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HERITABILITY AND GENETIC ADVANCE STUDIES FOR BIOCHEMICAL TRAITS IN F_{2-3} INTROGRESSED FAMILIES OF *BR*ASSICA

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Abstract

Higher heritability estimates along with high genetic advance values are effective in envisaging gain under selection in developing genotypes. The objective of the present study was to evaluate variability, heritability and genetic advance in 10 interspecific F_{2-3} families of *Brassica* species (*B. napus* × *B. juncea*, *B. napus* × *B. rapa*). These families were studied for heterospecific introgression of biochemical traits. Low to high heritability estimates were recorded for seed quality traits. Considerable variations within F_{2-3} families were observed for biochemical traits. Most of the F_{2-3} families for oil content and erucic showed moderate to high heritability indicating the slightest influence of environment thus modification of trait by selection would be more effective. Among F_{2-3} introgressed families *Bn*-510 x *Bj*-109 produced high oil i.e., 49.5% while *Bn*-532 x *Br*-118 (24.4%), *Bn*-533 x *Bj*-109 (24.1%) and high protein percentage in terms of mean performance. In the present research, individual segregating progenies of interspecific cross populations i.e., which possessed combination of desirable traits, were identified which could be incorporated in the future Breeding programs and it may facilitate varietal development.

Key words: Heterospecific introgression, Biochemical traits, Inter-specific hybridization, Brassica.

Introduction

Interspecific hybridization among different species of Brassica provides the breeder with new genetic combinations and more variability which is due to infiltration of genes from one species to another within the genus, the phenomenon is called introgression. "Genetic introgression" or "introgressive hybridization" is "introduction of alleles from one species into another species through hybridization" (Anderson & Hubricht, 1938). Introgression results in a complex mixture of genes from both parental lines which might be supported by selection and as a result it contributes to adaptive evolution within populations (Rieseberg & Carney, 1998). Inter-specific hybridization has been widely used in *B*rassica species to increase genetic diversity and to introgress desirable traits from one gene pool to another genetic background. Thus, interspecific hybridization is a source of speciation in crop sciences. Plant Breeder designs a planned hybridization to combine desirable genes found in two or more different species, through carefully selected plants within or among species (Saleem *et al*., 2013; Sidra *et al*., 2014). *B*rassica oil seed species have high economic value and are vital source of vegetable oil. *B*rassica oil seed species stand third important oilseed crop globally after palm oil and soybean (Haq *et al*., 2014; Zang & Zhou, 2006).

Heritability estimation predicts the effects of phenotypic variation in the population that arise from two sources i.e., average differences between the genotypes and the phenotypic variance that each genotype reveals due to environmental variation. Heritability findings help in the proper selection criteria and assessment of genetic improvement in the succeeding population. Heritability estimates could be used to predict gain from selection. Higher heritability estimates along with better genetic advance values are useful in predicting the gain under selection in developing genotypes (Ghimirary & Sarkar, 2000).

In brassica high oil and yield and low levels of detrimental compounds (as GSL, erucic acid) is an ultimate objective of oilseed breeder. In order to improve the production of edible oil, analysing heritability and genetic advance using biochemical parameters is core goal of a plant breeder in Breeding programs (Laila *et al*., 2014). The presence of substantial amount of genetic variability and heritability is key to successful crop improvement program (Sidra *et al*., 2014; Laila *et al*., 2014; Adnan and Farhatullah, 2013; Khan *et al*., 2008) because the ultimate goal is to develop hybrid cultivars that can potentially use the total amount of heterosis available.

Keeping in view these perspectives, the current research was conducted to determine evaluate the range of genetic variability, estimate Broad sense heritability and determine genetic advance in introgressed F_{2-3} families for various quality traits.

Materials and Methods

Plant materials: In the year 2009, two male parental lines of *B. juncea* (foreign accession from USA) and *B. rapa* (an accession from NARC) were crossed with eight local *B. napus* accessions collected from different sites of Khyber Pakhtunkhwa and Punjab provinces. Twelve out of 16 crosses showed introgression in F_1 and were advanced to F_2. On the basis of results of F_2 populations, some of the introgressed crosses were found to be exceedingly promising for seed quality traits such as oil and protein content (%) and were categorized as " specialized introgressed crosses □ (Sidra *et al*., 2014).

In the current research, 10 out of 12 F_2 "specialized introgressed" populations (Table 1) were advanced to F_{2-3} to further study the inheritance pattern and to estimate heritability for quality traits.

Table 1. List of experimental material comprised parental lines and their $F_{2\text{-}3}$ introgressed families.

*B*rassica species	Site of collection	Origin	$F_{2\text{-}3}$ introgressed families
Female lines			
Bn-510	Okara	Pakistan	*Bn*-510 × *Bj*-109
Bn-514	Rajanpur		*Bn*-514 × *Bj*-109
Bn-532	Rawalpindi		*Bn*-532 × *Bj*-109
Bn-533	Swabi		*Bn*-533 × *Bj*-109
Bn-547	Haripur		*Bn*-547 × *Bj*-109
Bn-525	Khaiabad		
Bn-531	Diamer		
Male lines			*Bn*-525 × *Br*-118
Bj-109	UC Davis	USA	*Bn*-547 × *Br*-118
Br-118	Islamabad	Pakistan	*Bn*-532 × *Br*-118
			Bn-533 × *Br*-118
			Bn-531 × *Br*-118

B*rassica napus* (*Bn*), *Brassica junceae* (Bj), *Brassica rapa* (*Br*)

Field trials: The $F_{2\text{-}3}$ interspecific families and their parents were planted in field trials as ten different populations. The experimental unit had four rows, each consisting of $F_{2\text{-}3}$ family with their respective parental lines. The spacing between rows was 60 cm. Single plant sowing was done having 30 cm space between plants within a row. Row length was 5 meters. Data was taken on every single plant of each family of $F_{2\text{-}3}$ progenies from the interspecific cross combinations.

Broad sense heritability was calculated for each population and each trait by using the following formula in analogy with Mehmood & Kramer (1951):

$$h^2 = VF_3 - \sqrt{Vp1 \times Vp2} \,/\, VF_3$$

Genetic advance was calculated according to Allard (1964):

$$GA = i\, h^2 \sqrt{Vp}$$

where i= selection intensity, Vp= phenotypic variances, h ^{2}= heritability

Results and Discussion

Estimation of heritability, genetic variability and genetic advance contribute in devising efficient selection criteria in crop improvement programs (Aytaç & Kinaci, 2009).

Oil concentration (%): High oil concentration in Brassica species is of immense value since it is largely consumed as edible oil as well as for industrial purposes. Oil content ranged from 45.5% (*Br*-118) to 51% (*Bn*-531) trailed by 50.6% (*Bn*-525) among the parental genotypes. The highest oil content (49.5%) was recorded for $F_{2\text{-}3}$ family *Bn*-510 × Bj-109, while the minimum (43.9%) for *Bn*-532 × *Br*-118. Genotype number 260 within $F_{2\text{-}3}$ family *Bn*-532 × *Br*-118 had the highest (55.3%) oil concentration followed by the individual introgressed genotype number 208 (55.1%) within $F_{2\text{-}3}$ family *Bn*-547 × Bj-109 (Table 6). Fayyaz *et al*. (2014) also reported 47.07% oil content in F_2 interspecific populations of Brassica. $F_{2\text{-}3}$ family *Bn*-510 × *Bj*-109 carried plants with the highest oil content (55.3%) while plants with the minimum oil content (22.9%) were produced by the cross *Bn*-547 × *Br*-118. Results of Ali *et al*. (2013) and Iqbal *et al*. (2014) are nearly alike to the present finding are nearly alike to the present findings. They reported 44 to 43.1% oil contents in *B. carinata* and *B.rapa* genotypes respectively. In comparison to the currents results, Tuncturk & Ciftci (2007) found lower percentage of oil (34-38%) in rapeseed genotypes. Among the $F_{2\text{-}3}$ families, the highest variance (23.05) was obtained for *Bn*-532 × *Br*-118 population (Table 4).

Protein concentration (%): Mean performance for parental lines ranged from 24.3% (*Br*-118) to 17.9% (*Bn*-525). For $F_{2\text{-}3}$ families, mean values spelled out that $F_{2\text{-}3}$ families *Bn*-532 × *Bj*-109 and *Bn*-533 × *Bj*-118 had the maximum protein contents with the percentages 24.4 and 24.3, respectively. The lowest (21.7) protein content was present in seeds of group *Bn*-510 × *Bj*-109. Mean values established no major shift in protein contents of $F_{2\text{-}3}$ families from parental genotypes (Table 2). The results are in agreement with Laila *et al*. (2014) who reported 21.27% protein content in interspecific hybrids of *B*rassica, whereas Mahasi & Kamundia (2007) got lower protein content (18%) in rapeseed genotypes. Genotype number 135 within the family *Bn*-532 × *Bj*-109 had maximum (31.3%) protein content among all and thus selected among superior genotypes for high protein content (Table 6).

Glucosinolate content (µ mol g^{-1}): Glucosinolates (GSL) are organic compounds containing sulphur and nitrogen. High content of GSL have damaging effects on human and animal nutrition, also it adds to the pungent flavour of Brassica, therefore; low GSL content is desirable in Brassica species (Agnihotri & Kaushik, 1999). *Bn*-514 produced the lowest GSL content (70.4 µ mol g^{-1}), followed by *Bn*-547 (87.34 µ mol g^{-1}) and *Bn*-532 (87.48 µ mol g^{-1}). Among $F_{2\text{-}3}$ introgressed populations, *Bn*-532 × *Bj*-109 exhibited the lowest content GSL i.e. 84.34 µ mol g^{-1} followed by *Bn*-510 × *Bj*-109 (88.2 µ mol g^{-1}) while the highest GSL of 101.5 µ mol g^{-1} were extracted from seed of *Bn*-525 × *Br*-118 (Table 2). In compliance to the recent findings, Zhang & Zhou (2006) and Laila *et al*. (2014) also reported high levels of GSL in Brassica. Ranges for all $F_{2\text{-}3}$ families shows that the lowest GSL is observed for the individual genotypes within two families *Bn*-532 x *Br*-118 (18.3 µ mol g^{-1} for genotype number 190) and *Bn*-525 x *Br*-118 (28.6 µ mol g^{-1} for genotype number 32).

Table 2. Mean performance and ranges for various seed quality traits of parental lines and F_{2-3} families.

Genotypes	Oil content (%)		Protein content (%)		Glucosinolate content (µ mol g-1)	
	Range	Mean	Range	Mean	Range	Mean
Parents						
Bn-525	50.1 – 51.1	50.6	17.6 – 18.3	17.9	79.6 – 82.1	80.86
Br-118	41.4 – 49.9	45.5	20.3 – 27.4	24.7	90.1 – 110.3	97.04
Bn-547	49.6 – 50.6	50.2	19.1- 20.1	19.8	79.1 – 106.2	87.34
Bn-532	40.3 - 50.1	44.2	20.2 – 26.9	22.9	76.5 – 100.1	87.48
Bj-109	43.5 – 49.8	47.2	22.7 – 27.8	24.3	82.1 – 118.8	98.76
Bn-533	45.2 – 50.9	48.5	17.6 – 22.6	18.8	92.6 – 103.2	97.64
Bn-510	50.3 – 50.7	50.5	18.9 – 19.7	19.3	93.8 – 97.1	95.92
Bn-514	47 – 51.3	49	17.1- 20.5	18.9	70.4 – 87.4	70.4
Bn-531	49.8 – 54.1	51.1	17.5 – 18.7	18.1	87.5 – 90.9	89.1
F_{2-3} families						
Bn-525 ×*Br*-118	33.7 – 54.4	47.2	18.7 – 29.8	22.9	28.6 – 192	101.5
Bn-547 × *Br*-118	22.9 – 53.1	46.4	16.9 – 29.9	22.8	60.2 – 122.1	91.31
Bn-532 × *Bj*-109	34.6 – 51.6	46	18.7 – 31.3	23.3	103.5 – 123.9	84.34
Bn-532 × *Br*-118	33.8 – 55.3	43.9	17.1 – 30	24.4	18.3 – 123.8	88.79
Bn-547 × *Bj*-109	39.8 – 55.1	47	17.8 – 27.8	23.3	46.8 – 115.5	89.17
Bn-533 × *Br*-118	39.6 – 52.7	46.8	19.9 – 28.9	23	72.8 – 89.4	110
Bn-533 × *Bj*-109	36.7 – 51.1	45.2	20.1 – 28.1	24.1	60.7 – 123.2	91.75
Bn-510 × *Bj*-109	44.7 – 52.9	49.5	19.6 – 24.3	21.7	73.1 – 104	88.2
Bn-514 × *Bj*-109	40 – 54.3	47.8	17.4 – 27.2	22.5	70.5 – 108	91.1
Bn-531 × *Br*-118	41.6 – 53.4	46.7	20.75 – 26.6	22.2	80.8 – 118.3	99.9

Oleic acid (per-cent of fatty acids): Oleic acid belongs to the class of monosaturated omega-9 fatty acids. High oleic acid content in Brassica is desirable for nutritional purpose (Iqbal *et al*., 2014). Range of means for oleic acid among parental lines varied from 32 (*Bn*-533) to 50.2% (Br-118). According to the mean performance of all F_{2-3} families, *Bn*-510 × *Bj*-109 possessed the highest (48.9%) oleic acid. F_{2-3} families *Bn*-547× *Bj*-109 (43.9%) and *Bn*-514 × *Bj*-109 (43.9%) contained the minimum oleic acid content (Table 3). These results are supported by the earlier findings of Iqbal *et al*. (2014) who found 43.7 and 48.7% oleic acid in F_2 interspecific populations *Bn*-510 × *Bj*-109 and 531 × 118 respectively. Khan *et al*. (2008) observed comparatively high levels of oleic acid (52.7%) in $F_{3:4}$ interspecific populations of Brassica.

Linolenic acid (per-cent of fatty acids): Linolenic acid is nutritionally essential omega-3 fatty acid. It has potential benefits for health and thus high percentage of this fatty acid is advantageous (Simopoulos, 1991). Mean values for linolenic acid varied from 7.7 (*Bn*-525) to 10.24% (*Bj*-109) among the parental genotypes. F_{2-3} family *Bn*-514 × *Bj*-109 had the highest (10.38%) linolenic acid content. The minimum linolenic acid percentage was recorded for two populations *Bn*-510 × *Bj*-109 (8.91%) and *Bn*-533 × *Bj*-118 (8.93%) (Table 3). Khan *et al*. (2008) represented 9.9% linolenic acid in interspecific populations of Brassica which is nearly comparable to our findings. In contrast to the present observations, Laila *et al*. (2014) reported high linolenic acid content in F_2 Brassica populations.

Erucic acid (per-cent of fatty acids): Erucic acid is a crystalline monosaturated omega-9 fatty acid which is present in the form of glycerides in Brassica species (Davis, 2011). Low erucic acid content is desirable in Brassica varieties due to its harmful effects (Khan *et al*., 2008). Erucic acid percentage for parental lines was in the range of 52.3 (*Bj*-109) to 57.9% (*Bn*-531). Among F_{2-3} families, the lowest (44.8%) levels of erucic acid was detected in two populations *Bn*-532 × *Bj*-109 and *Bn*-532 × Br-118 whereas the highest (57.7%) in *Bn*-514 × *Bj*-109. Over all, F_{2-3} families exhibited high levels of erucic acid. Nasim & Farhatullah (2013) and Iqbal *et al*. (2014) also reported high erucic acid in rapeseed (37.73-57.50%) and F_2 interspecific progenies (33.7-44.4%) respectively. Introgressed genotypes within the F_{2-3} families *Bn*-532 x *Bj*-109 (24% for genotype number 165) and *Bn*-525 x *Br*-118 (29.1% for genotype number 32) exhibited the lowest erucic acid content among all (Table 3).

Heritability and genetic advance: High heritability estimates along with the high genetic advance indicates that there are more chances that a character is controlled by additive genes and selection for improvement is more successful. Oil content was affirmed as most heritable trait in F_{2-3} family *Bn*-547 × *Br*-118 with the highest genetic advance (6.19). All the other families exhibited medium to low heritability values. Singh *et al*. (2013) observed high heritability and comparatively lower genetic advance values in their experiment on association of yield components in Indian mustard, which is almost similar to the findings of the present project. Gosh & Gulati (2001) also reported high heritability for oil content in Indian mustard.

The highest genetic advance results in high gain from selection in breeding programs. Marjanovic *et al*. (2011) and Khan *et al*. (2006) also quantified high genetic advance values in rapeseeds. Iqbal *et al*. (2014) found in their experiment with F_2 introgressed population of *Bn*-533 × *Br*-118 having highest heritability for protein content. These results are in agreement with Khan *et al*. (2008) who reported low heritability in $F_{2:3}$ Brassica interspecific populations for protein oil. Iqbal *et al*. (2014) and Aytac & Kinaci (2009) observed moderate to high heritability values for protein.

Table 3. Mean performance and ranges for various seed quality traits of parental lines and F_{2-3} families.

Genotypes	Oleic acid (% of fatty acid)		Linolenic acid (% of fatty acid)		Erucic acid (% of fatty acid) (µ mol g-1)	
	Range	Mean	Range	Mean	Range	Mean
Parents						
Bn-525	43.7 – 46.1	44.4	7.3 – 8.1	7.7	48.1 – 49.3	48.7
Br-118	48 – 54.1	50.2	8.1 – 10.3	9.44	40.1 – 52.4	46.4
Bn-547	47.2 – 48.6	47.8	8.8 – 9.7	9.34	46.3 – 50.1	44.8
Bn-532	35.3 – 50	44.2	7.8 – 10.2	9.18	42.1 – 56.9	49.8
Bj-109	41.4 – 43.6	42.5	9.5 – 11.4	10.24	44.3 – 55.8	52.3
Bn-533	28.9 – 35.8	32	7.3 – 8.5	7.82	44.1 – 55.3	50
Bn-510	46.1 – 47.3	46.7	7.6 – 8.1	7.88	54.8 – 57.5	55.6
Bn-514	43.5 – 49.3	46.1	6.3 – 8.3	7.14	41.6 – 56.1	26.7
Bn-531	36.5 – 39.5	38.1	8.5 -9.8	9.13	56.2 – 59.4	57.9
F_{2-3} families						
Bn-525 ×*Br*-118	32.5 – 51.1	45.2	2.3 – 12.9	9	29.1 – 66.4	50.7
Bn-547 × *Br*-118	40.4 – 59.5	47	7.7 – 12.1	9.71	37.7 – 59.9	49.1
Bn-532 × *Bj*-109	40.1 – 68.9	47.6	4.8 – 12.7	9.77	24.8 -51.6	44.8
Bn-532 × *Br*-118	33.6 – 57.1	45.5	0.4 – 12	9.44	31.9 – 56.3	44.8
Bn-547 × *Bj*-109	39.6 – 52.2	43.6	7.9 – 12.8	10.5	46.4 – 60.8	52.5
Bn-533 × *Br*-118	44 – 52	48.2	7.7 – 10.8	9.42	49.2 – 59.5	48.5
Bn-533 × *Bj*-109	38.9 – 53.9	46	3.4 – 11	8.93	31.3 – 56.6	47.9
Bn-510 × *Bj*-109	41.4 – 54.6	48.9	7.4 -11.4	8.91	46.4 – 58.8	52.2
Bn-514 × *Bj*-109	40 – 50.1	43.9	8.2 – 11.5	10.38	49 – 64.8	57.7
Bn-531 × *Br*-118	38.1 – 52.5	45.7	9.1 – 11.5	10.36	49 - 60	52.2

Table 4. Variance, heritability estimates and genetic advance for various seed quality taits of parental lines and F_{2-3} families.

Genotypes	Oil Content (%)			Protein content (%)			Glucosinolate content (µ mol g^{-1})		
	Variance	h^2	GA	Variance	h^2	GA	Variance	h^2	GA
Parents									
Bn-525	0.16	--	--	0.08	--	--	1.13	--	--
Br-118	9.58	--	--	8.39	--	--	213.65	--	--
Bn-547	0.15	--	--	0.16	--	--	136.33	--	--
Bn-532	25.7	--	--	8.17	--	--	130.04	--	--
Bj-109	5.92	--	--	4.28	--	--	236.86	--	--
Bn-533	6.2	--	--	4.51	--	--	17.4	--	--
Bn-510	0.02	--	--	2.08	--	--	1.75	--	--
Bn-514	2.87	--	--	2.01	--	--	49.32	--	--
Bn-531	2.89	--	--	0.23	--	--	2.02	--	--
F_{2-3} families									
Bn-525 ×*Br*-118	13.96	0.91	4.76	6.35	0.86	3.06	409.76	0.97	27.68
Bn-547 × *Br*-118	21.91	0.94	6.19	6.99	0.83	3.09	125.04	0.16	2.65
Bn-532 × *Bj*-109	14.46	0.14	0.78	7.8	0.24	0.94	322.7	0.45	11.47
Bn-532 × *Br*-118	23.05	0.31	2.14	14.83	0.44	2.38	396	0.74	20.73
Bn-547 × *Bj*-109	14.43	0.93	4.96	8.63	0.9	3.71	210.02	0.14	2.92
Bn-533 × *Br*-118	14.62	0.77	2.53	8.14	0.24	0.97	146.13	0.74	12.62
Bn-533 × *Bj*-109	12.42	0.51	2.52	5.16	0.14	0.47	290.81	0.77	18.6
Bn-510 × *Bj*-109	6.33	0.93	3.3	3.1	0.8	1.99	74.2	0.72	8.74
Bn-514 × *Bj*-109	9.71	0.57	2.51	5.95	0.5	1.73	87.19	0.24	3.26
Bn-531 × *Br*-118	11.5	0.54	2.57	2.69	0.48	1.1	73.36	0.82	9.92

h^2 = Heritability (BS), GA= Genetic Advance (% of mean)

Very low to high heritability estimates were observed for glucosinolate content among F_{2-3} introgressed families. Zhang & Zhou (2006) and Fayyaz *et al*. (2014) also reported high levels of GSL in Brassica. High heritability estimates were recorded for *Bn*-525 × *Br*-118 and *Bn*-531 × *Br*-118 with heritability values 0.97 and 0.82 respectively (Table 4). Population *Bn*-525 × *Br*-118 also demonstrated the maximum genetic advance value i.e. 27.68. Iqbal *et al*. (2014) also reported high heritability for all F_{2-3} introgressed population of Brassica. Similar results were reported by Khan *et al*. (2008) and Bradshaw & Wilson (1998) who found high heritability values for GSL content in inter specific *Br*assica populations and *B. napus* genotypes respectively whereas Schierholt & Becker (2001) observed low heritability for GSL in winter oil seed rape.

Most of the $F_{2\text{-}3}$ populations under study exhibited high heritability estimates for oleic acid content. The highest heritability for oleic acid was displayed by $F_{2\text{-}3}$ family *Bn*-514 × *Bj*-109 (0.97), followed by *Bn*-510 × *Bj*-109 (0.96). In contrast to these results, Iqbal *et al*. (2014) reported moderate to low heritability values for same populations in two F_2 families i.e. *Bn*-514 × *Bj*-109 (0.62) and *Bn*-510 × *Bj*-109 (0.34). Moderate heritability was evinced for $F_{2\text{-}3}$ family *Bn*-532 × *Bj*-109 (0.68) while the lowest for *Bn*-533 × *Br*-118 (Table 5). The lowest *B*road sense heritability shows that this character is highly influenced by environment and selection for this trait may not be more beneficial. In comparison to the present study, Khan *et al*. (2008) and Schierlot & Becker (2001) also realized high heritability for this trait. $F_{2\text{-}3}$ family *Bn*-533 × *Br*-118 gave the highest (4.93) genetic advance value in comparison to other families. High genetic advance shows that character is governed by additive genes and selection for improvement is more effective for such characters.

Most of the $F_{2\text{-}3}$ families showed high heritability assessments for linolenic acid composition, however medium and low heritability values were also observed. Among $F_{2\text{-}3}$ families heritability values ranged from 0.90 (*Bn*-547 × *Br*-118, *Bn*-510 × *Bj*-109) to 0.12 (*Bn*-525 × *Br*-118) (Table 5). In consistency to the results of high heritability in this study, Schierholt & Becker (2001) and Khan *et al*. (2008) reported high heritability estimates while Sidra *et al*. (2014) found low to medium values for linolenic acid percentage in F_2 populations. The highest genetic gain was observed for *Bn*-532 × *Br*-118 and *Bn*-547 × *Br*-118 with values of 2.67 and 2.27, respectively.

Heritability estimates for erucic acid varied from 0.97 (*Bn*-547 × *Br*-118) to 0.31 (*Bn*-532 × *Bj*-109). The maximum genetic gain (23.03) for erucic acid was also recorded for $F_{2\text{-}3}$ family *Bn*-547 × *Br*-118 (Table 5). Khan *et al*. (2008), Chauhan & Tyagi (2002) and Iqbal *et al*. (2014) reported high heritability estimates for erucic acid. High heritability with high genetic gain reveals rewarding selection for improvement.

Table 5. Variance, heritability estimates and genetic advance for various seed quality traits of parental lines and $F_{2\text{-}3}$ families.

Genotypes	Oleic acid (% of fatty acid)			Linolenic acid (% of fatty acid)			Erucic acid (% of fatty acid)		
	Variance	h^2	GA	Variance	h^2	GA	Variance	h^2	GA
Parents									
Bn-525	0.93	--	--	0.8	--	--	0.28	--	--
Br-118	6.03	--	--	0.08	--	--	27.36	--	--
Bn-547	0.42	--	--	0.12	--	--	2.35	--	--
Bn-532	44.3	--	--	1.48	--	--	39.92	--	--
Bj-109	0.63	--	--	0.56	--	--	21.57	--	--
Bn-533	8.09	--	--	0.34	--	--	24.32	--	--
Bn-510	0.36	--	--	0.03	--	--	1.13	--	--
Bn-514	7.63	--	--	0.68	--	--	26.71	--	--
Bn-531	1.46	--	--	0.23	--	--	1.9	--	--
$F_{2\text{-}3}$ families									
Bn-525 ×*Br*-118	16.83	0.85	4.93	2.26	0.88	1.86	34.7	0.91	7.58
Bn-547 × *Br*-118	12.69	0.87	4.35	3.25	0.9	2.27	286.56	0.97	23.03
Bn-532 × *Bj*-109	16.65	0.68	3.89	1.71	0.46	0.85	33.95	0.13	1.1
Bn-532 × *Br*-118	21.43	0.23	1.53	5.62	0.8	2.67	40.98	0.19	1.73
Bn-547 × *Bj*-109	9.83	0.94	4.15	1.13	0.76	1.13	15.47	0.54	2.97
Bn-533 × *Br*-118	8.19	0.14	0.58	0.73	0.28	0.34	220.9	0.88	18.38
Bn-533 × *Bj*-109	11.49	0.8	3.8	3.37	0.86	2.23	44.7	0.48	4.56
Bn-510 × *Bj*-109	12.16	0.96	4.68	1.4	0.9	1.5	18.124	0.72	4.33
Bn-514 × *Bj*-109	8.11	0.72	2.9	0.83	0.25	0.32	15.9	0.17	0.96
Bn-531 × *Br*-118	19.12	0.84	5.17	0.49	0.12	0.12	15.39	0.53	2.91

h^2 = Heritability (BS), GA= Genetic Advance (% of mean)

Conclusions and recommendations

On the basis of results, $F_{2\text{-}3}$ families *Bn*-510 x *Bj*-109, *Bn*-532 x *Br*-118 and *Bn*-533 x *Bj*-109 are recommended to be used in further *B*reeding programs for progressing genotypes with high oil and high protein contents. Some of the genotypes within the $F_{2\text{-}3}$ families *Bn*-525 x *Br*-118 and *Bn*-532 x *Br*-118 had low levels of GSL (as 28.6, 18.3 μ mol g^{-1}); $F_{2\text{-}3}$ families *Bn*-532 x *Bj*-109 and *Bn*-525 x *Br*-118 had genotypes with the lowest erucic acid percentage (as 24.8%, 29.1%). These individual genotypes may help in advancement of lines with low GSL and erucic acid. It is observed that on the basis of mean performance parental species are high in oil, protein content, erucic acid, glucosinolates and some other yield related traits in comparison to the successive generation but in the $F_{2\text{-}3}$ families, such genotypes are present on the individual level that showed supreme performance than their parental lines.

Table 6. Introgressed segregates within F_{2-3} families selected on the basis of superior performance for various seed quality traits.

Traits	F_{2-3} Families	F_{2-3} introgressed segregates
High Oil %	*Bn*-252 × *Br*-18	34, 17, 19, 27, 16, 46, 48, 58
	Bn-547 × *Br*-118	123, 130, 336, 335
	Bn-547 × *Bj*-109	208, 210, 209, 296, 299, 295
	Bn-532 × *Br*-118	260, 262, 265
High Protein %	*Bn*-532 × *Bj*-109	135, 172, 151, 139, 150, 132, 133, 131,165
	Bn-532 × *Br*-118	191, 192, 193, 189, 194
	Bn-547 × *Br*-118	109 , 90, 108, 77
Low GSL content (µ mol g^{-1})	*Bn*-532 × *Bj*-109	178, 153, 187, 155, 183
	Bn-547 × *Bj*-109	206, 221, 209
	Bn-533 × *Bj*-109	250, 270
	Bn-525 × *Br*-118	32, 34
	Bn-532 × *Br*-118	190, 264
Low Erucic acid %	*Bn*-532 × *Bj*-109	153, 172, 187, 170, 165, 172
	Bn-532 × *Br*-118	258, 251, 263, 198, 250
	Bn-547 × *Br*-118	86
	Bn-525 × *Br*-118	1, 32

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