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Heritability and interrelationship among traits of twenty Brassica genotypes

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Abstract

The genetic potential, heritability, selection response and correlation were studied during 2011-12 in brassica cultivars at the University of Agriculture, Peshawar, Pakistan. Data were recorded on days to maturity, plant height, pods per main raceme, pod width and 100-seed weight. Analysis of variance showed highly significant *($P\leq 0.01$)* differences for all the traits. Mean ranges were days to maturity (178 to 205 days), plant height (174.7 to 215 cm), pods per main raceme length (27.0 to 56.3), pod width (0.3 to 0.5 cm) and 100-seed weight (0.25 to 0.41 g). Heritability and selection response were; days to maturity (0.70; 8.11), plant height (0.35; 8.7), pods main raceme^{-1}, (0.68; 9.11), pod width (0.60; 0.06) and 100-seed weight (0.57; 0.04), respectively. Days to maturity revealed significant positive with plant height (r= 0.661**), pods per main raceme (r= 0.302*) and non-significant with 100-seed weight. Plant height revealed positive significant correlation with 100-grain weight (r= 0.375**) and non-significant with pods per main raceme and pod width. Similarly pods per main raceme exhibited positive non-significant correlation with 100-seed weight and negative with pod width. Whereas, pod width manifested negative correlation with 100-grain weight. Results revealed that the studied genotypes with larger genetic potential, positive relationship between yield and yield contributing traits and moderate to high heritability could guide intensive selection and improvement and could further be studied to identify better performing lines for Peshawar division.

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Introduction

The genus *Brassica* L. holds the most economically valuable position in the tribe Brassiceae, which is a part of family Brassicaceae (Rakow, 2004). This genus consists of a versatile batch of species that includes major oilseed crops and vegetables (Rich, 1991; Christopher *et al.*, 2005). This family comprises of 338 genera and 3709 species (Warwick *et al.*, 2006). The species of genus Brassica are generally classified into two main groups commonly known as rapeseed and mustard. It also contains six economically valuable species with huge genetic and morphological variation and is cultivated in all over the world (Shah *et al.*, 2008). Among these, three species are diploid (*Brassica oleracea*, 2n = 18; *Brassica rapa*, 2n = 20; *Brassica nigra*, 2n = 16), and three are amphidiploid (*Brassica napus*, 2n = 38; *Brassica juncea*, 2n = 36; *Brassica carinata*, 2n = 34). Rapeseed-mustard (*Brassica napus, Brassica campestris and Brassica juncea*) are grown all over the world as an important source of edible oil (Downey and Rakow, 1987).

Genetic parameters i.e variability, heritability and correlation analysis are very important for plant breeders to move in a right direction. To run a progressive breeding program, the locally available germplasm are genetically evaluated.

The local germplasm have more chance of variability than others and can be easily manipulated in a varietal developmental process. These genetic estimations could be on various yield and yield related traits to understand its potential (Ali *et al.*, 2013; Azam *et al.*, 2013). These yield and yield related traits are not only controlled by its genetics but are also greatly influenced by its environment in which they survive because of polygenic inheritance (Gaines *et al.*, 1996; Novoselovic *et al.*, 2004).

Thus heritability is a tool which could easily differentiate between the genetic and environmental influences and also helps in the rate of transmission of a trait into next generation. So through heritability estimation, we may predict and select in coming generations easily (Khan *et al.*, 2003). Selection response tells us the rate of increase in a trait under various selection pressures and have direct relationship with heritability. So, selection response is an important tool for a breeder in the isolation and selection process in a breeding program (Shukla *et al.*, 2004). Correlation analysis tells us the magnitude of interrelationship between various sets of traits and thus there is a little possibility for any sets of traits to be separately controlled. In view of the above facts and figures the present research was conducted to estimate heritability and correlation between yield and yield components of brassica.

Materials and methods

The current study consisted twenty Brassica genotypes sown at the University of Agriculture, Peshawar in a randomized completely block design with three replications in 2011-12 with an objective to evaluate its genetic potential through various yield and yield related traits. Ten plants per genotype in a single replication were selected for data recording. Data were recorded for each trait on its proper time and all agronomic practices were done at specified time.

Statistical analysis

Estimation of genetic parameters and correlation

Genotypic and phenotypic variances, heritability (broad sense) and genetic advance were computed according to Burton and Devane (1953), Johnson *et al.* (1955) and Singh and Chaudhary (1985).

Data were recorded on days to maturity, plant height, pods per main raceme, pod width and 100-seed weight. Data were subjected to analysis of variance (ANOVA) according to Steel *et al.* (1997).

After getting the significant variations among genotypes performance for various parameters, the means for each trait were further separated and compared by using the least significant difference (LSD) test at 5% level of probability. The correlation of 100-seed weight with other traits was worked out according to Kwon and Torrie (1964).

$$\text{Genetic variance }(Vg) = \frac{\text{Genotypes mean squares }(GMS) - \text{Error mean squares }(EMS)}{\text{Number of replications }(r)}$$

$$\text{Evironmental variance }(Ve) = \text{Error mean squares }(EMS)$$

Phenotypic variance (Vp)= Vg + Ve

Heritability broad sense (H^2) on entry mean basis was calculated as:

$$H^2 = \frac{Vg}{Vp}$$

The expected response to selection (Re) for each trait was calculated as under:

$$\text{Re} = k\sqrt{vp}\,H^2$$

Where:

k = 1.40 at 20% selection intensity for a trait.

V_P = Phenotypic variance for a trait.

h^2 = Broad sense Heritability for a trait.

Results and discussion

Analysis of variance showed highly significant *($P \leq 0.01$)* differences for days to maturity, plant height, pods per main raceme, pod width and 100-seed weight (Table 1).

Table 1. Mean squares table for yield and yield related traits in twenty Brassica genotypes.

Traits	Replication	Genotypes	Error	CV %
Days to maturity	110.15	156.505**	19.887	2.29
Plant height	187.8	515.308**	199.168	7.28
Pods per main raceme	25.317	202.372**	27.001	11.88
Pod width	0.058	0.011**	0.002	11.12
100-seed weight	0.008	0.005**	0.001	11.9

For days to maturity and plant height significant differences in brassica genotypes which were confirmed by (Sinha *et al.*, 2001; Zare and Sharafzadeh 2012; Samad and Khaleque, 2000; Ali *et al.*, 2003). Similarly pods per main raceme and pod length revealed significant differences for the said attributes in brassica germplasm (AytacandKinaci 2009; Nazeer *et al.*, 2003and Tahir *et al.*, 2006). Finally 100-seed weight exhibited results which were in close conformity with (Akbar *et al.*, 2007; Aytaçand Kınacı, 2009; Sadat *et al.*, 2010; Nasim *et al.*, 2013).

Mean performance of brassica genotypes

Days to maturity ranged from 178 to 205 days. Maximum days to maturity were observed in genotype J.615 (205 days), whereas minimum days were found in genotype J.602 (178 days)(Table 2). Plant height ranged from 174.7 to 215 cm. Genotype J.603 exhibited maximum plant height (215 cm), while genotype J.611 revealed lowest value (174.7 cm)(Table 2).Pods per main raceme ranged from 27.0 to 56.3. Maximum pods per main raceme were observed in genotype J.610 (56.3), whereas genotype J.618 exhibited least number of pods per main raceme (27.0) (Table 2).

Table 2. Ranges with best genotypes table for yield and yield related traits in twenty Brassica genotypes.

Traits	Ranges	Best Genotype
Days to maturity	178-205	J.602
Plant height (cm)	174.7-215	J.610
Pods Main Receme^{-1}	27-56	J.610
Pod Width (cm)	0.3-0.5	J.606
100-Seed Weight (g)	0.25-0.41	J.608

Pod width ranged from 0.3 to 0.5 cm. Widest pods were recorded ingenotypesJ.606, J.602 and J.604 (0.5), however thinnest pods (0.3) were revealed by genotypes J.600, J.611, J.612, J.615, J.616 and J.619 (Table 2).

100-seed weight ranged from 0.25 to 0.41 g. Maximum 100-seed weight was observed in genotype J.608 (0.41 g), whereas minimum weight was found in genotypesJ.611 and J.615 (0.25 g) (Table 2).

Table 3. Variances, broad-sense heritability and selection response table for yield and yield related traits in twenty Brassica genotypes.

Trait	Ve	Vg	Vp	h^2	Re
Days to maturity	19.89	45.54	65.43	0.70	8.11
Plant height (cm)	199.17	105.38	304.55	0.35	8.7
Pods Main Receme^{-1}	27	58.46	85.46	0.68	9.11
Pod Width (cm)	0.002	0.003	0.005	0.60	0.06
100-Seed Weight (g)	0.001	0.001	0.002	0.57	0.04

Heritability

Genetic variance (45.54) was greater than environmental variance (19.89) for days to maturity. Moderate broad-sense heritability (0.70) with moderate selection response (8.11) was recorded for the said trait, which clearly manifested the importance of genetic variance in the inheritance and improvement of days to maturity (Table 3) (Bilal *et al.,* 2015). Genetic variance (105.38) was muchlowerin magnitude than environmental variance (199.17) for plant height with moderate broad-sense heritability and selection response (0.35 and8.70) (Ali *et al.*, 2013; Nasim *et al.*, 2013).

For pods main raceme genetic variance (58.46) was higher than environmental variance (27.00) for pods per main raceme. Moderate broad-sense heritability (0.68) and selection response (9.11) were recorded for pods per main raceme. These results for high broad-sense heritability are similar with the findings of Mahmood *et al.*, 2003 who also reported high heritability for pods main raceme^{-1}. Genetic variance (0.00) was equal in amount with environmental variance (0.00) for pod width. Moderate broad-sense heritability (0.60) and low selection response (0.06) were obtained for the said trait. Genetic variance (0.00) was equal in amount with environmental variance (0.00) for 100-seed weight. Moderate broad-sense heritability (0.57) and low selection response (0.04) were found for 100-seed weight (Ali *et al.*, 2003; Nazeer *et al.*, 2003; Zhang and Zhou, 2006).

Table 4. Correlations table for yield and yield related traits in twenty Brassica genotypes.

Traits.	Plant height	Pod main raceme	Pod width	100-Seed Weight
Days to maturity	0.661**	0.302*	-0.267*	0.146
Plant height		0.026	0.075	0.375**
Pods Main Receme^{-1}			-0.003	0.022
Pod Width				-0.006

Correlation

Days to maturity showed significant and positive correlation with all the traits but was negatively correlated with pod width (Table 4). Positive correlation were resulted by Bilal *et al.*, 2015 among days to maturity and 100-seed weight which strengthen our findings. Plant height showed highly significant positive correlation with 100-seed weight (r = 0.375**). Our current results are strongly supported by the findings of (Nasim *et al.*, 2013; Azam *et al.*, 2013) by reporting positive correlation among plant height and 100-seed weight.

Pods per main raceme showed highly significant positive correlation with days to maturity (r = 0.302*), while non-significant positive with 100-seed weight. Ali *et al.*, (2013) resulted non-significant positive correlation between pods per main raceme and 100-seed weight and strengthen our findings for the said trait. Pod width showed significant negative correlation with days to maturity (r = -0.267*). Nasim *et al.*, (2013) obtained highly significant differences and moderate heritability for pod width which elaborated our findings. 100-seed weight showed highly significant positive correlation with plant height (r = 0.3759**), while non-significant positive correlation with days to maturity (r = 0.146). Bilal *et al.*, (2015) obtained positive correlation among 100-seed weight and days to maturity.

Conclusions

It is concluded that sufficient amount of variability is present in the studied germplasm. Days to maturity, plant height and pods per main racemes hould be used as a selection criteria to improve 100-seed weight. Based on mean performance and genetic parameters, genotypes J.608 and J.610 are recommended to be used in future breeding programs.

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