HL, is found in six-rowed, where as cultivated two-rowed barleys have dominant alleles for *Vrs1*.

The gain in barley yield has come largely due to manipulating genes responsible for lodging and disease resistance which made barley plant responsive to agronomic practices. Thus, the realized increase in barley productivity is to be maintained. Further efforts to increase yield have become relatively difficult because of the fact that the ongoing breeding methods such as pedigree method are limited due to several drawbacks like limited parent participation, low genetic variability, reduced recombination, and rapid fixation of genes following selfing. The improvement following such method may further be restricted due to association between genes for desirable and undesirable characters and there is no chance to regain desirable genes that may have lost in the selected plants. 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. Different mating designs have been suggested to exploit the hidden variability by breaking the linkages in the breeding materials of self pollinated crops. One of these designs is the biparental mating in the early segregating generations, mostly in 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 fostered recombination in rice (Manickavelu *et.al*., 2006; Mahalingam *et al*., 2011a; Mahalingam *et al*., 2011b), in wheat (Yunus and Paroda, 1982; Verma, 1989) and in six row-barley (Prakash and Verma, 2006). However, the information is scanty in case of barley. Therefore, the present investigation was designed to investigate the relative efficiency of inter-mating and selfing in breaking the undesirable linkage blocks between the yield component traits to affect association among those component traits.

Materials and Methods

The experimental materials used for the first crop season of this study during 2012-13 comprised of F_2 generation of three inter-varietal crosses of barley, namely, cross I (IBON-W-61/DWR91- two-row / two-row), cross II (BH935/BH902 - two-row / six-row) and cross III (BH902/DWRUB64 - six-row / six row). From each cross 1,000 F_2 plants were space planted in 2012-13 *rabi* season at the research station of the department of Genetics and Plant breeding, CCS Haryana Agricultural University, India. Out of F_2 populations 60 plants were selected from each cross for paired crossing to generate biparental populations (BIPs) and to get selfed generations from 30 female parent plants. Crossing was conducted following the normal hand emasculation procedure and more than five tillers of the maternal plants were allowed to self pollinate for production of F_3 selfed seed. Then, seeds of 30 BIPs and the respective selfs were harvested separately to grow the next experiment.

In the *rabi* season of 2013-14, 30 families in two populations (BIPs and their respective F_3s) in each cross along with their parents and checks were grown in a compact family block design with three replications. In each replication, two compact blocks were set for each population and each compact block was further partitioned to 33 plots for families, parents and checks. In each cross, families were randomized with in replication and progenies with parents and checks were randomized with in family block following the standard procedure for the design (Nageswara, 2007). Each plot consisted of a single row with 3 meters length and the spacing between rows and plants were 30 cm and 15 cm, respectively.

Data was recorded on days to heading, days to maturity, plant height, spike length, grains per spike, effective tiller number per plant, biomass yield per plant, grain yield per plant, harvest index and 1000 grain weight. Days to heading was recorded when ears of 50% the plants in the plot were fully emerged from the flag leaf sheath, while days to maturity was recorded when the plants of plot had fully turned to yellow on plot bases. The rest traits were measured from five competitive selected plants from the middle of the row after maturity of the crop.

The data recorded on quantitative characters of yield and its components were subjected to statistical analysis. For the mean data collected, separate analysis of variances between families for each population in every cross was carried out using the standard ANOVA procedure for the randomized complete block design (Nageswara, 2007). Following ANOVA, the nature and extent of association between yield and its component traits was examined by computing phenotypic and genotypic correlation coefficients for each population in every cross using the Plant Breeding Tools software version 1.1 (PBTools, 2013) as suggested by Miller *et al*. (1958) and Kwon and Torrie (1964) as:

$$r_{pxy} = \frac{\operatorname{cov} pxy}{\sqrt{(\sigma^2 px)(\sigma^2 py)}}$$

$$r_{gxy} = \frac{\operatorname{cov} gxy}{\sqrt{(\sigma^2 gx)(\sigma^2 gy)}}$$

where r_{pxy} is phenotypic correlation coefficient and r_{gxy} is genotypic correlation coefficient between characters x and y; cov_{pxy} and cov_{gxy} are phenotypic covariance and genotypic covariance between characters x and y, respectively; σ^2_p and σ^2_g are phenotypic and genotypic variance, respectively, for the respective character.

Results and Discussion

Analysis of variance

The analysis of variance results for mean family of ten characters studied in biparental and selfed populations of three crosses revealed significant variation among families as source of variation for most the assessed traits in BIP and F_3s of three crosses (Table 1). Hence, all the families in both populations of all three crosses differed significantly from each other with respect to all the assessed characters. Previous research findings indicated that biparental mating generated adequate variability in crops like rice (Amudha *et al*., 2006; Mahalingam *et al*., 2011a; Mahalingam *et al*., 2011b), wheat (Yunus and Paroda, 1983; Fredrickson and Kronsrad, 1985; Verma, 1989; Nematualla and Jha, 1993;), barley (Prakash and Verma, 2006), sesame (Vinayan and Govindarasu, 2010) and okra (Raju *et al*., 2010; Guddadamath *et al*., 2011).

Correlation of characters

Correlation of traits signifies that when one trait is selected, the other associated trait is also changed. The short-term response to selection depends not only on the heritabilities of the selected traits but also on the genetic and phenotypic covariances among traits (Falconer, 1989). Genetic correlations between traits, which arise due to pleiotropy or linkage relations among genes controlling the traits, are considered factors affect the direction of short term phenotypic evolution (Norry *et al*., 2000). The correlation between traits can be negative or positive in which a negative (for genes to increase one trait and decrease the other one) correlation arises from repulsion linkage of genes controlling the two traits while the positive (genes increase both traits) association occurs due to coupling phase of linkage (Sharma, 2008). In general the genotypic correlation varies from one population to another and also over time.

In the present investigation, the phenotypic and genotypic correlation coefficient analysis was carried out for combinations of all measured traits in three crosses for two populations (Tables 2, 8 & 9), and the result revealed that for most of the character associations, the genotypic correlation coefficients were higher, in magnitude, than the corresponding phenotypic correlation coefficients for both populations in three crosses. This indicated that the association between characters was, in general, inherited or controlled genetically. However, there are certain cases that the phenotypic correlation coefficients were closer to, or greater than (like biomass with effective tiller number and grain yield per plant in all crosses) the corresponding genotypic coefficients suggesting that environment had effect on those correlations. Most of the previous research findings also confirm higher magnitude of genotypic correlation coefficient compared to the corresponding phenotypic one (Yunus and Paroda, 1982; Waitt and Levine, 1998; Al-Tabbal and Al-Fraihat, 2012).

The considerable shift of correlations in the biparental populations compared to selfed progenies was observed in this investigation. When comparing the phenotypic and genotypic correlation coefficients among characters between BIP and F_3 selfs, the situation varied depending on traits associated and crosses. As many as 20, 16, and 14 new associations (either from non-significant to significant or vice versa) appeared in BIPs compared to selfed progenies in cross I, cross II, and cross III, respectively.

In BIPs of cross I, grain yield/ plant showed a significant positive association with spike length and grains per spike in F_3 were broken and changed to non-significant correlation in biparental progenies. The grain yield/plant's positively significant correlation coefficient with traits such as effective tiller /plant, harvest index and 1000-grain weight showed increment; however, its association reduced to positively significant with biomass yield/plant. In cross II, the association of grain yield/plant with plant height, spike length and days to heading was reduced to non-significant in intermated population from a significant positive association in selfed progenies; but its association with effective tiller per plant and harvest index was significantly and positively improved in BIPs form non-significant correlation in F_3 while its association with biomass yield/plant, 1000-grain weight and days to maturity improved in magnitude towards positive and significant in BIPs form significant positive association in F_3. The association of grains/spike with grain yield/plant was changed towards significant negative association in biparental from significant positive correlation in selfed progeny. The association of grain yield/plant with other traits in cross III revealed significantly and positively improved association with effective tiller number/plant, slightly reduced with significant positive magnitude when associated with biomass yield/plant and harvest index, and the correlation was significantly reduced to non-significant correlation with 1000-grain weight in BIPs compared to F_3. Yunus and Paroda (1982) reported the improvement of association of grain yield with days to heading, days to maturity and plant height towards a positively significant correlation coefficient in BIPs in one cross of bread wheat. Similarly, Nematualla and Jha (1993) noticed in wheat that the significant association of grain yield/plant with plant height, number of tillers per plant, spike length, number of spikelets/spike, grains per spike and 1000-grain weight was considerably reduced in magnitude in BIPs compared to F_3. Verma (1989) also demonstrated considerable improvement of correlation coefficient in magnitude in BIPs for association of grain yield/plant with tillers per plant, 1000-grain weight and biomass yield/plant in one cross of bread wheat, while the correlation coefficient considerably reduced with 1000-grain weight in the other cross.

Grains per spike established significant positive association with plant height, spike length and harvest index in F_3 reduced in magnitude in BIPs, while its significant positive correlation with effective tiller number per plant, 1000-grain weight and days to heading in F_3 was broken and became non-significant in BIPs in cross I. In cross II, grains/spike had significant positive association with plant height and biomass yield in selfed was broken to non-significant in BIPs. However, previous research report showed significant positive association between grains/ear with plant height and days to maturity in wheat (Yunus and Paroda, 1982). The magnitude of significant negative association of grains/spike with 1000-grain weight in F_3 was increased in BIPs which was in line with findings of Verma (1989) and Yunus and Paroda (1982) in bread wheat. The non-significant association of harvest index and days to heading with grains/spike in selfed progenies was changed to significant correlation in BIPs to negative (harvest index) and positive (days to maturity) directions. In cross III, the significant positive correlation of grains/spike with plant height in F_3 was broken to non-significant in BIPs but its association with spike length considerably increased. However, the significant correlation of days to heading (negative) and days to maturity (positive) with grains/spike appeared in BIPs from non-significant correlation in F_3.

The significant positive association of plant height with spike length in F_3 was broken in cross I and reduced in magnitude in crosses II & III in BIPs. Similarly, in cross I, effective tiller number per plant showed increased significant positive associations with harvest index and 1000-grain weight in BIPs from significant correlation in F_3 while the magnitude reduced when it was associated with biomass yield/plant. In crosses I & III, the association of biomass yield/plant and 1000-grain weight with effective tiller numbers/plant was changed to significant positive association in biparental from non-significant correlation in selfed progenies. Association of biomass yield per plant with 1000-grain weight in F_3 was broken in cross I, reduced in magnitude in cross III, and significantly improved in cross II. Thousand grain weight established a significant positive association with harvest index in BIPs in cross I and cross III. The significant decrease or increase as well as magnitude change in correlations between different yield contributing characters have also been reported in different crops like sesame (Martinez and Cordoba, 2004; Vinayan and Govindarasu, 2010), in cotton (Meredith and Bridge, 1971; Tyagi, 1987), in pearl millet (Singh and Murty, 1973), in safflower (Naike *et al*., 2009) and in okra (Guddadamath *et al*., 2012).

From the above elaboration, it is evident that reshuffling of genes responsible for correlations (Yunus and Paroda, 1982) at genotypic level amongst some of the characters in three crosses resulted in new recombination, probably due to changes from coupling to repulsion phase linkage or vice versa. An increase in a genetic correlation coefficient can be obtained if linkages were in a predominant repulsion phase (Meredith and Bridge, 1971; Tyagi, 1987). Miller and Rawlings (1967) suggested that breakage of coupling phase linkages tended to decrease the correlation, whereas that of repulsion phase linkages increased their magnitude (ignoring the sign). Form those suggestions, the results of the present investigation indicate to have involved both repulsion and coupling phase linkage as both decreases and increases the correlation. For some of the associations between characters, more changes will likely to occur in these populations following successive intermating (Nematualla and Jha, 1993). In rare cases, the correlation has been changed from significant positive in F_3 to significant negative in BIPs in cross I for traits between effective tiller number per plant & plant height and spike length & biomass; however in cross III, the association between biomass yield/plat and days to heading changed from significant negative in F_3 to significant positive in BIPs which indicates the breakage of repulsion linkage phase in both biparental mating and selfing approaches following recombination.

In conclusion, the new correlations appeared in biparental compared to selfed progenies changed from either significant to non-significant or non-significant to significant either in desirable or undesirable association. And it was evident that reshuffling of genes responsible for correlations which might have involved both repulsion and coupling phase linkage that decreases and increases the correlation, respectively. This warranted that selection may be resorted to initiate subsequent cycles of intermating which may lead to further improvement.

Table 1. Mean square due to families for BIPs and F_3s across three crosses

Agronomic Trait	**Mean squares due to families**					
	Cross I		**Cross II**		**Cross III**	
	BIP	**F_3**	**BIP**	**F_3**	**BIP**	**F_3**
Days to heading	9.2**	33.5**	37.4**	31.0**	7.64	5.4
Days to maturity	2.96**	12.3**	7.5**	21.1**	3.1**	2.71
Plant height (cm)	53.3*	165.1**	94.1**	93.85**	32.95*	64.9**
Spike length (cm)	0.5*	1.6**	0.71**	1.23**	0.64	0.95**
Grains/spike	5.3**	9.75**	53.8**	35.8**	37.1**	43.7**
Effective tiller number	5.8*	5.52**	8.24*	5.35**	6.01**	2.36**
Biomass yield/plant (g)	242.7*	295.6**	408.4*	206.6**	385.5**	178.1**
Harvest index (%)	26.1**	29.1**	35.3	27.6**	26.9**	17.9**
1000 grain weight (g)	15.1**	39.1**	82.9**	84.1**	125.2**	79.9**
Grain yield/plant (g)	45.2**	53.0**	67.7**	29.3*	66.8**	41.1**

* and **, value is significant at 5 and 1% level, respectively

Table 2. The genotypic (above diagonal) and phenotypic (below diagonal) correlations of traits in F_3 and BIP families of cross I

	PH	SL	GPS	ETN	BM	GY	HI	TGW	DH	DM	Population
PH		0.605**	0.722**	0.475**	0.247	0.329	0.307	0.758**	0.374*	-0.076	F_3
		0.235	0.713**	-0.625**	-0.647**	-0.110	0.313	0.015	0.004	-0.085	BIP
SL	0.555**		0.603**	0.404*	0.371*	0.610**	0.687**	0.423*	0.224	0.130	F_3
	0.155		0.587**	0.013	-0.644**	-0.236	0.246	0.230	0.587**	-0.026	BIP
GPS	0.652**	0.612**		0.529**	0.263	0.555**	0.737**	0.425*	0.539**	0.248	F_3
	0.502**	0.554**		-0.002	-0.208	0.212	0.472**	0.255	0.236	0.153	BIP
ETN	0.345	0.315	0.410*		0.779**	0.770**	0.413*	0.700**	-0.173	-0.188	F_3
	-0.374*	0.048	0.023		0.657**	0.778**	0.568**	0.809**	0.053	0.063	BIP
BM	0.242	0.318	0.239	0.729**		0.864**	0.282	0.756**	-0.364*	-0.045	F_3
	-0.337	-0.197	-0.032	0.675**		0.774**	0.182	0.232	0.011	0.402*	BIP
GY	0.282	0.500**	0.470**	0.760**	0.870**		0.723**	0.793**	-0.161	-0.040	F_3
	-0.133	-0.060	0.184	0.745**	0.785**		0.751**	0.835**	0.121	0.030	BIP
HI	0.194	0.504**	0.567**	0.373*	0.166	0.626**		0.439*	0.206	-0.004	F_3
	0.128	0.104	0.275	0.395*	0.063	0.661**		1.000**	0.121	-0.403*	BIP
TGW	0.502**	0.270	0.270	0.462*	0.446*	0.543**	0.375*		-0.313	-0.655**	F_3
	0.105	0.247	0.324	0.458*	0.225	0.596**	0.664**		0.346	0.055	BIP
DH	0.271	0.239	0.444*	-0.082	-0.255	-0.136	0.133	-0.224		0.731**	F_3
	0.028	0.392*	0.181	-0.010	0.035	0.080	0.050	0.206		0.519**	BIP
DM	-0.085	0.144	0.200	-0.121	-0.020	-0.042	-0.043	-0.38*	0.540**		F_3
	-0.016	0.079	0.138	-0.042	0.197	0.016	-0.246	0.064	0.361*		BIP

* and ** , the correlation coefficient is significant at 5 and 1%, respectively; DH, days to heading; DM, days to maturity; PH, plant height; SL, spike length; GPS, grains per spike; ETN, Effective tiller number; BM, biomass yield/plant; HI, Harvest index; TGW, 1000-grain weight; GY, grain yield/plant.

Table 3. The genotypic (above diagonal) and phenotypic (below diagonal) correlations of traits in F_3 and BIP families of cross II

	PH	SL	GPS	ETN	BM	GY	HI	TGW	DH	DM	Population
PH		0.566**	0.545**	0.325	0.791**	0.658**	-0.367*	0.130	0.018	-0.060	F_3
		0.437*	0.284	0.026	0.390*	-0.073	-0.807**	0.163	0.234	0.155	BIP
SL	0.486**		0.239	-0.152	0.566**	0.430*	-0.311	0.355	0.155	0.175	F_3
	0.328		0.062	0.213	0.212	0.074	-0.21	0.11	0.298	0.151	BIP
GPS	0.389*	0.236		-0.085	0.371*	0.445*	0.015	-0.444*	-0.183	-0.059	F_3
	0.193	0.058		-0.191	-0.140	-0.430*	-0.738**	-0.758**	0.388*	0.234	BIP
ETN	0.173	-0.068	-0.056		0.195	0.227	-0.036	-0.076	-0.083	-0.098	F_3
	0.071	0.205	-0.145		0.998**	0.959**	0.014	0.886**	0.196	-0.073	BIP
BM	0.506**	0.467**	0.309	0.404*		0.744**	-0.573**	0.211	0.333	0.352	F_3
	0.324	0.201	-0.066	0.596**		0.970**	0.050	0.716**	0.523**	0.626**	BIP
GY	0.359	0.339	0.295	0.458*	0.824**		0.116	0.438*	0.394*	0.453*	F_3
	0.016	0.103	-0.271	0.515**	0.868**		0.369*	0.615**	0.224	0.549**	BIP
HI	-0.282	-0.250	-0.026	0.046	-0.363	0.223		0.197	-0.025	0.013	F_3
	-0.580**	-0.202	-0.435*	-0.148	-0.265	0.239		-0.298	-0.308	0.149	BIP
TGW	0.136	0.322	-0.323	-0.002	0.238	0.336	0.123		0.2583	0.154	F_3
	0.103	0.105	-0.560**	0.547**	0.558*	0.513**	-0.105		0.008	0.115	BIP
DH	0.072	0.162	-0.198	-0.041	0.254	0.273	0.005	0.176		0.835**	F_3
	0.195	0.209	0.264	0.111	0.276	0.127	-0.278	-0.004		0.965**	BIP
DM	0.014	0.191	-0.044	-0.057	0.300	0.330	0.028	0.127	0.719**		F_3
	0.204	0.206	0.199	0.028	0.341	0.292	-0.101	0.076	0.769**		BIP

* and ** , the correlation coefficient is significant at 5 and 1%, respectively; DH, days to heading; DM, days to maturity; PH, plant height; SL, spike length; GPS, grains per spike; ETN, Effective tiller number; BM, biomass yield/plant; HI, Harvest index; TGW, 1000-grain weight; GY, grain yield/plant.

Table 4. The genotypic (above diagonal) and phenotypic (below diagonal) correlations of traits in F_3 and BIP families of cross III

	PH	**SL**	**GPS**	**ETN**	**BM**	**GY**	**HI**	**TGW**	**DH**	**DM**	**Population**
PH		0.907**	0.531**	-0.329	0.132	-0.029	-0.281	-0.156	0.064	0.268	F_3
		0.431**	0.333	-0.008	-0.229	-0.131	0.125	-0.091	-0.947**	0.592**	BIP
SL	0.602**		0.823**	-0.085	0.031	-0.121	-0.281	-0.363*	-0.166	0.323	F_3
	0.307		0.963**	-0.083	0.144	0.021	-0.208	0.013	-0.336	0.292	BIP
GPS	0.397*	0.759**		0.066	0.180	0.041	-0.179	-0.186	-0.283	0.006	F_3
	0.262	0.869**		-0.008	0.078	-0.079	-0.273	-0.093	-0.396*	0.423*	BIP
ETN	-0.156	-0.065	0.025		0.053	0.074	0.072	0.084	-0.106	-0.100	F_3
	-0.049	0.041	0.017		0.720**	0.716**	0.192	0.593**	0.724**	0.049	BIP
BM	0.137	0.056	0.102	0.299		0.866**	0.206	0.800**	-0.980**	-0.330	F_3
	-0.168	0.155	0.062	0.746**		0.833**	-0.076	0.559 **	0.442*	0.067	BIP
GY	0.033	-0.051	0.011	0.281	0.894**		0.664**	0.811**	-0.767**	-0.268	F_3
	-0.083	0.077	-0.044	0.748**	0.857**		0.486**	0.876**	0.319	0.026	BIP
HI	-0.155	-0.201	-0.148	0.096	0.208	0.621**		0.355	-0.026	0.004	F_3
	0.130	-0.121	-0.191	0.205	-0.038	0.478**		0.667**	-0.166	-0.036	BIP
TGW	-0.078	-0.264	-0.173	0.167	0.670**	0.712**	0.369*		-0.263	-0.233	F_3
	-0.034	0.012	-0.096	0.519**	0.517 **	0.789 **	0.633**		0.463**	-0.059	BIP
DH	0.125	-0.080	-0.092	-0.043	-0.412*	-0.370*	-0.098	-0.158		0.264	F_3
	0.049	0.125	0.067	0.230	0.180	0.166	0.004	0.201		-0.550**	BIP
DM	0.208	0.270	0.012	-0.082	-0.250	-0.212	0.002	-0.205	0.150		F_3
	0.384	0.267	0.362*	0.055	0.073	0.040	-0.033	-0.045	0.052		BIP

* and ** , the correlation coefficient is significant at 5 and 1% , respectively; DH, days to heading; DM, days to maturity; PH, plant height; SL, spike length; GPS, grains per spike; ETN, Effective tiller number; BM, biomass yield/plant; HI, Harvest index; TGW, 1000-grain weight; GY, grain yield/plant.

Reference

Al-Tabbal JA and Al-Fraihat AH (2012). Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *J. Agri. Sci*. 4 (3): 193-210.

Amudha K, Arumugachamy S and Thiyagarajan K, (2006). Studies on selfed and biparental progenies involving upland rice genotypes. *Crop Res*. 31(1): 157-159.

Anonymous (2012). Barley. Consultative Group for International Agricultural Research Centres (CGIAR). *http://www.cgiar.org/our-research/crop-factsheets/barley/*. Accessed on 20/11/2013.

Comstock RE and Robinson HF (1952). Estimation of average dominance of genes, pp. 494-515. In: *Heterosis*, Gowen, J.W. (Ed), Iowa State College Press-Ames.

Falconer DS (1989). Introduction to quantitative genetics, 3rd edition John Wiley, New York.

Fredrickson LJ and Kronsrad WE (1985). A comparison of intermating and selfing following selection for heading date in two diverse winter wheat crosses. *Crop Sci*. 25: 555-560.

Guddadamath S, Mohankumar HD and Salimath PM (2011). Genetic analysis of segregating populations for yield in okra [*Abelmoschus esculentus* (L) Moench]. *Karnataka J. Agric. Sci.* 24 (2): 114-117.

Guddadamath SG, Mohankumar HD and Salimath PM (2012). Effect of biparental mating on association pattern among quantitative characters in okra [*Abelmoschus esculentus* (L.) Moench]. *Int. J. of Hort.* 2(5): 21-24.

Hayes PM, Castro A, Marquez-Cedillo L, Corey A, Henson C, Jones BL, Kling J, Mather D, Matus I, Rossi C and Sato K (2003). Genetic diversity for quantitatively inherited agronomic and malting quality traits. *Developments in Plant Gent. Breed.* 7: 201-226.

Khan M (1985). Inheritance of awns and rows in barley. *Pakistan J. Agric. Res*. 6(2): 93-96.

Kwon SH and Torrie JH (1964). Heritability and interrelationships among characters of two soybean populations. *Crop Sci*. 4: 196-198.

Mahalingam A, Robin S and Rabindran R (2011a). Genetic studies on enhanced disease reaction of biparental progenies (BIPs) to blast disease of rice (*Oryza sativa* L.). *J. Rice Res*. 4(1 & 2): 15-19.

Mahalingam A, Robin S, Mohanasundaram K and Pushpam R (2011b). Studies on genetic architecture of biparental progenies for important yield attributes in rice (*Oryza sativa* L.). *J. Plant Breed. Crop Sci*. 3(12): 296-301.

Manickavelu A, Gnanamalar RP, Nadarajan N and Ganesh SK (2006). Genetic variability studies on different genetic populations of rice under drought condition. *J. Plant Sci*. 1(4): 332 -339.

Martínez JF and Córdoba (2004). Correlation studies in F_2, F_3 and BIPS Populations of sesame (*Sesamum indicum* L.). Sesame and Safflower Newsletter 19, FAO, Italy, Rome.

Meredith WR and Bridge RR (1971). Breakup of linkage blocks in cotton *Gossypium hirsutum* L. *Crop Sci.* 11:695-698.

Miller PA and Rawlings JO (1967). Breaking up of initial linkage blocks through intermating in cotton population. *Crop Sci*. 7: 637-640.

Miller PA, Williams JC, Robinson HF and Comstock RE (1958). Estimates of genetic and environmental variance and covariance and their implication in selection. *Agron. J.* 50:126-131.

Nageswara RG (2007). Statistics for Agricultural sciences. B.S. Publications, Hyderabad, India.

Naik VR, Bentur MG and Parameshwarappa KG (2009). Impact of biparental mating on genetic variability and path analysis in safflower. *Karnataka J. Agric. Sci.* 22(1): 44-46.

Nematualla and Jha PB (1993). Effect of biparental mating in wheat. *Crop Improve*. 20(2): 173-178.

Norry FM, Vilardi JC and Hasson E (2000). Negative genetic correlation between traits of the *Drosophila* head, and interspecific divergence in head shape. *Heredity* 85: 177–183.

Palmer SA, Moore JD, Clapham AJ, Rose P and Allaby RG (2009). Archaeogenetic evidence of ancient Nubian barley evolution from six to two-row indicates local adaptation. *PLoS ONE* 4(7): e6301. doi:10.1371/journal.pone.0006301.

PBTools (2013). Plant Breeding Tools, version 1.1. International Rice Research Institute, Los Banos, Laguna, Philippines.

Pourkhiranandish M and Komatsuda T (2007). The importance of barley genetics and domestication in global perspective. *Annals of Bot.* 100: 999-1008.

Prakash V and Verma RPS (2006). Comparison of variability generated through biparental mating and selfing in six-rowed barley (*Hordeum vulgare* L.). *Crop Improve*. 33(1): 49-52.

Raju C, Satish RG, Rajesab Shanthakumar G and Nayak A (2010). Genetic variability created through biparental mating in bhendi [Abelmoschus esculentus (L.) Moench]. *Gregor Mendel Found*. J. 1: 33-35.

Sharma JR (2008). Statistical and biometrical techniques in plant breeding. New age international publishers, New Delhi, India.

Singh BB and Murty BR (1973). A comparative analysis of biparental mating and selfing in pearl millet (*Pennisetum typhoïdes*). *Theor. Appl. Genet*. 43(1): 18-22.

Tyagi AP (1987). Correlation studies on yield and fibre traits in upland cotton (*Gossypium hirsutum* L.). Theor Appl Genet. ;74 (2) **:**280-283.

Verma RPS, Kharub AS, Sarkar B and Dinesh K (2011). Barley: A crop for changing climate in India. *Progressive Agri.*, 11: 63-73.

Verma RPS, Kharub AS and Mishra B (2008). Dual purpose barley for green fodder and grain in dry areas of India. Poster presented in *10th Int. Barley Genetics Symposium*, Alexandria during 5-10 April, 2008.

Verma SR (1989). Studies on methods of generating variability and genetic analysis of yield and its component traits in bread wheat (*Triticum aestivum* L.em. Thell). *PhD Thesis*, Haryana Agricultural University, Hisar.

Vinayan MT and Govindarasu R (2010). Relative efficiency of biparental mating, single capsule descent, selected bulk and random bulk selections in sesame (*Sesamum indicum* L.). *Electronic J. of Plant Breed*. 1(4): 666-674.

Waitt DE and Levin DA (1998). Genetic and phenotypic correlations in plants: a botanical test of Cheverud's conjecture. *Heredity* 80: 310-319.

Yunus M and Paroda RS (1982). Impact of biparental mating on correlation coefficients in bread wheat. *Theor. Appl. Genet*. 62: 337-343.

Yunus M and Paroda RS (1983). Extent of genetic variability created through biparental mating in wheat. *Indian J.Plant Gen. Breed*. 43 (1): 76-81.