

Analysis of genetic parameters and correlations for physiological and quality characters in Indian mustard [*Brassica juncea* (L.) Czern. & Coss.]

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Abstract

The present investigation was carried out to assess heritability, genetic advance and *inter se* associations of physiological, oil and seed meal quality characters in diverse accessions of Indian mustard. Significant mean sum of squares indicated genotypic differences for all the physiological and oil and seed meal quality characters investigated except protein content. Estimates of heritability and genetic advance were high for harvest index, specific leaf weight and total dry matter at 50% flowering suggesting the dominant role of additive gene action in their inheritance. The phenotypic and genotypic correlations of seed yield with biological yield/plant and harvest index were positive and significant indicating the usefulness of these characters in selection. Reduction in erucic acid would also bring forth correlated increase in oleic, linoleic and linolenic fatty acids owing to its negative associations with all the fatty acids except eicosenoic acid.

Key words: Genetic parameters, correlations, physiological and quality characters, Indian mustard, *Brassica juncea* L.

Rapeseed-mustard crops are important sources of edible oil in Indian diet. Indian mustard followed by toria and yellow sarson is the major rapeseed-mustard crop in India. Despite the increased production of rapeseed-mustard in India, much needs to be done to feed the ever-growing human and livestock population with minimal nutritional requirement and also to meet the demand of industries. Hence, development of high

yielding cultivars of rapeseed-mustard especially Indian mustard is foremost and a continuous process. Knowledge of genetic parameters is vital for the effectiveness of selection for improvement of target character. Interrelationship among characters is highly useful in selecting characters, which are not easily observed or genotypic values of which are modified by the environmental effects. It also helps the breeders to know the nature, extent and direction of selection pressure among the characters. However, information on such aspects involving physiological parameters of Indian mustard is lacking. In view of the aforesaid, the present investigation was undertaken with objectives to estimate genetic parameters (heritability and genetic advance) and associations for various physiological and quality (oil, glucosinolate content and fatty acid profile) characters.

The materials for the present investigation comprised 60 germplasm accessions from China (8), India (27), Australia (25) and 5 check varieties (Bio-902, Bio-772, PCR-7, Rohini and Varuna) of Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] grown in an augmented block design [1] with 4 blocks during *rabi* 2007-2008. In each block, there were 15 accessions and 5 checks planted in 3 rows of 5 m length with plant-to-plant distance at 10 cm. Standard agronomic practices were followed to raise the crop

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with two irrigations at 36 days interval. Plant protection measures were adopted as and when required.

To study different growth parameters, plant samples from 30 cm running length were harvested above ground level at 50 % flowering and full flowering stage. The shoot and leaves were separated and leaf area was recorded. Shoot and leaves were dried in an oven ($65^{\circ} \pm 2^{\circ}\text{C}$) for at least 72 hours till constant weight was achieved. The samples were weighed and dry matter of leaves, shoot as well as shoot + leaves was expressed in g/m^2 . For recording photosynthesis, transpiration and SPAD chlorophyll meter readings (SCMR), 4th fully expanded leaf from the top was used from three randomly selected plants in each block. Transpiration quotient (TQ), ratio of transpiration and photosynthesis was expressed as m moles/i mole. Leaf area index (LAI), specific leaf weight (SLW) was computed using leaf area and dry weight of leaves. Biological yield/plant (g) and harvest index (%), oil and protein content were recorded on a composite sample of 10 plants using near infrared reflectance spectroscopy. Two plants were selfed in each accession and seeds were harvested separately. The fatty acid profile was analyzed using selfed seeds [2] and open pollinated seed of the same plant was used for glucosinolate analysis following the method of Kumar *et al.* [3].

The mean data for agro-morphological and physiological characters were subjected for analysis of variance of an augmented block design as suggested by Federer [1]. The data were analyzed using software SPAD (IASRI, New Delhi). Heritability (in broad-sense), genetic advance expressed as

percentage of mean were computed following Hanson *et al.* [4]; Lush [5] and Johnson *et al.* [6], respectively. The genotypic and phenotypic correlation coefficients were calculated on the basis of adjusted and unadjusted means, respectively, using the formula given by Johnson *et al.* [6].

Analysis of variance indicated significant mean sum of squares for all the physiological and oil and seed meal quality characters investigated except protein content, thereby suggesting genotypic differences. Estimates of heritability and genetic advance were high for harvest index, SLW and TDM at 50 % flowering (Table 1) thereby suggesting the dominant role of additive gene action in the inheritance of these characters. Thus, selection would be effective for their improvement in early segregating generations. Moderate to high heritability associated with moderate to high genetic advance for biological yield/plant, LAI and SLW at full flowering, SCMR and TQ (inverse of water use efficiency) at 50% and full flowering indicated role of both additive and non-additive gene action in the genetic control of these characters. Such characters could be amenable for improvement through selection in advance generations. High heritability but low genetic advance was recorded for oil content. The low genetic advance might be due to low variability in the experimental materials. Therefore, simple selection would not be effective for its improvement. The results of the present investigations were in agreement with those of previous studies [7] where high heritability and genetic advance were recorded for harvest index and biological yield/plant. No information is available on estimates of genetic parameters for physiological characters like SLW, LAI, TQ and SCMR. The present

Table 1. Heritability (in broad-sense), actual genetic advance (Ga) and as % of mean (Gs) for physiological characters in Indian mustard

Character	Heritability (%)	Ga	Gs
Leaf area index (Full flowering)	60.0	119.4	51.2
Specific leaf weight (50 % flowering)	93.4	412.1	110.5
Specific leaf weight (Full flowering)	71.9	257.6	40.2
Total dry matter (50 % flowering)	81.0	1279.5	94.7
Transpiration quotient (50 % flowering)	56.5	9.8	28.3
Transpiration quotient (Full flowering)	62.3	7.0	18.9
SCMR (50 % flowering)	61.5	249.2	5.3
Biological yield/plant	60.8	2269.3	40.3
Harvest index	80.6	677.7	36.2
Oil Content	72.1	152.4	3.9

study is probably the first such published report.

Genotypic and phenotypic correlations were in the same direction. The genotypic correlations were classified as low ($r < 0.30$), moderate ($r = 0.31-0.65$) and high ($r > 0.65$). Genotypic correlations were, in general, higher than phenotypic correlations. Seed yield/plant had significant and positive correlations with biological yield/plant ($r_p = 0.858^{**}$) and harvest index ($r_p = 0.276^*$). The genetic correlation of seed yield with was positive but of moderate strength ($r_g = 0.284$) with harvest index and strong with biological yield/plant ($r_g = 0.822$). However, Patel *et al.* [8] reported significant positive relationship between harvest index and seed yield but negative correlation of seed yield with biological yield. Specific leaf weight at 50% and full flowering were positively associated ($r_p = 0.687^{**}$). The SLW at 50 % and full flowering exhibited positive and highly significant association with TDM at 50 % ($r_p = 0.744^{**}$ and $r_p = 0.798^{**}$). The TQ at full flowering and SLW at 50% flowering ($r_p = 0.399^*$) and full flowering ($r_p = 0.445^{**}$) were positively and significantly correlated. The SCMR at 50% flowering had significant and positive association with SLW at full flowering ($r_p = 0.435^*$). At genotypic level, SLW at 50 % flowering showed moderate ($r_g = 0.5334$) and high correlation ($r_g = 0.766$), respectively, with SLW at full flowering and TDM at 50 % flowering. TQ at full flowering and SLW at 50 % flowering were also positively associated ($r_g = 0.379$). High positive association was also observed between SLW at full flowering and TDM at 50 % flowering ($r_g = 0.818$). TDM at 50 % flowering and TQ at full flowering were positively correlated ($r_g = 0.369$). The TQ at full flowering and 50 % flowering were negatively correlated ($r_g = -0.309$).

The TDM at 50 % flowering was positively and significantly related to plant height ($r = 0.465^*$), main shoot length ($r = 0.454^*$) and biological yield/plant ($r = 0.474^*$). SLW at full flowering showed positive and significant relationship with 1000-seed weight ($r = 0.656^{**}$) but negative and significant association with main shoot length ($r = -0.433^*$). The negative correlation of TQ at full flowering with main shoot length ($r = -0.483^*$) and biological/plant ($r = 0.442^*$) suggested that high water use efficiency is reflected in production of high biological yield which in turn resulted in increased seed yield. The study also revealed that excessive tall plants might use more water to produce dry matter as indicated by positive association of TQ with plant height ($r = 0.572^{**}$). Therefore, for efficient use of available water, genotypes with short plant stature

should be selected and also exploit genotypic variability in TQ, i.e., selecting genotypes with low TQ for hybridization. The SLW at 50 % and full flowering and TDM at 50 % flowering were also positively correlated. A low positive genetic correlation of SLW at 50 % and full flowering with TQ at full flowering and SCMR at 50 % and full flowering but significant correlations at phenotypic level suggested that association among SLW, TQ and SCMR was relatively more influenced by environmental conditions. Although positive correlation between SCMR and SLW might be of interest as the later has been reported to be positively associated with water use efficiency [9, 10] and thus could be used as indirect selection criterion for water use efficiency. The present study is probably the first report dealing with association analysis among physiological characters in Indian mustard. The results of the present investigation suggested that for yield enhancement in Indian mustard greater emphasis in the selection programme should be laid on biological yield/plant and harvest index.

Oil and seed meal quality characters

The fatty acid profile and relative proportion of saturated and unsaturated fatty acids determine oil quality whereas; glucosinolate and protein content determine the quality of seed meal. Saturated fatty acid (palmitic + stearic acid) had positive and significant association with unsaturated fatty acid, oleic ($r = 0.331^*$), linolenic acid ($r = 0.478^{**}$) and oil content ($r = 0.314^*$). Their association with erucic acid ($r = -0.527^{**}$) and glucosinolate content ($r = -0.549^{**}$) was negative and significant. Oleic and linoleic acid were positively and significantly correlated ($r = 0.493^{**}$). But oleic acid had highly significant and negative association with eicosenoic ($r = -0.520^{**}$), erucic acid ($r = -0.844^{**}$) and glucosinolate content ($r = -0.812$). Similarly, linoleic acid exhibited negative and significant correlation with eicosenoic ($r = -0.526^{**}$), erucic acid ($r = -0.761^{**}$) and glucosinolate content ($r = -0.748$). Linolenic acid also had significant but negative relationship with erucic acid ($r = -0.385^{**}$) and glucosinolate content ($r = -0.372^{**}$). Erucic acid had positive and highly significant associations with eicosenoic acid ($r = 0.427^{**}$) and glucosinolate content ($r = 0.951^{**}$). The relationship of glucosinolate content was highly significant and positive with eicosenoic acid ($r = 0.533^{**}$). Negative and significant correlations of erucic acid with all the fatty acids except eicosenoic acid were observed in the present study. However, Patel *et al.* (2003) recorded positive and significant associations of erucic acid with all other fatty acids.

Oleic acid had positive and significant association with linoleic acid and supported the similar observations of Chaudhary *et al.* [11] in *Brassica juncea*. Both oleic and linoleic acid showed negative and significant relationship with eicosenoic acid and glucosinolate content. Glucosinolate content was negatively and significantly correlated with all the fatty acids except eicosenoic and erucic acid. Palmer *et al.* [12] also observed positive association of glucosinolate content with oil content and erucic acid. The discrepancy between the results of the present study and the earlier reports might due to different genetic background of the experimental materials and/or g x e interactions. In a subsequent 3 year study, Chauhan *et al.* [13] analysed the effects of environmental factors and concluded that the pattern of correlations of oil content and quality (fatty acid profile and glucosinolate content) was affected by the prevailing temperature, humidity and sunshine duration during the post flowering period. Maximum temperature up to 42 days after flowering and oil content was negatively and significantly correlated. Similarly, correlation coefficients of erucic acid with mean temperature prevailing between 15-28 days after 50% flowering were significant. Mean relative humidity during 15–28 days after flowering had negative and significant relationship with linoleic acid but significantly positive with linolenic acid. However, the physiological characters studied in the present investigation neither influenced oil content or fatty acid profile. The findings of the present study suggested that reduction in erucic acid would also bring forth correlated increase in desirable fatty acids such as oleic, linoleic and linolenic acid owing to their negative associations.

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