Heritability Estimates in Intra and Inter-Specific F₂ Populations of Brassica

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Abstract

Six F₂ derived inter and Intra-specific Brassica populations along with their parents were evaluated to estimate heritability at The University of Agriculture, Peshawar during 2012-13. Maximum plant height was 181.62 cm for 560 x 867 (*B. napus x B. campestris*), primary branches plant⁻¹ was 12.47 for 525 x 905 (*B. napus x B. olaracea*), main raceme length was 76.40 cm for 525 x 905 (*B. napus x B. olaracea*), pods main raceme⁻¹ was 80.03 for 525 x 905 (*B. napus x B. olaracea*), pod length was 52 mm for 525 x 905 (*B. napus x B. olaracea*), pod width was 3.79 mm for 525 x 925 (*B. napus x B. olaracea*), seed pod⁻¹ was 16.63 for 614 x 616 (*B. juncea x B. juncea*), 1000-seed weight was 3.45 g for 609 x 616 (*B. juncea x B. juncea*). Higher heritability values were found for most of the quantitive traits. In F₂ population maximum heritability estimates were recorded 0.789 in 609 x 616 (*B. juncea x B. juncea*) for plant height, 0.570 in 609 x 616 (*B. juncea x B. juncea*) for primary branches plant⁻¹, 0.660 in 609 x 616 (*B. juncea x B. juncea*) for main raceme⁻¹, 0.902 in 615 x 617 (*B. juncea x B. juncea*) for pod length, 0.756 in 609 x 616 (*B. juncea x B. juncea*) for pod width, 0.833 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for seed pod⁻¹, 0.902 in 614 x 616 (*B. juncea x B. juncea*) for 1000-seed weight in Intr

INTRODUCTION

Oilseed crops are grouped as conventional and non-conventional. The conventional oil seed crops include rapeseed mustard, ground nut, linseed, castor oil, sesame: whereas cotton, canola, sunflower, soybean and safflower are the non-conventional. The *Brassica* species (*B. napus, B. juncea, B. rapa or B. campestris*) are now the third most important source of edible oil after palm and soybean, but in Pakistan, Brassica stands second in edible oil production after cotton. In *Brassica*, oil quality refers to low levels of erucic acid, glucosinolate and linolenic acid and high levels of protein, oil and oleic acid. Despite the significant amount of high valued nutrient, use of rapeseed in human diet or in animal feeding has been limited, mainly because both oil and protein in rapeseed are accompanied by certain anti-nutritional factors (Renarid and McGregor, 1976).

Brassica campestris is also one of the major oil seed crop in the Indian sub-continent. It is highly selfincompatible and relies on cross-pollination from other plants. It is the predominant cruciferous species and has been widely grown throughout the rain-fed areas of Khyber Pakhtunkhwa. It has great yield potentials for semi arid conditions and known to be more drought tolerant and shattering resistant than *B. napus*. It matures earlier than *B. napus* and consequently escapes the attack of insect pest. *B. napus* is rather recent and one of the most important species, its cultivation as a seed crop is confined to NWFP (now Khyber Pakhtunkhwa) and some areas of Punjab (PARC, 1991).

In Brassica crops various techniques are used for the development of improved genotype of desirable characteristics. Inter-specific, inter-generic hybridization and heterosis are simple tools for the production of desirable genotypes and improvement of rape and mustard crops. For improving genotypes of desirable traits, as a first step information available on genetic analysis of important characters is collected. To carry out a genetic analysis it is necessary to collect data from a number of successive generations or from the different mating systems. A sufficient number of lines are crossed in all possible combinations including inter-specific hybridization, selfing, reciprocal crossing etc from where best desirable families/lines are selected and forward for fixing and improvement.

The present study was thus designs to estimates heritability of various traits in inter and intra specific crosses of Brassica and to check and compare the performance of *B. juncea* in inter and intra specific crosses.

MATERIAL AND METHODS

This study pertains to "Heritability estimates in segregating population of *Brassica*". The experimental material was comprised of six F_2 population obtained from F_1 plants of intra and inter-specific crosses with their respective parents and was evaluated at Malkandhar Research Farm, Peshawar. The data were recorded on 30 plants of each cross and their parents having 30 cm row-to-row and 4-5 cm plant-to-plant distance.

The following generation/ population were evaluated during the experiments.

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PARENTS

Accessions	
609, 616, 614, 615, 617, 625	B. juncea
825, 867	B. campestris
525, 560	B. napus
905	B. olaracea
F₂ POPULATIONS	
Inter-specific crosses	
Accession#	
825 x 625	B. campestris x B. juncea
525 x 905	B. napus x B. olaracea
560 x 867	B. napus x B. campestris
Intra-specific crosses	
Accession#	
609 x 616	B. juncea x B. juncea
614 x 616	B. juncea x B. juncea
615 x 617	B. juncea x B. juncea

Data were recorded on plant height, primary branches plant⁻¹, main raceme length, pods main raceme⁻¹, pod length, pod width, seeds pod⁻¹, 1000 seed weight.

STATISTICAL ANALYSIS

The broad sense heritability of each trait was calculated by the following formula for each trait using *Mahmud and Kramer* (1951).

Heritability (B.S) =
$$VF_2 - \frac{\sqrt{VP_1 \times VP_2}}{VF_2}$$

RESULTS AND DISCUSSION

Primary branches plant⁻¹

The numbers of pods bearing branches plant⁻¹ is the result of combined effect of genetic make up of the genotype and environmental conditions, which play a remarkable role towards the final seed yield of the crop. The value recorded for number of primary branches plant⁻¹ showed a range of 5.8 to 16.6 branches for parents, in which the minimum branches were produced by 525 (*B. napus*) 5.8 and the maximum for 905 (*B. olaracea*) (Table 2). Data regarding F₂ populations ranged from 7.34 to 12.47 branches. The maximum primary branches plant⁻¹ (12.47) was recorded for population 525 x 905 (*B. napus x B. olaracea*), while the minimum (7.34) primary branches plant⁻¹ was observed for population 560 x 867 (*B. napus x B. campestris*) (Table 2). Heritability estimates for primary branches plant⁻¹ in Inter-specific F₂ population were in the range of 0.409 to 0.420, while in Intraspecific F₂ population were in the range of 0.506 to 0.570. The maximum and minimum heritability for primary branches in Inter-specific F₂ populations were estimated in 525 x 905 (*B. napus x B. olaracea*) and 560 x 867 (*B. napus x B. campestris*) 0.420 and 0.409 respectively (Table 2), similarly in Intra-specific F₂ populations, the maximum and minimum heritability estimated were in 609 x 616 (*B. juncea x B. juncea*) and 615 x 617 (*B. juncea x B. juncea*) 0.570 and 0.506 respectively (Table 2). High heritability estimate obtained for the primary branches plant⁻¹ in the current studies were supported by the results of Gosh and Gulati (2001) who reported higher heritability in Indian mustard.

Table 2. Mean, variance and heritability of primary branches plant⁻¹ of P₁, P₂, F₂ of *Brassica* species (where serial # 525 and 560 are *B. napus*; 609, 614, 616 and 617 are *B. juncea*; 825 is *B. campestris* and 905 is *B. olaracea*).

		Inte	er-specific cro	sses	Intra-specific crosses		
		825 x 625	525 x 905	560 x 867	609 x 616	614 x 616	615 x 617
	P ₁	11.80	5.80	11.40	8.80	14.00	9.40
Means	P ₂	13.80	16.60	12.40	13.20	13.20	13.60
	F ₂	12.38	12.47	5.97	11.47	10.06	10.31
Variance	P1	2.70	3.70	2.30	3.20	4.50	3.30
	P2	3.70	2.30	2.80	3.70	3.70	2.80
	F ₂	5.40	5.03	4.30	8.00	8.83	6.16
Heritability (B	BS)	0.415	0.420	0.409	0.570 0.538 0.506		0.506

Main raceme length (cm)

Main raceme length contributes significantly towards number of pods $plant^{-1}$ in crops. The data exhibits that main raceme length in parents was in the range of 50.74 cm to 94.18 cm; while for F₂ populations were 41.13 cm to 76.40 cm. Parent 560 (*B. napus*) attained maximum main raceme length of 94.18 cm, while parent 867 (*B. campestris*) attained minimum main raceme length of 50.74 cm (Table 3). In F₂, population 525 x 905 (*B. napus x B. olaracea*) produces maximum main raceme length of 76.40 cm, while population 560 x 867 (*B. napus x B. campestris*) produces minimum main raceme length of 40 cm (Table 3). Heritability estimates for main raceme length in Inter-specific F₂ populations were in the range of 0.559 to 0.584, while in Intra-specific F₂ populations were in the range of 0.60 to 0.66. The maximum and minimum heritability for main raceme length in Interspecific F₂ populations was estimated in 525 x 905 (*B. napus x B. olaracea*) and 560 x 867 (*B. napus x B. campestris*) 0.584 and 0.559 respectively (Table 3), similarly in Intra-specific F₂ populations, the maximum and minimum heritability estimated were in 609 x 616 (*B. juncea x B. juncea*) and 615 x 617 (*B. juncea x B. juncea*) 0.66 and 0.60 respectively (Table 3). The results of current studies are supported by the earlier findings of Gosh and Gulati (2001). Similarly, Ali (1985) reported heritability estimated ranged from 0.51 to 0.95.

Table 3. Mean, variance and heritability of main raceme length of P₁, P₂, F₂ of *Brassica* species (where serial # 525 and 560 are *B. napus*; 609, 614, 616 and 617 are *B. juncea*; 825 is *B. campestris* and 905 is *B. olaracea*).

		Inte	er-specific cro	sses	Intra-specific crosses		
		825 x 625	525 x 905	560 x 867	609 x 616	614 x 616	615 x 617
	P ₁	52.56	53.62	94.18	69.06	66.06	77.64
Means	P ₂	69.18	79.38	50.74	81.48	81.48	64.84
	F ₂	49.53	76.40	41.13	46.75	84.71	63.41
Variance	P1	37.03	24.59	44.86	37.00	27.79	35.79
	P2	34.92	29.90	50.93	37.27	37.27	32.75
	F ₂	81.68	65.11	108.42	46.75	84.71	63.41
Heritability (H	BS)	0.560	0.584	0.559	0.660 0.620 0.600		0.600

Pods main raceme⁻¹

The number of pods main raceme⁻¹ is key and major yield determining component of Brassica species and contributes substantially towards seed yield. It depends upon the factor like variety, suitable soil and environmental condition. The data collected for pods main raceme⁻¹ indicated that parents had ranged 58.00 to 114.40 pods, where the maximum pods were produced by 560 (B. napus) 114.40 pods, while the minimum pods were produced by 867 (B. campestris) 58 pods (Table 4). Number of pods for F₂ populations ranged from 42.93 to 80.03 pods where maximum value was recorded for population 525 x 905 (B. napus x B. olaracea) 80.03 pods, and minimum for 609 x 616 (B. juncea x B. juncea) 42.93 pods (Table 4). Heritability estimates for pods main raceme⁻¹ in Inter-specific F_2 population were in the range of 0.601 to 0.659, while in Intra-specific F_2 population were in the range of 0.689 to 0.722. The maximum and minimum heritability for pods main raceme⁻¹ in Inter-specific F₂ populations was estimated in 525 x 905 (B. napus x B. olaracea) and 825 x 625 (B. campestris x B. juncea) 0.659 and 0.601 respectively (Table 4), similarly in Intra-specific F₂ populations, the maximum and minimum heritability estimated were in 614 x 616 (B. juncea x B. juncea) 0.722 and 0.689 respectively (Table 4). The results of current studies have higher heritability for pods main raceme⁻¹. Our findings are supported by the earlier findings of Mahmood et al. (2003) who obtained higher heritability for siliquae plant⁻¹ in mustards. Similarly, Gosh and Gulati (2001) reported higher heritability for number of pods main shoot⁻¹ in Indian mustard. High heritability combined with high selection response is reported by Ali (1985) in mustard germplasm.

Table 4. Mean, variance and heritability of pod main raceme⁻¹ of P_1 , P_2 , F_2 of *Brassica* species (where serial # 525 and 560 are *B. napus*; 609, 614, 616 and 617 are *B. juncea*; 825 is *B. campestris* and 905 is *B.*

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Inter-specific crosses			sses	Intra-specific crosses			
		825 x 625	525 x 905	560 x 867	609 x 616	614 x 616	615 x 617
	P ₁	63.40	75.00	114.40	85.00	81.60	71.00
Means	P ₂	74.20	104.20	58.00	72.40	72.40	78.40
	F ₂	55.53	80.03	51.34	42.97	73.06	61.63
	P1	29.30	34.00	40.30	37.50	28.30	48.50
Variance	P2	42.70	30.70	44.50	32.80	32.80	36.80
	F ₂	88.64	94.68	107.78	118.03	109.48	135.66
Heritability (E	BS)	0.601	0.659	0.607	0.703 0.722 0.689		0.689

Pod length (mm)

Pod length play vital role for seed setting and seed yield of a crop. Pod length ranged from 34.40 to 53.40 mm for parents, in which the maximum pod length was recorded for 560 (*B. napus*) 53.40 mm and the minimum for 614 (*B. juncea*) 34.40 mm (Table 5). Pod length for F_2 populations ranged from 34.89 mm to 52 mm where maximum pod length recorded by 525 x 905 (*B. napus x B. olaracea*) 52 mm, while minimum pod length recorded by 615 x 617 (*B. juncea x B. juncea*) 34.89 mm (Table 5). Heritability estimates for pod length in Interspecific F_2 populations were in the range of 0.808 to 0.848, while in Intra-specific F_2 populations were in the range of 0.878 to 0.902. The maximum and minimum heritability for pods length in Inter-specific F_2 populations were in the range of 0.878 to 0.902. The maximum and minimum heritability for pods length in Inter-specific F_2 populations were in the range of 0.878 to 0.902. The maximum and minimum heritability for pods length in Inter-specific F_2 populations were in 615 x 617 (*B. juncea x B. olaracea*) and 825 x 625 (*B. campestris x B. juncea*) 0.848 and 0.848 respectively (Table 5), similarly in Intra-specific F_2 populations, the maximum and minimum heritability estimated were in 615 x 617 (*B. juncea x B. juncea*) and 614 x 616 (*B. juncea x B. juncea*) and 0.902 and 0.878 respectively (Table 5). High heritability value obtained for pod length in the current studies were supported by the result of Zhang and Zhou (2006) who estimated heritability 0.952 for pod length in F_2 population. Similarly, our results are also in agreement to the earlier findings of Nazeer *et al.* (2003) who reported variable heritability estimates ranging from very low to high.

Table 5. Mean, variance and heritability of pod length of P1, P2, F2 of *Brassica* species (where serial # 525 and 560 are *B. napus*; 609, 614, 616 and 617 are *B. juncea*; 825 is *B. campestris* and 905 is *B. olaracea*).

		Inte	er-specific cro	sses	Intra-specific crosses		
		825 x 625	525 x 905	560 x 867	609 x 616	614 x 616	615 x 617
	P ₁	48.20	68.40	63.40	36.80	34.60	36.00
Means	P ₂	41.20	42.00	47.40	34.60	34.60	36.40
	F ₂	39.43	52.00	46.92	35.49	50.88	34.89
Variance	P1	7.70	8.80	5.30	2.20	5.80	3.50
	P2	8.20	7.50	6.80	4.30	4.30	3.30
	F ₂	41.34	52.37	36.50	29.87	39.01	34.80
Heritability (H	BS)	0.808	0.845	0.836	0.897	0.872	0.902

Pod width (mm)

Pod width ranged from 3.64 to 4.98 mm for parents, in which the maximum pod width was recorded for parent 560 (*B. napus*) 4.98 mm and the minimum pod width was recorded for parent 625 (*B. juncea*) 3.64 mm (Table 6). Pod width for F_2 populations ranged from 2.89 mm to 3.79 mm where maximum pod width was recorded by 525 x 925 (*B. napus x B. olaracea*) 3.79 mm, while minimum pod width was recorded by 609 x 616 (*B. juncea x B. juncea*) 2.89 mm (Table 6). Heritability estimates for pod width in Inter-specific F_2 populations were in the range of 0.650 to 0.707, while in Intra-specific F_2 populations were in the range of 0.744 to 0.756. The maximum and minimum heritability for pod width in Inter-specific F_2 populations were estimated in 525 x 905 (*B. napus x B. olaracea*) and 560 x 867 (*B. napus x B. campestris*) 0.707 and 0.650 respectively (Table 6), similarly in Intraspecific F_2 populations, the maximum and minimum heritability estimated were in 609 x 616 (*B. juncea x B. juncea*) and 615 x 617 (*B. juncea x B. juncea*) 0.756 and 0.744 respectively (Table 6). High heritability estimate obtained for the pod width in the current studies were supported by the results of Gosh and Gulati (2001) who reported higher heritability in Indian mustard.

Table 6. Mean, variance and heritability of pod width of P1, P2, F2 of *Brassica* species (where serial # 525 and 560 are *B. napus*; 609, 614, 616 and 617 are *B. juncea*; 825 is *B. campestris* and 905 is *B. olaracea*).

		Inter-specific crosses			Intra-specific crosses		
		825 x 625	525 x 905	560 x 867	609 x 616	614 x 616	615 x 617
	P ₁	3.86	4.24	4.98	4.30	3.76	3.90
Means	P ₂	3.64	3.94	4.12	3.80	3.80	3.78
	F ₂	3.55	3.79	3.61	2.89	3.72	3.62
Variance	P1	0.033	0.098	0.107	0.035	0.063	0.015
	P2	0.028	0.073	0.062	0.015	0.015	0.037
	F ₂	0.097	0.289	0.233	0.094	0.122	0.092
Heritability (B	BS)	0.686	0.707	0.650	0.756 0.748 0.744		0.744

Seed pod⁻¹

The number of seed pod⁻¹ contributes significantly towards the final seed yield in canola. The data exhibits that the number of seed pod⁻¹ for parents was in the range of 11.40 to 19.40 seeds; whereas the maximum number of seed pod⁻¹ was observed for 525 (*B. napus*) 19.40 seeds and the minimum for 617 (*B. juncea*) 11.40 seeds (Table 7). Seed pod⁻¹ for F₂ populations was ranged between 11.53 to 16.63 seeds. Population 614 x 616 (*B. juncea x B. juncea*) produced maximum 16.63 seed pod⁻¹ and population 615 x 617 (*B. juncea x B. juncea*) produced minimum 11.53 seed pod⁻¹ (Table 7). Heritability estimates for seed pod⁻¹ in Inter-specific F₂ populations were in the range of 0.571to 0.709, while in Intra-specific F₂ populations were in the range of 0.805 to 0.833. The maximum and minimum heritability for seed pod⁻¹ in Inter-specific F₂ populations was estimated in 560 x 867 (*B. napus x B. campestris*) and 825 x 625 (*B. campestris x B. juncea*) 0.709 and 0.571 respectively (Table 7), similarly in Intra-specific F₂ populations, the maximum and minimum heritability estimated were in 614 x 616 (*B. juncea x B. juncea*) and 615 x 617 (*B. juncea x B. juncea*) 0.833 and 0.805 respectively (Table 7). The high value of estimated heritability in broad sense for seed pod⁻¹ in the current studies were supported by the earlier findings of Zhang and Zhou (2006) who reported 0.972 heritability for seed pod⁻¹. Similarly Gosh and Gulati (2001) also reported higher heritability in Indian mustard.

Table 7. Mean, variance and heritability of seed pod^{-1} of P_1 , P_2 , F_2 of *Brassica* species (where serial # 525 and 560 are *B. napus*; 609, 614, 616 and 617 are *B. juncea*; 825 is *B. campestris* and 905 is *B. olaracea*).

		Inte	er-specific cro	sses	Intra-specific crosses		
		825 x 625	525 x 905	560 x 867	609 x 616	614 x 616	615 x 617
	P ₁	19.60	19.40	18.20	13.60	14.80	14.40
Means	P ₂	14.00	18.00	18.40	15.00	14.60	11.40
	F ₂	11.91	13.09	16.16	11.78	16.63	11.53
Variance	P1	0.700	1.30	0.700	0.800	0.700	0.800
	P2	0.500	1.50	0.800	1.50	1.30	1.30
	F ₂	1.38	4.22	2.39	6.05	5.73	5.22
Heritability (B	BS)	0.571	0.669	0.687	0.819 0.833 0.805		0.805

1000- seed weight (g)

The weight of seed expresses the magnitude of seed development that is an important yield determinant and plays a decisive role in showing off the yield potential of a genotype. The seed weight for parents was in the range of 3.11 to 4.18 g, while for F₂ populations were 3.31 to 3.45 g. Parent 560 (B. napus) attained maximum 1000-seed weight of 4.18 g, while parent 905 (B. olaracea) attained minimum 1000- seed weight of 3.11 g (Table 8). In F₂, population 825 x 625 (B. campestris x B. juncea) produced a maximum 1000-seed weight of 3.45 g and 609 x 616 (B. juncea x B. juncea) produced minimum 1000-seed weight of 3.31 g (Table 8). Heritability estimates for 1000-seed weight in Inter-specific F₂ populations were in the range of 0.843 to 0.879, while in Intra-specific F₂ populations were in the range of 0.892 to 0.902. The maximum and minimum heritability for 1000-seed weight in Inter-specific F_2 populations were estimated in 560 x 867 (B. napus x B. campestris) and 825 x 625 (B. campestris x B. juncea) 0.879 and 0.843 respectively (Table 3-b, 1-b), similarly in Intra-specific F_2 populations, the maximum and minimum heritability estimated were in 614 x 616 (B. juncea x B. juncea) and 615 x 617 (B. juncea x B. juncea) 0.902 and 0.892 respectively (Table 8). High values of heritability for 1000-seed weight were supported by Zhang and Zhou (2006) who estimated 0.987 heritability. Our results are also in agreement to the earlier findings of Singh et al (1996) who recorded high heritability estimate for 1000-seed weight. Similarly, Ali (1985) reported maximum heritability of 0.95 for 1000-seed weight in mustard.

Table 8	Mean, variance and heritability of 1000 seed weight of P1, P2, F2 of Brassica species (where serial #
	525 and 560 are <i>B. napus</i> ; 609, 614, 616 and 617 are <i>B. juncea</i> ; 825 is <i>B. campestris</i> and 905 is <i>B.</i>
	olaracea

		Inte	er-specific cro	sses	Intra-specific crosses		
		825 x 625	525 x 905	560 x 867	609 x 616	614 x 616	615 x 617
	P ₁	3.22	3.68	4.18	3.32	3.29	3.31
Means	P ₂	3.35	3.11	3.28	3.34	3.34	3.33
	F ₂	3.45	3.32	3.39	3.31	3.40	3.35
Variance	P1	0.052	0.026	0.037	0.042	0.035	0.037
	P2	0.057	0.070	0.035	0.040	0.040	0.042
	F ₂	0.347	0.310	0.297	0.400	0.383	0.363
Heritability (B	BS)	0.843	0.862	0.879	0.898 0.902 0.892		0.892

CONCLUSIONS

On the basis of results obtained from the experiment it can be concluded that high heritability estimates were recorded in Intra-specific as compared to Inter-specific F_2 populations for traits. Inter-specific F_2 population 525 x 905 (*B. napus x B. olaracea*) were found superior being higher primary branches, main raceme length, pods main racme⁻¹, pod length and pod width. *B. juncea* performed better in Intra-specific crosses rather than Interspecific crosses.

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