ISSN 2709–3662 (Print)
ISSN 2709–3670 (Online)
https://doi.org/10.52587/JAF040301
Journal of Agriculture and Food
2022, Volume 3, No.1, pp. 36-

Genetic Interaction and Selection Strategy for different Traits in *Brassica Campestris*

Salsabeel Rauf[1*], Muhammad Ahsan Iqbal[1], Hafeez Ahmad Sadaqat[1], Nisar Ahmed[2]

Abstract

Generation mean analysis through 6 parameter model for three parents along with four generations viz F_1, F_2, BC_1 and BC_2 of two crosses of *Brassica campestris* was studied and evaluation was done in Randomized Complete Block Design (RCBD) with three replications in 2019. Additive variance was noted for 1000 seed weight in cross Span × Toria and for days to 50% flowering in cross TR8 × Toria. Hence selection at early generation may be helpful for the improvement of these traits. Negative dominance effect was present for glucosinolate in cross TR8×Toria which might be supportive for the reduction of this trait. Genetic interactions were found fixable for plant height, siliqua length, days to 50% flowering, days to maturity, number of seeds per siliqua, yield, oleic acid and erucic acid in cross Span × Toria and for plant height, siliqua length, days to 50% flowering, days to maturity, oil contents, oleic acid, linoleic acid, erucic acid and glucosinolate in cross TR8 ×Toria. The traits showed fixable interaction mass selection and progeny selection would be effective while for others exploitation of heterosis breeding may be effective and selection would be delayed to attain homozygosity.

Keywords: Brassicaceae , Canola, *Brassica rapa*., Toria, Scaling tests

Article History: **Received:** 20th January, 2022; **Revised: 22**th March 2022, **Accepted: 25**th March, 2022

[1]Department of Plant Breeding and Genetics, University of Agriculture Faisalabad; [2]Centre of Agricultural Biochemistry and Biotechnology (CABB), University of Agriculture Faisalabad.
[1*]corresponding author; easahafiz44@gmail.com

Introduction

Brassicaceae is among the ten families having species supplying humanity food and enjoy great popularity among growers due to their greater economical return throughout the world (Caballero et al., 2003). The production of brassica was increased throughout the world due to development of varieties with low erucic acid and glucosinolates called as "LEAR" or double zero and marketed with brand name called as "CANOLA" (Abdelsatar et al., 2021).

Pakistan produced only 21 percent of total edible oil demand while remaining 79 percent was imported from various countries including Malaysia and Argentina which was of worth 1 billion $ (MINFAL, ???). In Pakistan, oilseeds brassicas are cultivated in wheat growing areas, therefore its competition is not only with wheat but also with fodder for the use of water and other resources. Farmer prefer to grow wheat because it is staple food and get more support price. As a result, oilseeds brassicas faces shortage of water and other inputs. Oilseeds crops are cultivated on marginal lands, therefore their production is not meeting the demand of people. This alarming situation demands the breeders to develop local varieties with high oil contents and better quality to fill this gap.

The understanding of genetics or type of genetic variability associated with economical traits is important which may help to apply specific population program to develop elite breeding material in *Brassica* species

The study of genetic behaviour for the enhancement of yield as well as yield contributing traits is utmost breeding objective in oilseed brassicas. Oil contents, protein contents, oleic acid, linolenic acid, linoleic acid, erucic acid and glucosinolate (in oil free meal) are the important traits of brassica oilseeds. The objectives of present study were to understand the genetic mechanisms governing the inheritance of plant performance and oil quality traits as well as to develop high yielding along with high oil content lines with double characteristics.

Materials and Methods

The experiments were sown in the field area of the department of Plant Breeding and Genetics at University of Agriculture, Faisalabad for the period of 2016-2019. The research material consisted of four parental lines of *Brassica rapa*. Among these two have low erucic acid and one with high erucic acid contents but high yielding. The parents were sown in the field and during flowering, hybridization was done by utilizing hand emasculation technique and controlled pollination by Span (Canola type) × Toria (Non canola type) and TR-8 (Canola type) × Toria (Non canola type). In the next season F_1 were sown in the field. F_1 plants were covered to control pollination and back crosses were made for each mentioned cross. Seeds were harvested and kept them separately to grow them next year. Some F_1 plants were covered at flowering to avoid foreign pollination and obtained pure F_2 seeds that was sown in the following growing season.

Three parents along with four generations viz F_1, F_2, BC_1 and BC_2 were sown in Randomized Complete Block Design (RCBD) as replicated three times. A distance of 15cm between plants and 45cm between rows was maintained. Recommended dose of fertilizers and three number of irrigations were applied. Different rows were allocated for different generations. One row was sown by each parent and their subsequent F_1, ten

rows for F_2 and three rows for BC_1 and BC_2. The length of each row was 500 cm. Ten plants were selected randomly and tagged for each of parents and F_1, hundred plants of F_2 and fifty plants each of BC_1 and BC_2 generations from each replication for recording the observations on different characters (Pandey et al., 2013).

Numerous plant traits i.e., Days to 50% flowering, days taken to maturity, plant height (cm), number of branches per plant, siliqua length, number of seeds per siliqua,1000 Seed weight, seed yield per plant (g), oil contents (%), protein contents(%), oleic acid contents (%), linolenic acid contents (%), linoleic acid contents (%), erucic acid contents(%), glucosinolate contents (%) were noted. Data was analysed statistically to determine genetic variability as described by Steel et al., (1997). Every character was genetically analysed by using Generation Mean Analysis (Mather and Jinks, 1982). Scaling tests A, B and C were used to determine presence or absence of non- allelic interactions as described by Mather (1949).

Results

The data were subjected for the analysis of variance. The results showed significant to highly significant differences among parents and their generations (P_1, P_2, F_1, F_2 BC_1, BC_2) in both crosses studied (Tables 1-2).

Table 1. Mean Square values of six generations from Analysis of Variance for various morpho-phenological, yield related and biochemical traits in Span × Toria of *Brassica campestris*

Source of variation		REP	GEN	P_1 vs P_2	P's vs F_1	BC_1 vs BC_2	F_2 vs BC's	P's, F_1 vs BC's ,F_2	Error
Traits	**DF**	2	5	1	1	1	1	1	10
Morpho-phenological traits	PH	0.8	452**	303**	1734**	77**	74.**	69**	0.9
	Bran.	0.5	1750**	4940**	1697**	3*	4*	2104**	0.5
	SL	0.0	1**	0**	2**	2**	0**	0**	0.0
	DTF50%	9*	185**	14*	412**	100**	190**	211**	1
	DTM	7*	30**	28**	6.	19**	85**	14*	2
Yield related traits	NSS	0	7**	2**	16**	7**	1*	11**	0
	1000-SM	0	0**	1**	0*	0**	0*	0**	0
	SYP	0	26**	0	105**	0**	2**	24**	0
Biochemical traits. (quality traits)	OC (%)	0	24**	4**	38**	30**	1**	46**	0
	PC(%)	0	28**	62**	27**	0**	1**	47**	0
	Ol (%)	0	319**	69**	570**	55**	156**	746**	0
	Lino (%)	0	1**	1**	3**	1**	1**	0**	0
	Lin (%)	0	3**	1**	1**	3**	0*	12**	0
	Eruc (%)	0	495**	1378**	69**	415**	119**	493**	0
	Gluco	0	3622**	2318**	1764**	857**	138**	130**	0

*=Significant ($p<0.05$); **highly significant ($p<0.01$)Rep = Replication, GEN = Generation, P_1= Parent-1, P_2 = Parent-2, BC_1 = Backcross-1, BC_2 = Backcross-2, vs = Verses, P's = Parents, F_1 = First Filial Generation, F_2 = Second Filial Generation.

Table 2. Mean Square values of six generations from Analysis of Variance for various morpho-phenological, yield related and biochemical traits in TR8 × Toria of Brassica campestris

Source of variation		REP	GEN	P_1 vs P_2	P's vs F_1	BC_1 vs BC_2	F_2 vs BC's	P's, F_1 vs BC's ,F_2	Error
Traits	**DF**	2	5	1	1	1	1	1	10
Morpho-phenological traits	PH	4	118.17**	303.31**	12*	72**	125**	79**	2
	Branches	1	1600.17**	4825.74**	1570**	1	2	1603**	1
	Siliquae length	0	2**	0.06	4**	0**	1**	4**	0
	DTF50%	10**	256**	915**	73**	130**	56**	109**	1.
	DTM	3*	268**	924**	21**	342**	51**	4*	1
Yield related traits	NSS	0	27**	2**	121**	7**	1**	2**	0
	1000SM	0	0**	1**	0**	0	0	1**	0
	SYP	0	0*	0	0**	0	0.	0	0
Biochemical traits. (quality traits)	OC(%)	0	38**	3**	87**	2**	29**	71**	0
	PC (%)	0	29**	61**	59**	0**	2**	25**	0
	Ol %	0	523**	64**	1225**	304**	220**	804**	0
	Lino%	0	2**	1**	5**	2**	1**	0*	0
	Linol%	0	9**	1**	4**	32**	5**	4**	0
	Eru%	0	503**	1378**	395**	569**	160**	15**	0
	Gluc%	0	2020**	2318**	57**	2529**	2076**	3120**	0

*=Significant ($p<0.05$); **highly significant ($p<0.01$)Rep = Replication, GEN = Generation, P_1= Parent-1, P_2 = Parent-2, BC_1 = Backcross-1, BC_2 = Backcross-2, vs = Verses, P's = Parents, F_1 = First Filial Generation, F_2 = Second Filial Generation.

Mean square values of six generations were found highly significant when comparison was made between parents for all morpho-phenological and yield related traits i.e., days to 50% flowering, days to 70% maturity, plant height, number of branches, siliqua length, number of seeds per siliqua, 1000 seed weight and seed yield in both crosses except siliqua length and seed yield in cross TR8 × Toria.

When parents were compared with first filial generation, significant mean squares appeared to be pronounced for days to 50% flowering in two crosses, days to maturity in cross TR8 × Toria except in cross Span × Toria, plant height, number of branches in both crosses, while siliqua length remained non-significant in cross TR8 × Toria, for yield related traits i.e., number of seeds per siliqua, 1000 seed weight and seed yield/ plant for both crosses

In cross Span × Toria, all significant differences were found for all morpho-phenological and yield related traits when BC_1 was compared to BC_2;$F_; F_2$ was compared BC's and P's; F_1 was compared to BC's and F_2. In cross TR8 × Toria showed significant differences for days to 50% flowering, days to 70 % maturity, plant height and for number of seeds per siliqua when BC_1 was compared with BC_2 and F_2 was compared

with BC's. When a comparison was made between P's, F_1 vs BC's, F_2 significant differences were found for all morpho-phenological and yield related traits except seed yield.

Both crosses showed highly significant differences when comparisons were made between parents, backcrosses, P's vs F_1, F_2 vs BC's and P's, F_1 vs BC's, F_2 for all biochemical traits studied . The Scaling Tests (A, B, C) for both crosses (Table 3-4) studied indicated the existence of epistasis for all the traits studied except for the seed yield in TR8 × Toria.

Five and six genetic parameter models were found to be fit for the inheritance of days to 50% flowering in both crosses studied. Both additive and non-additive gene action was responsible for the said trait while dominance effects was higher in two crosses studied. In cross Span × Toria while TR8 × Toria had more magnitude of additive effects than dominance effects and additive × additive gene effects have greater value than others. It also has the negative sign which indicated the presence of negative genes in parents. Results from analysis of gene effects showed existence of additive and non-additive components for expression of number of days to maturity in both crosses studied. Dominance with greater magnitude was present and opposite sign of (h) and (l) revealed the existence of duplicate epistasis in both crosses.

Table 3. Gene action for various morpho-phenological, yield related and biochemical traits in Span × Toria, where plant height (PH), number of branches (Branc.), silique length (SL), days to 50% flowering (DTF 50%), days to maturity (DTM), number of seed silique^{-1} (NSS), 1000-seed mass (1000-SM), seed yield plant^{-1} (SYP)

Traits	Scaling Test			Genetic Effects						χ^2(df)
	A	**B**	**C**	**[m]**	**[d]**	**[h]**	**[i]**	**[j]**	**[l]**	
PH	-28** ±3	1* ±3	-52** ±3	124** ±1	7** ±1	55** ±2	26** ±2	-14 ±2		0(1)
Bran	-62** ±1	-7** ±1	-63** ±2	41** ±0	29** ±0	-95** ±2		-27** ±1	65** ±1	10 (1)
SL	0 ±0	-1** ±0	-2** ±0	4** ±0	0 ±0	2** ±0	1** ±0	1* ±0		0 (1)
DTF 50%	9** ±1	-4** ±1	44** ±1	89** ±1	2** ±0	-59** ±4	-39** ±1	7** ±1	34** ±2	0 (0)
DTM	-0 ±1	-3** ±1	23** ±1	128** ±2	2** ±0	-53** ±4	-26** ±2		29** ±3	5 (1)
NSS	5** ±1	-1 ±1	6** ±1	14** ±0	-1 ±0		-3** ±0	3** ±1		1 (2)
1000-SM	0 ±0	0** ±0	0 ±0	2** ±0	0* ±0	0 ±0			-0 ±0	2 (2)
SYP	-7** ±0	-8** ±0	-12** ±0	10** ±1	0 ±0	-15** ±2	-2** ±0		19** ±1	1 (1)
OC%	2* ±0	9** ±1	8** ±1	39** ±0	-1* ±0	14** ±1		-4** ±1	-9** ±1	3 (1)
PC%	-8** ±0	-1** ±0	-12** ±0	24** ±0	3** ±0	-15** ±0		-3** ±0	11** ±0	25 (1)**
Ol%	23** ±1	29** ±1	17** ±2	-7** ±2	-4** ±0	138** ±6	35** ±2		86** ±4	8 (1)**
Linolei	-3** ±0	0 ±0	1 ±0	6** ±0	0 ±0.		-0 ±0	-2** ±0	1* ±0	16 (1)**

Lino.	-2** ±0	-4** ±1	-6** ±1	15** ±0	0 ±0	-7** ±1		1 ±0	6** ±1	1 (1)
Eur %	14** ±1	-50** ±0	-66** ±1	-18** ±0	15** ±0	39** ±0	33** ±0	32** ±0		10 (1)**
Gluc	136** ±2	49** ±3	218** ±3	63** ±0	-20** ±0	235** ±2		41** ±2	-205** ±2	67 (1)**

Table 4. Gene action for various morpho-phenological, yield related and biochemical traits in TR8 × Toria

Traits	Scaling Test			Genetic Effects						χ^2 (df)
	A	**B**	**C**	**[m]**	**[d]**	**[h]**	**[i]**	**[j]**	**[l]**	
PH	-16** ±2	12** ±2	-36** ±3	133** ±1	8** ±1	15** ±2	18** ±1	-15** ±2		22 (1)**
Bran.	-55** ±1	-0 ±2	-60** ±1	41** ±0	28** ±0	-86** ±1		-27** ±1	58** ±1	4 (1)*
SL	-22** ±0	-1** ±0	-6** ±0	3** ±0	0 ±0		2** ±0	-1 ±0	3** ±0	1 (1)
DTF 50%	1 ±1	7** ±1	30** ±1	74** ±1	12** ±0	-8** ±1	-14** ±1	-3** ±1		26 (1)
DTM	9** ±1	4** ±1	-8** ±1	92** ±1	12** ±0	49** ±3	20** ±1	3** ±0	-33** ±2	0.00 (0)
NSS	-6** ±1	-3** ±1	-6** ±1	11** ±0	-1 ±0			-2* ±0	8** ±0	6 (2)
1000 SM	1** ±0	1** ±0	2** ±0	2** ±0	0 ±0	2** ±0		-0 ±0	-2** ±0	0.02 (1)
SYP	0 ±0	-0 ±0	-0 ±0	6** ±0			0 ±0			3 (4)
OC (%)	10** ±0	6** ±1	1** ±1	23** ±1	-1* ±0	56** ±2	16** ±1		-33** ±2	31. (1)**
PC (%)	-7** ±1	0 ±1	-3** ±1	24** ±0	3** ±0	-10** ±1		-4** ±1	5** ±1	3.83 (1)
Ol. (%)	29** ±1	-6** ±2	65** ±2	59** ±1	-3** ±0	-7** ±1	-31** ±1	16** ±1		18 (1)**
Linol. (%)	1 ±0	-1 ±1	-2** ±1	5** ±0	0 ±0	2.58** ±0.32	1 ±0	1 ±0		2.23 (1)
Lino. (%)	1 ±1	-8** ±1	-0.47 ±1	21.66** ±1	-19** ±3		-6** ±1	5** ±0	14** ±2	7 (1)**
Eur. (%)	3** ±0	11** ±1	-22** ±1	-17** ±1	-15** ±0	61** ±2	32** ±1		-43** ±1	152 (1)**
Gluco.	12** ±4	54** ±5.41	195** ±5.49	158** ±2.71	-20** ±0.16	-102** ±3.80	-95** ±2.72	-26** ±2.93		21 (1)**

Fixable interaction (i) was present in both crosses. Five and six parameters model elaborated the genetic differences in this trait. The number of parameters that explain the genetic differences were four and five in crosses studied for the plant height. This trait was controlled by both additive and non-additive gene effects in both crosses. So it becomes the complex. The magnitude of dominance effects was higher than the additive effects.

Five components of generation mean showed genetic variation for number of branches. Both additive as well as non-additive gene effects explained gene actions with higher magnitude of dominance effects. Duplicate epistasis was found in both crosses studied. In epistatic interactions, (i) was found missing while (j) and (l) was present in both

crosses. Selection should be delayed. Siliqua length in cross TR8 × Toria showed significant dominance effects while TR8 × Toria showed epistatic interactions with non-dominance effects. Additive × additive was found in both crosses. Span × Toria and TR8 × Toria showed (i) and (j) interactions of epistasis. TR8 × Toria showed a little high magnitude of (l) than (i) that expressed importance of dominance x dominance interaction for controlling the trait under discussion Four and five parameter model were the best fit for number of seeds per siliqua. Significant value of dominance × dominance (l) for TR8 × Toria showed that parents had dispersal of alleles for number of seeds per siliqua. Cross Span × Toria had (i) and (j) interactions with high but negative magnitude of (i) for number of seeds per siliqua. Seed yield per plant **r**esults showed that additive and dominance model were prevalent in expressing the trait in two crosses with high degree of dominance. Dominance effect was many times more than additive effect in cross Span × Toria and showed duplicate epistasis while cross TR8 × Toria showed only (i) interaction.

In both crosses, five parameter model explained the genetic variability of oil content. Additive and non-additive genetic components were found significant. Additive and dominance effects along with epistasis effect were observed in both crosses. The magnitude of dominance effect was found greater than additive and epistatic effects in both crosses, suggesting hybrid breeding for the improvement in the character. Dominance × dominance (l) was present in both crosses. Duplicate type of epitasis was found in both crosses.

Additive and dominance gene effects with epistatic interactions were found significant for protein contents in both crosses. The amount of dominance effects was greater than additive effects in both crosses. The opposite signs of dominance (h) and dominance × dominance (l) effects showed the existence of duplicate epistasis. The additive × dominance (j) interaction effect was found in both crosses. Five parameter model justified the genetic variability for oleic acid. Additive main effects and dominance main effects along with additive × additive (i) and dominance × dominance (l) was observed for oleic acid in Span × Toria. In this cross, magnitude of dominance main effects was found higher than other effects. TR8 × Toria had complimentary type of gene action. TR8 × Toria fixable epistasis i.e., additive × additive (i) effects showed high magnitude. Additive main effects were observed negative sign illustrated that lower value alleles were over dominant.

Linolenic acid had five parameter models to illustrate genetic variability in both crosses. In Span × Toria dominance effects were absent. Although additive main effects were found in this cross but their share was found smaller than (j) i.e., additive × dominance and showed complementary type of epistasis. In cross TR8 × Toria, dominance effects were found significant so heterosis breeding may be adopted. Additive and non-additive effects along with interactions effects were found responsible for expression of linoleic acid in both crosses. Dominance main effect showed high magnitude value in Span × Toria and also showed epistasis of duplicate nature as dominance (h) and dominance × dominance (l) showed the opposite signs. So heterosis breeding method may be followed for improvement of this trait. Four parameter model fits for the expression of this trait in both crosses under studied. In TR8 × Toria, additive main effects showed high magnitude than others. Dominance main effects was not observed in this cross. So

selection should be done at early stage in this cross. Negative sign of additive main effects in TR8 × Toria showed that alleles controlling less value traits were found over-dominant than high values.Five parameter model described in both crosses studied for erucic acid. i.e; anti nutritional components in human diet. Additive and dominance effects were found in both crosses. Dominance effects have high magnitude than additive effects. Duplicate type of epistasis was found in TR8 × Toria. In epistatic interactions additive x additive (i) were found in both crosses. Dominance × dominance (l) was found in TR8 × Toria.

In both crosses, five parameter model were found the best for determination of genetic variability of glucosinolate contents. Additive and dominance main effects along with epistatic effects were found in both crosses. Dominance main effects showed many times high magnitude than additive in both crosses. Duplicate non allelic interaction was found in Span × Toria.

Discussion

Presence of variability in breeding material is the prerequisite for the improvement of a trait. Results revealed that days to 50% flowering was under the control of additive gene action in cross TR8 × Toria which suggested that selection at early generation may be effective for earliness in flowering. Negativity in the trait of days to 50% flowering showed earliness in flowering. As early flowering varieties was desired so it is very valuable trait for a breeder, and selection should be done at early stage because fixable epistatic effects were present in TR8 × Toria. Kemparaju et al., (2009) and Maurya et al., (2012) also observed the same effects. Akanksha et al., (2017) noted duplicate epistasis and value of dominance effect was found more than the others for days to 50% flowering. Kant et al., (2001) and Shrimali et al., (2017) reported that additive gene effects was more important for days to flowering. Hybrid breeding for early maturing is suggested because dominance effects had the greater magnitude. The results of Kemparaju et al., (2009) were in corroboration while Singh and Yadeve (1980) and Cheema and Sadaqat (2003) found presence of non-additive effects for the trait. Patel et al., (1996) reported additive type of gene action for days to maturity. Sachan and Singh (1987) found di-genics model and duplicate epistasis for maturity. They also found all interactions of epistasis significantly for this trait. Kant et al., (2001) found additive × additive effects for days to 75% maturity. Shrimali et al., (2017) reported that days to maturity was controlled additively. . Reciprocal recurrent selection is suggested for the improvement of plant height. Singh and Singh (1994) and Sabaghnia et al., (2010) also reported non-additive type of genetic components for the control of plant height. Akanksha et al., (2017) depicted that duplicate epistasis is responsible for plant height. Shrimali et al., (2017) reported that plant height was controlled additively. Preponderance of dominance effects for number of branches as demonstrated by Singh et al., (2007). Akanksha et al., (2017) reported duplicate epistasis for number of branches per plant. It also showed dispersal of alleles for siliquae length in particular cross. Five parameter model was fitted for genic variation of siliquae length in both crosses. Results were supported by Singh et al., (2007). Results of Sheikh and Singh (1998) contradicted the present research and detected additive gene action for this traits. Akanksha et al., (2017) reported presence of duplicate epistasis for this trait. Singh et al., (2003) showed

that additive gene effects were responsible for the number of seeds per siliqua. Selection in early generation could be successfully performed.
Results of Thakur and Sagwal (1997), Varsha et al., (1999), Ghosh et al., (2001) and Rameeh (2012a) were in corroboration to present study. While Kemparaju et al., (2009) concluded that duplicate epistasis was more powerful for controlling the seed yield. Results showed that selection should be postponed to later generations and suggested heterosis breeding would be rewarding. Kant et al., (2001) found additive x additive effects more important for seed yield per plant.
The quality characters of oilseed brassicas showed that genetic variation was due to significant and non-significant variation**.** The presence of these variations are very precious for oilseed breeder to develop high quality varieties especially for double low varieties in brassica. Oil contents, protein contents, oleic acid, linolenic acid, linoleic acid, erucic acid and glucosinolate (in oil free meal) are the important traits of brassica oilseeds. F_2 population showed significantly genetic variation for linolenic acid, oil content, erucic acid, glucosinolate and oleic acid (Khan et al., 2008). In both crosses negative sign of additive main effects (d) showed that alleles responsible for less oil content trait were over dominant over the alleles controlling the high value. Sheikh and Singh (1998), Rameah et al., (2003) and Wang et al., (2010) reported the same results. Some researchers reported that oil contents were governed additively or dominance gene action was responsible. (Iqbal et al., 2003, Zaho et al., (2006). Kant et al., (2001) found additive × additive non-allelic interaction for oil contents. Ahmad et al., (2015) reported additive effects were dominated for oil contents. Reciprocal recurrent selection or heterosis for the improvement of protein contents may be useful. High magnitude of dominance (h) showed that genes are dispersed in the parent and association was not found. Heterosis may lead to improve this trait. Turi et al., (2010) confirmed the non-additive effects for protein contents. Ahmad et al., (2015) noted that protein contents were non-additively controlled in one cross studied while non-additively controlled in the other cross and selection in early generation may be productive in that cross and it was additively controlled and heterosis breeding may be useful in other crosses. Results suggested reciprocal recurrent selection procedure for improvement in oleic acid traits. Coonrod et al. (2008) concluded that this trait was controlled additively. Harvey and Downey (1964) and Kondra and Stefansson (1965) confirmed the present results. Ahmad et al., (2015) depicted non-additive type of gene action for the control of oleic acid and proposed selection in later stages for the oleic acid. So these crosses should be taken forward for development of low linolenic varieties. Ahmad et al. (2015) reported negative dominance for the control of linolenic acid. Coonrod et al. (2008) and Shrimali et al., (2017) discovered that this trait was additively controlled. Results of Coonrod et al., (2008) was in contradictory to this research as they mentioned additive as well as additive × additive epistatic interactions for linoleic acid and additive effect had profound effect than interaction. High magnitude of dominance effect suggest either selection should be done in later stages or hybrid breeding for development of low erucic acid varities. Zhang et al. (1996) and Iqbal et al. (2003) reported that erucic acid was under the control of additive effects. Ahmad et al. (2015) reported additive gene action in one cross and non-additive in other cross for erucic acid. Ze-su et al. (2012) reported

that erucic acid did not follow the additive-dominance model and was under control of two major genes. Chauhan et al., (2002) concluded that erucic acid was under the control of additive and additive x additive interactions and selection may be fruitful in early generations either for low or high erucic acid. Negative sign of additive main components in both crosses illustrated lower value alleles are dominant and it may help in breeding for low value parent. The results showed that this trait was controlled by additive as well as non-additive genetic attributes. Ahmad et al. (2015) reported negative dominance for the control of glucosinolate. He also reported persistence of negative dominance for glucosinolate and for linolenic acid. One to more non allelic interactions and three major genes were reported by Ze-su et al. (2012) for glucosinolate contents.

Conclusion

Genetic interactions were found fixable in both crosses i.e. Span × Toria and TR8 ×Toria for the traits, plant height, siliqua length, days to 50% flowering, days to maturity, number of seeds per siliqua, yield, oleic acid and erucic acid except glucosinolate, oil contents and linoleic acid in cross TR8 ×Toria

Therefore mass selection and progeny selection may be useful for improvement in these traits. All other traits studied showed non fixable interactions and exploitation of heterosis breeding may be effective through biparental crosses.

Acknowledgement

Author acknowledges government of the Punjab for providing opportunity of studies

References

Abdelsatar, M. A., Hassan, T. H., Ahmed, A. A., & Aboelkassem, K. M. (2021). Generation means analysis of seed yield and its components in canola. *Egyptian Journal of Agricultural Research*, *99*(1), 37–48.

Ahmad, S., Sadaqat, H. A., Tahir, M. H. N., & Awan, F. S. (2015). An insight in the genetic control and interrelationship of some quality traits in Brassica napus. *Genetics and Molecular Research*, *14*(4), 17941–17950.

Akanksha, P. K., Verma, O. P., & Kumar, K. (2017). Genetic analysis for seed yield and its related attributes in Yellow Sarson (Brassica rapa var. Yellow Sarson). *Journal of Oilseed Brassica*, *1*(1), 43–51.

Anonymous. (1998). NIR calibration in practice. Available: http; //dx.doi. org/1:1051/ analysis: 199826040038.

Caballero, B., L. C. Trugo, and P.M. Finglas. (2003). Encylopedia of food scienes and nutrition. Academic.

Chauhan, J. S., Tyagi, P., Tyagi, M. K., & Tyagi, P. (2002). Inheritance of erucic acid content in two crosses of Indian mustard (Brassica juncea L.). *SABRAO Journal of Breeding and Genetics*, *34*, 19–26.

Coonrod, D., Brick, M. A., Byrne, P. F., DeBonte, L., & Chen, Z. (2008). Inheritance of long chain fatty acid content in rapeseed (Brassica napus L.). *Euphytica*, *164*(2), 583–592.

Ghosh, S. K. and S. C. Gulati. (2001). Genetic variability and association of yield components in Indian mustard (Brassica juncea L.). *Crop Research*, 21, 345–349.

Harvey, B. L., & Downey, R. K. (1964). The inheritance of erucic acid content in rapeseed (Brassica napus). *Canadian Journal of Plant Science*, *44*(1), 104–111.

Iqbal, M. M., Din, R., & Khan, S. J. (2003). Use of Diallel Analysis to Examine the Mode of Inheritance of Agronomic and Quality Parameters in F 1 Generation of Brown Mustard (Brassica juncea L. Czern and Coss). *Asian Journal of Plant Sciences* 2, 1040–1046.

Kant, L., Gulati, S. C., & Kant, L. (2001). Genetic analysis for yield and its components and oil content in Indian mustard (Brassica juncea L. Czern and Coss). *Indian Journal of Genetics*, *61*(1), 37–40.

Kemparaju, K. B., Yadava, D. K., Sujata, V., Yadav, A. K., Bhagwan, D., Giri, S. C., & Prabhu, K. V. (2009). Genetic analysis of yield and yield-attributing traits in Indian mustard (*Brassica juncea*). *Indian Journal of Agricultural Sciences*, *79*(7), 555–558.

Khan, S., Farhatullah, R., Khalil, I. H., Khan, M. Y., & Ali, N. (2008). Genetic variability, heritability and correlation for some quality traits in F3: 4 Brassica populations. *Sarhad Journal of Agriculture*, *24*(2), 223–231.

Kondra, Z. P., & Stefansson, B. R. (1965). Inheritance of erucic and eicosenoic acid content of rapeseed oil (Brassica napus). *Canadian Journal of Genetics and Cytology*, *7*(3), 505–510.

Mather, K., and J.L. Jinks. (1982). Introduction to Biometrical Genetics. 3rd editoion.

Maurya, N., A.K. Singh and S.K. Singh. (2012). Analysis of combining ability in Indian mustard (*Brassica juncea* L). *Indian Journal of Plant Sciences*, 1(2-3), 116–123.

Pandey, S., Kabdal, M., & Tripathi, M. K. (2013). Study of inheritance of erucic acid in Indian mustard (Brassica juncea L. Czern & Coss). *Octa Journal of Biosciences*, *1*(1) 77–84.

Patel, M. C., Malkhandale, J. D., & Raut, J. S. (1996). Combining ability in interspecific crosses of mustard (Brassica spp.). *Journal of Soils and Crops*, *6*, 49–54.

Poehlman, J. M. and D. A. Sleeper. (1995). Breeding Field Crops. 4th Ed. Panima, Pub. Corp., New Delhi, 75–76.

Rameah, V., Rezai, A., & Saeidi, G. (2018). Estimation of genetic parameters for yield, yield components and glucosinolate in rapeseed (Brassica napus L.). *Journal of Agriculture Science and Technology*, 5, 143–151.

Sabaghnia, N., Dehghani, H., Alizadeh, B., & Mohghaddam, M. (2010). Heterosis and combining ability analysis for oil yield and its components in rapeseed. *Australian journal of crop science*, *4*(6), 390–397.

Sachan, J. N., & Singh, B. (1987). Generation mean analyses for flowering and maturity in Indian mustard (Brassica junces (L.) Czern & Coss). *Theoretical and applied genetics*, *73*(4), 571-574.

Sadaqat, H. A., Tahir, M. H. N., & Hussain, M. T. (2003). Physiogenetic aspects of drought tolerance in canola (Brassica napus). *International Journal of Agriculture and Biology*, *5*(4), 611-614.

Salunkhe, D. K. (1992). World oilseeds. Springer Science and Business Media.

Sheikh, A., & Singh, J. N. (1998). Combining ability analysis of seed yield and oil content in Brassica juncea (L.) coss & czern. *Indian Journal of Genetics & Plant Breeding*, 58, 507–11.

Shrimali, T. M., Chauhan, R. M., Gami, R. A., & Patel, P. T. (2017). Components of Genetic Variation and Graphical Analysis (Wr-Vr) in Indian Mustard (Brassica juncea L. Czern & Coss.). *International Journal of Current Microbiology and Applied Sciences*, 6(2), 535–545.

Hari, S., & Yadav, C. K. (1980). Gene action and combining ability for seed yield, flowering and maturity in rapeseed. *Indian Journal of Agricultural Science*, *50*(9), 655–658.

Singh, K. H., Gupta, M. C., Srivastava, K. K., & Kumar, P. R. (2003). Combining ability and heterosis in Indian mustard. *Journal Of Oilseeds Research*, *20*, 35–39.

Singh, R. K., & Dixit, P. (2007). Heterosis and Combining Ability Studies for Seed Yield, its Attributes and Oil Content in Indian Mustard [Brassica Juncea (L) Czern & Coss]. *Crop Improvement*, *34*(2), 192–196.

Singh, R. P., & Singh, D. P. (1994). Genetic variation in the growth pattern, partitioning of dry matter, and harvest index in Brassica juncea (L.), Czern and Coss. *Tropical Agriculture*, *71*, 62–62.

Steel, R.G. D., J. H. Torrie and D.A. Dickey. (1997). Principles and Procedures of Statistics: A Biometrical Approach. McGraw-Hill. New York. USA.

Thakur, H. L., & Sagwal, J. C. (1997). Heterosis and combining ability in rapeseed (Brassica napus L.). *Indian Journal of Genetics and Plant Breeding*, *57*(02), 163–167.

Turi, N. A., Raziuddin, F., Khan, N. U., Munir, I., & Khan, S. (2010). Combining ability analysis in Brassica juncea L. for oil quality traits. *African journal of Biotechnology*, *9*(26), 3998–4002.

Varsha, I., D.R. Satija, and P. Singh. (1999). Gene effects for seed yield and its components in crosses involving exotic parents in Brassica napus. Crop Improvement, 26(2), 188–192.

Wang, X., Liu, G., Yang, Q., Hua, W., Liu, J., & Wang, H. (2010). Genetic analysis on oil content in rapeseed (Brassica napus L.). *Euphytica*, *173*(1), 17–24.

Ze-su, H., Paisan, L., Thitiporn, M., Ze-hui, C., Wen-dong, D., Rong, T., & Dezhen, L. (2012). Inheritance of erucic acid, glucosinolate, and oleic acid contents in rapeseed (Brassica napus L.). *Journal of Northeast Agricultural University*, *19*(2), 1-8.

Shufen, Z., Wenguang, S., Lejian, R., Baoming, T., Yancheng, W., Jianmin, L., & Jianping, W. (1996). Studies on hereditary capacity of quantitative characters and gene effects of CMS double low *Brasica napus*. *Oil Crop of China, 18(3)*, 1–3.

Zhao, J., Becker, H. C., Zhang, D., Zhang, Y., & Ecke, W. (2006). Conditional QTL mapping of oil content in rapeseed with respect to protein content and traits related to plant development and grain yield. *Theoretical and Applied Genetics*, *113*(1),33–38.

Citation of Article

Rauf, S., Iqbal, M.A., Sadaqat, H.A., Ahmed, N. (2022). Genetic Interaction and Selection Strategy for different Traits in *Brassica Campestris. Journal of Agriculture and Food, 3(1)*, 36–48.