# An insight in the genetic control and interrelationship of some quality traits in *Brassica napus*

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**ABSTRACT.** A study on three leading lines (KN-256, KN-257, and KN-258) of *Brassica napus* and an approved variety, Punjab-Sarson, was conducted to gain insight into the genetic control of some quality traits using generation mean analysis. Our results showed that additive gene action predominated in the inheritance of oil content and erucic acid in cross KN-256 x KN-257 and in that of glucosinolates in KN-258 x Punjab-Sarson, indicating that these traits may be improved through selection in early segregating generations. Negative dominance can be exploited through heterosis breeding for the development of lines with low glucosinolates in cross KN-256 x KN-257. Protein content and oleic acid in cross KN-256 x KN-257, and oil content, protein content, and erucic acid in cross KN-258 x Punjab-Sarson depicted non-additive gene action and require further improvement in the later segregating generations. Most of the traits displayed high heritability estimates;

 

glucosinolate content in both the crosses and erucic acid in cross KN-258 x Punjab-Sarson also displayed high genetic advance, reflecting improvement of the trait in the early segregating generations. All the quality traits were positively correlated with oil content and with one another at both (genotypic and phenotypic) levels in KN-256 x KN-257. Negative correlation was observed between glucosinolate and erucic acid, oleic acid and erucic acid, and linolenic acid and oil content in cross KN-258 x Punjab-Sarson. Thus, gene action changed with the material, and cross KN-258 x Punjab-Sarson carried favorable combinations compared to KN-256 x KN-257.

**Key words:** *Brassica napus;* Correlation coefficients; Gene action; Heritability; Quality traits

## INTRODUCTION

Pakistan has been facing severe scarcity of edible oil for the past several years. Although much progress has been made in the improvement of field crops such as wheat, rice, sugarcane, the oilseed sector has not shown improvement. There is a dearth of varieties with higher seed yield and seed oil contents. Pakistan is able only to meet 25% of its edible oil requirement and the remaining is imported thereby incurring large expenditures. In 2012-2013 (Anonymous, 2014), Pakistan spent over Rs. 200 billion on the import of edible oil. This figure is expanding at the rate of 5% every year, due to increasing population and per capita consumption (Fahimullah et al., 2013). There is a huge gap between local production and national demand. *Brassica* species, particularly those grown for their oil-rich seeds, are native to this continent and have the potential to fill this crucial gap.

Oil quality is determined by its fatty acid profile. Some important fatty acids are oleic acid, linolenic acid, and erucic acid. Oleic acid, a monounsaturated fatty acid, is known to reduce the level of blood cholesterol, which is a major cause of various heart ailments (Grundy, 1986). Oleic acid not only improves oil quality but also enhances its thermo stability. Brassica is next only to olive oil as the biggest source of oleic acid. Rapeseed oil and mustard oil also have considerable unsaturated fatty acid contents while they only have approximately 7% saturated fatty acid content - one of the lowest levels among oilseed crops. These also contain appreciable levels (20-25%) of essential fatty acids like linolenic acid. Rapeseed and mustard oils have a good ratio of omega 3-6 fatty acids to natural antioxidants, and play vital role in lowering the risk of cardiac diseases (Shyam Prakash et al., 2001).

Erucic acid, one of the undesirable fatty acids, increases blood cholesterol and disturbs myocardial activities by reducing coagulation time. Rapeseed meal after oil extraction is a source of calcium and protein; in particular, it is rich in lysine and methionine (Mailer et al., 1998). Besides these components, this meal also contains glucosinolates a sulfur-containing compound responsible for cardiac and respiratory diseases. Various oil quality characteristics are also important with respect to non-food uses of *Brassica* oil or as biodiesel (Jham et al., 2009). For edible purposes, development of varieties having high seed oil percentage, high monounsaturated fatty acid content, low polyunsaturated and very low saturated fatty acids content is required (Rakow and Raney, 2003). The main objective in *Brassica* breeding is to increase the seed oil content and improve the fatty acid profile to meet food and industrial demands.

A purposeful crop improvement program is dependent on the existence of sufficient genetic variability, heritability, correlation, and genetic gain in selection (Khan et al., 2006). Heritability not only determines the transmission of trait but also partitions the total variance into genetic and environmental components. Correlation studies among different traits are helpful in designing a breeding program envisaged for simultaneous improvement of a number of traits (Kumar, 2013). Plants having considerable variability, and high heritability coupled with genetic advance would be valuable for crop improvement (Aytac and Kinaci, 2009). The type of gene action governing a trait facilitate in choosing a breeding method for the improvement of a particular trait. The development of high yielding varieties is based on a thorough evaluation of the available genetic variability, heritability and genetic advance of the breeding material (Mahmood et al., 2003). Owing to the paramount importance of edible oil and its inadequate indigenous production, the present study was conducted to estimate genetic variability, heritability, genetic advance and genotypic and phenotypic correlation among quality parameters of some *Brassica napus* genotypes. Correlation studies have been reported for quantitative characters in *B. napus* (El-Beltagi and Mohamed, 2010) and in *B. carinata* (Belete, 2011).

## MATERIAL AND METHODS

This study was performed in the field area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, for a period of 3 years (2010-2013). The experimental material comprised of three elite lines (KN-256, KN-257, and KN-258) and one approved variety (Punjab-Sarson) of *B. napus*. Parental material was raised in pots under greenhouse conditions in December 2010. During January and February 2011, at the time of flowering, hybridization through emasculation and controlled pollination was performed in the following manner: 1) KN-256 x KN-257 and 2) KN-258 x Punjab-Sarson. Second filial generation ($F_2$), back cross one ($BC_1$) and back cross two ($BC_2$) generations were developed by sowing parent one ($P_1$), parent two ($P_2$) and first filial generation ($F_1$) seed in the field during 2011-2012. $BC_1$ and $BC_2$ were the crosses of $F_1$ with $P_1$ (KN-256) and $P_2$ (KN-257) in cross KN-256 x KN-257 and of $F_1$ with $P_1$ (KN-258) and $P_2$ (Punjab-Sarson) in cross KN-258 x Punjab-Sarson. Finally, six generations ($P_1$, $P_2$, $F_1$, $F_2$, $BC_1$, and $BC_2$) for both the crosses were developed for further study following generation mean analysis.

The six generations developed were evaluated during 2012-2013 in the field experiment. This field experiment was laid out in a triplicate randomized complete block design (RCBD). Inter-row and intra-row distances were maintained at 45 and 15 cm, respectively. Recommended doses of fertilizer (nitrogen = 28 kg, phosphorus = 28 kg, and potash = 25 kg per acre), three irrigations, and other cultural practices were applied to all the experimental units uniformly. At maturity, 10 plants each from $P_1$, $P_2$, and $F_1$ and 100 plants each from $BC_1$, $BC_2$, and $F_2$ per replication were selected for data recording on oil, protein, glucosinolate, oleic acid, linolenic acid, and erucic acid contents.

The oil, protein, and glucosinolate contents (%), and oil profile were determined using a near-infrared reflectance spectroscopy (NIRS) Foss NIRS Systems model 6500 (NIRS Systems Inc., Silver Springs, M D, USA). The samples were scanned on a mono-chromator, which is equipped with a sample auto-changer. The standard ring cup, requiring a seed volume of about 5 g, was used. The reflectance spectrum (log 1/R) from 400 to 2500 nm was recorded at 2-nm intervals for each sample. Calibration and validation procedures were performed using the ISI software, version 1a.1 (Infra Soft International) as described by Anonymous (1998).

## Biometrical approaches

The procedure described by Steel et al. (1997) was followed to perform analysis of variance using the GLM procedures of the SAS software. Heritability in the narrow sense were estimated following the method described by Warner (1952). For convenience, an arbitrary scale as given below was generated for estimating narrow sense heritability: high heritability >0.6; medium heritability = 0.4-0.6; and low heritability <0.4.

Genetic advance was calculated at 20% selection intensity (*i* = 1.4) following the method described by Poehlman and Sleeper (1995). Genetic advance was described as low, moderate, and high, according to Johnson et al. (1955), as following: low <10%; moderate 10-20%; and high >20%. Generation mean analysis was performed following the method described by Mather and Jinks (1982). Analysis of correlation in all possible combinations considering all quality traits was performed according to the method described by Kown and Torrie (1964).

# RESULTS

## Genetic variability

Table 1 depicts that $P_1$ *vs* $P_2$; $P_1$, $P_2$ *vs* $F_1$; $BC_1$ *vs* $BC_2$; $P_1$, $P_2$, $F_1$ *vs* $F_2$, $BC_1$, $BC_2$; and $F_2$ *vs* $BC_1$, $BC_2$ were highly significant for all the traits, with a few exceptions in both the crosses, i.e., $P_1$, $P_2$ *vs* $F_1$ was non-significant for linolenic acid, erucic acid, and glucosinolate content in cross KN-256 x KN-257, and $P_1$, $P_2$, $F_1$ *vs* $F_2$, $BC_1$, $BC_2$ were non-significant for oil and protein content in cross KN-258 x Punjab-Sarson (Table 1).

**Table 1.** Mean squares and their significance from analysis of variance of different quality traits in various generations of *Brassica napus* in two crosses.

| Trait | Generation | $P_1$ *vs* $P_2$ | $P_1$,$P_2$ *vs* $F_1$ | $BC_1$ *vs* $BC_2$ | $P_1$, $P_2$, $F_1$ *vs* $F_2$, $BC_1$, $BC_2$ | $F_2$ *vs* $BC_1$, $BC_2$ | Error | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | d.f. | MS |
| Cross KN-256 x KN-257 | | | | | | | | |
| Seed oil content | 10.86** | 20.39** | 0.99** | 5.39** | 13.86** | 13.67** | 154 | 0.18 |
| Oleic acid | 45.84** | 203.78** | 3.18** | 0.67** | 11.84** | 9.73** | 154 | 0.08 |
| Linolenic acid | 0.57** | 2.23** | 0.009 | 0.23** | 0.003** | 0.38 | 154 | 0.006 |
| Erucic acid | 204.15** | 678.41** | 0.26 | 149.67** | 154.10** | 38.33** | 154 | 0.56 |
| Protein content | 3.20** | 5.64* | 1.73** | 0.26** | 5.21** | 3.17** | 154 | 0.007 |
| Glucosinolate content | 71.03** | 245.76** | 0.40 | 0.08 | 101.56** | 7.38** | 154 | 1.25 |
| Cross KN-258 x Punjab-Sarson | | | | | | | | |
| Seed oil content | 4.26** | 1.19** | 0.36** | 18.61** | 0.07 | 1.08** | 154 | 0.07 |
| Oleic acid | 7.72** | 2.89** | 1.17** | 4.73** | 12.94** | 16.84** | 154 | 0.04 |
| Linolenic acid | 0.61** | 0.33** | 0.12** | 2.18** | 0.15** | 0.29** | 154 | 0.003 |
| Erucic acid | 6.40** | 7.78** | 0.53** | 0.07 | 4.34** | 19.29** | 154 | 0.07 |
| Protein content | 0.52** | 0.08** | 0.21** | 2.20** | 0.003 | 0.08** | 154 | 0.005 |
| Glucosinolate content | 370.86** | 148.32** | 796.27** | 16.23** | 890.23** | 3.27** | 154 | 0.39 |

* = significant at P = 0.05, ** = significant at P = 0.01.

## Gene action

Components of generation means presented in Tables 2 and 3 made it clear that for cross KN-256 x KN-257, four-parameter models for oil and erucic acid content, and five-parameter models for protein, glucosinolate, linolenic acid, and oleic acid content were found, whereas two, three, four, and five-parameter models were found fit for oleic acid, oil and glucosinolate, linolenic acid and erucic acid, respectively, in cross KN-258 x Punjab-Sarson.

**Table 2.** Heritability, genetic advance, and gene actions for different quality traits in cross KN-256 x KN-257 *Brassica napus.*

| Cross | $h^2$ (NS) | G.A (% age of mean) | (m) | (d) | (h) | (i) | (j) | (l) | $\chi^2$ | d.f. |
|---|---|---|---|---|---|---|---|---|---|---|
| Oil content | 0.52 | 4.02 | 41.92 ± 1.57 | 1.82 ± 0.36 | 7.33 ± 1.83 | 6.49 ± 1.64 | - | - | 0.74 | 2 |
| Protein content | 0.70 | 5.97 | 17.19 ± 1.22 | 0.94 ± 0.08 | 15.45 ± 2.80 | 4.73 ± 1.22 | - | -9.79 ± 1.62 | 1.25 | 1 |
| Glucosinolate content | 0.64 | 30.58 | 50.00 ± 0.18 | 6.40 ± 0.18 | 19.46 ± 3.20 | - | -6.06 ± 1.82 | -19.91 ± 3.19 | 1.13 | 1 |
| Linolenic acid | 0.73 | 13.50 | 6.13 ± 0.68 | 0.58 ± 0.06 | 3.98 ± 1.57 | 1.74 ± 0.68 | - | -2.29 ± 0.91 | 1.49 | 1 |
| Oleic acid | 0.77 | 8.24 | 58.65 ± 0.95 | 5.81 ± 0.17 | -6.89 ± 0.97 | -5.64 ± 0.98 | -5.19 ± 0.72 | - | 1.33 | 1 |
| Erucic acid | 0.43 | 30.33 | 13.59 ± 4.48 | 10.63 ± 0.29 | 18.11 ± 4.86 | 17.75 ± 4.86 | - | - | 0.03 | 2 |

All $\chi^2$ values are significant, d.f. = degrees of freedom, (m) = mean, (d) = additive, (h) = dominance, (i) = additive x additive, (j) = additive x dominance = (l) = dominance x dominance, GA = genetic advance.

**Table 3.** Heritability, genetic advance and gene actions for different quality traits in cross KN-258 x Punjab-Sarson *Brassica napus.*

| Cross | $h^2$ (NS) | GA (% age of mean) | (m) | (d) | (h) | (i) | (j) | (l) | $\chi^2$ | d.f. |
|---|---|---|---|---|---|---|---|---|---|---|
| Oil content | 0.73 | 6.19 | 44.60 ± 0.16 | 0.34 ± 0.16 | - | - | 6.33 ± 1.30 | - | 1.91 | 3 |
| Protein content | 0.53 | 15.61 | 22.98 ± 0.10 | 0.22 ± 0.09 | -2.26 ± 0.59 | - | - | 3.03 ± 0.61 | 1.17 | 2 |
| Glucosinolate content | 0.73 | 24.83 | 64.87 ± 1.33 | 4.98 ± 0.47 | - | -21.55 ± 1.41 | - | - | 2.29 | 3 |
| Linolenic acid | 0.64 | 11.68 | 8.68 ± 0.06 | 0.23 ± 0.06 | 2.19 ± 0.41 | - | - | -1.95 ± 0.42 | 0.35 | 2 |
| Oleic acid | 0.67 | 6.16 | 57.60 ± 0.13 | 1.14 ± 0.45 | - | - | - | - | 7.74 | 4 |
| Erucic acid | 0.77 | 35.94 | 27.64 ± 2.93 | 1.09 ± 0.16 | -31.54 ± 6.63 | -11.89 ± 2.92 | - | 19.11 ± 3.82 | 1.58 | 1 |

All $\chi^2$ values are significant, d.f. = degrees of freedom, (m) = mean, (d) = additive, (h) = dominance, (i) = additive x additive, (j) = additive x dominance, (l) = dominance x dominance, GA = genetic advance.

Dominance was of over-dominance type for protein content in cross KN-256 x KN-257 and erucic acid in cross KN-258 x Punjab-Sarson and it was directed towards the lower parent.

Oleic acid and glucosinolates were controlled by additive gene action in cross KN-258 x Punjab-Sarson. Negative dominance persisted for glucosinolates in cross KN-256 x KN-257 and for linolenic acid in both the crosses. Additive genetic variance has more contribution in the inheritance of oil and erucic acid content in cross KN-256 x KN-257 and oleic acid and glucosinolates in cross KN-258 x Punjab-Sarson. Oleic acid linolenic acid and protein content in cross KN-256 x KN-257 and oil content and protein content in cross KN-258 x Punjab-Sarson showed a complex type of gene action. Glucosinolate content in cross KN-256 x KN-257 and linolenic acid and erucic acid in cross KN-258 x Punjab-Sarson showed the preponderance of dominance variance.

## Heritability

High heritability estimates were observed for protein content in cross KN-256 x KN-257 and for oil content and erucic acid in cross KN-258 x Punjab-Sarson and for glucosinolate content, linolenic acid and oleic acid in both the crosses (Tables 2 and 3). Oil content and erucic acid in cross KN-256 x KN-257 and protein content in cross KN-258 x Punjab-Sarson displayed medium heritability values. Genetic advance was comparatively higher for glucosinolates and erucic acid in both the crosses and medium for protein content in cross KN-256 x KN-257 and for linolenic acid in both the crosses, whereas protein content in cross KN-256 x KN-257 and oil content and oleic acid in both the crosses exhibited low genetic advance.

## Correlation

Protein content showed a positive and significant association with all other quality traits such asoil, glucosinolate, oleic acid, linolenic acid, and erucic acid contents at both (genotypic and phenotypic) levels, except oil and erucic acid contents, in which the correlation was only at genotypic level in cross KN-256 x KN-257 (Table 4). Protein content was found negatively and significantly correlated with glucosinolate and oil contents at the genotypic level in cross KN-258 x Punjab-Sarson. Protein content also showed a significant and positive correlation with linolenic acid at both levels.

Glucosinolate content was found positively and significantly correlated with oil, oleic acid, linolenic acid, and erucic acid contents at the genotypic as well as the phenotypic levels in cross KN-256 x KN-257 (Table 4). Glucosinolate also developed a positive and significant correlation with oleic acid and oil content only at genotypic level in cross KN-258 x Punjab-Sarson (Table 4). Moreover, glucosinolates showed a negative and significant association with erucic acid at genotypic level in this cross.

Oleic acid showed significant and positive correlation with protein, glucosinolates, erucic acid and oil content mostly at both genotypic and phenotypic levels in cross KN-256 x KN-257 (Table 4). Oleic acid developed a positive and significant correlation with glucosinolates at genotypic level, and a negative and significant correlation with erucic acid at both levels in cross KN-258 x Punjab-Sarson (Table 4).

Linolenic acid had a significant and positive correlation with oil, protein, glucosinolate, oleic and erucic acid contents each at both levels in cross KN-256 x KN-257 (Table 4). Linolenic acid developed a positive and significant correlation with protein content at both levels and significant and negative correlation with erucic acid at genotypic level and with oil content at both levels in cross KN-258 x Punjab-Sarson (Table 4).

Erucic acid was positively and significantly associated with oil content and other quality traits such asprotein, glucosinolate, oleic, and linolenic acid content at both levels, except protein content, which showed this correlation only at genotypic level in cross KN-256 x KN-257 (Table 4). Erucic acid showed a significant and negative correlation with glucosinolate and linolenic acid at genotypic level and with oleic acid at both the levels in cross KN-258 x Punjab-Sarson (Table 4).

**Table 4.** Genotypic and phenotypic correlation coefficients among quality traits in two crosses of *Brassica napus*.

| | | GC | | OA | | LA | | EA | | OC | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | C1 | C2 | C1 | C2 | C1 | C2 | C1 | C2 | C1 | C2 |
| PC | G | 0.91* | -0.36* | 0.57* | -0.24 | 0.77* | 0.97* | 0.32* | -0.18 | 0.39* | -0.90* |
| | P | 0.85** | -0.34 | 0.57* | -0.29 | 0.69** | 0.86** | 0.30 | -0.14 | 0.30 | -0.98** |
| GC | G | | | 0.90* | 0.38* | 0.80* | 0.14 | 0.57* | -0.22* | 0.42* | 0.29* |
| | P | | | 0.88** | 0.36 | 0.78** | 0.14 | 0.49* | -0.17 | 0.30 | 0.28 |
| OA | G | | | | | 0.84* | 0.1 | 0.65* | -0.92* | 0.40* | 0.26 |
| | P | | | | | 0.77** | 0.06 | 0.62** | -0.82** | 0.33 | 0.26 |
| LA | G | | | | | | | 0.80* | -0.55* | 0.76* | -0.96* |
| | P | | | | | | | 0.69** | -0.41 | 0.64** | -0.88** |
| EA | G | | | | | | | | | 0.93* | 0.19 |
| | P | | | | | | | | | 0.92** | 0.21 |

* = significant (P < 0.05); ** = highly significant (P < 0.01). C1 stands for cross KN-256 x KN-257, C2 for cross KN-258 x Punjab-Sarson, PC for protein content, GC for glucosinolate content, OA for oleic acid, LA for linolenic acid, EA for erucic acid, and OC for oil content.

## DISCUSSION

The variation indicated in Table 1 is of paramount importance for the breeder intending to develop lines with better seed oil content and quality traits. Marjenovic-Jeromela et al. (2011) and Abideen et al. (2013) also recorded significant variability in oil content and other quality traits in oilseed brassicas. Oil and erucic acid content (Tables 2 and 3) showed comparatively more involvement of additive genetic component in cross KN-256 × KN-257 whereas additive gene action was wholly controlling the inheritance of glucosinolate and oleic acid in cross KN-258 x Punjab-Sarson. Additive genetic component is a vital factor that a breeder looks for and it is beneficial that oil content and important quality traits were controlled by additive variance. Early selection for the improvement of these traits is preferable. Preponderance of additive gene action is considered for the traits having high heritability and genetic advance, thereby making the selection effective (Aytac and Kinaci, 2009). Negative dominance was prevalent for glucosinolate content in cross KN-256 x KN-257 and for linolenic acid in both crosses. The higher value of dominance (h) than that of additive factor (d) indicated dispersion of genes. The negative sign attached with dominance x dominance (l) interaction showed that dominance was directed towards the low value parent and it is possible to reduce these anti-nutritional components through hybrid breeding (Celine and Sirohi, 1998). Protein content and oleic acid in cross KN-256 x KN-257 and oil, protein and erucic acid content in cross KN-258 x Punjab-Sarson showed preponderance of non-additive gene action suggesting that selection for the improvement of these traits be delayed until later segregating generations. Epistatic effects were more for oleic acid in cross KN-256 x KN-257 and for erucic acid in cross KN-258 x Punjab-Sarson.

The inheritance pattern of oil content, glucosinolate content, oleic acid, and erucic acid showed that these traits were governed by different gene actions in their respective crosses, indicating that gene action changed with the cross/genetic material. Additive gene action for erucic acid and preponderance of additive and over-dominance effects for glucosinolate has been reported by Iqbal (2003). Shu-Fen et al. (2006) and Zhao et al. (2005, 2006) reported additive and over-dominance type of gene actions whereas Wang et al. (2010) reported additive and non-additive effects for oil content in *B. napus*. Coonrod et al. (2008) observed additive gene action for oleic acid and linolenic acid. Turi et al. (2010) reported non-additive gene action for protein content. Non-additive effects along with additive genetic variance played a prominent role in the expression of most of the quality traits in both the crosses.

High heritability estimates and high genetic advance for glucosinolates in both crosses and medium heritability along with high genetic advance for erucic acid in cross KN-256 x KN-257 and high heritability coupled with high genetic advance for erucic acid in cross KN-258 x Punjab-Sarson are helpful in the improvement of these traits in the early segregating generations (Singh and Narayanan, 2000). Additive gene action has a major role in the expression of the traits having high narrow sense heritability (Khulbe et al., 2000). Oil and erucic acid content in cross KN-256 x KN-257 and oleic acid and glucosinolates in cross KN-258 x Punjab-Sarson having medium to high heritability estimates and preponderance of additive gene action may be exploited for the development of lines having high seed oil content and low anti nutritional components (glucosinolates and erucic acid). Protein and oleic acid content in cross KN-256 x KN-257 and oil content in cross KN-258 x Punjab-Sarson carried high heritability but low genetic advance, which may be due to the involvement of non-additive gene action (Lark and Rajput, 2000). Ahmad et al. (2013) and Fayyaz et al. (2014) reported high heritability for oil content and glucosinolates, whereas Kumar et al. (2013) and Mekonnen et al. (2013) reported low to medium heritability estimates for oil content and linolenic acid.

Khan et al. (2008) and Marjenovic-Jeromela et al. (2011) reported significant and negative correlation, and Aytac and Kinaci (2009) found significant and positive correlation of protein content with oil content in *Brassica* oilseed. Significant and positive association has been reported between protein content and linolenic acid (Abideen, 2013), and between protein content and glucosinolates, erucic acid, and linolenic acid each (Ahmad, 2013). The differences between the results of the present study and those in previous studies could be due to the differences in the material and environmental conditions in which the studies were conducted.

In cross KN-256 x KN-257, selection for higher protein content will increase desirable seed oil and oleic acid contents with a simultaneous increase in undesirable erucic acid and glucosinolate content. However, in cross KN-258 x Punjab-Sarson, selection for higher protein content will reduce the glucosinolate and oil content. This correlation is desirable when the objective is to achieve oil cake with higher protein and lower glucosinolate content, instead of higher oil content. In cross KN-258 x Punjab-Sarson selection for higher glucosinolates will increase oleic acid and oil content with a simultaneous reduction in erucic acid and protein content. From the point of view of human consumption, this association is desirable, but for animal consumption, this association is undesirable because oleic acid and erucic acid are found in oil, and glucosinolates are present in oil cake.

A significant and positive correlation of oleic acid with glucosinolates and significant and negative correlation with erucic acid has been reported by Islam et al. (2009). A significant and negative correlation between oleic acid and oil content has also been found by Abideen (2013). The results presented in Table 4 demonstrated that selection for higher oleic acid content would also increase oil and protein content with a simultaneous rise in undesirable components such as glucosinolates, erucic acid, and linolenic acid in cross KN-256 x KN-257. This aspect is comparatively better in cross KN-258 x Punjab-Sarson because selection for higher oleic acid content will cause a simultaneous decrease in erucic acid content. Reduction in the erucic acid content increases glucosinolate content, which is undesirable for animal consumption. Under such circumstances, oil quality may be improved with respect to human consumption but not with respect to animal consumption; high levels of glucosinolates lower the quality of the oil cake, which can then be used for manure purposes only.

Khan et al. (2008) and Tonguc and Erbas (2012) reported significant and negative correlation of erucic acid with oleic acid whereas Abideen (2013) reported a significant and positive correlation between erucic acid and oil content. Islam et al. (2009) and Tonguc and Erbas (2012) reported significant and negative correlation of linolenic acid with oil content, whereas Kumar et al. (2013) observed significant and positive association of linolenic acid with oil content and glucosinolate contents. The correlation aspect of linolenic acid is approximately the same in both the crosses because selection for lower linolenic acid will increase oil and erucic acid content and will reduce protein content. Higher oil content is desirable but higher erucic acid is harmful for oil quality and human health. Therefore, in order to increase oil quantity, the quality of the oil needs to be compromised. This type of oil (with high erucic acid content) is useful for industrial purposes.Erucic acid and glucosinolate contents having additive gene action and high heritability estimates coupled with high genetic advance can be improved in the early segregating generations. Gene action differed with the change in material/cross for most of the traits. Cross KN-258 x Punjab-Sarson can be utilized for the development of lines with high oil, low glucosinolate, and low erucic acid content.

## Conflicts of interest

The authors declare no conflict of interest.

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