

GENETIC VARIABILITY STUDIES IN BRASSICA F₂ POPULATIONS DEVELOPED THROUGH INTER AND INTRA-SPECIFIC HYBRIDIZATION

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Abstract

Assessment of variability and the heritable proportion of this variability are crucial to estimate the genetic advance in oilseed Brassica improvement, as in all crops. These may be variable in different segregating populations, including the F₂ populations of different crosses and should be studied to select the appropriate segregating population for further improvement. We; therefore, report on the estimation of variability, heritability and genetic advance for ten parental lines and the four intraspecific and four interspecific F₂ populations of brassica at New Developmental Farm, of the University of Agriculture, Peshawar for biochemical parameters. The experimental material studied was grown in the 1st week of October, 2010 in a randomized complete block design with three replications. In all genotypes highly significant ($p \leq 0.01$) differences were recorded for protein, glucosinolates, oleic acid, oil, erucic acid and linolenic acid content. Parental genotypes N-507, N-542 and N-2740 were superior in high oil, protein and oleic acid contents. Parental lines C-118, N-2740, N-532 were better for lower glucosinolate, linolenic and erucic acid contents. All the F₂ populations were comparatively better than their respective parental genotypes for oil, glucosinolate, erucic acid, protein, oleic acid and linolenic acid content. F₂ populations N-502×N-507, N-540×J-109 had high range of genetic variability, heritability and genetic advance.

Introduction

Edible oil is one of the most important commodities imported into Pakistan from abroad due to low domestic production. Oilseed Brassica species (*Brassica napus*, *B. campestris* and *B. juncea*) are now the 3rd most important source of edible vegetable oil worldwide after Palm and Soybean (Zhang & Zhou, 2006). *B. campestris*, cultivated in India and Pakistan, contains more concentration of erucic acid (40-50%) and high glucosinolates (80-160 $\mu\text{m g}^{-1}$) (Agnihotri & Kaushik, 1999) that make it unsuitable for human and animal (Inamullah *et al.*, 2013). Therefore there is need to develop new varieties, containing low erucic acid (<2%) and glucosinolate (<30 $\mu\text{m g}^{-1}$) and higher yield potential (Kaushik, 1998).

Traits which have high range of genetic variability, heritability and genetic advance would be an effective tool to improve seed yield (Ali *et al.*, 2013). To improve the production of edible oil the main goals of plant breeders in any breeding program are to estimate genetic diversity and its inheritance using agro-morphological characters. Experiments were conducted to determine the extent of genetic variability and relationships among the Brassica carinata germplasm (Zada *et al.*, 2006). In breeding program the high amount of heritability alone cannot bring incredible change in selection therefore it should be accompanied with genetic advance to do reliable selection (Shulka *et al.*, 2006). The traits having high heritability with high genetic advance are considered under control of additive genes, whereas with high heritability and low genetic advance are under the control of non-additive (dominant and/or epistatic) genes which limits the scope of improvement through selection (Akbar *et al.*, 2003). Considerable work has been done in Brassica species to estimate heritability and genetic advance of biochemical traits. Lower heritability (0.89 and 0.86) has been reported by (Schierholt and Becker

2001) for glucosinolate. Zhang *et al.*, (2006) also reported lower heritability for yield and biochemical traits, which may be due to difference in genotypes or environmental influence. Chauhan *et al.*, (2002) also reported moderate to high heritability with high genetic advance (45.0-62.5%) for erucic acid content.

Once the variability is determined, the estimation of the heritable proportion of this variability is crucial to estimate the genetic advance. These may be variable in different segregating populations, including the F₂ populations of different crosses should be studied to select the appropriate segregating population for further improvement. Thus like all quantitative traits, the improvement of edible oil production could be attained through estimation of genetic diversity and its inheritance not only to the traits related to edible oil, but also in other traits. The present study was thus designed to assess the variability and heritability in various F₂ populations and their parents.

Materials and Methods

The tested germplasm included 10 parental lines and eight F₂ populations of Brassica were grown at the University of Agriculture, Peshawar, Pakistan in the 1st week of October, 2010. The F₂ populations included both intra and inter specific crosses. Seeds obtained from F₁ hybrids of the four intra-specific crosses *i.e.*, *B. napus* × *B. napus* (N-501×N-2740), (N-502×N-507), (N-507×N-501), (N-548×N-501) and four interspecific crosses *i.e.*, *B. napus* × *B. campestris* (N-501×C-118), (N-542×C-118) and *B. napus* × *B. juncea* (N-532×J-109), (N-540×J-109) were space planted along with their parental lines to raise F₂ populations. Plant to plant distance was 20 cm and row to row distance was 60 cm. Row length was 5m. At maturity data was recorded on oil (%), protein (%), glucosinolate ($\mu\text{mol g}^{-1}$), erucic

acid (%), oleic acid (%) and linolenic acid (%) contents. Analysis was made for means, variability, broad sense heritability and genetic advance. Broad-sense heritability was estimated as (Mahmud & Kramer, 1951). Heritability values were categorized as < 20% = low, 20-50% = moderate and > 50% = high (Stansfield, 1986). Expected genetic advance for these traits were calculated according to (Allard, 1999) at 20% selection intensity. Genetic advance as percent mean was categorized as low = 0-10%, moderate = 10-20% and high = 20% and above (Johnson *et al.*, 1955). Coefficient of variations was also worked out for the above mentioned traits. Although both parental lines and F₂ populations were sown in randomized complete block designs, separate analyses of variance was carried out for parents and F₂ populations, as the segregating populations could not be repeated.

Results

Analyses of variance (Table 1) of the parental lines revealed non-significant differences for all the studied parameters except oleic acid while the segregating population F₂ was highly significant ($p \leq 0.01$). Among parents maximum oil contents (49.8 %) were observed in genotype (N-540) and minimum oil contents (41.3%) were attained by genotype (N-502). In F₂ populations cross (N-548×N-501) had minimum of 48.2% oil content while cross (N-502×N-507) had the maximum of 49.8% oil content (Table 2). The protein content ranged from 21.1% for genotypes (N-540), (N-542) to 31% for genotype (N-507) among parents. In F₂ populations highest amount (22.2%) of protein were found in (N-501×N-2740) while lowest amount (20.9%) was present in (N-532×J-109). The maximum glucosinolates (121.6 $\mu\text{mol g}^{-1}$) were found in genotype (C-118) whereas, minimum glucosinolates contents (72.4 $\mu\text{mol g}^{-1}$) were observed in (N-502). In F₂ populations the cross (N-502×N-507) had the maximum (116.2 $\mu\text{mol g}^{-1}$) glucosinolate content and cross (N-540×J-109) had minimum (102.3 $\mu\text{mol g}^{-1}$) glucosinolate content. Mean (Table 2) shows that parental genotype (C-118) had low value (33.8%) of oleic acid, while (N-2740) had high value (50.4%) for

oleic acid. In F₂ populations cross (N-501×N-2740) had minimum (32.9%) oleic acid while the hybrid (N-542×C-118) had the maximum (38.9%) oleic acid. Means (Table 2) shows that parental genotype (N-2740) had minimum (6.2%) linolenic acid while (J-109) had the maximum content. In F₂ populations cross (N-501×C-118) and (N-542×C-118) had minimum (15.5%) linolenic acid and cross (N-540×J-109) showed the maximum (19.2%) linolenic acid. Among parents minimum erucic acid contents (29%) were observed in (N-532) and the maximum erucic acid contents (49.4%) in (N-507). In F₂ populations cross (N-501×N-2740) had minimum (27.6%) erucic acid while cross (N-532×J-109) had the maximum percentage of (37.4%) erucic acid content.

The heritability estimate (broad sense) was studied in F₂ populations and was found high for all the parameters. It were high for oil in all the crosses (>50%) (Table 3). The genetic advance recorded as per cent mean for oil content of each cross was moderate ranged from (11.11-19.08). Heritability for protein ranged from (79.93-92.11%). The highest genetic advance as a percent mean for protein (27.09%) in this study was predicted for hybrid (N-502×J-109). Heritability was high for glucosinolate content in all F₂ populations which ranged from 71.75-98.16%. Genetic advance for glucosinolate was high in some crosses like (N-501×C-118), (N-501×N-2740), (N-532×J-109) and (N-540×J-109) while the remaining crosses showed moderate genetic advance. Heritability for oleic acid in F₂ populations ranged from (84.49 - 91.8%). Genetic advance for oleic acid was high in some crosses like (N-507×N-501), (N-501×N-2740), (N-502×N-507), and (N-542×C-118) while the remaining crosses showed moderate genetic advance. Heritability for linolenic acid in F₂ populations ranged from (84.15-99.6%). Genetic advance as a percent mean was high in all crosses for linolenic acid. Heritability for erucic acid in F₂ populations ranged from (86.71- 95.4%). Genetic advance was high in all crosses except in cross (N-540×J-109). Coefficients of variability were high in oil and linolenic acid, moderate in glucosinolate and low in protein and oleic acid.

Table 1. Mean squares for biochemical parameters of parents and F₂ populations in brassica.

Source of variation	df	Oil	Protein	Glucosinolates	Oleic acid	Linolenic acid	Erucic acid
Replications	2	3.52	1.37	74.69	1.45	4.91	22.74
Genotypes	17	61.61	20.43	533.60	94.56	39.82	96.94
Parents (P)	9	31.57ns	0.50ns	60.30ns	14.02*	4.72ns	39.05ns
F ₂	7	84.84**	29.57**	804.36**	145.01**	54.66**	132.82**
P vs F ₂	1	62.74	77.61	1409.94	14.02	152.00	179.23
Error	34	31.71	1.12	81.92	204.40	6.19	49.70
C.V (%)		15.94	4.64	8.50	5.78	17.25	20.53

*, **, = Significant at 0.05 and 0.01 level, respectively
ns = Non-significant

Table 2. Means for biochemical parameters of parents and F₂ populations of *Brassica*.

Genotypes	Oil (%)	Protein (%)	Glucosinolates ($\mu\text{M g}^{-1}$)	Oleic acid (%)	Linolenic acid (%)	Erucic acid (%)
Parents						
N-548	44.6	21.8	113.2	35.5	15.5	42.3
C-118	45.1	22.2	121.6	33.8	16.5	34.6
N-501	42.6	24.7	86.6	49.1	7.0	41.3
N-532	48.9	21.3	109.7	36.5	15.0	29.0
N-507	47.4	31.0	97.9	36.7	13.2	49.4
N-2740	42.3	25.2	82.1	50.4	6.2	37.4
J-109	45.2	24.7	115.6	35.8	16.7	30.1
N-540	49.8	21.1	111.6	33.9	16.5	30.5
N-502	41.3	26.1	72.4	50.0	7.7	35.0
N-542	48.7	21.1	107.9	37.2	15.1	30.1
Mean (M)	45.59	23.92	101.86	39.89	12.94	35.97
Intraspecific crosses						
N-502×N-507	49.8	21.4	116.2	35.2	15.8	34.8
N-548×N-501	48.2	21.9	113.3	34.2	16.7	33.8
N-507×N-501	49.0	21.4	110.5	34.7	15.8	33.3
N-501×N-2740	49.5	22.2	114.8	32.9	15.6	37.4
Mean (M)	49.12	21.72	113.7	34.25	15.97	34.82
Interspecific crosses						
N-532×J-109	48.7	20.9	113.6	37.7	16.2	27.6
N-540×J-109	49.0	21.2	102.3	38.6	19.2	28.8
N-542×C-118	48.7	21.3	110.9	38.9	15.5	28.2
N-501×C-118	48.6	21.7	115.7	35.7	15.5	34.4
Mean (M)	48.75	21.27	110.62	37.72	16.6	29.75
F₂ Means	48.93	21.5	112.16	35.98	16.28	32.28
Grand (M)	47.07	22.84	106.43	38.15	14.42	34.33
LSD(0.05)	3.633	1.759	15.03	3.66	4.129	11.7

Discussion

Genetic variability, heritability, genetic advance and correlation contribute to success of any crop improvement program (Nasim *et al.*, 2013). Our results are also encouraged by the research of Ping *et al.*, (2003) who stated significant variation for seed oil concentration. Parents were non-significant which were supported by Inayat *et al.*, (2009). Alemayehu *et al.*, (2005) also strengthened our findings by reporting significant variation for oil, glucosinolate and protein from a diallel cross of six inbred lines of *B. carinata*. Ping *et al.*, (2003) have reported significant values for protein meal ranging from 30 to 46%. Inayat *et al.*, (2009) analyzed the genotypes which were non-significant at 5% level of significance for protein percentage. Our results are in agreement with Inayat *et al.*, (2009), who reported genotype (MRS-1) had high amount (90.97 $\mu\text{mol/gm}$) of glucosinolate while genotype (Siren) had the lowest amount (44.83 $\mu\text{mol/g}$) of glucosinolate. Similar observations have been reported by Khulbe *et al.*, (2000) and Bilgili *et al.*, (2002) who detected significant differences in it. Oleic acid content was highly significant at 1% level of significance (Inayat *et al.*, 2009). The oleic acid percentage observed for five genotypes viz. HS-98, Altex, Oscar, Dunkled and Rainbow showed significant result at 1% level of probability (Ahmad *et al.*, 2008). Khan *et al.*, 2008 revealed highly significant differences ($p \leq 0.01$) for linolenic acid content among genotypes. A minimum erucic acid of < 2% is desired for

good quality oil which increased taste and flavor (Mumtaz *et al.*, 2001). Inayat *et al.*, (2009) also confirmed our results by reporting significant variation for glucosinolate, oleic acid, and erucic acid in rapeseed.

High heritability with high genetic advance showed that selection could be made with great success. Ghosh & Gulati (2001) also reported high heritability estimates for oil content in brassica. According to Pradeepkumar *et al.*, (2001), only high broad sense heritability does not always entail better selection due to the occurrence of non-additive variance. In addition, genetic advance as percentage of the mean becomes a useful indicator of gain from selection in particular populations for specific traits (Kalia *et al.*, 2005). High heritability accompanied by high genetic advance in this population is suggestive of additive gene action. Khan *et al.*, (2008) reported 0.15 heritability values for protein content in nine *Brassica* genotypes i.e., six F_{3,4} populations and three standard checks. Glucosinolates content is an essential quality trait in *Brassica* species which affects the quality of rapeseed and mustard cake. Canola type varieties are more desirable as far as erucic acid and glucosinolates contents are concerned (Mumtaz *et al.*, 2001). Canola contains less than 30 $\mu\text{mol g}^{-1}$ of defatted meal (Kumar *et al.*, 2009). Higher heritability for oleic acid and linolenic acid is confirmed by Schierholt & Becker (2001) who also obtained the same extent of heritability. Chauhan *et al.*, (2002) also stated moderate to high heritability for erucic acid content and high genetic advance.

Table 3. Heritability (Broad sense) h^2 and genetic advance (GA) for biochemical parameters of F_2 populations of *Brassica*.

Crosses	Oil (%)	Protein (%)	Glucosinolates ($\mu\text{M g}^{-1}$)	Oleic acid (%)	Linolenic acid (%)	Erucic acid (%)
N-501×C-118						
h^2	89.5	84.72	93.47	85.99	84.15	91.30
GA	6.74	4.458	29.00	6.90	3.86	24.85
GA %	19.08	19.52	27.25	18.10	26.76	72.38
N-548×N-501						
h^2	77.4	85.61	87.63	88.48	86.78	92.61
GA	4.23	4.718	20.24	7.61	4.18	23.80
GA %	11.97	20.65	19.02	19.94	29.00	69.33
N-507×N-501						
h^2	80.50	79.93	86.18	91.27	90.12	93.04
GA	4.74	4.39	18.48	8.71	5.02	25.36
GA %	13.42	19.24	17.36	22.82	34.81	73.87
N-501×N-2740						
h^2	74.78	87.72	89.13	89.76	93.02	94.66
GA	3.93	5.96	22.04	8.34	6.15	24.76
GA %	11.11	26.13	20.71	21.87	42.67	72.11
N-532×J-109						
h^2	99.99	88.90	98.16	87.16	97.34	86.71
GA	8.09	6.18	64.11	7.48	13.33	22.41
GA %	13.01	27.09	60.24	19.62	92.37	65.25
N-502×N-507						
h^2	81.14	92.11	71.75	91.79	92.39	95.40
GA	5.15	5.96	13.01	9.01	6.59	27.84
GA %	14.58	26.13	12.22	23.63	45.72	81.08
N-540×J-109						
h^2	83.48	86.29	85.63	84.49	99.60	94.66
GA	6.14	5.93	21.59	6.97	16.05	6.62
GA %	17.40	25.97	20.28	18.28	24.83	10.66
N-542×C-118						
h^2	82.39	80.73	79.65	90.37	88.86	90.16
GA	4.98	3.39	18.53	9.00	4.98	26.32
GA %	14.11	14.80	17.41	23.58	34.52	76.66

Conclusions

The traits having high heritability with high genetic advance are considered under control of additive genes, whereas high heritability low genetic advance under control non-additive (dominant and/or epistatic) genes which limits the scope for improvement through selection (Akbar *et al.*, 2003). In the present study broad sense heritability was high (>50%) for all characters. Genetic advance as a percent mean was high to moderate in all the crosses indicating that improvement or selection could be made. The results from the current study showed that all the F_2 populations were comparatively better than their parental genotypes for oil, glucosinolate, erucic acid, protein, oleic acid and linolenic acid content. Parental genotypes (N-540), (N-502) and (N-2740) and F_2 populations (N-502×N-507), (N-501× N-2740) and (N-542×C-118) were found

superior with regards to high oil content, protein content and oleic acid content and parental genotypes (N-502), (N-2740), (N-532) and F_2 populations (N-540×J-109), (N-542×C-118), (N-501×C-118) and (N-532×J-109) were found superior with regards to lower glucosinolate, linolenic acid and erucic acid content.

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