

Exploring Genetic Variation in *Brassica rapa* for Improved Yield and Fatty Acid Profiles

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ABSTRACT

Brassica rapa is one of the most widely cultivated oilseed crop and is known for a variety of benefits across the globe. *Brassica rapa* is one of the key *Brassica* species. Together with significant oil concentrations, it is distinguished by a high concentration of macro and micro nutrients. Oilseed rape cultivars has high amount of erucic acid and glucosinolate which may increase health risks. The current study was carried out in 2021 in the research area of the department of Plant Breeding and Genetics at University of Agriculture, Faisalabad. The goal of the experiment was to find *Brassica rapa* accessions with improved yield and fatty acid-related characteristics from the germplasm by screening and choosing them. One hundred accessions of *B. rapa* were screened for better yield and fatty acid-related traits in a randomized complete block design. Data were obtained for many morphological and fatty acid-related characteristics. Analysis of variance, mean comparison, correlation, and principal component analysis were performed on the recorded data. Three testers; 26240, 26283, 26215 and ten lines; 28244, 40961, 40970, 40975, 40977, 40978, 40979, 40980, 40981 and 40982 were selected on mean performance basis. The highest mean value was shown by 40975, and 40977 lines for most of the traits. The findings demonstrated that there was significant genetic variation in the oil content and mix of fatty acids across the species under study. This suggests that the oil extracted from the seeds of these lines may be appropriate for both industrial and human use. The selected accessions should be further assessed for various yield and fatty acid-related traits to modify their value for edible purposes. They may also be utilized as a favorable germplasm in the breeding program.

Keywords: *Brassica rapa* accessions; screening; Correlation coefficient analysis, Erucic acid; Principal component analysis

INTRODUCTION

During 2022–2023, more than 200 million metric tons of vegetable oil was produced worldwide. Canola oil, sometimes referred to as rapeseed oil, is one of the most commonly used cooking oils [1]. The fourth-largest importer of edible oil is Pakistan [2]. To meet domestic demand, 75% of the edible oil used in Pakistan is imported. In 2021, 2.917 million tons of edible oil worth Rs. 662.657 billion was imported. A tentative estimate of 0.374

million tons of edible oil was produced locally during this time. Rapeseed and Mustard was cultivated on 2.22 mha that is reduced from 3.53 mha [3]. There was also decline in the production of edible oil while consumption kept increasing. This condition is becoming worse so, there is need to narrow down this gap between import and local production [4]. The study of genetic variability of new accessions of a crop species and screening of best genotypes for higher yield is the main objective of plant breeders. Screening on the basis of various quantitative and qualitative parameters provides clear image of diverse genotypes. The diversity of plant genetic resources is imperative for crop improvement and information on these reservoir can contribute to the pace of improvement [5]. The main factors influencing the success of any crop improvement programme are genetic changes, heritability, and variability during the selection stage [6]. Yield and fatty acids are quantitative traits so, interrelationship of various traits with yield and fatty acid should be determined [7, 8]. Correlation coefficient analysis was the method used

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since seed yield is a complex characteristic that can be determined by a number of factors showing a positive or negative effect upon this trait [9]. The component qualities of trait association have higher heritability and simpler inheritance, they are an important tool for yield improvement.

Thus, the goal of the current study was to screen for trait relationships among specific traits. In order to find appropriate lines, screening of the available germplasm under field conditions is required [10]. Given the significance of yield and the scarcity of edible oil in the nation, the main focus of this research was shifted to screen *Brassica rapa* in the field for characteristics related to yield and fatty acids.

MATERIAL AND METHODS

Collection of Germplasm

One hundred and fifty *Brassica* (*Brassica rapa* L.) accessions were collected from National Agricultural Research Center, Islamabad.

Screening of Germplasm

In the Department of Plant Breeding and Genetics at the University of Agriculture, Faisalabad, an experiment was conducted in 2019. The procured germplasm were evaluated in the field for different yield and quality related traits. A Randomized Complete Block Design with three replications was used to set up the experiment. The data was recorded for different quantitative and qualitative traits. The following characteristics were examined; No. of aborted siliques/plant, the No. of primary and secondary branches/plant, the No. of siliques /plant, the No. of seeds/silique, seeds yield/plant, and the 100 seed weight.

Bio-chemical Analysis of Seed for Fatty Acid Compositions

Following the manufacturer's instructions, all seed samples were analyzed using an NIR (Near Infra-Red) spectroscopy equipment FOSS 6500 outfitted with Infra Soft International's ISI version 1.02a software to ascertain the fatty acid contents of the collected *Brassica rapa* accessions. The seeds of each accession were pulverized in a blender after being dried in a vented oven at 40°C for four hours, resulting in a 5% moisture content for each replication. Using petroleum ether as a solvent for six hours, five grams of crushed seeds were extracted for oil using the Soxhlet equipment, following the AOCS method. Using petroleum ether as a solvent for six hours, five grams of crushed seeds were extracted for oil using the Soxhlet equipment, following the AOCS method [11, 12] and then oil content percentage was calculated for each sample. The presence of oil, protein, glucosinolate contents, and erucic acid contents were recorded among quality-related attributes in accordance with the guidelines provided by the International Board for Plant Genetic Resources

(IBPGR) and the ICRISAT descriptor list for *Brassica rapa*.

Statistical Analysis

ANOVA was conducted on the recorded data after [13] mean comparison for yield and fatty acid related traits and principle component analysis for yield and quality related traits to screen the tested accessions followed by [14], principal component analysis. The variance and covariance components were used to conduct the correlation coefficient analysis [15, 16, 17].

RESULTS AND DISCUSSION

Screening of Germplasm

There were notable variations observed between the accessions for each characteristic listed in (Table 1). All the accessions were found to be highly significant, different from each other for entire the yield and fatty acid related traits. It suggests that these genetic differences among the accessions for all traits can be exploited in next breeding program. Our findings coincide with those of Jan et al. (2017), who identified various genotypes of *Brassica rapa* L. for quantitative agro morphological features. It was proposed that morphological variations have an important role in the development of novel, promising genotypes [18, 19, 20, 21, 22, 23, 24].

Mean Comparisons of Yield and Quality Traits in *Brassica rapa* Accessions

Mean performance of accessions, and check cultivar is presented in Table 2. Mean performance for all the accessions of *Brassica rapa* were observed for different yield and fatty acid related traits. Range of days to flower initiation was observed from 57 to 91. The accession 28244 showed minimum days to flower initiation (57). While accession 26177 showed maximum days to flower initiation (91). Mean performance for days to flower completion ranged from 70 to 126.

Maximum days to flower completion were shown by the accession 28242 (126) while accession 40982 showed minimum days to flower completion (70). Mean performance of days to silique formation of some accessions were least as compared to check cultivar and it ranged from 80 to 120 and 90, respectively. Maximum days to silique formation were observed in accession 26155 (120) while accession 40970 showed minimum days to silique formation (80). Range of number of aborted silique per plant in accession was 3 to 5. Accessions 40980 and 40982 had minimum number of aborted silique per plant (3) while accession 28213 showed maximum number of aborted silique per plant (5).

Table 1. Analysis of Variance of accessions from 26155 to 41001 for yield and quality traits

SOV	DF	FID	FC D	SF D	ASPP	PH	PBPP	SBPP	SPP	SS	HSW	YPP		FID	FCD	SFD
Genotypes	150	751.51**	858.95**	15.28**	0.558	2519.25**	30.26**	71.93**	1666.10**	545.31**	626.17**	0.208**	26.828**	6.87**	409.70**	20.51**
Replications	2	1.39	1.23	1.95	0.113	6.32	6.33	4.292	1174.19	47.6	14.30	0.0119	29.14	4.932	17.00	48.67
Error	300	24.16	31.30	6.038	0.454	94.59	5.58	6.303	144.16	202.2	19.01	0.096	13.038	4.371	194.86	11.63

***= Highly, highly Significant at 0.001, SOV= Sources of variation, DF= Degrees of freedom, FID = Flower initiation days, FC = Flower completion days, SFD = Silique formation days, ASPP= No. of aborted silique per plant, PH= Plant height, PBPP= Primary branches per plant, SBPP= Secondary branches per plant, SPP= Silique per plant, SS = Seed/silique, HSW = One hundred seed weight, YPP = Yield/ plant, OP= Oil percentage, PP, Protein percentage, Glu= Glucosinolate percentage and EAP= Erucic acid percentage.

Table 2. Mean performance of accessions from 26155 to 41001 for yield and quality traits

Accessions Range	FID	FC D	SF D	ASPP	PH	PBPP	SBPP	SPP	SS	HSW	YPP	OP	PP	Glu. P	EAP
Accessions	26177	28242	26155	28213	26156	40978	40978	40982	40977	40977	40982	40981	26241	26287	26262
Maximum value	91	126	120	5	137 cm	25	8	7	46	12.9 g	578 g	51.3 %	33.9 %	97.3 %	50.3 %
Accessions	28244	40982	40970	40980 40982	40977	26172	26162	40977	26158	26166	40966	28206	26487	40982	28212
Minimum value	57	70	80	3	79 cm	8	2	5	19	5.9 g	168 g	37%	19.9 %	9.4 %	37%

FID = Flower initiation days, FC = Flower completion days, SFD = Silique formation days, ASPP= No. of aborted silique per plant, PH= Plant height, PBPP= Primary branches per plant, SBPP= Secondary branches per plant, SPP= Silique per plant, SS = Seed/silique, HSW = One hundred seed weight, YPP = Yield/ plant, OP= Oil percentage, PP, Protein percentage, Glu= Glucosinolate percentage and EAP= Erucic acid percentage.

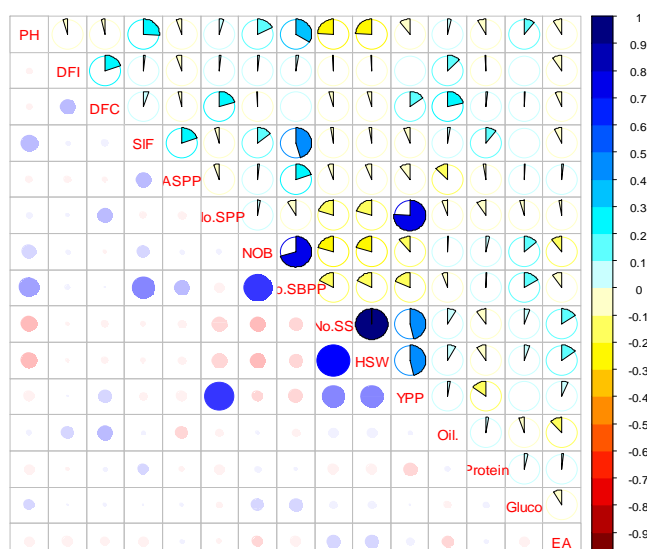


Figure 1. Correlation plot among the tested germplasm accessions for yield and fatty acid traits.

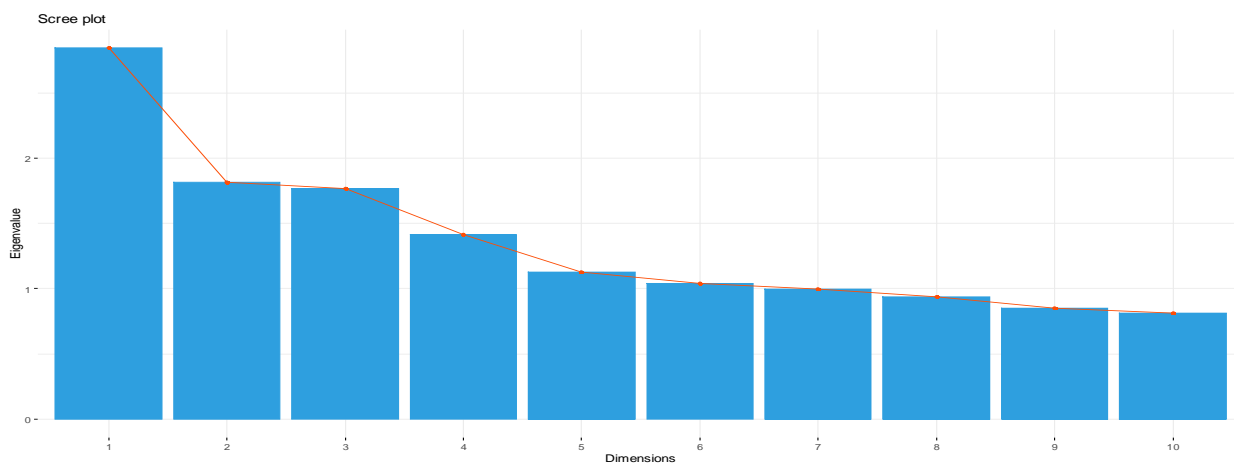


Figure 2. Screen plot for tested germplasm for yield and fatty acid traits.

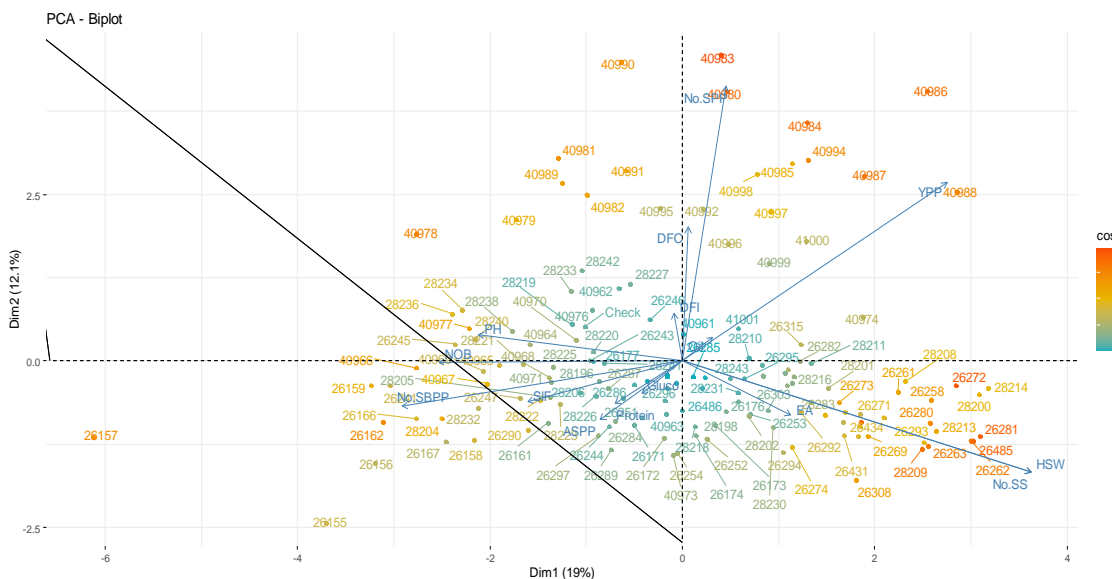


Figure 3. PCA of yield and quality traits in tested germplasm accessions.

Mean performance for plant height ranged from 79 cm to 137 cm. Maximum plant height was shown by accession 26156 while accession 40977 had shown the minimum value. Mean performance of the accessions for number of primary branches per plant was observed and it ranged from 8 to 25. The accession 40978 had the maximum number of primary branches per plant (25) while accession 26172 had minimum number of primary branches per plant (8) than the check cultivar. Mean performance of accessions for secondary branches per plant was observed. Accession 40978 had maximum number of secondary branches per plant (8) followed by 26162 (2). Mean performance of accession number of silique per plant was from 5 to 7 and 4 respectively. Accession 40977 had minimum number of silique per plant (5) while accession 40982 had maximum number of silique per plant (7). Range of accessions and check cultivar for number of seeds per silique was observed from 19 to 46. Maximum number of seeds per silique was observed in accession 40977 (46) while minimum number of seeds per silique was showed by accession 26158 (19). Range of accessions for number of hundred seed weight was from 5.9 g to 12.9 g and 5.9 g, respectively. The minimum mean performance was observed in accession 26166 while accession 40977 showed maximum hundred seed weight (12.9 g). Range of yield per plant 168 g to 578 g in accessions were observed and accession 40982 had maximum yield per plant (578 g) while 40966 showed minimum yield per plant (168 g) followed by 256 g of check cultivar. Mean performance of accessions and check cultivar for oil content was observed from 32.6% to 51.3% respectively. Accession 40981 showed maximum oil contents 51.3% while 28206 showed minimum oil content (37%). Accession 26241 had maximum protein content (33.9%) while 26487 showed minimum protein content (19.9%) followed by 25.8% of check cultivar. Glucosinolate contents decreased as compared to check cultivar range from 9.4% to 97.3%, respectively. Maximum glucosinolate contents were observed in 26287 (97.3%) while minimum in 40982 (9.4%). Mean performance of erucic acid content ranged from 37% to 50.3%, respectively. Accession 26262 had maximum erucic acid percentage (50.3%) while 28212 showed minimum erucic acid percentage (37%) followed by 43.2% of check cultivar.

Correlation Coefficient Analysis of Accessions from 26155 to 41001 for Yield and Quality Traits

A measure of the relationship between two variables is correlation. A correlation plot displays the association between all yield and fatty acid-related characteristics together (Fig. 1). There is significant high positive correlation of No. of silique/plant and

yield/plant, No. of branches/plant and No. of secondary branches/plant and No. of silique/plant and yield per plant, hundred seed weight and yield/plant. There is significant medium positive correlation of No. of secondary branches per plant, days to silique formation, No. of branches per plant and glucosinolate percentage with plant height, days to flower completion and oil percentage, days- silique formation and No. of secondary branches/plant. There is a significant high negative correlation of plant height with days to flower initiation, days- flower completion, No. of seed/silique and yield/plant, days-silique formation with yield/plant, No. of aborted silique/plant with yield/plant and protein percentage with yield/plant. Similar results were also observed by Islam et al., (2016) [25], in their study with twenty one F9 populations derived from inter-varietal crosses of *Brassica rapa* L. and Khan et al., (2013), during correlation and path co-efficient analysis using twenty genotypes to partition the cause and effect relationship into direct and indirect components in *Brassica napus* [26].

Principle Component Analysis (PCA) of Accessions from 26155 to 41001 for Yield and Quality Traits

All the principal components 1, 2, 3, 4, 5, 6, 7 and 8 showed Eigen value of greater than 1 i.e. significant while factor 8, 9 and 10 showed non-significant or less than 1 Eigen value. The contribution of PC1 to total variation for the trait under study showed different cumulative variability. (Fig. 3, 4) Shows accessions 26285, 40961, 41001, 28210, 26315, 26282, 28211, 40974, 40999 and 40996 falls in Quadrant III used as lines in the proceeding experiment. Accessions 28241, 26296 and 26287 used as testers as these were poor performing in Quadrant I. Current findings got support from past results about principal component analysis. Many breeders used principal component analysis for selection of various yield related traits [26, 27, 28]. All the studied accessions showed a vast range of variation for yield and fatty acid related traits. This could serve as major criteria for selection of promising *B. rapa* accessions for future. Our results were also supported by the past findings of [29] and [30], who described that genotypes with high variation for different yield and oil related traits were grouped together. Our findings were also in line with past findings of Choudhary et al., (2001) [31]. Results are also supported by the findings of Balkaya et al., 2005 and Mahendra et al., 2021 [32, 33 and 34] who reported highest positive significant correlation of seed yield and No. of silique/plant. So, it is concluded that selection based on any one of these characters either alone or in combination, would result in identification of high yielding accessions.

CONCLUSION

Selection for enhancing oil content and part of the fatty acid composition may be promising, as indicated by the significant genetic variation and high heritability for both traits. These results suggested that although accessions 28241, 26296 and 26287 showed significantly lower average oil content, accessions 26285, 40961, 41001, 28210, 26315, 26282, 28211, 40974, 40999 and 40996 might be a good source of genes to improve some fatty acid composition or other traits of rapeseed. For the purpose of improving *Brassica rapa*'s yield and fatty acid profile, genetic diversity among sources of variations can also be employed. Ten lines and three testers can be considered as possible parents for the development of breeding material based on principal component analysis for features linked to fatty acids and yield. These lines can also be further assessed under various climatic conditions to determine their value for improved oil and yield. Mean performance of accessions, and check cultivar was also observed for different yield and fatty acid related traits. Superior lines are considered as desirable selection for economic gain. This type of variability could be exploited for economic significance that could be used as a base line for future crop improvement programs.

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