



Genetic Variability for Morphological and Biochemical Traits among the Interspecific F₄₋₅ Populations of *Brassica* Species

**Barkat Ali^{a,b}, Sujon Kumar^{c*}, Waleed Ahmed^a, Muhammad Ayoub Khan^b,
Izhar Ullah^d and Md. Moshir Rahman^e**

^a College of Horticulture, Sichuan Agricultural University, Chengdu, Sichuan 611130, China.

^b Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar 25120, Pakistan.

^c Triticeae Research Institute, Sichuan Agricultural University, Chengdu, Sichuan 611130, China.

^d Department of Horticultural, Ondokuz Mayıs University, Samsun 55139, Turkey.

^e Bangladesh University, Dhaka 1207, Bangladesh.

Authors' contributions

This work was carried out in collaboration among all authors. Author BA designed the study and wrote the protocol and first draft. Authors SK, WA, IU and MMR performed the statistical analysis and wrote the first draft of the manuscript. Author MAK managed the analyses of the study and author SK revised the whole manuscript. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/JSRR/2022/v28i630524

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/87027>

Original Research Article

Received 15 March 2022

Accepted 18 May 2022

Published 26 May 2022

ABSTRACT

The study was carried out to determine genetic variability, heritability, and genetic progress among the F₄₋₅ population of *Brassica* species for several biochemical and morphological traits at Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, Pakistan, during the Rabi season 2018-19. In Pakistan, *Brassica* are economically important and high yielding oil seeds and it is needed to produce improved *Brassica* varieties for successful expansion of cultivation of oilseed crops. The genetic variability among 51 populations (genotypes) of four interspecific crosses Bn-531xBr-118, Bn-525xBr-118, Bn-514xBj-109 and Bn-510xBj-109 with six parents of *Brassica* species in paired rows of 4 m length with a spacing of 30 x 10-15 cm (row x plant). Data were recorded on ten different agro-morphological characters and six biochemical traits. The interspecific crosses of *Brassica* species highly performed all types of morphological traits in populations viz; 142, 129, 196, 186 and 142. Biochemical traits are highly performed in

*Corresponding author: E-mail: info.sujonkumar@gmail.com;

interspecific crosses of F_{4-5} populations other than parental genotypes. Majority had high to moderate heritability, whereas greatest had less environmental and genetic influence in the expression of these characters and had high heritability with substantial genetic advance. Interspecific crosses showed superior diversity for various traits and thus give a unique opportunity in further evaluation of these materials for profitable exploitation in next generations.

Keywords: *Brassica* species; heritability; genetic advance; morphological and biochemical traits.

1. INTRODUCTION

Oilseed *Brassica* is one of the most important and profitable oil crops in the world [1,2]. It is the most important source of edible oil [3], and consists of 380 genera and 3000 species [4] is one of the ten most economically important plant families with a wide range of agronomic traits [5,6]. In Pakistani, *Brassica* are economically important and high yielding oil seeds grown from long time that is why it is needed to produce improved oilseed *Brassica* varieties for successful expansion of cultivation of oilseed crops [7]. In Pakistan, Pakistan produced 207 thousand tonnes of rapeseed in 2016 by cultivating it on an area of 226 thousand hectare. The world average rapeseed production is 2.23tonnes/hectare. However in Pakistan the average production of rapeseeds per unit hectare is only 0.8548 tonnes/hectare, since last twenty year. In 2016 only 0.9144 tonnes/hectare yields was produced [8].

Seed yield of *Brassica* is the outcome of morphological and physiological belongings, the final concert of plant depends on the phonological stage and yield contributing traits, seed yield direct selection is not possible, and therefor indirect selection is the chief method for *Brassica* breeding program [9]. For a new varieties of plants to be released should always fulfill the criteria of distinctness, plant protection uniformity and stability as per the guidelines prepared by UPOV. DUS testing is one of the important criteria to test in-bred lines for distinctness, uniformity, and stability [10]. Increasing demand for edible oil in world markets and the pressure from the cost of buying and importing oil are among the factors that determine the importance of developing oilseed crops and expanding scientific research programs [11].

Future edible oil requirement can only be achieved through the improvement of seed quality by breeding *Brassica* species [12,13]. The reduced yield potential of the cultivated varieties needs an improvement of this crop for better

yield [14]. Moreover, it is a quality's measure between two variables. For plant breeders it is necessary to concentrate on the relationship between sets of characters keeping in mind the end goal to settle on the proper determination criteria for a breeding program [15]. The goal of study to evaluate potential interspecific crosses on the basis of morphological and biochemical traits and to quantify the heritability and association of *Brassica* species.

2. MATERIALS AND METHODS

2.1 Plant Material, Experimental Design and Location

The experimental materials were consisted of 51 populations (genotypes) of four interspecific crosses Bn-531×Br-118, Bn-525×Br-118, Bn-514×Bj-109 and Bn-510×Bj-109 and six parents (Tables 1 & 2). All 51 genotypes were grown in paired rows of 4 m length with a spacing of 30 × 10-15 cm (row × plant) at Department of Plant Breeding and Genetics form the University of Agriculture, Peshawar, Pakistan during Rabi season 2017-18. The coordinates of the experimental location are 34.04°N and 71.35°E with an altitude of 350m above sea level. The climate of the experimental location is subtropical with precipitation ranges 500-700mm of the growing season.

2.2 Observations and Evaluation

All the recommended package and practices were followed to raise the healthy crop. Observations were recorded on five random and competitive plants for ten agronomic and six biochemical traits viz; days to 50% flowering, plant height (cm), primary branches per plant (no.), main raceme length (cm), pod length (cm), seeds per pod (no.), number of pod on main raceme, days to maturity, hundred seeds weight (g), seed yield per plant (g) and Oil content (%), Protein content (%), Glucosinolates (%), Oliec acid (%), Linolenic acid (%), Erosic acid (%). To determine the chemical constituents of seed samples were scanned on Near Infrared (NIR)

Spectroscopy System (FOSS 6500 equipped with ISI version 1.02 a software of Infra Soft International) according to the manufacturer's protocol. Near infrared reflectance (NIR) spectroscopy, has been successfully applied as an alternative technique to gas chromatography for the analysis of biochemical analysis of oilseed crops [16,17,18]. The data was statistically analysed according to the appropriate method recommended for randomized complete block design [19]. Mean separation was carried out following LSD test. Broad sense heritability for a particular trait was computed using parental and F4-5 populations of each cross combination using the modified version of the formula suggested by Mahmud and Kramer [20]:

$$h^2 = \frac{VF_{4-5} - \sqrt{VP_1 \times VP_2}}{VF_{4-5}} \dots \dots \dots \text{Equation (1)}$$

Where, VF_{4-5} = Variance of F_{4-5} population for a specific trait. VP_1 and VP_2 = Variances of parent 1 and parent 2 of a specific F_{4-5} population.

Genetic advance was computed by using following formula as suggested by Panse and Sukhatme [21]:

$$GA = k. (\sqrt{\sigma^2P}) . h^2 \dots \dots \dots \text{Equation (2)}$$

Where, GA = Genetic advance, $K = 1.76$ for 10 % selection intensity, h^2 = Heritability coefficient (broad sense), $(\sqrt{\sigma^2P})$ = Phenotypic standard deviation.

3. RESULTS AND DISCUSSION

Brassica species was significantly improve F_{4-5} generation provides a measure of the degree of relatedness between individuals in an interspecific crossed populations [22] and it also plays a key role in genetic improvement through breeding methods [23]. Interspecific crosses gradually varied from parental genotypes of yield and yield contributing parameters ten agronomic traits is presented in Tables 3-8 and Figs. 1 & 2.

Table 1. Parental lines with their collecting sites

Sl. No.	Site of Collection	Code	Species
01	Okara	Bn-510	<i>Brassica napus</i>
02	Diamer	Bn- 531	<i>Brassica napus</i>
03	Rajanpur	Bn- 514	<i>Brassica napus</i>
04	Khairabad	Bn- 525	<i>Brassica napus</i>
05	Islamabad	Br- 118	<i>Brassica rapa</i>
06	USA	Bj- 109	<i>Brassica juncea</i>

Here, Br = *B. rapa*, Bn = *B. napus* and BJ = *B. juncea*

Table 2. List of various selected plants in F_4 populations

Sl. No.	F_5 populations	High OC	High PC	Low GSL	High OA	High LA	High EA	High SYPP	High GSL	Low EA	Total plants
1	Bn-531xBr-118		306 214	486 220					203 157 305		5
2	Bn-525xBr-118		265 268 502 487 502	47 241 240 486 442 252 261			471		494 487 225 268 502	471 442	21
3	Bn-514xBj-109	196 171				95 85					4
4	Bn-510xBj-109	110		141 132		95 85		144 84			21

Here, LA, Linolenic acid; OC, Oil content; OA, Oleic acid; PC, Protein content; EA, Erucic acid; SYPP, Seed yield per plant

Table 3. Variance (σ^2), heritability ($h^2_{(BS)}$) and genetic advance (GA) of morphological traits for parental lines and four interspecific crosses

Genotypes	DFFF			PH			PBPP			MRL			PL		
Parents	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA
Bn-531	9.3			167.5			0.3			132.5			0.912		
Bn-525	15.7			42.5			0.7			71.8			0.425		
Bn-514	15.5			167.5			0.2			25			0.517		
Bn-510	14.5			189.2			0.8			450			3.872		
Br-118	14.2			95			0.2			49.3			0.157		
Bj-109	30.2			211.2			0.3			50.7			0.185		
Crosses	-			-			-			-			-		
Bn-531 × Br-118	20.70	0.73	1.92	487.4	0.67	2.92	3.24	0.92	2.32	312.16	0.38	7.55	3.54	0.73	1.92
Bn-525 × Br-118	31.85	0.75	1.08	351.89	0.87	7.71	2.25	0.83	1.75	202.3	0.70	14.05	1.05	0.75	1.08
Bn-514 × Bj-109	58.91	0.77	1.25	263.83	0.66	5.05	1.67	0.85	1.54	191.46	0.81	15.76	1.35	0.77	1.25
Bn-510 × Bj-109	56.99	0.25	0.37	487.4	0.27	2.82	3.2	0.84	2.12	197.04	0.38	7.55	1.1	0.25	0.37
Genotypes	SPP			MR			DTM			HSW			SYPP		
Parents	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA
Bn-531	8.243			82.5			7.7			0.007416			2.42335		
Bn-525	4.597			75.3			2.2			0.006233			6.09457		
Bn-514	9.603			45.7			5.5			0.002394			5.54287		
Bn-510	53.23			73.2			10.8			0.00508			2.23008		
Br-118	5.403			49.3			3.3			0.002669			42.3342		
Bj-109	26.87			139.7			16.3			0.000447			1.80135		
Crosses	-			-			-			-			-		
Bn-531 × Br-118	9.61	0.67	2.92	354.04	0.82	21.83	7.71	0.34	1.34	0.001	0.54	0.075	17.87	0.43	2.56
Bn-525 × Br-118	39.73	0.87	7.71	243.3	0.74	16.36	6.78	0.60	2.2	0.006	0.35	0.039	68.57	0.76	8.87
Bn-514 × Bj-109	29.52	0.66	5.05	95.52	0.52	7.13	15.35	0.38	2.1	0.002	0.56	0.038	12.65	0.89	4.45
Bn-510 × Bj-109	52.33	0.27	2.82	169.8	0.6	11.08	22.26	0.40	2.66	0.008	0.81	0.1	18.14	0.80	4.78

DFFF, Days to 50% flowering; PH, Plant height (cm); PBPP, Primary branches per plant (no.); MRL, Main raceme length (cm); PL, Pod length (cm); SPP, Seeds per pod (no.); MR, Number of pod on main raceme; DTM, Days to maturity; HSW, Hundred seeds weight (g); SYPP, Seed yield per plant (g).

Table 4. Variance, heritability ($h^2_{(BS)}$) and genetic advance of biochemical traits for parental lines and four interspecific crosses

Genotypes	Oil content (%)			Protein content (%)			Glucosinolates (%)			Oleic acid (%)			Linolenic acid (%)			Erosic acid (%)		
	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA	σ^2	$h^2_{(BS)}$	GA
Parents																		
Bn-531	4.277			3.476			14.56			7.993			0.770			1.208		
Bn-525	4.570			3.444			10.13			1.493			1.076			4.875		
Bn-514	0.833			6.435			36.14			7.255			0.227			13.72		
Bn-510	2.433			4.878			10.18			5.065			0.435			3.827		
Br-118	6.958			6.503			188.70			7.083			0.947			4.702		
Bj-109	4.438			4.882			68.23			7.748			0.508			19.11		
Crosses																		
Bn-531×Br-118	18.72	0.70	4.30	22.67	0.79	5.26	262.40	0.80	18.14	19.06	0.60	3.7	1.44	0.41	0.69	14.64	0.83	4.48
Bn-525×Br-118	8.07	0.29	1.17	7.44	0.42	1.63	197.60	0.77	15.32	16.96	0.80	4.66	1.21	0.48	0.74	31.37	0.84	6.64
Bn-514×Bj-109	4.4	0.56	1.65	8.51	0.34	1.39	109.70	0.54	8.02	28.6	0.73	5.52	0.56	0.40	0.42	35.96	0.54	4.61
Bn-510×Bj-109	7.62	0.56	2.20	10.96	0.55	2.57	99.83	0.79	11.18	11.02	0.43	2.57	0.83	0.46	0.59	12.48	0.57	2.83

Table 5. Means and ranges of different biochemical traits for parental and interspecific crosses

Genotypes	Oil content (%)		Protein content (%)		Glucosinolates (%)		Oleic acid (%)		Linolenic acid (%)		Erosic acid (%)	
	Ranges	Means	Ranges	Means	Ranges	Means	Ranges	Means	Ranges	Means	Ranges	Means
Parents												
Bn-531	47.4-51.7	49.48	19.1-23.1	20.79	83.3-92.3	89.18	35.3-42.6	38.38	9.5-11.8	10.59	57.5-60	59.16
Bn-525	48.5-53.8	50.03	18.5-23.4	21.25	90-97.7	92.79	42.3-45.5	43.96	8.6-11.3	9.78	55.1-60	57.92
Bn-514	19.1-47	47.87	18.5-24.4	21.31	84.5-98.8	93.14	46-52.4	47.6	8.5-9.7	9.08	49.9-58.9	56.26
Bn-510	46.5-50.4	48.26	20.1-25.2	21.94	90-98.8	94.06	40.5-46.2	44.2	8.5-10.3	9.24	55.5-60	57.98
Br-118	45.8-51.4	48.58	16.8-22.4	20.7	60.5-91.2	77.12	43.7-49.7	47.66	9.8-11.4	10.44	54.4-59.9	56.08
Bj-109	45.1-50.7	48.04	19.7-25.2	22.58	77.5-99.8	90.58	42.1-49.3	45.36	8.3-10.3	9.26	49.4-60	56.02
Means	-	48.71	-	21.42	-	89.47	-	44.52	-	9.71	-	57.23
Crosses												
Bn-531×Br-118	49.6-52.7	48.91	17.6-20.3	21.2	71.7-83.8	84.90	45.1-52.1	46.83	8.5-11.4	10.62	40.7-60	55.81
Bn-525×Br-118	44.5-52.6	50.54	18.1-23.5	18.94	53.8-107.7	76.66	38.4-51.5	47.7	9.3-12.3	10.14	42.1-60	53.04
Bn-514×Bj-109	50.9-49.3	49.97	18.4-21.7	19.77	69.1-93.3	82.17	42.1-52.2	45.65	9.1-10.7	9.57	49.6-60	56.97
Bn-510×Bj-109	43.4-54.5	49.67	18.9-24.7	20.62	55.6-98.9	83.15	42.3-52.2	45.24	8.3-12.6	10.50	49.1-60	54.47
Means	-	49.77	-	20.13	-	81.72	-	45.35	-	10.20	-	55.07

Table 6. Means and ranges of morphological traits for parental and interspecific crosses

Genotypes	DFFF		PH		PBPP		MRL		PL	
Parents	Ranges	Means	Ranges	Means	Ranges	Means	Means	Means	Ranges	Means
Bn-531	129-136	133.6	100-135	119	4-6.36	4.67	Ranges	Means	Ranges	Means
Bn-525	125-135	130.2	130-145	141	6-7.5	6.6	50-80	62	4-6.36	4.67
Bn-514	135-144	139	100-135	119	3.3-5	4.48	55-70	60.6	6-7.5	6.6
Bn-510	127-135	131	120-150	132.8	4.6-9.8	7.12	55-65	60	3.3-5	4.48
Br-118	117-127	123.2	145-170	157	2.6-5	4.3	40-95	65	4.6-9.8	7.12
Bj-109	126-140	131.8	120-155	141.8	3.7-4.8	4.3	43-72	60	2.6-5	4.30
Means		131.46		135.1		5.24	58-77	65.8	3.7-4.8	4.30
Crosses	Ranges	Means	Ranges	Means	Ranges	Means	62.23	Ranges	Means	
Bn-531×Br-118	126-136	143.23	127-147	134.96	4.02-5.82	4.89	Ranges	Means	4.02-5.82	4.89
Bn-525×Br-118	124-145	130.82	109-162	142.15	3.16-6.56	3.16	55-67	59.20	3.16-6.56	3.16
Bn-514×Bj-109	127-145	136.75	133-116	124.55	5.04-6.3	5.57	48-77	64.48	5.04-6.3	5.57
Bn-510×Bj-109	136-155	130.57	89-156	131.03	5.2-7.8	5.76	50-69	58.40	5.2-7.8	5.76
Means		135.33		133.17		4.84		60.19		4.84
Genotypes	SPP		MR		DTM		HSW		SYPP	
Parents	Ranges	Ranges	Means	Ranges	Ranges	Means	Means	Ranges	Means	Means
Bn-531	15.3-22.6	22-46	32	0.415-0.65	11.5-15.8	13.64	0.525	189-196	193.2	19.16
Bn-525	23.3-28.6	35-55	43.4	0.47-0.68	2.02-8.53	5.59	0.556	173-177	174.8	25.82
Bn-514	19.3-26	40-56	49.2	0.45-0.57	10.4-15.9	13.70	0.522	188-193	191	22.16
Bn-510	6-24	29-50	40.8	0.45-0.65	2.23-5.65	3.61	0.556	184-192	189.4	17.20
Br-118	16-26.6	30-67	50.4	0.45-0.58	7.24-23.5	12.69	0.537	177-182	179.6	21.04
Bj-109	14-28	21-56	37	0.527-0.58	4.84-11.3	8.51	0.549	183-193	187.4	19.60
Means			42.13			9.62	0.540		185.90	20.83
Crosses	Ranges	Ranges	Means	Ranges	Ranges	Means	Means	Ranges	Means	Means
Bn-531×Br-118	9.98-24.8	39-57.8	36.0	0.52-0.32	5.8-11.9	7.10	0.503	186-190	184.6	17.6
Bn-525×Br-118	18.4-21.6	31-64	47.8	0.35-0.48	5.3-18.3	8.611	0.435	170-192	188.4	20.0
Bn-514×Bj-109	20.2-30	38.4-51.8	44.3	0.34-0.43	6.2-9.18	7.502	0.394	187-195	191.1	24.0
Bn-510×Bj-109	9.96-29.6	19-48.6	46.4	0.37-0.65			0.411	177-199	180.6	18.9
Means			43.6				0.435		186.3	20.1

DFFF, Days to 50% flowering; PH, Plant height (cm); PBPP, Primary branches per plant (no.); MRL, Main raceme length (cm); PL, Pod length (cm); SPP, Seeds per pod (no.); MR, Number of pod on main raceme; DTM, Days to maturity; HSW, Hundred seeds weight (g), SYPP, Seed yield per plant (g).

Table 7. Means and ranges values of different morphological and biochemical traits for the populations of *Bn-525xBr-118*

Pop ⁿ	DTFF	PH	PBPP	MRL	PL	SPP	MR	DTM	HSW	SYPP	OC	PC	GSL	OA	LA	EA
474	125	150.6	7.8	62	4.9	17.18	64	170	0.428	18.01	51.8	19.6	84.2	44.6	9.8	58.7
488	134	148.6	6.6	48.6	4	13.56	67.2	181	0.412	8.04	47.5	23.2	107.7	42.8	11.3	44.8
471	128	137	6.2	31	6.2	29.6	57.8	179	0.402	8.09	50.1	21.2	79.4	49.6	11.1	42.1
20	124	153	5.8	59.6	4.94	19.7	71	172	0.366	13.58	46.1	23.5	90.2	43.1	11.2	59.9
452	140	144.2	6.2	49.4	5.12	19.36	77	187	0.366	16.64	50.9	18.1	71.2	38.4	10.9	58.8
261	135	148	7.8	60.4	4.16	13.7	68.2	183	0.452	15.26	44.5	22.4	88.2	51.5	10.7	42.9
464	125	161.8	7.2	64	5.32	22.9	69.4	173	0.35	18.35	52.6	19.4	100.1	39.7	12.1	59.9
241	131	137.4	5	40.6	5.06	20.7	64.8	182	0.414	7.99	49.1	22.1	94.1	48.5	10.3	45.5
2	135	153	6.4	51.2	3.16	9.96	72.4	186	0.434	5.70	50.1	20.6	74.4	47.2	9.8	54.3
468	145	109	5.4	39.4	4.9	16.16	48	192	0.384	6.53	47.1	23.1	96.4	44.9	11	53.4
11	127	135	5.8	37.6	4.4	17.3	55	175	0.44	13.06	50.1	18.2	53.8	40.3	9.7	59.9
453	136	140.2	6.2	40.8	6.56	20.64	58.2	184	0.466	16.02	49.2	19.9	65.5	45.9	9.3	56.1
498	129	135.6	5.8	48.2	4.98	21.56	55.6	182	0.444	11.09	48.5	21.4	75.6	48.4	10.1	57.2
491	133	131.8	6	37.8	4.84	21.02	62.2	185	0.384	12.26	50.1	20.4	96.1	45.5	9.3	54.7
47	128	133.6	6.8	38.4	6.2	24.78	63	180	0.48	18.35	50.5	19.2	60.4	50.1	12.3	48.6
457	135	139.2	6.2	57	4.28	17.22	70.2	185	0.402	9.74	52.1	19.1	76.1	43.6	10.5	56.6
48	126	148.8	6.8	32.6	4.54	16.38	69.6	176	0.464	14.71	49.1	18.8	80.4	47.1	9.3	53.6
524	127	144.4	6.2	39.2	4.7	14.76	67.6	178	0.372	8.32	49.6	20.9	92.1	41.1	11.3	59.8
481	124	132.6	5.6	37.2	5.06	21.06	60	178	0.354	9.84	52.1	20.7	85.1	46.3	9.8	57.8
521	126	151.8	5.4	52.4	5.4	21.32	68.8	180	0.368	10.29	51.3	19.4	74.2	47.1	11.4	60.0
441	129	148.25	5	48	4.76	19.96	64.2	186	0.456	5.38	50.8	21.9	101.1	44.5	9.4	59.3
Ranges	124-	109-	5-7.8	31-	31.1-	9.9-	84-	170-	35-	5.3-	44.5-	18.1-	53.8-	38.4-	9.3-	42.1-
	145	161.8		64	6.5	29.6	77	192	48	18.3	52.6	23.5	107.7	51.5	12.3	60
Means	130.5	142.0	6.2	46.4	4.92	18.9	64.5	180.	0.411	11.77	49.6	20.6	83.15	45.2	10.5	54.4

DTFF, Days to 50% flowering; PH, Plant height (cm); PBPP, Primary branches per plant (no.); MRL, Main raceme length (cm); PL, Pod length (cm); SPP, Seeds per pod (no.); MR, Number of pod on main raceme; DTM, Days to maturity; HSW, Hundred seeds weight (g), SYPP, Seed yield per plant (g). OC, Oil content (%); PC, Protein content (%); OA, Oleic acid (%); LA, Linolenic acid (%); EA, Erucic acid (%).

Table 8. Means and ranges values of different morphological and biochemical traits for the populations of Bn-510xBj-109, Bn-531xBr-118 and Bn-514xBj-109

	Pop ⁿ	DHF	PH	PBP	MRL	PMR	PL	SP	DM	HSW	SYP	OC	PC	GSL	OA	LA	EA
Bn-510xBj-109	81	149	141.8	6.8	68.2	37.2	5.2	14.58	192	0.465	9.46	50.1	22.5	87.3	44.6	10.8	59.9
	144	145	155.8	5.4	70.2	45.2	6.24	21.6	188	0.449	7.69	50.7	19.9	92.2	47.7	10.7	56.2
	152	134	141.8	5.8	71.4	41.4	5.8	24.8	179	0.412	8.69	48.9	19.4	83.6	50.7	11.1	55.7
	127	154	137.6	4.6	64.4	41	5.32	22.8	197	0.479	5.13	51.1	20.1	85.1	44.5	10.8	60.0
	84	144	127.2	5.8	53.2	31.2	5.8	24	185	0.423	6.71	48.8	20.1	76.1	46.1	11.7	54.2
	130	132	115.8	3.8	57	28.8	5.52	22.8	177	0.456	9.33	51.6	19.9	85.4	50.9	10.5	52.4
	74	138	114.2	5.8	62.2	32.2	5.66	20.8	180	0.379	8.42	46.9	21.7	91.5	48.8	12.6	51.2
	80	155	99	4.4	38	19	5.2	9.98	199	0.436	2.28	47.7	21.6	86.4	49.3	10.1	55.1
	136	153	89	3.6	45.4	30.6	5.28	11.04	192	0.464	1.53	47.5	21.8	55.6	51.4	9.5	50.1
	103	136	137.2	7	50	32.6	7.8	21.88	180	0.654	11.63	50.4	20.6	93.1	46.6	8.3	59.8
	92	134	126	5.8	55	31.8	5.7	12.36	178	0.479	3.84	48.5	19.5	70.5	44.6	10.2	56.5
	137	151	145.2	6.4	69.8	48.4	5.7	13.58	190	0.528	7.05	49.6	20.7	78.6	47.8	10.9	54.2
	82	132	114	6	50.4	31.5	5.36	13.02	179	0.515	5.60	48.2	21.4	86.1	45.1	10.5	59.5
	151	152	142	7.2	64.5	40.2	5.28	12.92	192	0.543	5.81	49.1	21.4	93.8	43.2	9.7	59.1
	122	141	143	6.6	70.3	43.4	5.44	14.22	182	0.541	8.37	43.4	24.6	72.4	48.6	10.4	52.2
	110	143	145.6	7.6	55.6	38.2	5.2	19.96	185	0.524	10.14	48.8	21.1	98.9	43.6	10.5	58.8
	142	142	127.2	7.6	64.8	35.8	5.9	12.96	182	0.606	5.78	54.5	18.9	80.1	42.3	11.1	59.5
	87	140	148	8	57.2	19.2	7.08	19.18	178	0.564	11.63	48.2	23.3	83.1	46.8	10.1	58.6
	141	138	129.8	6	59.4	42.2	5.9	22.22	179	0.579	7.28	50.2	20.4	95.3	44.5	12.2	52.4
107	144	133.4	7.6	53	38.8	5.94	19.04	186	0.578	7.97	49.4	21.6	89.7	44.3	11.1	57.6	
129	132	136.4	5.6	53	48.6	5.72	15.7	178	0.490	4.70	43.7	24.7	89.8	52.2	10.4	49.1	
Ranges	136-155	89-155.8	3.6-8	38-71.4	19-48.6	5.2-7.8	9.98-24	177-199	0.3-0.6	1.53-11.6	43.4-54	18.9-24	55.6-98	42.3-52	8.3-12.	49.1-60	
Means	143.23	130.9	6.066	58.71	36.06	5.763	17.6	184.7	0.503	7.1	48.91	21.2	84.50	46.83	10.62	55.81	
Bn-531xBr-118	186	127	126.8	5.8	62.6	57.8	5.44	20.58	189	0.44	9.75	50.2	20.3	73.3	45.5	10.3	60.0
	328	136	130	5	55.2	40	5.82	18.4	190	0.32	5.824	49.7	18.8	71.7	47.3	10.2	52.5
	163	126	135.8	5.4	55	44.6	4.5	19.46	189	0.44	8.54	49.6	20.2	76.3	52.1	11.4	40.7
	340	130	147.2	6	56.6	57.6	4.7	19.92	186	0.452	11.994	50.5	17.8	78.2	48.5	10.3	54.4
	157	135	135	6	66.6	39	4.02	21.66	190	0.526	6.95	52.7	17.6	83.8	45.1	8.5	57.6
	Ranges	126-136	126.8-147	5.0-6.0	55-66.6	39-57.8	4.02-5.8	18.4-21	188-197	0.3-0.5	5.8-11.9	49.6-52	17.6-20	71.7-83	45.1-52	8.5-11.4	40.7-60
	Means	130.8	134.96	5.64	59.2	47.8	4.89	20.00	192.84	0.435	8.611	50.54	18.94	76.66	47.7	10.14	53.04

	Pop ⁿ	DHF	PH	PBP	MRL	PMR	PL	SP	DM	HSW	SYP	OC	PC	GSL	OA	LA	EA
Bn-514x Bj-109	196	127	126.6	5.6	68.8	51.8	5.04	30	187	0.348	7.584	49.3	18.4	69.1	52.3	9.1	49.6
	171	140	116	4.4	50	38.4	5.24	20.2	192	0.424	6.256	50.9	19.3	79.4	42.1	9.3	60.0
	158	145	122.6	4.2	54.8	41	5.32	22.2	195	0.432	6.542	49.9	21.7	93.3	42.1	10.7	58.6
	185	135	133	6.2	58	44.6	6.392	21.6	191	0.38	9.188	49.8	19.7	86.9	46.1	9.2	59.7
	Ranges	127-145	116-133	4.2-6.2	50-68.6	38.4-51	5.0-6.3	20.2-30	187-195	0.3-0.4	6.25-9.18	49.3-50	18.4-21	69.1-93	42.1-46	9.1-10.7	49.6-60
Means	136.75	124.53	5.13	58.4	44.33	5.57	24.03	191.16	0.394	7.50	49.97	19.77	82.17	45.65	9.57	56.97	

DTFF, Days to 50% flowering; *PH*, Plant height (cm); *PBPP*, Primary branches per plant (no.); *MRL*, Main raceme length (cm); *PL*, Pod length (cm); *SPP*, Seeds per pod (no.); *MR*, Number of pod on main raceme; *DTM*, Days to maturity; *HSW*, Hundred seeds weight (g), *SYPP*, Seed yield per plant (g). *OC*, Oil content (%); *PC*, Protein content (%); *OA*, Oleic acid (%); *LA*, Linolenic acid (%); *EA*, Erucic acid (%).

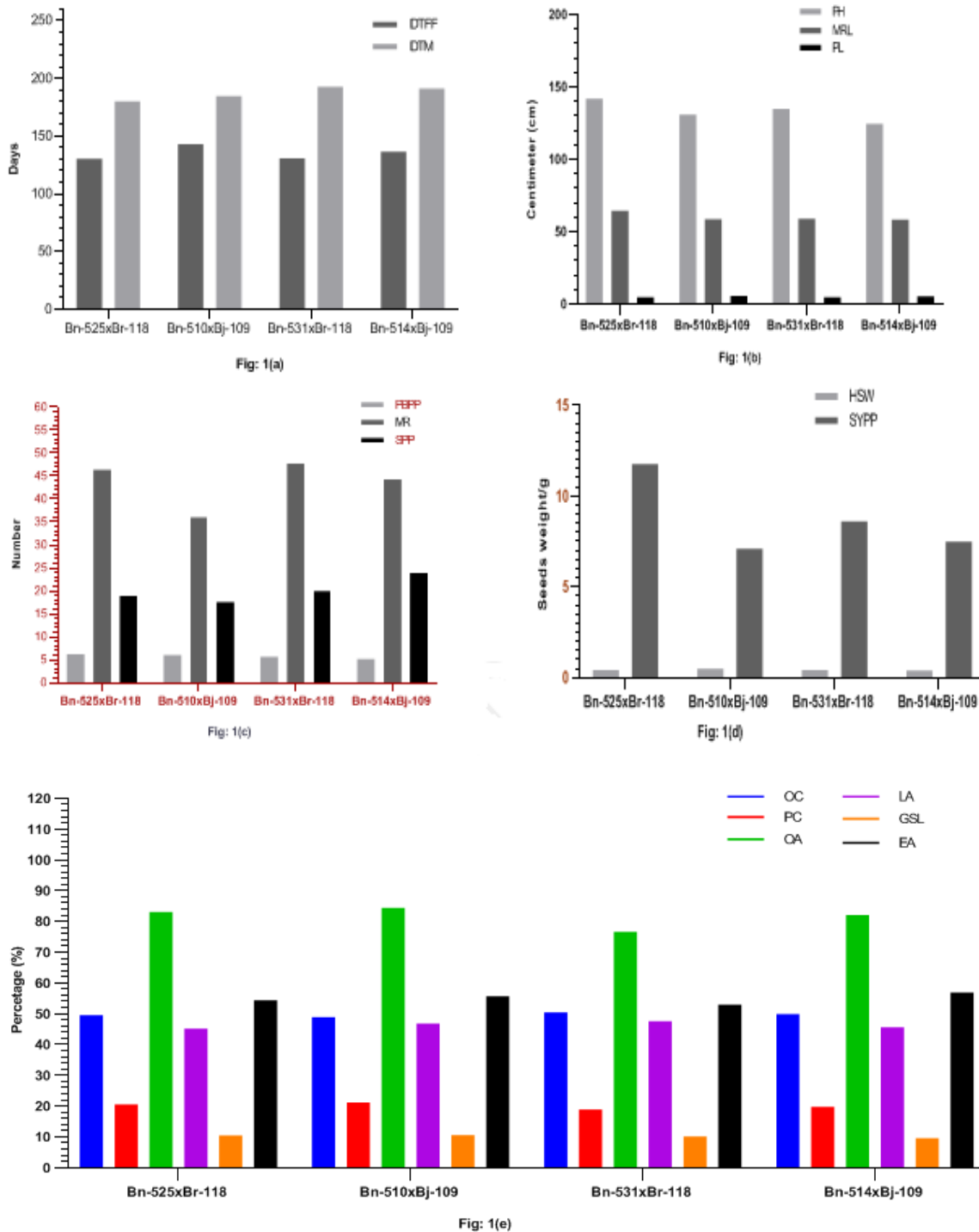


Fig. 1. Mean values of different morphological and biochemical traits for the populations of four interspecific crosses. 1(a) days to 50% flowering (DTFF) and days to maturity (DTM). 1(b) plant height (PH), main raceme length (MRL) and pod length (PL). 1(c) primary branches per plant (PBPP), number of pod on main raceme (MR) and seeds per pod (SPP). 1(d) hundred seeds weight (HSW) and seed yield per plant (SYPP). 1(e) oil content (OC), protein content (PC), oleic acid (OA), linoleic acid (LA), glucosinolates (GSL) and erucic acid (EA)

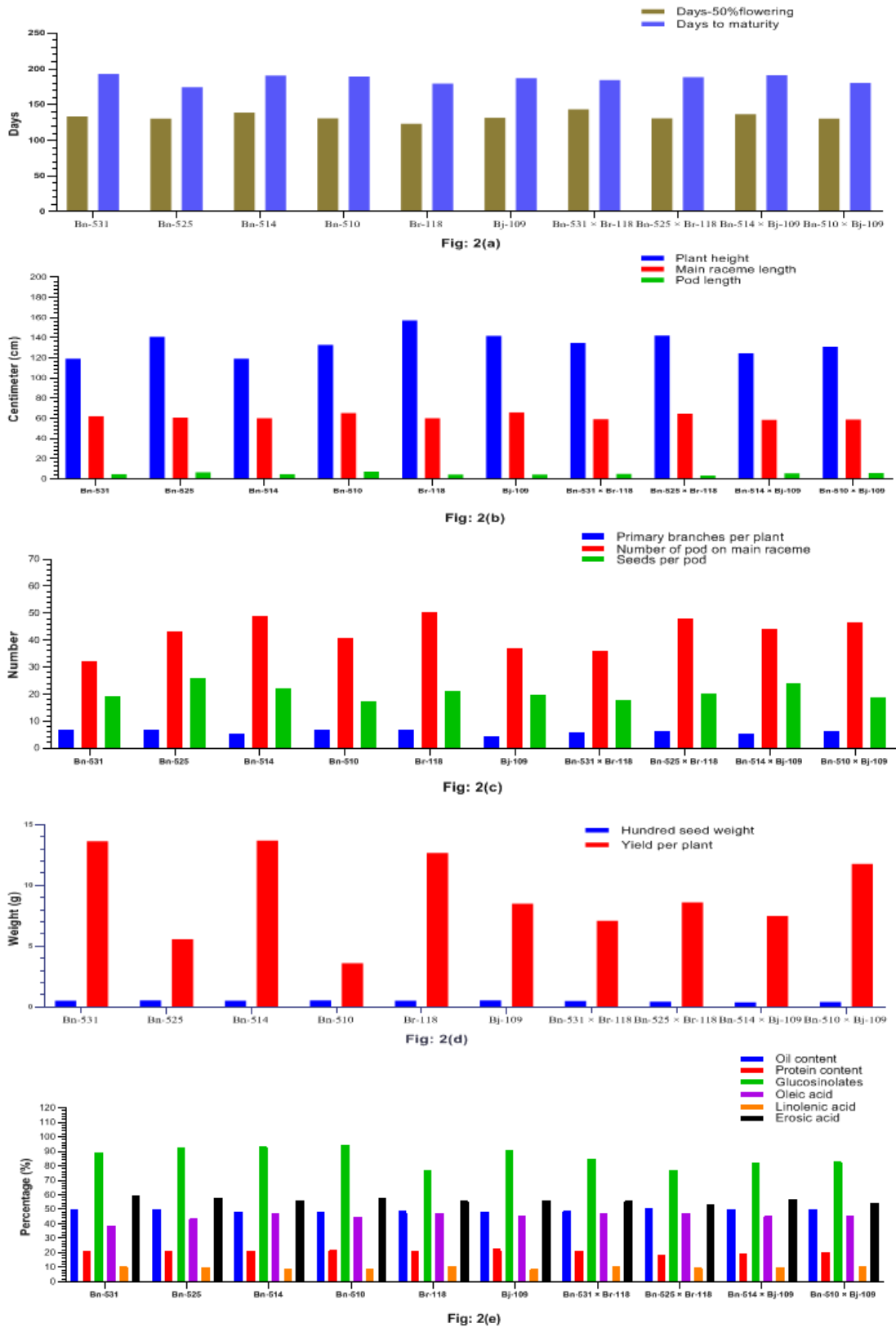


Fig. 2. Mean values of different morphological and biochemical traits of Parental and interspecific crosses

Akabari et al. [24] and Kumar et al. [25] reported almost similar results found in these traits of our present investigation. Days to 50% flowering (155) calculated in the cross Bn-510xBj-109 and variance (20.70) was estimated for the cross Bn-531xBr-118, all the interspecific crosses had high heritability with genetic advance (7.43) was found in the cross Bj-109xBn-514. The tallest plant (161.8 cm) were noted in the crosses Bn-525xBr-118, high heritability (0.92) coupled with low genetic advance (2.23) was analyzed for the cross Bn-514xBj-109. Longest main raceme length was (77 cm) measured in the cross Bn-510xBj-109 and variances (312.16) was calculated for the crosses Bn-531xBr-118. Heritability and genetic advance estimation was 0.81, 15.76 for the cross Bn-514xBj-109. Pod length was (7.8cm) recorded for the cross Bn-510xBj-109 and variance (3.54) was estimated for the crosses Bn-531xBr-118. All the crosses had high heritability with low genetic advance except Bn-510xBj-109. Seed per pod was calculated in the cross Bn-514xBj-109, variances was high (52.33) and showed heritability with high genetic advance (7.71). The important parameter main raceme pods (64) was counted for the cross Bn-525xBr-118 and variance (354.04) was calculated and showed high heritability (0.82) coupled with high genetic advance (21.83). Our results of heritability and genetic advance was also reported by Muhammad et al. [23]; Singh et al. [24]. Days to maturity (199) in the cross Bn-510xBj-109 and variance (22.26) was estimated in this cross. The heritability estimations was with low genetic advance in all the interspecific crosses. The hundred seed weight was (0.654) observed in the cross Bn-510xBj-109 and variance (0.008) analyzed for Bn-510xBj-109 and Bn-531xBr-118. High heritability (0.81) coupled with low genetic advance (0.1) was estimated in the cross Bn-510xBj-109, rest of the crosses also had high heritability estimations (0.56, 0.54 and 0.35) with genetic advance estimations (0.038, 0.075 and 0.039). Seed yield per plant (18.3g) found in the cross Bn-525xBr-118 and variance (68.57) was found in Bn-525xBr-118 and Bn514xBj-109. Maximum heritability and genetic advance (0.89 and 4.45) found in the cross Bn514xBj-109. Our findings of present experiments for high heritability and high genetic advance for seed yield and morphological traits was strongly supported by Sandhu et al. [26]; Gupta et al. [27]; Kumar et al. [25].

In *Brassica*, interspecific crosses genotypes are evaluated for biochemical traits wide range of

variability with respect to different traits (Table 2). Maximum oil content (54.5%) found in the cross Bn-510xBj-109 from population (142) and variance (18.72) was calculated in Bn-531xBr-118 with high heritability and genetic advance (0.70) and (4.3) for the cross Bn-531xBr-118. Highest protein content and variance was (24.7% and 22.67) found in population (129) in the crosses Bn-510xBj-109 with high heritability (0.79) and high genetic advance (5.26). The high glucosinolates content was (107.7 μ mol/g) showed by the cross Bn-525xBr-118 in population (11 and 488) with high heritability (0.80) and high genetic advance (18.14). The desirable component oleic acid maximum (52.3%) found in Bn514xBj-109, and high heritability (0.80) coupled with high genetic advance (4.66) was calculated for the cross Bn-525xBr-118. Linolenic acid was (12.6%) observed in population (74) for the cross Bn-510xBj-109 and high heritability (0.48) with low genetic advance (0.74) was estimated in the cross Bn-525xBr-118. Erucic acid (EA) content was minimum (49.1%) found in population (129) for the cross Bn-510xBj-109. Heritability estimation was maximum (0.84) coupled with high genetic advance (6.64) for the cross Bn-525xBr-118. The results of our present investigations of biochemical traits are mostly similar to the findings reported by Fayyaz et al. [28]; Khan et al. [29]; Amsalu et al. [30].

4. CONCLUSION

The 51 genotypes of four interspecific crosses studied exhibited wide genetic variations from morphological and biochemical level. Majority traits with high genetic progress had high heritability, indicating that the investigated qualities were less affected by environmental factors. Highest oil, protein, low glucosinolates and low erucic acid were observed in Bn-510xBj-109 in population (142 and 129), population (11) of crosses Bn-525xBr-118 and crosses Bn-531xBr-118 in population (163). Maximum yield in population (47) along with low glucosinolates (53.8 μ mol g⁻¹) found in population (11) were observed in crosses Bn-525xBr-118. Population (142 and 129) in Bn-510xBj-109, population (111 and 193) in Bn-525xBr-118 and 531xBr-118 should be forwarded to next generations for developing varieties with high oil and protein, low glucosinolates and low erucic acid content, respectively. To generate sergeants with a combination of desirable qualities, genotypes from distinct clusters with specific desirable traits

should be hybridized. The F₄₋₅ crosses analyzed demonstrated more variation for a variety of desired traits, and this knowledge can be utilized to improve the evaluation of available germplasm for future breeding operations.

DISCLAIMER

The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

ACKNOWLEDGEMENTS

The Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar (UAP), and Nuclear Institute for Food and Agriculture (NIFA) Pakistan is greatly acknowledged for providing the platform, all necessary equipment, and the agricultural field to conduct present research.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Hu Q, Hua W, Yin Y, Zhang XK, Liu LJ, Shi JQ, Zhao YG, Qin L, Chen C, Wang HZ. Rapeseed research and production in China. *The Crop Journal*. 2017;5:127-135.
2. Friedt W, Tu JX, Fu TD. Academic and Economic Importance of *Brassica napus* Rapeseed. *The Brassica napus Genome*. Cham. Springer. 2018;1–20.
3. Zhou WJ. Oilseed cultivation. In: Ding YS (Editor). *Cultivation of Crops*. Shanghai Sci. and Tech. Press. Shanghai. 1994;357-380.
4. El-Esawi M, Bourke P, Germaine K, Malone R. Assessment of Morphological Variation in Irish *Brassica oleracea* Species. *Journal of Agricultural Science*. 2012a;4:20–34.
5. Rich TCG. *Crucifers of Great Britain and Ireland*. Botanical Society of the British Isles, London. 1991;336.
6. Christopher GL, Andrew JR, Geraldine ACL, Clare JH, Jacqueline B, Gary B, German CS, David E. *Brassica* ASTRA: an integrated database for *Brassica* genomic research. *Nucleic Acids Res*. 2005;1: (33):656-659.
7. Khatri A, Khan IA, Siddiqui MA, Raza S, Nizamani GS. Evaluation of high yielding mutants of (*Brassica juncea* L.) cv. S-9 developed through Gamma rays and EMS. *Pakistan Journal of Botany*. 2005;37:279-284.
8. FAO statistics; 2018. Available:www.fao.org/statistics.
9. Sadat HA, Nematzadeh GA, Jelodar NB, Chapi OG. Genetic evaluation of yield and yield components at advanced generations in rapeseed (*Brassica napus* L.). *African Journal of Agricultural Research*. 2010;5: 1958-1964.
10. Yadav DK, Giri SC, Vignesh M, Vasudev S, Yadav AK, Das V, Singh R, Singh N, Mahapatra T, Prabu KV. Genetic variability and trait association studies in Indian mustard (*Brassica juncea*). *Indian Journal of Agricultural Sciences*. 2010;81(8):712-716.
11. Nematollahi Z, Saeidi G. Study of drought tolerance in some genotypes of flax (*Linum usitatissimum* L.). *Journal of Water Research in Agriculture*. 2011;25:57-65.
12. Becker HC, Löptien H, Röbbelen G. Breeding: An overview. In: *Biology of Brassica Coenospecies*. (Ed.): C. Gómez-Campo, Elsevier, Amsterdam. 1999;413-460.
13. Shengwu HU, Ovesna J, Kucera L, Kucera V, Vyvadilová M. Evaluation of genetic diversity of *Brassica napus* germplasm from China and Europe assessed by RAPD markers. *Plant Soil and Environment*. 2003;49:106-113.
14. Naz S, Siddiquiland MF, Raza S. Effect of different growth regulators on in vitro propagation of *Brassica napus* L. *Pak. J. Bot*. 2018;50(5):1871-6.
15. Engqvist MG, Becker HC. Correlation studies for agronomic characters in segregating families of spring oilseed rape (*Brassica rapa* L.). *Hereditas*. 1993;118: 211-216.
16. Reinhardt TC, Röbbelen G. Quantitative Analysis of Fatty Acids in Intact Rapeseed by Near Infrared Reflectance Spectroscopy. In *Proceedings of the 8th International Rapeseed Conference*. 1991; 1380-1384.

17. Panford JA, Man JMD. Determination of Oil Content by NIR: influence of fatty acid composition on wavelength selection. *Journal of the American Oil Chemists' Society*. 1990;67:473-482.
18. Velsaco L, Mollers C, Becker HC. Estimation of seed weight, oil content and fatty acid composition in intact single seeds of rapeseed (*Brassica napus* L.) by near-infrared reflectance spectroscopy. *Euphytica*. 1999;106:79-85.
19. Steel RGD, Torrie JH. Principles and procedures of statistics, a biological approach, 1980; 2nd ed. McGraw Hill, Inc. New York, Toronto, London.
20. Mahmud I, Kramer HH. Segregation for yield, height and maturity following a soybean cross. *Agron. J*. 1951;43:605-609.
21. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Indian Council of Agriculture Research. New Dehli. 1951;381.
22. Khan AH, Mahmood T, Shah SA. Path coefficient analysis of morphological parameters with seed yield in Raya. *Pakistan Journal of Agricultural Research*. 1992;13(4):334-337.
23. Garcia AA, Benchimol LL, Barbosa AM, Geraldi IO, Souza Jr CL, Souza AP. Comparison of RAPD, RFLP, AFLP and SSR markers for diversity studies in tropical maize inbred lines. *Genetics and Molecular Biology*. 2004;27(4):579-88.
24. Liu FM, Hong Z, Xu DP, Jia HY, Zhang NN, Liu XJ, Yang ZJ, Lu MZ. Genetic diversity of endangered endemic *Dalbergia odorifera* revealed by SSR markers. *Forests*. 2019;10:225.
25. Kumar S, Ali B, Khaldun ABM, Islam SS, Uddin MS, Akanda MAL, Miah MS. Genetic Diversity, Correlations and Path Coefficient Analysis among the F5 Populations of *Brassica* Species. *Asian Journal of Advances in Agricultural Research*. 2021;16:20-31.
26. Sandhu R, Rai SK, Bharti R, Kour A, Gupta SK, Verma A. Studies on genetic diversity among various genotypes of *Brassica napus* L. Using Morphological Markers. *International Journal of Current Microbiology and Applied Science*. 2017; 6:469-480.
27. Gupta M, Roy HS, Bhadauria SS. Genetic variability analysis in F2/F3 population derived through interspecific hybridization in oilseed *Brassica*. *Electronic Journal of Plant Breeding*. 2019;10:1275-1282.
28. Fayyaz LA, Afzal M. Genetic variability and heritability studies in indigenous *Brassica rapa* L. accessions. *Pakistan Journal Botany*. 2014;46:609-612.
29. Khan N, Farhatullah IH, Naheed HA, Abid SA. Heritability and genetic advance studies for biochemical traits in F2-3 introgressed families of *Brassica*. *Pakistan Journal of Botany*. 2015;47:883-888.
30. Amsalu F, Sentayehu A, Bulecha W. Genetic Variability, Heritability, Genetic advance, Genetic advance as Percent Mean and Character Association of Ethiopian Mustard (*Brasica carinata* A. Braun) Land races. *International Journal of Plant Breeding and Crop Science*. 2017;4:166-177.

© 2022 Ali et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:
The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/87027>