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ORIGINAL RESEARCH

Elucidating Genetic Variability of *Brassica napus* L. Progenitors and Their Crosses for Enhanced Qualitative Traits

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ABSTRACT: Evaluation of the breeding population is crucial for the selection of a superior genotype. Hence, the present study was conducted to assess genetic variation among five *Brassica napus* L. parents and their diallel hybrids to identify the best-performing parents and crosses. Heterosis and inbreeding depression were also assessed for the qualitative traits. Among the parental genotypes, Ancestor 2702 was identified as the best general combiner for protein (1.41%) and oleic acid content (1.21%). 2702×DUNCLED was the best specific combiner for oil content (0.78%), while 2702×2722 was recognized as best cross for linoleic acid content (1.3%). Similarly, DUNCLED×2702 was the best reciprocal cross for oil content (2.4%) and linoleic acid content (0.4 %), while P1-801×2702 was considered the best cross for protein content (2.2%) and oleic acid (1.7%). All the qualitative traits revealed a broad sense of heritability and non-additive type of gene action, which indicated the later generation selection for further improvement. High oleic acid content, preferred negative mid and best parent heterosis for erucic acid, glucosinolate and moisture contents was reported for 2702×DUNCLED. The favorable cross combination for protein and oil content was 2702×2722, which also yielded the positive mid and best parent heterosis. Inbreeding depression for qualitative traits ranged from -20.8% to 22.9%. It was concluded that among all the genotypes, accession 2702 was the best general, specific and reciprocal combiner, and the best parent heterosis for all traits when crossed with genotypes DUNCLED, P1-119 and 2722. It is also suggested that the screened crosses be carried to further generations to improve the quality related traits of *Brassica napus*. L.

KEYWORDS: *Brassica napus*, qualitative traits, diallel, combining ability, heritability, heterosis.

1. Introduction

Brassica napus. L is one of the particular canola cultivars, having a bright yellow flowering of the family Brassicaceae, cultivated widely for its rich source of oil. *Brassica napus* L. is an amphidiploid with an AACC genome (2n=38), developed by a cross between diploid species *B. rapa* L. with a AA genome (2n=20) and *B. oleracea* L. having CC genome (2n=18) (Iniguez & Fedrico, 2010). The Brassica genus has almost 100 species in which *Brassica napus* is commonly known as rape seed. It is not native to Australia and originated either in North Europe or the Mediterranean area. Rape seed is the third largest source of edible oil throughout the world. However, in

Pakistan, 0.25 million hectares of land produced 0.39 million tons of rapeseed and 0.23 million tons of rapeseed oil. Pakistan is facing a chronic deficit in edible oil production with better quality characteristics for value added products. Quality is the major constraint in *Brassica napus.*

Rape seed has shown little improvement in yield as well as in quality since 1980 due to the research work of breeders (Booth et al., 2005). Quality-related traits play an important role in expanding the cultivation of rape seed (Rameah et al., 2003). The usefulness and quality characteristics of seed oils are determined by the proportion of their main constituent fatty acids (Mcvetty et al., 2016). Consequently, one of the most important objectives in Brassica breeding is the genetic modification of seed oil by maximizing the proportion of specific fatty acids (Dar et al., 2010). Brassica oil is considered beneficial from a health point of view. It contains linoleic acid, which is desirable for nutritional purposes and oleic acid, which makes it desirable for cooking oil (Turi et al., 2010). High oleic acid oil tastes better and may also have health benefits. The oxidative stability of this fatty acid also makes it suitable for some industrial applications (Scarth & Mcvetty, 1999). Nevertheless, Brassica oil is characterized by significant amounts of erucic acid (about 50% of the total fatty acids), which is absent in any other commercial plant oils (Sharafi et al., 2015). Whereas, erucic acid in the oil is one of the most undesirable components associated with Brassica spp. High levels of erucic acid in rapeseeds produce fatty deposits in the heart, skeletal muscles, and adrenal glands of rodents and impeding growth (Afrin et al., 2011). On the other hand, high erucic acid oil is a valuable and renewable raw material used in the manufacture of many industrial products. Erucamide, a derivative of erucic acid is used as an anti-block and slip promoting agent in the production of plastic film (Suchindra & Singh, 2006). Linolenic acid is one of two essential fatty acids that are necessary for health and can only be acquired through diet. However, higher levels of linolenic acids in the oils are inappropriate for human usage because of the unstable oxidative nature of the fatty acids which disturb the flavor and quality of the oil, therefore lower levels of linolenic acid in edible oil are desirable (Gami & Chauhan, 2014).

Brassica napus is an especially self-pollinated crop, often outcrossing. The qualitative traits must be improved by the implementation of heterosis breeding (Ali et al., 2014). In breeding programs, the most prevalent tool is gene action, which is used to analyze the combining ability of parents along with F1 hybrids, to identify the most aggressive genotype to be utilized as an F1 hybrid or a way to find further improvements in rapeseed (Sabaghnia et al., 2010). Combining ability studies the predominant effect of GCA on production and attributes (Kang et al., 2013).

Due to these constraints, the present study was intended to boost the oil value responsible traits in *Brassica napus*. Existing studies were designed to expand the genetic potential and oil quality of *Brassica napus*. This study will create breeding measures and scientific evidence on breeding outlines, heritability and combining ability indexes to frame out upcoming selection strategies for the improvement of qualitative traits. Further, for developing better genotypes through intercrossing, the selection of reliable parents is of great concern to the breeders.

Keeping these points in view the experiment was designed to (1) analyze the qualitative traits under Near Infrared Reflectance Spectroscopy (NIRS) of diallel crossed *Brassica napus* genotypes, (2) estimate the combining ability and inbreeding depression among parental material (3) to find out the SCA and RCA of different intercrossed parents and (4) to evaluate the heterosis (mid parent and high parent) of different cross combinations of *Brassica napus* L. varieties and identify the best general combiner on the basis of quality and other attributes to be used in future breeding programs.

2. Material and Methods

The experiments related to *Brassica napus* L. were carried out at the Bacha Khan Agriculture Research Farm (BARF) Charsadda (34°08′11.6″N 71°50′17.5″E / 34.136556°N 71.838194°E) during 2017-2019. The experimental material consisted of five rapeseed genotypes i.e., Accession 2702, DUNCLED, P1-801, P1-119 and Accession 2722. Parental material was sown under field conditions in December 2017. During January and February 2018 at the time of flowering hybridization through emasculation and controlled pollination was carried out in 5×5 full diallel fashion. Sowing of the experimental material, which included of F1 hybrid seed resulting from intercrosses among these five varieties, including self, direct and reciprocals was carried out in a randomized complete block design (RCBD) having two replications during 2018-2019 sowing season at BARF Charsadda. At the maturity stage, five plants of each genotype from each plot were randomly chosen to record data on parents and F1 plants for different qualitative *parameters*.

3. 2.1 Measurement of qualitative traits

The erucic acid, glucosinolate, moisture content, oil content, protein content, oleic acid and linoleic acid content were determined by using Near Infrared Reflectance Spectroscopy (NIRS). The samples were kept in the ring cup which had a seed volume of 5g. Trials were looked over on a monochromator that was prepared with a sample autochanger. The measures were conceded with Infra Soft International (ISI) software, as determined by Anonymous, 1998.

2.2 Analytical protocol

The investigational records were exposed to the analysis of variance (ANOVA) applicable for RCB design using the statistical software DIAL-98. Having a significant F-value, the data were further exposed to diallel analysis, using the Griffing, (1956) model (fixed effect). The estimation of heritability was studied according to (Weber & Moorthy, 1952). Measurements for heritability: Broad sense heritability (Additive GA) and Narrow sense heritability (Non-additive GA). Inbreeding depression (ID) was premeditated by the following procedure (Haldane, 1948).

$$ID\% = [S_p - S_i] \times 100 / S_p$$

Where, S_p = Average mean of parent, and
S_i = Average mean of self's.

Heterosis (Falconer & Mackey, 1996) was calculated by using the following formula;

$$BP\ heterosis = F1 - BP / BP \times 100$$

Whereas F_1 and BP are the mean of F1 progenies and better parent in all replications.

4. Results and Discussion

3.1 Mean performance of qualitative traits

Brassica *napus* L. parents along with hybrids publicized non-significant and highly significant effects for different traits (Table 1). Erucic acid exhibited non-significant results for both parents and crosses. Contrary to our findings, Bashir et al. (2013) found significant differences among the genotypes evaluated for Erucic acid. Genotype DUNCLED showed maximum (55.6%) mean performance (Table 2) followed by P1-119 (47.3%), while 2722 revealed minimum mean value (41.8%), On the other hand for the same trait cross 2702×P1-801 indicated a maximum (59.4%) mean performance and 2702×P1-119 exhibited minimum (40.4%) value. Also, non-significant results were found for glucosinolate, our results are in contradiction to the findings of Khulbe et al. (2000), who revealed significant differences for glucosinolate. Maximum and minimum mean values were found for genotype 2702 (94.6%) and DUNCLED (61.3%), however, cross P1-119×2722 revealed maximum (91.7%) mean value and 2702×DUNCLED showed the lowest (43.7%) mean value for glucosinolate. Moisture content was also conveyed non-significant differences among genotypes and crosses, the highest and lowest moisture content revealed for genotype P1-801 (6.4%) and DUNCLED (5.5%), whereas for crosses maximum and minimum moisture content were exhibited for 2702×DUNCLED (7.1%) and 2702×2722 (6.1%), respectively. Highly significant differences were reported for oil content having good variation, this is in line with the findings of Sajid et al. (2008) and Bashir et al. (2013), genotype DUNCLED showed highest (51%) mean value followed by 2702 (50.6%) and minimum mean value presented for 2722 (45.6%), for the same trait DUNCLED×P1-119 revealed supreme (51.5%) and P1-801×P1-119 revealed lowest (46.9%) mean value. Protein content revealed highly significant differences among the genotypes evaluated, this is similar to the findings of Alemayehu and Becker (2005) who revealed significant differences for protein content among the cross of six inbred lines of *B.carinata*. Maximum and minimum protein content was presented for genotype 2702 (23.7%) and DUNCLED (21.5%), respectively 2702×P1-801 and 2702×2722 showed similar maximum (24.1%) protein content, despite the fact P1-801×P1-119 showed the poorest mean (21%) value for protein content. Highly significant differences were expressed for oleic acid (Bashir et la., 2013), all-out result was presented for genotype 2702 (54.1%) and least for DUNCLED (45%), conversely for crosses maximum mean value reported for 2702×DUNCLED (55.9%), while minimum mean value exposed for DUNCLED×P1-801 (46.2%). At the last highly significant mean value was observed for linoleic acid having the range 11% (P1-119) to 9.7% (2702), respectively. On the other hand, DUNCLED×P1-801 was considered the highest (11.1%) mean performer, while the lowest (8.5%) mean value was shown by 2702×DUNCLED. The earlier finding of *Brassica napus* quality traits both significant and non-significant differences was studied by Khan et al. *(*2010) and Fayyaz & Afzal, (2014)

3.2 Estimates of GCA of several Qualitative characters

Highly significant variation for GCA was considered among the genotypes for different

Table 1. Mean squares of Statistical ANOVA of different traits in a 5×5 diallel cross of Brassica Napus L.

SOV	D.F	EA	GSL	MC	OC	PC	OA	LA
Reps	1	29.26	0.90	0.708	11.022	4.84	0.09	0.320
Crosses	24	50.62	450.18	0.242	8.166**	6.22**	19.66**	1.495**
Error	24	32.77	242.29	0.165	2.495	2.32	6.91	0.458
CV (%)	…	12.1	19.8	6.4	3.2	7.3	5.2	6.7

Note: * , ** = significant at 0.05 and highly significant at 0.01 probability levels, respectively. EA= Erucic acid, GSL= Glucosinolate, MC= Moisture content, OC= Oil content, PC= Protein content, OA= Oleic acid and LA= Linoleic acid

Table 2. Mean performance Erucic acid , Glucosinolate content , Moisture content , Oil content , Protein Content , Oleic acid and Linoleic acid of five parents and diallel crosses.

S. No	Parents and Crosses	EA (%)	GSL (%)	MC (%)	OC (%)	PC (%)	OA (%)	LA (%)
1	2702	42.9	94.6*	6.3	50.6	23.7	54.1*	9.7
2	DUNCLED	55.6	61.3	5.5	51.0	21.5	45.0	10.3
3	P1-801	46.3	62.9	6.4	48.8	20.5	50.0	10.9
4	P1-119	47.3	91.5*	6.0	47.2	19.3	48.9	11.0*
5	2722	41.8	85.3	6.1	45.6	18.6	52.7	10.1
6	2702×DUNCLED	42.7	43.7	7.1*	50.7	23.2	55.9	8.5
7	2702×P1-801	59.4*	83.7	6.7	50.8	24.1**	46.5	9.5
8	2702×P1-119	40.4	66.5	6.5	51.0	23.0	54.2	10.0
9	2702×2722	53.7	78.4	6.1	51.2*	24.1**	50.3	8.8
10	DUNCLED×2702	45.8	85.0	6.4	51.0*	22.7	52.4	9.2
11	DUNCLED×P1-801	50.2	83.9	6.9*	51.0*	21.7	46.2	11.1
12	DUNCLED×P1-119	50.4	85.7	6.3	51.5*	21.5	48.7	9.9
13	DUNCLED×2722	49.6	75.8	6.4	50.9*	21.4	51.1	10.1
14	P1-801×2702	46.0	83.6	6.1	48.9	21.0	52.2	10.3
15	P1-801×DUNCLED	36.0	68.1	5.8	48.8	21.2	53.3	10.4
16	P1-801×P1-119	45.6	82.5	6.8	46.9	21.0	52.6	10.7
17	P1-801×2722	50.7	74.0	6.3	46.8	20.2	49.6	9.5
18	P1-119×2702	49.9	84.0	6.3	46.3	20.5	55.2*	9.3
19	P1-119×DUNCLED	49.4	68.6	6.1	46.5	18.4	46.1	10.0
20	P1-119×P1-801	43.0	44.1	6.1	46.8	19.1	56.0*	8.3
21	P1-119×2722	48.7	91.7*	6.4	47.4	21.1	50.7	10.0
22	2722×2702	50.2	110.7*	6.3	48.0	19.8	46.9	11.7*
23	2722×DUNCLED	43.8	86.3	6.0	47.9	18.7	51.6	11.5*
24	2722×P1-801	46.6	80.3	6.6	46.4	18.3	51.4	10.6
25	2722×P1-119	50.1	89.7*	6.1	46.4	20.4	50.2	9.7

Note: * , ** = significant at 0.05 and highly significant at 0.01 probability levels, respectively qualitative parameters (i.e., OC, PC, OA and LA content) to pinpoint the outstanding parent (Table 3). Significant GCA results revealed for oil content in different genotypes, positively maximum (1.19%) GCA were reported for DUNCLED followed by 2702 (1.04%), while negative minimum GCA presented for 2722 (-1.17%) agreed with Turi et al. (2010), who also reported significant differences for oil trait. However, Sabaghnia et al. (2010) revealed highly significant differences among genotype for the same trait. For protein content, the genotype 2702 superseded significant general combiner (1.41%) tracked by DUNCLED (0.36%), whereas the poorest GCA were found for the genotype 2722 having negative (-1%) GCA. (Naseem & Farhatullah, 2013) and (Abideen et al., 2013) reported the significant results for the above protein content trait. For oleic acid content the highest non-significant GCA results were exposed by 2702 (1.21%) tracked by P1-801 (0.95%), however significantly negative GCA were bared by DUNCLED (-1.87%), similar results were studied in *Brassica napus* L. by (Shehzad et al., 2015). An essential fatty acid, linoleic acid contents were found to be non-significant among different genotypes with maximum GCA revealed for 2722 (0.36%) followed by DUNCLED (0.07%), while negative GCA was reported for P1-119 (-0.28%), hence proving to be a poor combiner. The above results were in agreement with Shehzad et al. (2015) and Naseem & Farhatullah, (2013). General combing ability analysis revealed that parental lines Duncled and 2702 are good general combiners hence can be used as a heterotic group for the mentioned traits.

3.4 Estimations of SCA for various qualitative characters

The differences among SCA for 10 *Brassica napus* genotypes resulted from diallel fashion was shown in (Table 4). The most desirable trait oil content in rapeseed showed non-significant SCA for different combinations, genotype 2702×DUNCLED revealed positive high SCA (0.78) followed by P1-119×2722 (0.70), whereas the negative and poor SCA was reported for 2702×P1-119 (-1.69), Turi et al. (2010) also revealed desirable maximum SCA for said trait. Sabaghnia et al. (2010) and Ahmad et al. (2012) also reported related significant observations. Protein content are the most promising trait in *Brassica napus* L., the highest SCA were shown by the combination of P1-119×2722 (1.83) trailed by DUNCLED×P1-801 (0.72), whereas the poorest negative combination was observed DUNCLED×P1-119 (-1.59). Ahmad et al. (2012) and Shehzad et al. (2015) supported our findings. For oleic acid contents P1-801×P1-119 showed significant and high (4.17) SCA, followed by DUNCLED×P1-801 (3.19), however the poorest and highly significant (-5.29) SCA effects were studied for 2702×2722. Similar findings were observed by Abideen et al. (2013). For linoleic acid contents, promising (1.3) SCA effect and highly significant alterations were studied for 2702×2722, although negatively poor (-1.68) SCA with highly significance effects were revealed for P1-801×P1-119, these findings are in agreement with Naseem & Farhatullah, (2013).

Hence it is evident from the study that those parental lines which are good general combiners also used to be involved in

Table 3. Estimates of components of variance due to GCA in 5×5 diallel crosses of *Brassica napus* L.

Parents	OC	PC	OA	LA
2702	1.04	1.41*	1.21	-0.18
DUNCLED	1.19*	0.36	-1.87*	0.07
P1-801	0.05	-0.11	0.95	0.02
P1-119	-1.10*	-0.65	-0.15	-0.28
2722	-1.17*	-1.00	-0.13	0.36

Note: * and ** significant at 0.05 and 0.01 probability levels.

Table 4. Estimates of components of variance due to SCA in 5×5 diallel crosses of *Brassica napus* L.

Crosses	OC	PC	OA	LA
2702×DUNCLED	0.78	0.71	2.01	-0.85
2702×P1-801	-0.20	-0.53	-0.98	0.27
2702×P1-119	-1.69	-0.54	3.09	-0.42
2702×2722	0.11	-0.86	-5.28**	1.3**
DUNCLED×P1-801	-0.40	0.72	3.19	0.14
DUNCLED×P1-119	-1.57	-1.59	-2.96	-0.03
DUNCLED×2722	-0.12	-0.91	2.49	0.90
P1-801×P1-119	-0.18	-0.35	4.17*	-1.68**
P1-801×2722	-0.53	-0.87	-0.52	0.03
P1-119×2722	0.70	1.83	-0.55	-0.54

Table 5. Estimates of components of variance due to RCA in 5×5 diallel crosses of *Brassica napus* L.

Crosses	OC	PC	OA	LA
DUNCLED×2702	2.4**	1.3**	-0.5**	0.4*
P1-801×2702	1.6**	2.2**	1.7*	-1.5**
P1-801×DUNCLED	1.5**	1.3*	-0.2	-0.7**
P1-119×2702	-0.2	0.3	1.7*	-0.4
P1-119×DUNCLED	0.9*	1.6**	-2.8**	-0.4*
P1-119×P1-801	1.1*	0.3	-3.6**	0.3
2722×2702	1.6**	2.2**	1.7*	-1.5**
2722×DUNCLED	1.5**	1.3*	-0.2	-0.7**
2722×P1-801	0.2	0.9*	-0.9	-0.5*
2722×P1-119	0.5	0.4	0.2	0.1

development of superior crosses, as majority of the superior crossed involved parents having good general combining ability.

3.5 Estimations of RCA for various qualitative parameters

Reciprocal combining ability for 10 *Brassica napus* genotypes resulted from diallel fashion was shown in (Table 5). The most promising trait, oil content mostly showed significant and highly significant differences for all crosses. For oil content, the best (2.4) reciprocal combination was recorded for DUNCLED×2702, while the negatively lowest (-0.2) combination was reported for P1-119×2702. Yadav et al., (2009) and Turi et al., (2010) also revealed desirable maximum RCA for mentioned trait and also reported the highly significant differences among different crosses. Protein content is the most demanding trait in *Brassica napus* L., the highly significant maximum (2.2) RCA were shown by two combinations of P1-801×2702 and 2722×2702, whereas the weak combination was observed for two different combinations i.e., P1-119×2702 and P1-119×P1-801 having the value of (0.3). Turi et al., (2010) supported our findings related to oleic acid content, in which the significant maximum (1.7) RCA were recorded for three different crosses i.e., P1-801×2702, P1-119×2702 and 2722×2702, whereas the poor (-3.6) highly significant RCA was revealed by P1-119×P1-801. Effects were supported by Shehzad et al., (2015), while Turi et al., (2010) reported non-significant differences for oleic acid content. For LA contents, maximum (0.4) RCA effect and significant alterations were studied for DUNCLED×2702, although negatively poor (-1.5) RCA with highly significant effects were revealed for P1-801×2702 and 27722×2702, these findings are in agreement with Shehzad et al., (2015). Hence the performance of the reciprocal crosses also proved our previous analysis regarding the parental lines, as for majority of traits superior parental lines are involved in the production of superior reciprocal crosses as well.

3.6 Heritability and gene action

The heritability and gene action of qualitative traits are shown in table 6. The studied traits revealed higher phenotypic variance than genetic variance, which indicates environmental effects on the phenotypic expression of these traits. It was clear from the results that for all traits (OC, PC, OA and LA) there was low broad sense heritability and non-additive gene action. Results for quality traits are in agreement with Gosh & Gulati, (2011) and Chauhan et al., (2002). Contrary to our findings Kumar and Misra (2007) revealed high heritability for different qualitative traits. A trait having high heritability and high genetic advance is considered under the control of additive genes which highlights the usefulness of plant selection based on phenotypic performance.

3.7 Appraisal of mid-parent heterosis and heterobeltiosis

The negative estimation of heterosis (mid/best) is desirable for erucic acid because it is the most unattractive constituent in *Brassica napus* L. Appreciable negative -13.3 mid-parent heterosis (Ali et al., 2015) (Table 7) were observed for 2702×DUNCLED and unwanted positive (33.3) mid parent heterosis was studied for 2702×P1-801. Conversely, the promising negative (-23.3) heterobeltiosis was recorded by 2702×DUNCLED and undesirable maximum positive (28.3) heterobeltiosis was recorded for 2702×P1-801. To achieve the genotypes having less glucosinolate, the negative heterosis results could be used to accomplish the goal. Attractive negative (-43.9) heterosis over mid parent heterosis for glucosinolate were achieved by 2702×DUNCLED and unattractive positive (35.1) mid parent heterosis was perceived for DUNCLED×P1-801, although looked-for negative (-53.8) heterobeltiosis (Ali et al., 2015) was achieved by 2702×DUNCLED and unwanted positive

Table 6. Estimation of heritability and gene action of quality related traits of 5×5 diallel crosses of *Brassica napus* L.

Attributes	h^2B	h^2N	σ^2A	σ^2D	σ^2P
Erucic acid	0.19	0	o	9.57	47.9
Glucosinolate	0.15	0.13	47.2	9.54	361.6
Moisture content	0.05	0.004	0.0009	0.01	0.20
Oil content	0.38	0.38	2.60	0	7.60
Protein content	0.32	0.32	1.7	0	5.4
Oleic acid	0.40	0	0	6.1	15.2
Linoleic acid	0.20	0	0	0.21	1.05

Table 7. Heterotic manifestation of quality traits of *Brassica napus* L.

Traits	Erucic acid content (%)		Glucosinolate content (%)		Moisture content (%)		Oil content (%)	
Crosses	MP	BP	MP	BP	MP	BP	MP	BP
2702×DUNCLED	-13.3	-23.3	-43.9	-53.8	20.3	12.7	-0.3	-0.8
2702×P1-801	33.3	28.3	6.3	-11.5	5.1	4.3	2.2	0.3
2702×P1-119	-10.4	-14.6	-28.5	-27.3	6.1	3.6	4.3	0.8
2702×2722	26.9	25.3	-12.8	-8.1	-1.0	-2.8	6.5	1.2
DUNCLED×P1-801	-1.5	-9.7	35.1	33.3	16.4	8.2	2.2	0.0
DUNCLED×P1-119	-2.1	-9.5	12.2	-6.4	9.6	5.0	4.8	0.8
DUNCLED×2722	1.9	-10.8	3.5	23.8	10.6	5.3	5.3	-0.3
P1-801×P1-119	-2.5	-3.5	6.8	-9.9	8.9	5.5	-2.3	-3.9
P1-801×2722	15.0	9.4	-0.1	-13.2	0.2	-2.3	-0.7	-4.0
P1-119×2722	9.4	3.1	3.7	0.1	5.2	4.5	2.2	0.5

Table 8. Heterotic manifestation of quality traits of *Brassica napus* L.

Traits	Protein content (%)		Oleic acid content (%)		Linoleic acid content (%)	
Crosses	MP	BP	MP	BP	MP	BP
2702×DUNCLED	2.9	-1.8	12.9	3.4	-14.8	-17.3
2702×P1-801	9.1	1.9	-10.6	-13.9	-7.8	-12.9
2702×P1-119	7.1	-2.9	5.4	0.3	-2.7	-8.4
2702×2722	14.1	2.0	-5.9	-7.0	-11.2	-12.9
DUNCLED×P1-801	3.5	1.2	-2.7	-7.6	5.2	2.3
DUNCLED×P1-119	5.5	0.0	3.7	-0.5	-6.6	-9.6
DUNCLED×2722	6.5	-0.6	4.6	-3.1	-0.2	-1.2
P1-801×P1-119	5.7	2.4	6.4	5.2	-2.3	-2.7
P1-801×2722	2.9	-1.8	-3.4	-5.9	-8.9	-12.2
P1-119×2722	11.6	9.7	-0.2	-3.9	-4.8	-8.7

Table 9. Inbreeding depression values of qualitative traits of *Brassica napus* L.

Traits	Genotypes				
	2702	DUNCLED	P1-801	P1-119	2722
Erucic acid	8.2	10.4	5.5	7.9	2.4
Glucosinolate	-3.2	12.5	-2.1	-0.8	-11.1
Moisture content	1.6	-12.2	-20.8	4.8	6.5
Oil content	11.7	6.9	4.4	4.5	0.9
Protein content	-2.4	2.4	4.5	18.8	13.8
Oleic acid	3	6	7	15.7	15.5
Linoleic acid	16.1	4.2	20.2	22.9	20.2

(33.3) heterobeltiosis were attained by DUNCLED×P1-801.

Heterosis for moisture content also needed to be negative because more than 15% moisture can degrade the seed quality. Appropriate negative (-1) mid parent heterosis was recorded for 2702×2722 and unsuitable maximum positive (20) mid parent heterosis was obtained by 2702×DUNCLED, while desirable negative (-4) heterobeltiosis were observed for P1-801×2722 and positive (1.2) recorded for 2702×2722. Positive heterosis is desired for oil content to get promising oil producing variety. Maximum (6.5) mid parent heterosis were achieved by 2702×2722 and minimum negative -2.3 (Table 7) results recorded for P1-801×P1-119, on the other hand supreme 1.2% (Shen et al., 2005) heterobeltiosis results for oil content were attained by 2702×2722 and poorest (-4) findings were evident for P1-801×2722, However the conclusions aren't in settlement with Cuthbert et al., (2011), which showed up to 9% of oil content. Positive heterosis results (Table 8) are desirable for protein proportion in *Brassica napus* L. Maximum positive (14.1) mid parent heterosis were attained by 2702×2722 (Table 16) and minimum (2.9) results were reported for P1-801×2722 as reported by (Ali et al., 2015), while highest (9.7) heterobeltiosis were accomplished by P1-119×2722 and deprived negative (-2.9) heterobeltiosis calculated for 2702×P1-119. According to table 16, for oleic acid content maximum (12.9) mid parent heterosis secured by 2702×DUNCLED and lowest negative (-10.6) results were considered for 2702×P1-801, conversely highest (5.2) heterobeltiosis were gotten by P1-801×P1-119 and lowest negative (-13.9) heterobeltiosis were analyzed for 2702×P1-801. Uppermost (5.2) heterosis over mid parent heterosis were observed for DUNCLED×P1-801 and worse (-14.9) results considered for 2702 × DUNCLED, whereas 2702 × DUNCLED achieved the highest positive (2.3) heterobeltiosis and the lowest negative -17.3 (Gami & Chauhan, 2014) heterobeltiosis were recorded for 2702×DUNCLED.

3.9 Inbreeding depression of qualitative traits of *Brassica napus* L.

In qualitative traits (Table 9), the maximum (10.4%) inbreeding depression for erucic acid was noted for DUNCLED and the minimum (2.4%) inbreeding depression for 2722. The highest (12.5%) glucosinolate, inbreeding depression were recorded for DUNCLED, whereas the lowest (-11.1%) inbreeding depression was studied for 2722.

For moisture content, maximum (6.5%) and minimum (-20.8%) inbreeding depressions were recorded for 2722 and P1-801. As far as oil content is concerned, highest (11.7%) inbreeding depression was studied for 2702, while negligible (0.9%) inbreeding depression was reported for 2722. The highest (18.8%) protein content inbreeding depression was recorded for P1-119, on the other hand inferior (-2.4%) inbreeding depression were studied for 2702. The highest (15.7%) and lowest (3%) inbreeding depression for oleic acid content was noted for P1-119 and 2702, respectively. When linoleic acid was taken in to consideration maximum and minimum inbreeding depression was evident for P1-119 (22.9%) and DUNCLED (4.2%), respectively.

5. Conclusion

It was concluded from the results of diallel crosses of *Brassica napus* L. genotypes. That among all the parents 2702 were recognized as the superlative general combiner for PC and LA content, while got the average position in other traits. Afterward the best specific combiner 2702×DUNCLED was noted for oil content, while 2702×2722 were recognized as best specific cross for linoleic acid. DUNCLED×2702 was reported as the best reciprocal cross for oil content and linoleic acid, conversely P1-801×27022 was recoded as the best reciprocal cross for protein content and oleic acid content. However, DUNCLED×P1-801 showed average performance for all the qualitative traits. All qualitative traits had broad sense heritability and non-additive gene action, which indicates late generation selection for further improvement. For the heterotic study, 2702×DUNCLED revealed the wanted positive oleic acid and preferred negative mid and best parent heterosis for erucic acid, glucosinolate and moisture content. Regarding protein and oil content the favorable crossed combination was 2702×2722, which gave the positive mid and best parent heterosis. Inbreeding depression for qualitative traits ranged from -20.8% to 22.9%. It was concluded from the studies that among all the genotypes 2702 was the best general and specific combination along with the best parent heterosis with DUNCLED, P1-119 and 2722 for all the traits.

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M.A.S., and S.M.R., conceived the main idea. M.A.S., F.U.R., H.A., O.Y and F.U., designed the experiment, wrote the manuscript. All authors helped in data collection, data analysis and revising manuscript. The Author (s) read and approved the final manuscript.

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