Original Research Article

Genetic Diversity among the Interspecific F_{4-5} Populations of *Brassica* for Agronomic and Biochemical Traits

ABSTRACT

The study was carried out to determine genetic diversity, heritability, and genetic progress among the F_{4-5} population of *Brassica* 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 diversity 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 genotypes in paired rows of 4 m length with a spacing of 30 x 10-15 cm (row × plant). Data were recorded on ten different agro-morphological characters and six biochemical traits. The interspecific crosses of Brassica highly performed all types of morphological traits in populations *viz;* 142, 129, 196, 186 and 142. Biochemical traits are highly performed in interspecific crosses of F4-5 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.

Key words: Variability, Heritability, Genetic advance, Morphological and Biochemical traits, Brassica

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, it is cultivated over an area of 219 thousand hectare and produced 158 thousand tons seeds which in turn produced 51 thousand tons of edible oil during 2012-13 [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 [12, 13]. Estimation of the relationship between two variables is known as correlation. Measurable association alludes to a quantifiable relationship between two variables. 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 [14]. 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.

3. MATERIALS AND METHODS

3.1. 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. 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^{o}N and 71.35^{o}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.

3.2. 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 [15, 16, 17]. Heritability, estimates were calculated by the formula [18].

4. RESULT AND DISCUSSION

Genetic distance provides a measure of the degree of relatedness between individuals in a population [19] and it also plays a key role in genetic improvement through breeding methods [20]. Interspecific crosses gradually varied from parental genotypes of yield and yield contributing parameters ten agronomic traits is presented in Table 1 and Figure 1 & 2. Akabari *et al.* [21] and Kumar *et al.* [22] reported almost similar results found in these traits of our present investigation. Days to 50% flowering (155) calculated in the cross Bn-510×Bj-109 and variance (20.70) was estimated for the cross Bn-531×Br-118, all the interspecific crosses had high heritability with genetic advance (7.43) was found in the cross Bj-109×Bn-514. The tallest plant (161.8 cm) were noted in the crosses Bn-525×Br-118, high heritability (0.92) coupled with low genetic advance (2.23) was analyzed for the cross Bn-514×Bj-109. Longest main raceme length was (77 cm) measured in the cross Bn-510×Bj-109 and variances (312.16) was calculated for the crosses Bn-531×Br-118. Heritability and genetic advance estimation was 0.81, 15.76 for the cross Bn-514×Bj-109. Pod length was (7.8cm) recorded for the cross Bn-510×Bj-109 and variance (3.54) was estimated for the crosses Bn-531×Br-118. All the crosses had high heritability with low genetic advance except Bn-510×Bj-109. Seed per pod was calculated in the cross Bn-514×Bj-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-525×Br-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-510×Bj-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-510×Bj-109 and variance (0.008) analyzed for Bn-510×Bj-109 and Bn-531×Br-118. High heritability (0.81) coupled with low genetic advance (0.1) was estimated in the cross Bn-510×Bj-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-525×Br-118 and variance (68.57) was found in Bn-525×Br-118 and Bn514×Bj-109. Maximum heritability and genetic advance (0.89 and 4.45) found in the cross Bn514×Bj-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.* [25]; Gupta *et al.* [26]; Kumar *et al.* [22].

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-510×Bj-109 from population (142) and variance (18.72) was calculated in Bn-531×Br-118 with high heritability and genetic advance (0.70) and (4.3) for the cross Bn-531×Br-118. Highest protein content and variance was (24.7% and 22.67) found in population (129) in the crosses Bn-510×Bj-109 with high heritability (0.79) and high genetic advance (5.26). The high glucosinolates content was (107.7µmol/g) showed by the cross Bn-525×Br-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 Bn514×Bj-109, and high heritability (0.80) coupled with high genetic advance (4.66) was calculated for the cross Bn-525×Br-118. Linolenic acid was (12.6%) observed in population (74) for the cross Bn-510×Bj-109 and high heritability (0.48) with low genetic advance (0.74) was estimated in the cross Bn-525×Br-118. Erucic acid (EA) content was minimum (49.1%) found in population (129) for the cross Bn-510×Bj-109. Heritability estimation was maximum (0.84) coupled with high genetic advance (6.64) for the cross Bn-525×Br-118. The results of our present investigations of biochemical traits are mostly similar to the findings reported by Fayyaz *et al.* [27]; Khan *et al.* [28]; Amsalu *et al.* [29].

5. 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-510×Bj-109 in population (142 and 129), population (11) of crosses Bn-525×Br-118 and crosses Bn-531×Br-118 in population (163). Maximum yield in population (47) along with low glucosinolates (53.8µ mol g^{-1}) found in population (11) were observed in crosses Bn-525×Br-118. Population (142 and 129) in Bn-510×Bj-109, population (111 and 193) in Bn-525×Br-118 and 531×Br-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 F_{4-5} 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.

COMPETING INTERESTS DISCLAIMER:

Authors have declared that no competing interests exist. 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.

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. PBS. Pakistan oilseed development board. Pakistan Bureau of Statistics. 2013;22-23.
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;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. Gòmez-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. Engqvist MG, Becker HC. Correlation studies for agronomic characters in segregating families of spring oilseed rape (*Brassica rapa* L.). Hereditas. 1993;118:211-216.
15. 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.
16. 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.
17. 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.
18. 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.
19. 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.
20. 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.
21. Akabari VR, Sasidharan N, Kapadia VN. Inbreeding depression heritability and genetic advance for yield and yield components in Indian mustard. Journal of Pharmacognosy and Phytochemistry. 2017;6:755-760.
22. 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.
23. Muhammad A, Raziuddin MS, Bacha QU, Rahman AU, Khan SA. Combining Ability and Heritability Studies for Yield Contributing Traits in F4 Populations of *Brassica napus*. American-Eurasian Journal of Agricultural and Environmental Sciences. 2014;14:509-515.

24. Singh AP, Verma OP, Kumar K. Estimates of genetic variability parameters and interrelationships of morpho-physiological traits in yellow sarson (*Brassica rapa* L. var. yellow sarson). Electronic Journal of Plant Breeding. 2017;8:629-635.
25. 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.
26. 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.
27. Fayyaz LA, Afzal M. Genetic variability and heritability studies in indigenous *Brassica rapa* L. accessions. Pakistan Journal Botany. 2014;46:609-612.
28. 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.
29. 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.

Table 1. Variance (σ^2), heritability (h_{BS}) and genetic advance (GA) of morphological traits for parental lines and four interspecific crosses.

Genotypes		**DTFF**			**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			0.0074			2.4233		
Bn-525	4.597			75.3			2.2			0.0062			6.0945		
Bn-514	9.603			45.7			5.5			0.0023			5.5428		
Bn-510	53.23			73.2			10.8			0.0050			2.2300		
Br-118	5.403			49.3			3.3			0.0026			42.334		
Bj-109	26.87			139.7			16.3			0.0004			1.8013		
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

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).

Table 2. Variance, heritability (h_{BS}) and genetic advance of biochemical traits for parental lines and four interspecific crosses.

Genotypes	**Oil content (%)**			**Protein content (%)**			**Glucosinolates (%)**			**Oliec acid (%)**			**Linolenic acid (%)**			**Erosic acid (%)**		
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**	**σ^2**	**$h^2_{(BS)}$**	**GA**
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

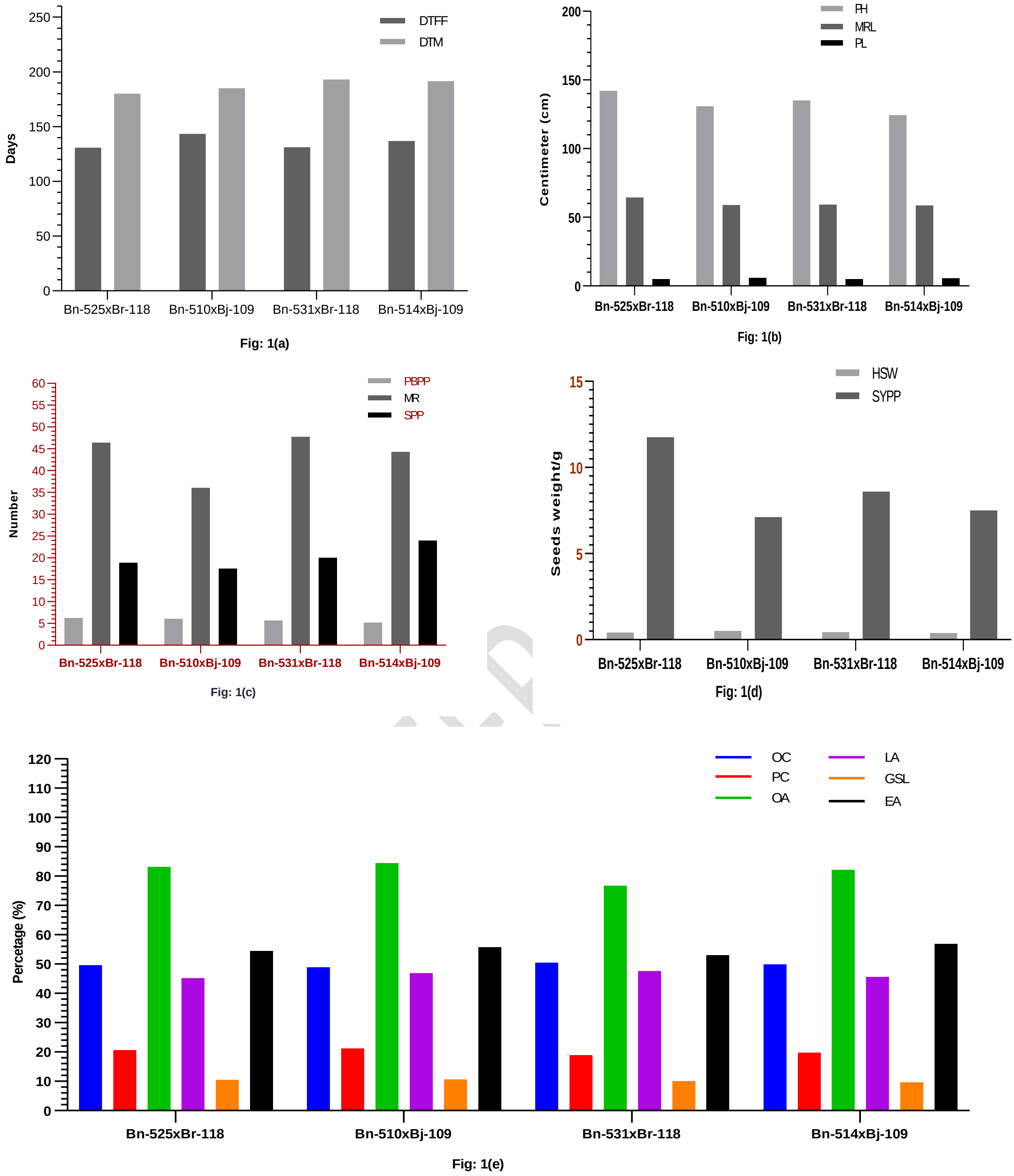


Fig: 1(a)

Fig: 1(b)

Fig: 1(c)

Fig: 1(d)

Fig: 1(e)

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).

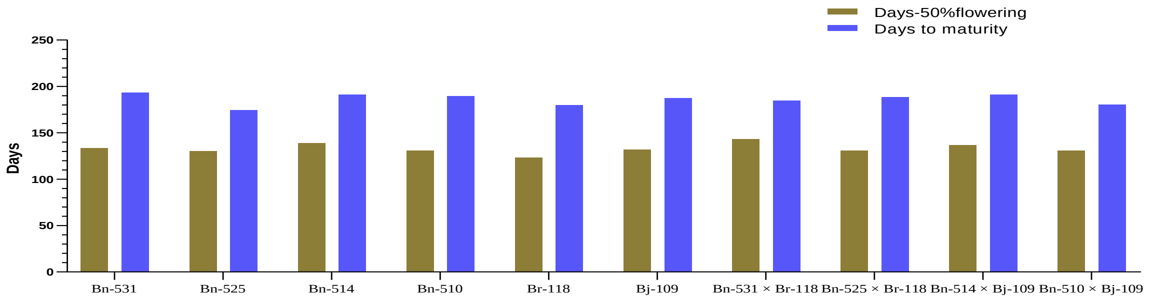
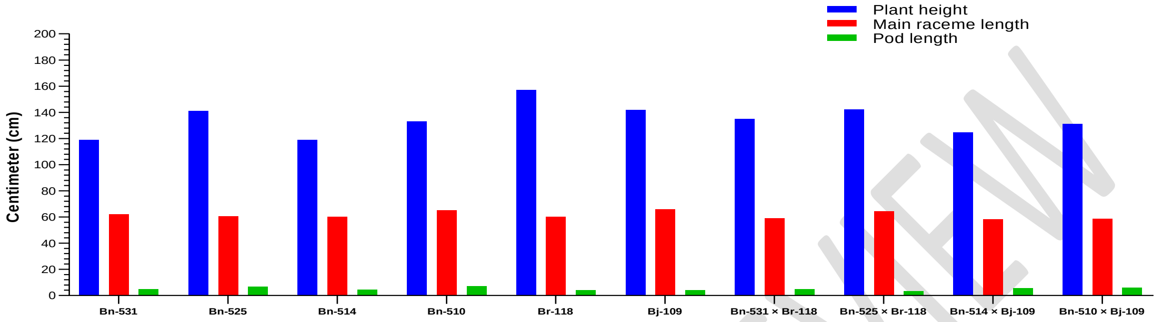


Fig: 2(a)



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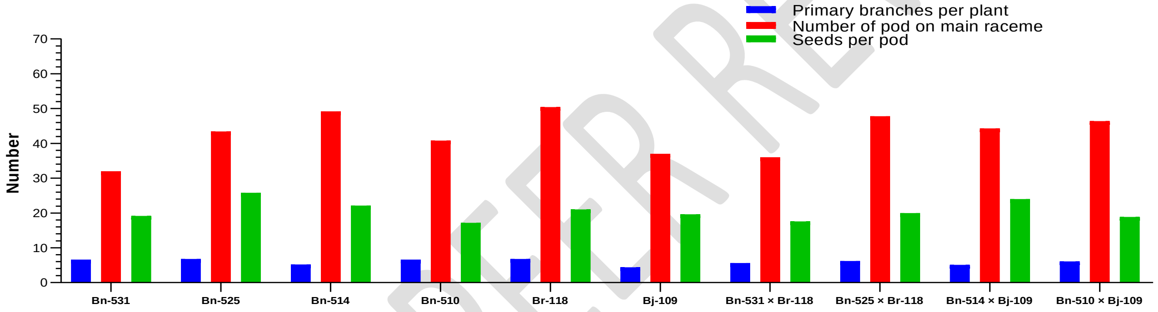

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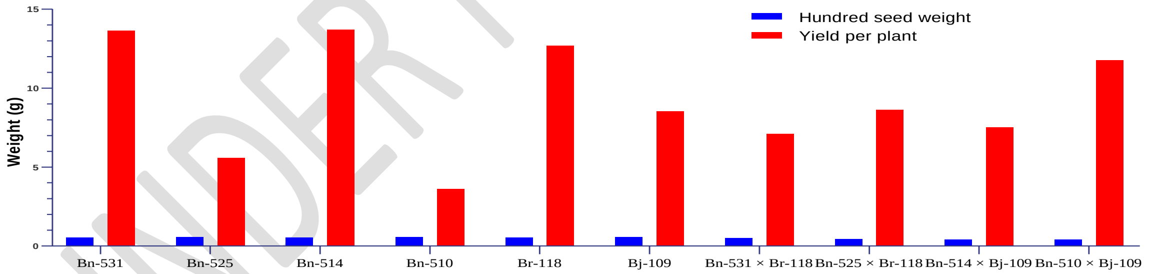

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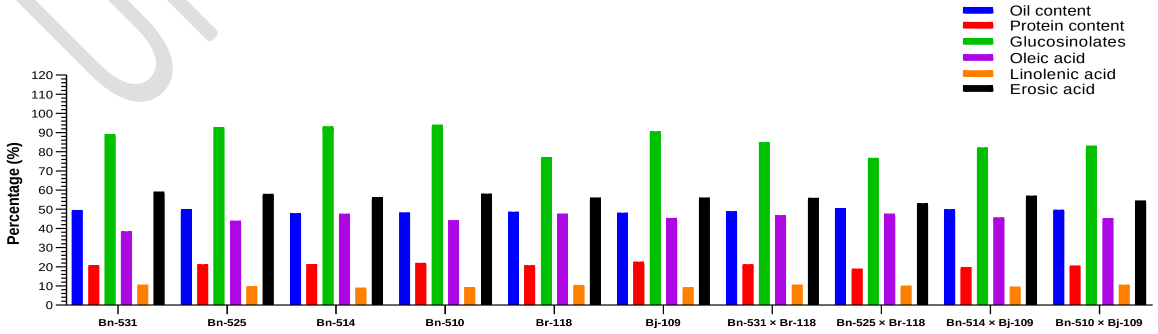

Fig: 2(e)

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