

Full Length Research Paper

Combining ability analysis in *Brassica juncea* L. for oil quality traits

Naushad Ali Turi, Raziuddin, Farhatullah*, Naqib Ullah Khan, Iqbal Munir², Abrar Hussain shah³ and Sajid Khan

¹Department of Plant Breeding and Genetics, NWFP Agricultural University, Peshawar-Pakistan.

²Institute of Biotechnology and Genetic Engineering (IBGE).

³Department of Horticulture, NWFP Agricultural University, Peshawar-Pakistan.

Accepted 30 April, 2010

This study was conducted in *Brassica juncea* L. for the determination of good combiners for quality associated traits using 8 x 8 diallel during 2004 - 2005 and 2005 - 2006. Analysis of variance revealed highly significant differences ($p \leq 0.01$) for all the studied traits. Components of combining ability analysis showed that general combining ability (GCA) was highly significant ($p \leq 0.01$) for oil percentage (%) and glucosinolates ($\mu\text{Molg-1}$) whereas the rest were non-significant. Specific combining ability (SCA) effects were highly significant for all traits except for oleic acids. Reciprocal combining ability (RCA) effects were highly significant ($p \leq 0.01$) for all traits except for oleic acid which was significant at ($p \leq 0.05$). The SCA effects were higher than RCA for oil %. The GCA effects were of greater magnitude than the SCA effects for glucosinolate, erucic acid and protein content. The parental genotypes NUM009, NUM123, NUM105 and NUM117 and their hybrids NUM009x NUM123, NUM103x NUM105, NUM113x NUM124 and NUM103x NUM120 had high GCA and SCA effects, respectively and therefore these could be exploited for further selection of high yielding progenies. The overall study reveals the importance of both additive and non-additive genetic variability suggesting the use of integrated breeding strategies which can efficiently utilize the additive as well as non-additive genetic variability.

Key words: Combining ability, general combining ability, specific combining ability, reciprocal combining ability, *Brassica juncea* L, diallel, yield.

INTRODUCTION

Since Pakistan imports large quantity of edible oil by spending huge amount of foreign exchange, the importance of oilseed crops in the country increases with every passing day. The share of oil extracted from species belonging to Brassicaceae family is the second highest after cotton seed. Of these species, rape and mustard are the two most important species. Brassica is a major source of edible oil used in several parts of the world. Oil of *Brassica juncea* (Czern. and Coss.), the Indian mustard is consumed in large quantity and the production ranks second among all oilseeds (Chopra and Prakash, 1991). Due to the presence of undesirable long chain fatty acids like erucic acid (50%) in the seed oil, it

becomes detrimental to human health. Erucic acid increases blood cholesterol, interferes in myocardial conductance and shortens coagulation time (Renard and McGregor, 1992). European economic committee has restricted cultivation of *Brassica* crop that contains more than 10% erucic acid content in their oil (Dhillon et al., 1992). Several works through selection, mutation as well as conventional breeding and modern biotechnological techniques have been reported for developing mustard variety containing low erucic acid (18: 2) (Anand and Downey, 1981; Chen et al., 1988). Both linoleic and linolenic acids are essential fatty acids; however, less than 3% linolenic acid is preferred for oil stability.

Advancement in the yield of mustard requires certain information regarding the nature of combining ability of parents available for use in the hybridization program and also the nature of gene action involved in the expression of quantitative and qualitative traits of economic importance. Information on general and specific combining ability effects is very important in making the next phase of a

*Corresponding Author E-mail: aliawaisj@hotmail.com.

Abbreviations: GCA, General combining ability; SCA, specific combining ability; RCA, reciprocal combining ability.

Table 1. Analysis of variance for oil quality traits of *B. juncea*, studied at NWFP, Pakistan.

S/N	Characters	Replication (df = 1)	Mean squares genotype (df = 63)	Error (df = 63)
1	Oil %	9.41**	12.34**	0.16
2	Glucosinolate	0.61**	210.12**	24.89
3	Erucic acid	0.12ns	230.43**	0.88
4	Protein	4.06*	6.06**	0.04
5	Oleic acid	30.62**	16.50**	0.2

*p < 0.05, **p < 0.01.

Table 2. Analysis of variance for combining abilities in eight *B. juncea* genotypes and their F₁s.

S/N	Characters	GCA (df = 7)	SCA (df = 28)	RCA (df = 28)	Error (df = 126)
1	Oil %	18.41**	4.55**	18.38**	0.2
2	Glucosinolate	758.57**	133.26**	154.66**	0.01
3	Erucic acid	290.69 ^{ns}	131.30**	253.51**	0.07
4	Protein	8.12 ^{ns}	5.50**	6.58**	1.18
5	Oleic acid	17.0 ^{ns}	11.91 ^{ns}	16.15*	9.53

breeding program.

Many people working on combining ability have reported general combining ability (GCA) and specific combining ability (SCA) effects for yield and yield components in different crops (Nassimi et al., 2006; Dorrel and Downey, 1964; Harvey and Downey, 1964; Kondra and Stefansson, 1995; Brown et al., 1999; Smith and Donald, 1988; Satwinder et al., 2000). With a few exceptions, all the studies showed significant GCA and SCA effects for yield and component characters indicating that both additive and non-additive gene action were important in the inheritance of these traits.

The main objective of the present study is to identify the best combiners and their crosses on the basis of their general, specific and reciprocal combining ability for oil and its associated traits.

Materials and Methods

The experiment was conducted at NWFP Agricultural University, Peshawar. Eight *B. juncea* L. genotypes were selected from the pool of the national uniform mustard yield trail. These genotypes were labeled as NUM009, NUM103, NUM105, NUM113, NUM117, NUM120, NUM123 and NUM124 in the text and were crossed manually in all possible combinations in an 8 x 8 diallel fashion during the Rabi season 2004 - 2005. In 2005 - 2006, seeds of 56 F₁ hybrids and their parental lines were sown in a randomized complete block design with two replications. Each plot comprised of 8 F₁s or parent plants having row length 4 m while the distance between row to row was 1 m and plant to plant was 30 cm. The experimental crop was irrigated when needed. Plants were grown with normal agricultural practices.

Data were recorded on oil percentage (%), glucosinolate, erucic acid, protein% and oleic acid content. The quality analysis for oil and its associated traits were determined through nuclear infrared spectroscopy (NIRS) at the Nuclear Institute for Food and Agriculture (NIFA) Tarnab Peshawar, Pakistan. The data were subjected to analysis of variance according to Steel and Torrie (1980).

Combining ability effects were computed according to Griffing (1956).

RESULTS AND DISCUSSION

Analysis of variance presented in Table 1 showed that for genotypes, highly significant differences ($p \leq 0.01$) were obtained for all traits studied viz., oil%, glucosinolate, erucic acid, protein and oleic acid. Since genotypic variations were significant for all the characters, these variations were partitioned into variation components, for example, GCA, SCA and reciprocal combining ability (RCA) effects (Table 2). In Tables 3 and 4, diagonal values represent the GCA effects, above diagonal SCA effects and below diagonal reciprocal effects.

Oil content (%)

Data for oil% in different genotypes of *B. juncea* indicated that the range for parental genotypes was 39.2 to 45%, in which the lowest percentage was exhibited by NUM105 while the highest was by NUM117 with a mean value of 42.5%. For crosses involving NUM103, oil% ranged from 39.8 to 43.5% where lowest value was recorded in NUM103 x NUM120 and highest in NUM103 x NUM117. For crosses of NUM009, data was in the range of 38.4% in NUM009 x NUM120 to 42.3% in NUM009 x NUM103. For crosses concerning NUM124, range was 43.2 to 48.8% whereas lowest oil was recovered from NUM124 x NUM113 and the maximum from NUM124 x NUM103. For crosses pertaining NUM113, oil% ranged from 42.7% for NUM113 x NUM120 to 47% in NUM113 x NUM124. For crosses with reference to NUM123, range was 42.1%

Table 3. Estimates of general combining ability effects for oil quality traits in an 8 x 8 diallel cross of *B. juncea* genotypes.

Parents	Oil %	Protein	Glucosinolate	Erucic acid	Oleic acid
NUM009	-0.86	0.1	0.51	-2.37	1.08
NUM103	-0.19	-0.04	-7.27	-4.89	-0.16
NUM105	-0.85	-0.51	7.05	3.63	0.7
NUM113	1.05	-0.49	-4.92	-3.93	-0.15
NUM117	0.92	-0.03	3.5	5.41	0.46
NUM120	-0.48	0.68	5.28	-1.16	-0.7
NUM123	-0.67	0.52	0.46	1.02	-0.17
NUM124	1.07	-0.23	-4.61	2.32	-1.07

Table 4. Estimates of specific combining ability effects for oil quality traits in an 8 x 8 diallel cross of *B. juncea* genotypes.

Cross Combination	Oil %	Protein	Glucosinolate	Erucic acid	Oleic acid
NUM009 x NUM124	-0.03	-0.78	6.06	-7.37	0.76
NUM009 X NUM113	0.24	-0.02	-3.82	-3.28	-1.45
NUM009 x NUM123	-0.54	-0.08	10.55	-2.03	1.82
NUM009 x NUM117	1.37	-1.83	4.11	-11.01	-0.11
NUM009 x NUM105	1.25	-0.4	-4.15	13.72	1.46
NUM009 x NUM120	-0.78	0.86	-0.32	1.67	1.1
NUM103 x NUM009	-0.57	0.37	6.27	1.14	-0.85
NUM103 x NUM124	0.7	-1	-13.71	-3.85	2.45
NUM103 X NUM113	-0.48	0.96	2.21	4	-1.07
NUM103 x NUM123	-0.01	-0.45	-5.32	-3.61	-0.3
NUM103 x NUM117	0.35	-0.6	-1.21	7.01	-0.43
NUM103 x NUM105	-0.02	-0.42	3.59	-0.56	2.99
NUM103 x NUM120	0.1	-1.31	6.21	0.08	-0.72
NUM105 x NUM120	-0.38	0.56	-1.36	-0.89	-5.09
NUM113 x NUM123	0.35	-1.9	4.25	-1.97	1.79
NUM113 x NUM117	-0.52	0.06	-1.7	-2.65	4.66
NUM113 x NUM105	2.63	-1.41	-0.71	-2.18	-2.52
NUM113 x NUM120	-1.69	-0.31	3.02	-4.28	0.42
NUM117 x NUM105	-1.48	-0.18	5.07	-3.81	0.07
NUM117 x NUM120	-0.86	0.38	-6.3	-3.06	1.58
NUM123 x NUM117	1.38	0.59	-2.83	1.7	1.82
NUM123 x NUM105	0.35	0.72	-15.34	-2.38	-0.6
NUM123 x NUM120	0.18	-1.02	6.54	3.37	1.29
NUM124 X NUM113	-0.39	-0.55	0.3	7.99	-1.54
NUM124 x NUM123	0.23	-0.61	0.27	-0.86	1.64
NUM124 x NUM117	-0.06	-0.06	7.03	2.81	-2.82
NUM124 x NUM105	0.12	0.32	7.27	-2.27	0.6
NUM124 x NUM120	1.74	-0.47	-0.85	-0.03	-1.96

(NUM123 x NUM105) to 44.4% (NUM123 x NUM117). Data for crosses pertaining to NUM117 ranged from 37% (NUM117 x NUM120) to 47.6% (NUM117 x NUM009). For crosses relating to NUM105, the range was 39.2%

(NUM105 x NUM117) to 45.8% (NUM105 x NUM113). For crosses of NUM120, data ranged from 41.8 to 45.8%, in which the lowest oil was recorded in NUM120 x NUM113 and highest in NUM120 x NUM103. The mean value of

oil% for F_1 s was 43.5% and grand mean, 43.0%.

Glucosinolate content (μMolg^{-1})

Data for glucosinolate contents ranged from 100.1 to 132.2 μMolg^{-1} for parental genotypes in which the lowest level was found by NUM009 and highest by NUM105, with a mean value of 113.3 μMg^{-1} . Data for the crosses of NUM103 ranged from 102.6 to 132.5 μMg^{-1} with the lowest for NUM103 x NUM123 and highest for NUM103 x NUM120. For crosses relating to NUM009, range was 105.3 μMg^{-1} in NUM009 x NUM113 to 132 μMg^{-1} for NUM009 x NUM105. For crosses pertaining NUM124, range was from 95.1 μMg^{-1} (NUM124 x NUM103) to 123.7 μMg^{-1} (NUM124 x NUM117). For crosses with reference to NUM113, data ranged from 87 to 123.5 μMg^{-1} where minimum was attained by NUM113 x NUM105 and maximum by NUM113 x NUM120. For crosses pertaining NUM123, data ranged from 108.7 to 137.5 μMg^{-1} where lowest value was exhibited by NUM123 x NUM103 and highest by NUM123 x NUM105. For crosses relating to NUM117, range was 108.7 μMg^{-1} in NUM117 x NUM103 to 128.8 μMg^{-1} in NUM117 x NUM009. For crosses involving NUM105, range was from 119.4 μMg^{-1} in NUM105 x NUM009 and NUM105 x NUM113 to 132.9 μMg^{-1} in NUM105 x NUM123. For crosses relating to NUM120, data ranged from 111.5 to 133.2 μMg^{-1} where the lowest amount was recorded in NUM120 x NUM103 and the highest in NUM120 x NUM105. The mean value for F_1 s was 119.1 μMg^{-1} and grand mean was 116.2 μMg^{-1} .

Erucic acid content (%)

Data for erucic acid content ranged from 13.6 to 47.4% for parental genotypes in which the lowest was recorded in NUM103 and the highest in NUM117. The mean value for erucic acid content of parental genotypes was 29.7%. For crosses concerning NUM103, data ranged from 11.6 to 31.6% while the lowest amount was recorded for NUM103 x NUM113 and highest for NUM103 x NUM123. For crosses relating to NUM009, range was from 11.5% (NUM009 x NUM117) to 41.5% (NUM009 x NUM105). For crosses involving NUM124, values were in the range of 16.4% for NUM124 x NUM103 to 44.5% for NUM124 x NUM117. For crosses of NUM113, range was 10.8% in NUM113 x NUM120 to 33.8% in NUM113 x NUM103. Data for the crosses of NUM123 ranged from 8.6% in NUM123 x NUM103 to 42.3% in NUM123 x NUM120. For crosses involving NUM117, range was from 17.2% (NUM117 x NUM120) to 48.2% (NUM117 x NUM103). For crosses relating to NUM105, data ranged from 19.6 to 44.1% in which the lowest value was exhibited by NUM105 x NUM117 and highest by NUM105 x NUM009. For crosses concerning NUM120, range was 17.1 to 40.3% where the lowest was noted for NUM120 x NUM124 and the highest for NUM120 x NUM117. The

mean value for F_1 s was 27.3% and the grand mean was 28.5 %.

Protein content (%)

Data for protein% indicated that the range for parental genotypes was 25.6 to 29.6% in which the lowest percentage was exhibited by NUM105 while the highest was by NUM123 with a mean value of 28.00%. For crosses involving NUM103, protein% ranged from 26.1 to 27.6% where lowest value was recorded in NUM103 x NUM009 and NUM103 x NUM105 and highest in NUM103 x NUM124. For crosses of NUM009, data was in the range of 24.8% in NUM009 x NUM117 to 28.2% in NUM009 x NUM120. For crosses concerning NUM124, range was 21.5 to 25.6% where lowest protein was recovered from NUM124 x NUM103 and the maximum from NUM124 x NUM123. For crosses pertaining NUM113, protein% ranged from 22.6% in NUM113 x NUM123 to 26.4% in NUM113 x NUM120. For crosses with reference to NUM123, the range was 25.1% (NUM123 x NUM103) to 28% (NUM123 x NUM105). Data for crosses pertaining to NUM117 ranged from 22.8% (NUM117 x NUM103) to 28.5% (NUM117 x NUM123). For crosses relating to NUM105, range was 23.5% (NUM105 x NUM113) to 27.0% (NUM105 x NUM120). For crosses of NUM120, data ranged from 23.8 to 27.4 % in which the lowest protein was recovered from NUM120 x NUM103 and the highest from NUM120 x NUM117. The mean value of protein% for F_1 s was 25.5% and grand mean, 26.75%.

Oleic acid (%)

Data for oleic acid contents ranged from 33.3 to 37.8% for parental genotypes in which the lowest ranged was presented by NUM120 and highest by NUM117, with the mean value of 35.9%. Data for the crosses of NUM103 ranged from 35.3 to 45.7% with lowest for NUM103 x NUM113 and highest for NUM103xNUM105. For crosses relating to NUM009, range was from 37.1% for NUM009 x NUM113 to 41.3% for NUM009 x NUM123. For crosses pertaining NUM124, range was from 31.8% in NUM124 x NUM123 to 41.2% in NUM124 x NUM113. For crosses with reference to NUM113, data ranged from 35.4 to 47.0% where minimum oleic acid was found in NUM113 x NUM124 and maximum in NUM113 x NUM117. For crosses pertaining to NUM123, data ranged from 38.4 to 40.5% where lowest value was exhibited by NUM123 x NUM103 and highest by NUM123 x NUM120. For crosses relating to NUM117, range was 33.6% in NUM117x NUM123 to 41.2% in NUM117 x NUM105. For crosses involving NUM105, range was from 34.8% in NUM105 x NUM113 to 41% in NUM105 x NUM009. For crosses relating to NUM120, data ranged from 36.1 to

41.3% where the lowest amount was presented by NUM120 x NUM123 and the highest by NUM120 x NUM105. The mean value for F_1 s was 38.8% and grand mean was 37.35 %.

In the present study, majority of the traits present significant differences which indicate that there is enough variability available for an effective selection. Our results are strengthened by the early findings of Ghosh and Gulati (2001), whose study on genetic variability and association among 12 yield components, also found significant variation for qualitative traits in *B. juncea*. Our result is further supported by the findings of Nazer et al. (2003), who studied variability and genetic advance, correlation and path analysis of seed yield and yield components. They found significant differences among genotypes for most of the traits. Similarly, Hu et al. (1988) found significant variation for oil, glucosinolate and protein from a diallel cross of six inbred lines of *Brassica carinata*. Similarly, Ping et al. (2003) also reported significant variation for seed oil concentration however, oil concentration of seed ranged from 36 to 46%. Bradshaw and Wilson (1998) and Krzymanski et al. (1999) found significant variation among brassica lines for glucosinolate content. Nassimi et al. (2006) studied population variation during three cycles of selection for increased meal protein content and quantify the relationships of protein with oil.

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