

## A Review on Genetics of Seed Yield and Quality Related Traits in *Brassica* Group

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**Abstract:** Pakistan is facing severe shortage of edible oil and expended heavy cost on the import of edible oil. Rapeseeds and Mustards (*Brassica* group) crops are important oilseed crops. These can be a good source for fulfilling the gap between local production and consumption due to their adaptability to Pakistani climate. Major problems in current *Brassica* varieties are low quality oil with high percentage of erucic acid, low yielding, aphid attack, white rust of crucifer and shattering at maturity and lodging problem due to rain and winds. For overcoming these problems it is necessary to get knowledge about genetics of *Brassica* group. There are many contradictions in genetics of *Brassica* group i.e., genetic control of seed color, additive and dominance control of traits and maternal effects etc. That's why in this research paper information from previous literature of *Brassica* is discussed.

**Key words:** Combining ability • Diallel • General combining ability (GCA) • Heterosis • Specific combining ability (SCA)

### INTRODUCTION

Pakistan is facing a severe shortage of domestic edible production than its demand. Production of edible oil is 34% (0.606 million tons) of its total requirement (2.325 million tons). Pakistan spent Rs.1.719 billion on the import of edible oil. Share of rapeseeds share in the local production is 0.068 million tons (about 11.22%) [1]. Due to this alarming situation immediate attention is needed.

Rapeseed and mustards (*Brassica* oilseeds) crops is the 2<sup>nd</sup> larger producer of vegetable oil after cottonseed in Pakistan. They can be good source for fulfilling the gap between production and consumption. They have oil contents 35 to 46 % [2].

They cover 0.183 million hectares in 2013 in comparison to the area of wheat and rice (8.693 million and 2.311 million hectares, respectively). The share of remaining oilseed crops (i.e. sunflower and soybean) is very low in local production of edible oil [1].

Major problems in current *Brassica* varieties are low quality oil with high percentage of erucic acid, low yielding, aphid attack, white rust of crucifer and shattering

at maturity and lodging problem due to rain and winds. Development of varieties with seed yield of economic value and high percentage of high quality oil is needed badly.

Their economic return is also a big problem for farmers. But with varieties of minimum life cycle, high quality oil percentage and highest yield, its area and production will be increased and farmers can be attracted towards it. Yellow seeded varieties have potential of more oil [2]. So breeding of high yielding yellow seeded varieties is very beneficial and needed for increasing oil yield.

The present research was an effort of gathering and developing information on genetics of different quality traits of *Brassica* which should be helpful for researchers to improve its oil quality. The relevant literature pertaining to study variability, gene action and heterosis for descriptive, seed yield and quality traits in *Brassica* species is briefly reviewed here.

**Genetics of Descriptive Traits:** Mohammad *et al.* [3] studied two Indian cultivars i.e., toria and brown sarson. They reported that the seed color is controlled by three

genes  $br_1$ ,  $br_2$  and  $br_3$ . If  $br_1$  loci is dominant, the color will be brown, if the  $br_2$  loci is dominant then the color will be red brown and if the dominance is at  $br_3$  loci results in yellow brown. The pure yellow color only appears when all the loci are in recessive form in toria.

Vera *et al.* [4] studied seed coat color inheritance in *B. Juncea*. They found that 8 out of 10  $F_1$ 's were of brown in color and 2 were of yellow color. They also found that in  $F_2$  and  $BC_1$ , the color was brown and yellow without any intermediate and ratio was 1/4 or 1/16 and  $0^{0.5}$  or 1/4, respectively which showed that brown color was dominant over yellow color. They concluded that seed coat color was controlled by two duplicate pairs of genes ( $R_1$  and  $R_2$ ), if any of them is present then brown color appears and yellow color appears only when both are in recessive form.

Stringam [5] investigated the seed inheritance color in one Swedish and three Canadian cultivars of *B. rapa*. Who observed consistent segregation in  $F_2$  and backcrosses. Who also reported that 2 independent genes  $Br_1$  and  $Br_3$  controlled the seed color inheritance. If dominance is present at  $Br_1$  locus then the color will be brown and if  $Br_3$  locus is dominant and  $Br_1$  locus is homozygous recessive, the color will yellow-brown. If both the loci are in homozygous recessive condition, the yellow color develops.

Hawk [6] studied association between hypocotyl color and seed color in turnip rape. Who crossed a green hypocotyl yellow seeded stock of early flowering with a cultivar torch. Who also found a complete association between these two characters. Who concluded that by transferring single recessive gene, yellow seeded varieties can be produced by taking benefit of the association.

Schwetka [7] studied seed color inheritance in turnip rape (*B. rapa*). Who made crosses between one brown seeded and seven yellow seeded lines of *B. rapa*. Who observed that seed color differences in all crosses were due to one or two genes and an epistatic effect. Who also observed that maternal parent has effect on seed color inheritance but it was not completely influenced by it. He found two genes ( $Br_1br_1$  and  $Br_6br_6$ ) having epistatic effects and four genes ( $Br_3br_3$ :  $Br_4br_4$ :  $Br_5br_5$  and  $Br_7br_7$ ) having hypostatic effects. Who found two recessive genes for yellow color inheritance ( $Br^1$  and  $Br^2$ ) which were present at  $Br_2br_1$  locus and also one other allele  $Br^1_6$  for yellow color which was present at  $Br_6Br_1$  locus.

Zhang *et al.* [8] studied inheritance of seed color in *B. napus*. They did conventional genetic analysis in  $F_1$ ,  $F_2$ ,  $F_3$ ,  $BC_1$ , which were derived from a yellow seeded (2127-17) and nine black seeded varieties. They found that

seed color was controlled by maternal genotype but also influenced by maternal, endosperm and embryonic genotype interactions. In combination of yellow seeded and four black seeded lines 1141B, 94560, 94545, SW0780, they found that the yellow seeded was partially dominant over black with two or three dominance epistasis ratio. However the yellow color resulted from these crosses was slightly darker than original parent 2127-17 yellow color. They also found that yellow seeded gene Y in *B. napus* showed epistatic effects on Black color genes B and C. But in the remaining crosses (HS No. 3, HS No.4, 94570, ZS No.10, XY No.15) the black seed was dominant over yellow. They discovered a new dominant gene D of black seed color which inhibits the action of dominant yellow color gene. Finally they concluded that seed color inheritance in *B. napus* is controlled by four genes, combination of Y, B, C and inhibitor gene D.

Rahman and Tahir [9] investigated seed coat color in  $F_1$ ,  $F_2$ ,  $F_3$  and back cross progenies of Ethiopian mustard (*B. carinata*). They made crosses between yellow and brown pure lines. They found that xenia effect was not present in seed coat color. They observed the segregation pattern according to monogenic incomplete dominance model. They concluded that yellow-brown and light yellow seeds were due to brown seed coat color gene and dominant repressor gene (Rp) interaction.

Rahman and McVetty [10] reviewed the seed color in Brassicas. They studied that seed quality of *Brassica* regarding oil, protein content, fiber contents might be improved by developing yellow seeded varieties. They concluded that seed color in *B. rapa* is controlled by two genes, seed color in *B. Juncea* in controlled by two duplicate genes and in *B. rapa* three genes controlled seed color in *B. napus*. They also found that yellow color appears in *B. carinata* because the normal color is suppressed by one gene and when that gene is absent then the resulting color would be brown.

Rather *et al.* [11] investigated inheritance of yellow seed coat color in brown sarson. They made crosses among two brown cultivars Gulchin and KOS-1 and one yellow cultivar Yellow Sarson-1. They concluded that there is monogenic control of seed coat color and black color is dominant over yellow color. They set up five yellow seeded brown sarson populations (three from Gulchin x Yellow Sarson-1 and two from KOS-1 x Yellow Sarson-1) and by considering Gulchin as check variety, they observed higher seed weight and high oil content than check in  $BC_2F_3$ . Among these four populations second population was high in oil yield than check.

Finally, they concluded that yellow seed coat color is controlled by single gene and development of yellow seeded varieties is a very best approach for increasing oilseed production in brown sarson.

Rahman [12] studied the inheritance of leaf hairiness and seed color in  $F_1$ ,  $F_2$ ,  $F_3$  and backcross progenies of a hairiness and brown seeded line of a *B. rapa* subsp. *Chinensis* and non-hairy yellow seeded line *B. rapa* var. *trilocularis*. He examined the leaf hairiness, seed color segregation and their joint effect in  $F_2$  and backcross populations. Who observed a color pattern of brown, yellow-brown and yellow in segregating population and also observed that leaf hairiness was dominant over non-hairiness. Who found seed color was under digenic control and leaf hairiness was under monogenic control. Who concluded that genes controlling leaf hairiness and seed color are inherited independently.

#### **Genetics of Plant and Seed Yield Related Traits:**

Dorn and Olds [13] found a strong positive correlation among flowering height and flowering date in *B. rapa*. They did not found any plant which are tall and early flowering present in them. They also found that plant size and flowering height are positively correlated with seed yield. They concluded that the small size plants evolve due to early flowering and large size plants evolved due to late flowering.

Iqbal *et al.* [14] found highly significant variation for almost all seed yield related traits in among parents and their hybrids in *B. Juncea*. Variation was not observed significant in days taken to maturity. They observed additive gene action days taken to flowering. They concluded that days taken to flowering were controlled by dominant gene action. They finally concluded that non-allelic interaction was absent as regression line deviated non-significantly from the unit slope.

Oghan *et al.* [15] found significant variation for yield and yield related traits, morphological traits, harvest index and 1000 seeds weight. They observed additive gene effects involved in genetic control of duration to flowering, number of seeds per siliqua and days to complete flowering, while non-additive gene effects were found to be more important for number of biological yield, siliqua per plant and days to maturity. They concluded that 100 seeds weight, plant height, number of branches and days to initial flowering were controlled by additive and non-additive gene action. They also concluded that additive and non-additive effects are equally important in

controlling seed yield. They also found high broad sense heritability for all traits and moderate narrow sense heritability for number of seeds per siliqua and 1000 seeds weight.

Pankaj *et al.* [16] reported significant SCA variances for all the traits. They observed non-significant GCA variances for siliqua length and plant height while for all other traits it was significant. They found greater reciprocal variances for SCA and GCA variances for number of primary branches per plant, siliqua length, siliqua on main shoot, seeds/ siliqua and plant height which indicated that maternal effects is more important in expression of these traits. They recommended the genotypes PT-9701, PT-9700, PT-9600 and PT-30 as good general combiners.

Ahmed [17] observed significant relationship in variability and G x E interaction in *B. rapa*. Who observed high phenotypic and genotypic coefficients for number of seeds per siliqua, secondary branches per plant, primary branches per plant and moderate phenotypic and genotypic coefficients for days to maturity. Who found positive phenotypic and genotypic correlation of seed yield per plant with all the traits. Who also found positive association between harvest index and seed yield per plant; number of seeds per siliqua and 1000 seeds weight; seed yield per plant and siliqua per plant; Seed yield per plant and number of seeds per siliqua. He concluded that General combining ability and specific combining ability both were important in inheritance of desired traits as GCA and SCA variances were found to be significant. Who also found significant better and mid parent heterosis for most of traits and observed highest heterosis for seed yield. Who concluded that heterosis breeding is a very economical and feasible method for production of commercial hybrids in *B. rapa*.

Sabaghnia *et al.* [18] estimated heterosis and combining abilities (GCA and SCA) in nine genotypes of five countries, i.e., Germany, Denmark, Iran, France and Sweden, crossing in a diallel design. The experimental material has been sown in two years in simple lattice design. They observed highly significant GCA and SCA mean squares. SCA genetic variance was found greater than GCA which showed non-additive gene action predominant. They found significant SCA × year interaction in overall analysis of variance in all traits inheritance and significant GCA × year interaction only for oil percentage and number of seeds per siliqua. They observed significant positive mid parent and high parent

heterosis for all the traits in different crosses. They concluded that parental genotypes (Opera and Talaye) had best GCA effects and any one of both as a parent produced excellent hybrids with valuable SCA for oil yield. They also concluded that F<sub>1</sub> hybrids Zarfam × Orient, Talaye × Orient and Talaye × Opera performances were best in heterosis and SCA and GCA determination. They recommended these genotypes could be used as source population for further selection or utilized as F<sub>1</sub> hybrids.

Sinhamahapatra *et al.* [19] developed lines of yellow seeded varieties and created improved breeding lines by transferring the multilocular siliqua character from a spontaneous erectophyle multilocular siliqua mutant. They concluded that the bilocular types yield higher number of siliqua per plant and tetralocular types gave higher number of seeds per siliqua. They increased the number of branches by crossing these lines spontaneous basal branching mutant and concluded that it helped in increasing number of siliqua per plant. They transferred the apetalous character from a spontaneous apetalous mutant and in result of this the waxy apetalous character gave higher yield than the others. Finally, they concluded that by transferring morphological characters to the elite lines of *B. rapa*, its yield can be improved.

Dar *et al.* [20] estimated heterosis for seed yield related traits in brown sarson (*B. rapa*). They used ten diverse genotypes (KOS-101, KOS-1, CR-1617, CR-2638, CR-2871, CR-2677, CR-1485, CR-1607 and CR-1630) for this estimation. They found CR-1485 × CR-1607 most desirable cross combination for seed yield and also estimated desirable better and mid parent heterosis for primary branches of plant and 100 seed weight. They observed the highest mid and better parent heterosis in KOS-1 × CR-2638 for number of siliqua on main raceme, CR-1607 × CR-1485 for primary branches/plant, CR-KOS-101 × CR-1630 for secondary branches/plant, KOS-1 × CR-1607 for days to maturity and CR-2871 × CR-1630 for number of siliqua/plant.

Rameeh [21] estimated narrow sense heritability, high parent heterosis, GCA and SCA effects in *B. napus* cultivars for seed yield, yield components and plant height. They observed significant variance for seed yield and siliqua per plant which indicated the importance of non-additive gene action in controlling the studying traits. They found significant average heterosis for almost all traits except seeds per siliqua. They estimated high narrow sense heritability for all traits except seeds per

siliqua which indicated the importance of additive gene effect for all traits except seeds per siliqua. They concluded that efficiency of high parent heterosis effect were more than SCA for all traits except siliqua per plant for superior cross combinations determination.

Ahsan *et al.* [22] estimated combing ability and heterosis in five lines and three testers of *B. napus* for 100 seeds weight, seed yield per plant, number of primary branches, number of secondary branches and plant height. They found significant genetic variation among the genotypes (parent and their crosses) for seed yield and yield components. Average heterosis was also found to be significant for all except plant height. High GCA and SCA ratio was observed which indicated the more importance of additive gene action for all except plant height. They observed significant positive SCA and GCA estimates. They concluded that in most of the crosses significant positive better parent heterosis was present for seed yield and recommended these hybrids as suitable candidate for improving seed and plant related traits.

Ali *et al.* [23] observed highly significant genetic variation for different traits in *B. carinata* lines. They estimated genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) of about 3.2-38.1% and 4.92 to 28.24% respectively. They recorded highest heritability for siliqua length and siliqua on main raceme of about 0.83 and 0.82 respectively. They observed highest genetic advance for siliqua on main raceme and seed yield per plant and significant positive phenotypic correlation for seed yield per plant with primary branches per plant and plant height and seed yield per plant with seeds per siliqua. They recommended *carinata*-83, *carinata*-45, *carinata*-38, *carinata*-29, *carinata*-7 and *carinata*-47 as superior genotypes for seed and yield traits. On overall basis, they recommended *carinata*-83 and *carinata*-70 best lines for use in future breeding programs.

Nasim *et al.* [24] conducted an experiment for estimating heritability, genetic variability, correlation and genetic advance for morphological traits in ten *Brassica* genotypes. Significant differences were observed among genotypes which indicated high genetic variability presence. They observed high genetic advance and high heritability plant height, flowering completion, 50% flowering and initiation of flowering, 100 seeds weight and seeds per siliqua. They observed positive correlation for seeds per siliqua with siliqua width and siliqua length; siliqua length with 100 seeds weight and siliqua width.

They recommended that siliqua length, seeds per siliqua, 100 seeds weight and plant height could be used as selection criteria for future breeding programs.

Zada *et al.* [25] estimated the genetic variability and relationships among agro-morphological characters of *B. carinata* germplasm. The germplasm consists of 134 accessions collected from abroad and from different climates of Pakistan. From seedling emergence to crop maturity 33 agro-morphological characters were characterized. They analyzed data by cluster and principle component analysis. They observed largest variation in seed yield and moderate variation in plant height, siliqua per main raceme and main raceme length. All accessions were categorized in seven clusters by hierarchical analysis. Total variability of 39.03% was observed in all accessions for agro-morphological traits. They recommended four genotypes (26190, 25994, 25942 and 25939) for future breeding program on the basis of seed yield per plant, greater yield potential and 100 seeds weight.

Muhammad *et al.* [26] performed 4 x 4 diallel for estimating heritability and combining ability in *B. napus*. They observed significant differences among entrees for siliqua length, plant height, main raceme length and days to 50% flowering. They observed highest GCA in G9 parents for main raceme length. They recommended G6 parents a good general combiner for plant height, siliqua length and days to 50% flowering and G4 x G2 crosses best specific combination for siliqua length, plant height. And also for reciprocal effects they recommended G4 x G6 cross best combination for main raceme length. They concluded that main raceme length and plant height were highly heritable traits and best for use in future breeding programs and additive and non-additive effects could be exploited efficiently for making breeding strategies for above traits.

**Genetics of Quality Traits:** Chen and Heneen [27] determined the fatty acid composition of *B. napus* resynthesized lines which were raised through the four crosses of *B. rapa* and *Brassica alboglabra*. They observed that high oleic acid contents might be partially hypostatic or transgressive epistatic over low palmitic acid contents depending upon parent erucic acid contents. They observed additive gene action for low erucic acid contents, partial epistasis for low lenolenic acid and epistasis for high eicosenoic acid over low eicosenoic acid. They also observed epistasis in three out

of four crosses for high erucic acid contents and in one remaining cross hypostasis was observed. They concluded that for oleic acid *B. Juncea* have 2 genes, one from *B. rapa* and other from *B. oleracea*.

Iqbal *et al.* [14] found highly significant variation for almost all quality traits in among parents and their hybrids in *B. Juncea*. They observed additive gene action for erucic acid. They concluded that oil contents and glucosinolate contents were controlled by dominant gene action. They finally concluded that non-allelic interaction was absent as regression line deviated non-significantly from the unit slope.

Alemayehu and Heiko [28] found significant differences among parents and their hybrids. They also found significant cytoplasmic, dominance and additive effects for all traits in *B. carinata*. They accounted 40% variation in additive genetic variance almost twice as compared to dominance genetic variances. They also observed inbreeding depression for oil contents. They noticed partial dominance, also some level of over dominance for glucosinolate contents. They concluded that cytoplasmic effects in addition to nuclear genes were also responsible for inheritance of traits. They finally concluded that there were two dominant genes which have a decreasing effect on glucosinolate, while their recessive genes had a counter effect.

Oghan *et al.* [15] found significant variation for %age of oil. They observed additive gene effects involved in genetic control of %age of oil. They also concluded that additive and non-additive effects are equally important in controlling oil content. They also found high broad sense heritability for %age of oil.

Pankaj *et al.* [16] reported significant SCA variances for oil contents. They observed non-significant GCA variances oil contents. They found that maternal effects less important in expression of these traits. They recommended the genotypes PT-9701, PT-9700, PT-9600 and PT-30 as good general combiners.

Davik and Heneen [29] determined erucic acid inheritance in *B. rapa*, *B. alboglabra* and *B. napus*. They observed significant variation in 20 lines of *Brassica alboglabra* and classified them as high erucic acid types. They did not find any polymorphism in erucic acid genes. They observed that the erucic acid contents were controlled by one major gene in *B. rapa*. This gene showed partial dominance in three out of four crosses. They also made reciprocal crosses to check maternal effects in *B. rapa* and observed that the function of erucic

acid in cytoplasm is more efficient. They found more zero erucic acid individuals in F<sub>2</sub> of those crosses where females parent were of low erucic acid. They observed two loci controlling erucic acid in resynthesized *B. napus*. They found no maternal effects in *B. napus* but deviation was observed in F<sub>1</sub> hybrids which they concluded as partial dominance effect.

Ahmed [17] observed significant relationship in variability and G x E interaction in *B. rapa*. Who found negatively correlation in oil contents and maturity days. He concluded that General combining ability and specific combining ability both were important in inheritance of desired traits as GCA and SCA variances were found to be significant. He also found significant better and mid parent heterosis for oil contents. He finally concluded that heterosis breeding is a very economical and feasible method for production of commercial hybrids in *B. rapa*.

Dar *et al.* [20] estimated heterosis for oil contents in brown sarson (*B. rapa*). They used ten diverse genotypes (KOS-101, KOS-1, CR-1617, CR-2638, CR-2871, CR-2677, CR-1485, CR-1607 and CR-1630) for this estimation. They found KOS-101 x KOS-1 for oil contents.

Ali *et al.* [23] observed highly significant genetic variation for different traits in *B. carinata* lines. They estimated genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) of about 3.2-38.1% and 4.92 to 28.24% respectively. They observed highest genetic advance for oil contents with erucic acid. They recommended *carinata*-70 best for oil quality traits. On overall basis, they recommended *carinata*-83 and *carinata*-70 best lines for use in future breeding programs.

Nasim and Farhatullah [30] estimated combining ability in *B. rapa* accessions, collected from Swat, Punjab and Chitral, Pakistan using 6 x 6 diallel cross for oil, glucosinolate, erucic acid, protein, oleic acid and linolenic acid contents. They found significant difference in all characters except glucosinolate and protein contents. They found non-significant GCA means while SCA and RCA means were found to be significant in all traits except in oil and oleic acid contents. They reported that maternal effects were more important in oleic acid and non-additive genetic control was detected in all other traits and ACC-909 and ACC-403 as good general combiner for linolenic acid, oil contents and ACC-1500 for oleic acids. ACC-265 was concluded as worse general combiner for erucic acid contents. They classified different crosses for oil quality traits, ACC-1500 x ACC-403 and ACC-909 x ACC-265 for

oil contents; ACC-902 x ACC-909 and ACC-1500 x ACC-909 for oleic acid contents; ACC-1500 x ACC-403 for linolenic acid contents and ACC-1500 x ACC-909, ACC-403 x ACC-265 and ACC-902 x ACC-265 for erucic acid contents.

Zada *et al.* [25] estimated the genetic variability and relationships among agro-morphological characters of *B. carinata* germplasm. The germplasm consists of 134 accessions collected from abroad and from different climates of Pakistan. They analyzed data by cluster and principle component analysis. They observed largest variation in erucic acid and glucosinolate contents. All accessions were categorized in seven clusters by hierarchical analysis. Total variability of 39.03% was observed in all accessions for agro-morphological traits. They recommended four genotypes (26190, 25994, 25942 and 25939) for future breeding program on the basis of oil contents, oleic acid and protein contents.

Iqbal *et al.* [31] estimated broad sense heritability and variability in 10 brassica genotypes and 12 F<sub>2</sub> progenies for seed quality traits. They found highly significant variation among genotypes for oleic acid, erucic acid, glucosinolate contents, oil contents and linolenic acid. They observed highly variable trend in heritability for all traits except erucic acid and glucosinolate which showed high heritability. They recommended 547 x 118 (cross combination of (*B. napus* × *B. rapa*)) a good interspecific hybrid for having high heritability of beneficial traits.

The previous literature showed that there are many contradiction related to genetics of *Brassica* group. Seed color is said to be controlled by monogenic, digenic and even trigenic controlled by different scientist. Some said it completely dominant, some as intermediate dominant and some as epistatic trait. Leaf hairiness is said to be monogenic controlled but it is still confused. Also there are confusions about maternal control of seed color. For seed yield related traits, some confusions are seen in previous literature almost all scientist reported highly significant variation for all seed yield related traits but non-significant variation i.e., number of seeds per siliqua is also reported. Some scientist reported that some seed yield related traits i.e., 100 seeds weight, biological yield and number of siliqua/ primary branches of plant, number of siliqua/ secondary branches of plant and total number of siliqua per plant are controlled by additive genetic effects and some reported them as non-additive genetic effect.

There are also some contradictions in literature relevant of quality traits. Majority scientist reported highly significant variations in quality traits but some also reported non-significant variation in some traits i.e., oil %age. Some scientists observed dominance behavior, some additive and some epistatic behavior. Also variations are present in studying narrow sense and broad sense heritability for all traits. Due to these contradictions it is necessary to study the genetics of these traits for removing confusions.

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