ONLINE ISSN: 3007-3197 | PRINT ISSN: 3007-3189

http://amresearchreview.com/index.php/Journal/about

Annual Methodological Archive Research Review

http://amresearchreview.com/index.php/Journal/about

Volume 3, Issue 5 (2025)

Study On Correlation And Heritability Analyses For Morphological And Yield Associated Traits In Mustard (*BRASSICA JUNCEA*L.) Genotypes

Piar Ali Shar*[1], Munaiza Baloch[2], Ayaz Ali Soomro[3], Nawal Naz[4], Bebagar[5], Zarnaz[6], Laiba Ashfaq[7], Majid Ali[8], Suneel Kumar[9].

Article Details

Keywords: Correlation, Heritability, Mustard genotypes, Yield performance

[1]Piar Ali Shar*
Department of Plant Breeding and genetics Faculty of Crop Production Sindh Agriculture University Tando jam pasher@sau.edu.pk
[2]Munaiza Baloch
Department of Plant Breeding and genetics Faculty of Crop Production Sindh Agriculture University Tando jam
[3]Ayaz Ali Soomro
Campus Umer Kot Department of Plant Breeding and Genetics Sindh Agriculture University Tando Jam
[4]Nawal Naz
Department of Plant Breeding and genetics Faculty of Crop Production Sindh Agriculture University Tando jam
[5]Bebagar
Directorate General Agriculture Extension Balochistan, Quettabibagrmb@gmail.com
[6]Zarnaz
Department of Plant Breeding and genetics Faculty of Crop Production Sindh Agriculture University Tando jam
[7]Laiba Ashfaq
Centre of Agricultural Biochemistry and Biotechnology, University of Agriculture Faisalabad, Pakistan.
[8]Majid Ali
Department of Plant Breeding and genetics Faculty of Crop Production Sindh Agriculture University Tando jam
[9]Suneel Kumar
Department of Plant Breeding and genetics Faculty of Crop Production Sindh Agriculture University Tando jam

ABSTRACT

Mustard is an important oil seed crop in Pakistan, however there is limited information about improved genotypes of mustard. So, we examined the correlation and heritability of ten genotypes including 69-9172, Gaj-Sarhein, A.H. 2001, NRT-02/9, UCD-11/1, Canola-II, P-23-R.2, UCD-22, P-62. R5 and Early Raya at Oilseeds Research Institute (ARC) Tando jam. Result showed significant difference ($P<0.05$) for growth and yield characteristics among the genotypes. Days to 75% flowering showedhighly positive and significant relationship with days to 90% maturity, plant height and seed yield plant^{-1}. A significant and positive association was found with the number of branches plant^{-1} and number of pods plant^{-1}. Days to 90% maturity was positive and highly significant with the number of branches plant^{-1}, number of pods plant^{-1} and seed yield plant^{-1}. Plant height resulted in the highly positive significant correlation with the number of branches plant^{-1} and seed yield plant^{-1} with correlation coefficient value of r = 0.7361** and 0.6024** respectively. The positive significant association was observed with the number of pods plant^{-1} and oil content. Number of branches plant^{-1}showed highly significant and positive association with number of pods plant^{-1}, seed yield plant^{-1} and seed index. Number of pods plant^{-1} showed the highly significant and positive relationship with seed yield plant^{-1}. Seed yield plant^{-1}resulted highly significant and positive relationship with seed index and positively significant with oil content. High heritability ratios for studied characters suggested that the observed differences were under the genetic control and were less affected by environment.

Introduction

Mustard (Brassica juncea L.) comes under the family of Cruciferae and genus Brassica. Mustard is third important oil seed crop grown after soybean and oil palm in more than 60 countries of the world. It contents 38 to 42% oil and 24% protein. Raiis very famous between mustard and rapeseed because of its greater yield and tolerance against lodging, shattering, scarcity, hotness, salinity and some other factors like diseases respectively. Rapeseed-mustard also performs well in unfavorable conditions like soil acidity, low available nutrient content, poor drainage and drought (Maurya et al., 2019). Mustard is grown in typically both tropical and subtropical areas. It is grown as quietly tolerant to acidity of soil, favoring a pH from 5.7 to 6.7, grow well in region with hot days and cool night and can grow up in moderately weather scarcity. Mustard-rapeseed usually grown in low water (250–400mm) which can be fitted healthy in the rainfed cropping systems (Shekhawat et al., 2012). During July 2020, the imported value of 2.750 million tons of edible oil was Pakistani rupees about 321.555 billion ($2.039 billion). In 2019-20 the local production was assessed about 0.506 million tons. The total available amount of edible oil production was recorded nearly about 3.249 million tons (GoP, 2019).World producing mustard in assessed area about 33.2 million hectares and the total production of 60.8 million tons. The evaluated mean of total yield is about 1842 kg per hectare (Singh et al., 2015). Pakistan is confronting a lack of eatable oil and local oil production. The local oil production is about 18% national demand while the remaining 82% is trade in at the cost of enormous foreign exchange (Anonymous, 2015). All rapeseed-mustard species and also brassica genus cultivars grown in most countries of the world as green feed crop and oil extraction. These crops are mostly cultivated as conventional feed crops. Brassica crops production for green feed production can available in various places, including soils. Mustardis good for digestibility at 80 to 90% which deals with fine alfalfa at 75%. Its leaves rich in crude protein, which contains about 18 to 25%, whereas the roots of brassica contain about 7 to 12% crude protein respectively. It has been grown as fodder for cattle for many years, leaves and root are delicious feed for sheep and cattle. Mustard can be improved the richness of soil, its permits growers to increase their cropping season. It provides fine soil cover winter to adhere soil erosion, produces huge quantity of biomass, overwhelms herbs and alsoprovides to soil core with root system (Maurya et al. 2019). Mustard is self-pollinated crop, however only 3-15% of cross pollination can be achieve through honeybees (Ompal et al., 2018). It contains of many economically valuable species which have edible leaves, stems, root, buds, and their seeds used as condiment. Leaves and immature stem of plant are commonly cooked as vegetable (Ganapur et al., 2009). Oil seed crops are essential due to their uses in different medicines preparation for many years because of their harmless effects and medicinal formulations like pills, capsules, creams, mixtures, perfumes, flavors, balms, plasters, intramuscular vaccinations and other makeup stuffs (Saeed-ul-Hassan et al., 2014). Oil and fats play major role in human diets, they are essential stuffs and supply energy, increase cooking zest and deliciousness of food. Pakistan is slow in making of cooking oils and this shortfall is rising day by day due to rising up population and living standard of humans (Minfal, 2005) and (Vessar et al.,2025). The main reason of shortage of edible oil is desired genotypes are not easily available (Nasimi et al., 2006). Breeders using many statistical techniques in modeling yields crop such as correlation coefficient analysis, factor analysis, path analysis, linear regression analysis and cluster analysis (Aytac et al., 2008). A successful crop improvement program for specific trait through selection needs genetic variability among the genotypes in association with high heritability. Correlation studies suggest a good knowledge to understand the association between different characters, and can help breeders to formulate a proper breeding plan to improve a number of traits concurrently (Priyamedha et al., 2018). Correlation coefficient analysis techniques deliver a well knowledge to obtain degree and direction of linkage among two or more than two variables (Kumar et al., 2019). Correlation studies between yield and

yield component is of formulating the selection criteria under crop improvement. Selection of any required trait is generally achieved based on the phenotypic value of the plants, which is comparatively determined by genotypes, which is heritable, and comparatively by environment which is non-heritable. Therefore, it is obligatory to know the several components of the yield and its mutual correlation with other independent traits. This is because; selection was having affected if it was based upon some components which are less sensitive to environment. Several components of seed yield usually show different degree of associations with seed yield and among themselves. Correlation coefficients analysis between characters impacting directly or indirectly for seed yield however is not only a sufficient approach (Chaurasiya et al., 2019). Heritability studies play a major role in breeding, as a guide it expresses the depend ability of phenotype breeding value. Phenotypic value evaluated directly when individual values of breeding are taken from proper analysis. Breeding value can help to determine that how much phenotype would be forwarded to the next generation (Rehman & Alam, 1994). Hence the aim of the recent research was to examine the correlation and heritability analysis between yield and yield associated traits in mustard genotypes.

Materials and Methods

The study "correlation and heritability analysis for yield and yield associated traits of mustard genotypes" was conducted at experimental field of Oilseeds Research Institute (ARI) Tando jam in the year 2020.

Experimental design

The plot was prepared in Randomized Complete Block Design (RCBD) with three replications. Plot size was put 5x1.35 meters and plant to plant and row to row space maintained at 45 cm to 75 cm respectively.

Statistical analysis

Analysis of variance was applied to the data according to the method suggested by **(Gomez & Gomez, 1984)** and the means was compared using Least Significant Difference (LSD).
Correlation coefficient (r) was computed according the methods of (Snedecor & Cochran, 1980) by using the formula.

$$\text{Correlation coefficient (r)} = \frac{\text{Covariance}}{\text{Geometric mean of covariance}}$$

$$r = \frac{\Sigma xy}{\sqrt{(\Sigma x)2\_(\Sigma y)2}}$$

$$\Sigma xy = \frac{\Sigma xy\_(\Sigma x)\_(\Sigma y)}{N}$$

$$\Sigma x2 = \frac{\Sigma x2\_(\Sigma x)2}{N}$$

$$\Sigma y2 = \frac{\Sigma y2\_(\Sigma y)2}{N}$$

Whereas:

X	=	Independent variable
Y	=	Dependent variable
N	=	Number of observation

Heritability was calculated according to the formula given by **(Falconer, 1989).** Heritability formulas are given below.

Environmental variance (Ve) = *(VP1 + VP2)/3*
Genetic variance (Vg) = *MSg-MSe/3*
Phenotypic variance (Vp) = *Vg+Ve*

Genetic Variance (vg)

$$h^2 = \frac{X\ 100}{Phenotypic\ Variance\ (vp)}$$

Whereas:
Ve = *Environmental variance*
Vg = *Genetic variance*
Vp = *Phenotypic variance*
h2 % = *Heritability percentage in broad sense*

Results
Analysis of variance
The mean squares for grain yield and its components of mustard genotypes are exhibited in Table 01. The mean performance of grain yield and related characters presented in Table 02. Correlation analysis between qualities parameters of economic importance results are displayed in Table 03. The estimation of heritability results are displayed in Table 04.
Table 01 exhibited the results of all recorded parameters including days to 75% flowering, days to 90% maturity, plant height (cm), branches plant^{-1}, pods plant^{-1}, seed yield plant^{-1}, seed index and oil content (%) which were significantly different ($P<0.05$) between the genotypes.

Table 1. Mean squares of different yield and yield related traits in mustard genotype

Source of variance	D.F	Days to 75% flowering	Days to 90% maturity	Plant Height (cm)	Number of branches plant^{-1}	Number of pods plant^{-1}	Seed yield plant^{-1}	Seed index	Oil Content (%)
Replications	2	5.83	0.70	65.43	0.006	188.51	3.43	1.19	7.25
Genotypes	9	72.45**	18.99**	4249.93**	1.27**	6414.49**	5.15**	0.61**	7.50**
Error	18	3.98	0.88	78.57	0.13	410.63	0.22	0.05	1.27
Total	**29**	-	-	-	-	-	-	-	-

**=Highly Significant at P ≤ 0.01 level

Mean performance

The mean performance of the ten examined genotypes is presented in Table-02. The results showed that the most of the days 75% to flowering (65.25 days) were taken by the genotype 69-9172 followed by the genotype NRT-02/9 (64.21 days), whereas the genotype Early Raya evidenced the least flowering days (49.39 days). The maximum 90% maturity (130.27 days) was taken by the genotype A.H 2001 followed by the genotype P-62-RS (126.42 days) and the minimum days to 90% maturity (120.33 days) was noted by Early Raya genotype. In case of plant height, tallest plants (226.38 cm) were articulated by the A.H 2001 genotype followed by P.62.R5 genotype (216.82 cm), despite the fact the shortest plants (108.50 cm) were detected by Gaj-Sarhien. Furthermore, the most branches plant^{-1} (9.71) found in the genotype P.62.R5 followed by the genotype A.H 2001 (9.52). However, the minimum observations of these traits were found in the mustard genotype P.23. R2 (7.36). For pods plant^{-1}, the most pods plant^{-1} (490.54) were calculated by the genotype A.H 2001 followed by P.62.R5 (464.41), and the minimum pods plant^{-1} were obtained in the genotype canola II (409.67). According to the examination, the maximum seed yield plant^{-1} (27.57) was observed in the genotype A.H 2001 followed by P.62.R5 (26.67), and the minimum seed yield plant^{-1} were explored in the genotype UCD-22 (23.37). In the results of seed index, the most assesses for seed index (5.09 g) was found by A.H 2001 followed by P.62.R5 (5.06 g), while the minimum assesses for seed index was shown by UCD-22 (3.76 g). As a final point, the highest oil content (36.69%) was achieved by the genotype A.H 2001 followed by the Early Raya genotype (36.46%), while the minimum oil content was produced by the genotype UCD-22 (31.37%).

Table 2. Mean performance of different yield and yield related traits in mustard genotypes

Varieties	Days to 75% flowering	Days to 90% maturity	Plant height (cm)	Number branches plant^{-1}	Number of pods plant^{-1}	Seed yield plant^{-1}	Seed index	Oil content (%)
69-9172	65.25	125.20	215.42	8.46	452.0	25.52	4.43	35.70
Gaj-Sarhein	53.33	124.67	108.50	7.66	445.67	23.65	4.23	32.85
A.H. 2001	58.37	130.27	226.38	9.52	490.54	27.57	5.09	36.69
NRT-02/9	64.21	125.24	204.85	8.46	463.23	25.36	4.07	33.36
UCD-11/1	56.31	126.12	216.20	8.65	462.32	25.63	4.17	34.24
Canola-II	54.07	124.27	214.96	8.33	409.67	24.46	3.93	33.10
P-23-R2	56.41	123.38	159.63	7.36	442.04	24.44	4.26	34.73
UCD-22	53.01	123.15	201.57	8.33	427.67	23.37	3.76	31.37
P-62. R5	56.13	126.42	216.82	9.71	464.41	26.67	5.06	35.61
Early Raya	49.39	120.33	200.63	8.12	431.67	24.49	4.53	36.46
LSD at (0.05%)	**3.42**	**1.61**	**0.09**	**0.16**	**47.68**	**0.03**	**0.07**	**0.04**

CORRELATION (r)

Days to 75% flowering

Results suggested that 75% flowering days was significantly positive connection with the 90% maturity (0.4201**), plant height (0.4254**) and seed yield plant-^{1} (0.5001**) where the significant level was estimated higher in these traits. On the other hand, a significantly positive correlation was determined in the branches plant^{-1} (0.4146*) and the pods plant^{-1} (0.3863*). However, a positively non-significant correlation in oil content with the ratio of (0.1631^{NS}) and the negative non-significant ratio was estimated in seed index with the ratio of (-0.059^{NS}) respectively.

Days to 90% maturity

Present study revealed that a positive and strongly significant correlation was presented in the branches per plant, pods per plant, and in the seed yield with correlation measurement level of r = 0.6737**, 0.5237**, and 0.7504**. Positive and significant association with seed index (0.4013*). On the other hand, non-significantly positive correlation between height of plant (0.2869^{NS}) and oil content (0.2243^{NS}) was recorded.

Plant height

Results identified that the plant height had a significantly positive association with other traits including the branches^{-1}plantand seed yield plant^{-1}. Analysis results suggested the ratio of correlation coefficient r = 0.7361** and 0.6024** in above-mentioned traits, while significant ratio remained higher in the correlation of these traits. A significantly positive relationship among the charactersincluding oil content (0.4096*) and the pods per plant (0.4135*) was examined. However, a positively non-significant association was recorded by the character seed index (0.2552^{NS}).

Branches plant^{-1}

The results of analysis suggested the highly significant and positive linkage of this trait with the pods plant-^{1} (0.6283**), seed yield plant-^{1} (0.8330**) and seed index (0.6597**) respectively. The positive association and significant was observed with trait oil content (0.4102*).

Pods plant^{-1}

The results of this trait exhibited the positive association and highly significant relationship and with seed yield plant-^{1} (0.6552**). The relationship of this parameter was positive and significant were recorded with seed index (0.4188*) and oil content (0.3979*).

Seed yield plant-^{1}

Present study of this parameter disclosed the positive and highly significant connection with seed index (0.7443**) and positively significant with oil content (0.4123*).

Seed index

Seed index showed the highly significant and positive relationship with oil content (0.7501**).

Table 3. Correlation among various traits in mustard genotypes

Traits	Days to 75% flowering	Days to 90% maturity	Plant height (cm)	Number of branches plant^{-1}	Number of pods plant^{-1}	Seed yield plant^{-1}	Seed index
Days to 90% maturity	0.4291**						
Plant height (cm)	0.4254**	0.2869^{NS}					
Number of branches plant^{-1}	0.4146*	0.6737**	0.7361**				
Number of pods plant^{-1}	0.3863*	0.5237**	0.4135*	0.6283**			
Seed yield plant^{-1}	0.5001**	0.7504**	0.6024**	0.8330**	0.6552**		
Seed index(g)	-0.0595^{NS}	0.4013*	0.2552^{NS}	0.6597**	0.4188*	0.7443**	

Oil content (%)	0.1631^{NS}	0.2243^{NS}	0.4096*	0.4102*	0.3979*	0.4123*	0.7501**

** = Highly significant at P ≤ 0.01 probability level * = Significant at P ≤ 0.05 probability level
NS = Non-significant at P ≥ 0.05 probability level

Heritability Estimates
The estimation of heritability (h^2) in broadsense (b.s), the genetic variance(δ^2g), and phenotypic variance(δ^2p)from modification components for many characters calculated are included inTable-04.

Daysto 75% flowering
The analysis of this trait exhibited the genetic variance (δ^2g) (22.82) was lower than phenotypic variance (δ^2p) (26.08), which showed the high heritability estimates (h^2=85.14%).

Days to 90% maturity
The present perimeter showed the value of genetic variance (δ^2g) (6.03) and phenotypic variance (δ^2p) (6.91), which gave the high heritability estimates (h^2=87.26%).

Plant height
Plant height manifested that genetic variance (δ^2g) (1390.45) was lower than phenotypic variance (δ^2p) (1469.02), which resulted high heritability estimates (h^2=94.65%).

Branches plant^{-1}
For this character the value of genetic--variance--(δ^2g) was (0.34) and phenotypic--variance--(δ^2p) was (0.47), which gave the high--heritability estimates (h^2=72.34%).

Pods plant^{-1}
The calculation of this character showed the genetic variance (δ^2g) was (2001.28) and phenotypic variance (δ^2p) (2411.91), which revealed high heritability estimates (h^2=82.97%).

Seed yield plant^{-1}
The genetic variance (δ^2g) of this trait was observed of (1.21) and phenotypic variance (δ^2p) which was recorded of (1.43) resulted high heritability estimates (h^2=84.61%).

Seed index
Index of seed evaluated that the value of geneticvariance (δ^2g) was (0.25)and thephenotypicvariance(δ^2p) was (0.30), while itestimated highheritability (h^2=83.33%).

Oil content (%)
For the character oil content (%), the value of genetic-variance- (δ^2g) -was (2.66) and the value of phenotypic-variance- (δ^2p) was- (3.01), while it showed-high -heritability- estimates- (h^2=88.59%).

Table 4. Heritability estimates in broad sense for various characters of mustard genotypes

Traits	Environmental Variance (Ve)	Genotypic Variance (δ^2g)	Phenotypic Variance (δ^2p)	Heritability (%) (Broad sense)
s to 75% flowering	3.98	22.82	26.08	85.14
s to 90% maturity	0.88	6.03	6.91	87.26
t height (cm)	78.57	1390.45	1469.02	94.65
nber of branches plant^{-1}	0.13	0.34	0.47	72.34
nber of pods plant^{-1}	410.63	2001.28	2411.91	82.97
l yield plant^{-1}	0.22	1.21	1.43	84.61
l index (%)	0.05	0.25	0.30	83.33
content (%)	1.27	2.66	3.01	88.59

Discussion

The breeding material was composed of ten genotypes of mustard. The ten genotypes, namely 69-9172, Gaj-Sarhein, A.H 2001, NRT-02/9, UCD-11/1, Canola-II, P-23-R.2, UCD-22, P-62. R5 and Early Raya. The parameters were recorded for the days to 75% flowering, days to 90% maturity, plant height (cm), branches plant^{-1}, pods plant^{-1}, seed yield plant^{-1}, seed index (thousands seed weight in grams) and oil content(%) respectively. The aim of this study was to estimate the correlation and heritability analysis for yield and its contributing traits of mustard genotypes. The result exhibitedin (Table No.1) significant variances in the mean squares from investigation of variance atp $\leq$0.01level. Studied genetic lines may reference for further evaluation in genetic and breeding programs. Our results are related with Lodhi et al (2014); Meckonnen et al (2014) and Tiwari et al (2016) who also testified the significant variation of mustard genotypes.

Correlation coefficient

Correlation statistical technique plays a vital role for breeders in section crop plants for greater yields. The results exhibited significant ($P \leq 0.05$) and positive association between different characteristics such as days to 75% flowering displayed the highly positive also significant relationship with days to 90% maturity (0.4201**), plant height (0.4254**) and seed yield plant^{-1} (0.5001**). Whereas significantly positive connection was found with branches plant^{-1}(0.4146*) and pods plant^{-1} (0.3863*). Non-significantly positive was found with oil content (0.1631^{NS}) and non-significantly negative relation with index of seed (-0.059^{NS}). Days to 90% maturity exposed positive and highly significant relationship with amount of traits including branches plant^{-1}, pods plant^{-1}, and seed yield plant^{-1}, where value of correlation coefficient was recorded as r = 0.6737**, 0.5237**, and 0.7504** respectively and positive and significant association was observed with seed index (0.4013*). On the contrary, non-significantly positive linkage of this trait was detected with plant height (0.2869^{NS}) and oil content (0.2243^{NS}). Another trait plant height showed a highly significant and also positive correlation with some of traits such as the branches plant^{-1} and seed yield plant^{-1} with the values of r = 0.7361** and 0.6024** respectively. The pods plant^{-1} (0.4135*) and oil content (0.4096*) were observed with significantly positive correlation, while positive and non-significant association was recorded with seed index (0.2552^{NS}). Branches plant^{-1} displayed the highly significant and positive linkage with pods plant^{-1} (0.6283**), seed yield plant^{-1} (0.8330**), seed index (0.6597**). Positively significant connection of this attribute was observed with oil content (0.4102*). Pods plant^{-1} displayed the positive and highly significant linkage with seed yield plant^{-1} (0.6552**). The podsplant^{-1} resulted in significantly positive correlation with seed index (0.4188*) and oil content (0.3979*). Seed yield plant^{-1} exhibited the highly significant and positive connection with these traits including seed index (0.7443**) and significantly positive with oil content (0.4123*). Seed index displayed the highly significant and positive connection with oil content (0.7501**).

Heritability (h^2)

Heritability techniques is a major part of breeding; asaguide it expresses the dependability of phenotype breeding value. Phenotypic value evaluated directly when individual values of breeding are taken from proper analysis. Breeding value can help to determine that how much phenotype would be forwarded to the next generation. For the trait of daysto75% flowering the genetic variance (δ^2g) was (22.82) and phenotypic variance (δ^2p) value was (26.08) respectively, it gave high heritability estimate (h^2=85.14%). Nasim et al (2012) who also reported high results of heritability. The days to 90% maturity of genetic variance (δ^2g) was (6.03) and phenotypic variance (δ^2p) was (6.91), while it gave the high heritability estimate (h^2=87.26%). Plant height manifested that genetic variance (δ^2g) (1390.45) was lower than phenotypic variance (δ^2p) (1469.02), which resulted high heritability estimates (h^2=94.65%). The branches plant^{-1} showed the genetic variance (δ^2g) of (0.34) that was found lower than phenotypic variance (δ^2p) which was detected (0.47). In results, analysis showed high heritability estimates (h^2=72.34%). In pods plant^{-1} the genetic variance (δ^2g) was (2001.28) and phenotypic variance (δ^2p) (2411.91), which revealed high heritability estimates (h^2=82.97%). These results are related with (Khan et al., 2013) who reveal high heritability in pods plant^{-1}. For the parameter of seed yield plant^{-1} the genetic variance- (δ^2g) (1.21) was lower- and -phenotypic- variance (δ^2p) (1.43) –was high, -which resulted high heritability (h^2=84.61%). For the seed index, the genetic variance- (δ^2g) value was (0.25) and phenotypic variance (δ^2p) value was (0.30). Highheritability was estimated for this trait at (h^2=83.33%). For the character oil content (%), the geneticvariance value (δ^2g) -was (2.66) which was low than the value of phenotypic-variance (δ^2p) (3.01). High-heritability was estimated

at (h^2=88.59%). The present study supported the study of Sohail et al (2017) and Singh et al (2018).

Conclusions

Current study revealed that all mustard genotypes had significant results for most of the traits including days to 75% flowering, days to 90% maturity, plant height (cm), branches plant^{-1}, pods plant^{-1}, seedyield plant^{-1}, seed index and oil content (%) respectively. These examined results suggested the potentiality of genotype A.H 2001 as it was noticed during the comparative examinations between multiple traits of different genotypes.Correlation analysis suggested that the days to 90% maturity was under positive and highly significant with other traits including branches plant^{-1}, pods plant^{-1}, and seed yield plant^{-1} respectively. while plant height was found positively correlated and highly significant with branches plant^{-1} and seed yield plant^{-1}. However, it disclosed a positive and significant relationship with pods plant^{-1} oil content and positive with non-significant level was observed in seed index. Similarly, branches plant^{-1} was observed with highly significant and positive correlation with podsplant^{-1}, yield plant^{-1} and seed index respectively. Oil content had positive and significant association. Pods plant^{-1} was estimated positive and highly significant association with seed yield plant^{-1} and seed index. High heritability estimates (h^2 broad sense) was calculated for all studied characters, high heritability ratios for studied characters specified that they were genetically controlled and were not as much of affected by environment.

Conflict of interest

The authors declare that they have no conflict of interest for the publication of the manuscript.

Author contributions

Asadullah Laghari and Piar Ali Shar designed the experiment, Sohail Ahmed Otho and Ghulam Hassan Bahalkani collected field data, Asadullah Laghari wrote the original manuscript, Abdul Hafeez laghari, Ayaz Ali soomro and Akhtar Hussain Shar analyzed field data and edited the manuscript, Ghulam Hussain Talpur revised the analyses and manuscript, Piar Ali Shar supervised the project.Syeda Mahvish Zahra read, approved and submitted the final version of manuscript.

Acknowledgements

We are thankful to Mr. Abrar Ahmed Shaikh (Director of Oil Seed Research Institute, SAU Tandojam) and his staff for their valuable guidance during conducting experiment.

References

Anonymous (2015). Pakistan Economic Survey. Ministry of Finance, Government of Pakistan, Islamabad.

Aytaç Z, Kinaci G and Kinaci E (2008). Genetic variation, heritability and path analysis of summer rapeseed cultivars. *J App Bio Sci* 2(3):35-39.

Chaurasiya JP, Mahak S and Tomor P (2019). Genetic variability, heritability, genetic advance and character association of Indian mustard (*Brassica juncea* L.). *J Oil Bra* 10(2): 80-86.

Falconer DS (1989). Introduction to Quantitative Genetics. Richard Clay Ltd. Bungay Suffolk,

Great Britain pp.129-185.

Gangapur DR, Prakash BG, Salimath PM, Ravikumar RL and Rao MSL (2009). Correlation and path analysis in Indian mustard (Brassica juncea L. Czern and Coss). *Karnataka J Agri Sci* 22(5): 971-977.

Gomez KA and Gomez AA (1984). Statistical Procedures for Agriculture Research. John Wilely and Sons. New York.

Govt of Pakistan (2019-20). Pakistan Economic Survey. Ministry of Finance, Economic Advisor's Wing, Islamabad.

Khan FU, uddin R and Khalil IA (2013). Heritability and genetic potential of brassica napus genotypes for yield and yield components. *American-Eurasian J Agri & Envi Sci* 13(6): 802-806.

Kumar R, Kaur S, Bala K, Kaur S and Sharma L (2019). Assessment of genetic variability, correlation and path analysis for yield traits in F1 hybrids of Indian mustard [*Brassica Juncea* (L.) Czern&Coss.] *J Agri ways* 7(1): 1-7.

Lodhi B, Thakral NK, Avtar R and Singh A (2014). Genetic variability, association and path analysis in Indian mustard (*Brassica juncea*). *J Oil Bra* 5(1): 26-31.

Maurya JK, Avanish K, Archana S and Sriom (2019). Quantitative analysis of selection parameters in vigour contributing traits of in Indian mustard (*Brassica juncea* L. *Czern&Coss*.) Germplasm. *International J Chem Sci* 7(3): 4728-4731.

Mekonnen TW, Wakjira A and Genet T (2014). Correlation and path coefficient analysis among yield component traits of Ethiopian mustard (*Brassica carinata a. brun*) at Adet, northwestern, Ethiopia. *JPS* 2(2): 89-96.

Minfal 2005. Daily NEWS, Islamabad, Pakistan. pp.10.

Nasim A, Farhatullah, Iqbal S, Shah S and Azam SM (2013). Genetic variability and correlation studies for morpho-physiological traits in *brassica napus* L. *Pak. J Bot* 45(4): 1229-1234.
Nassimi AW, Raziuddin, Ali N, Ali S and Bakht J (2006). Analysis of combining ability in *Brassica napus* L. lines for yield associated traits. *Pakistan J Bio Sci* 9(12): 2333-2337.

Ompal, Kerkhi SA, Chand P, Singh SK and Yadav MK (2018). Study of correlation and path coefficient analysis in Indian mustard (*Brassica juncea* L. Czern&Coss). *J Phar &Phy*7(6): 890-894.

Priyamedha, Hyder ZA, Arun K, Ram B, Singh VV and Rai PK (2018). Analysis of genetic parameters and correlation for yield and quality traits in Indian mustard (*Brassica juncea* L.) *J Oil Bra* 9(2): 146-150.

Rehman A and Alam K (1994). Principles of crop breeding. M.Sc dissertation, University of

Agric., Faisalabad, Pakistan, pp. 4-9.

Saeed-Ul-Hassan S, Muhammad TA, Imran T, Arshad AS and Sohail A (2014). Evaluation of physicochemical parameters of selected brands of pharmaceutical oils sold in punjab, Pakistan. *Latin American J Phar* 33(1).115-122.

Shekhawat K, Rathore SS, Premi OP, Kandpal BK and Chauhan JS (2012). Advances in agronomic management of Indian mustard (*Brassica juncea* L.) Czernj. Cosson): *International J Agro.*

Singh D, Prasad R and Bairwa B (2015). Screening of brassica germplasm and breeding material against Altenaria brassicae causing Alternaria blight under artificial condition. *J Pure & Appl Micro* 8(6): 1-5.

Singh SK and Singh AK (2018). Inter-relationship and path analysis for seed yield in Indian mustard. *Indian J Eco* 37: 8-12.

Snedecor GW and Cochran WG (1980). Statistical Methods. 7th Edition, Iowa State University Press, Ames.

Sohail AJ, Shinwari ZK, Rabbani MA, Niaz IA and Shah SH (2017). Assessment of quantitative agro-morphological variations among *brassica rapa* diverse populations. *Pakistan J Bot* 49(2): 561-567.

Tiwari AK, Singh SK, Tomar A and Singh M (2016). Heritability, genetic advance and correlation coefficient analysis in Indian mustard (*Brassica Juncea* (L.) Czern&Coss). *J Phar &Phy* 6(1): 356-359.

Vessar, Y. N., Soomoro, N. S., Khan, H., Baloch, S. K., Kaler, A. A., & Tunio, S. A. (2025). Evaluation of Mustard (Brassica spp.) Genotypes for Yield and Oil Content in Tandojam, Sindh, Pakistan. Indus Journal of Bioscience Research, 3(1), 847–850.

Annual Methodological Archive Research Review
http://amresearchreview.com/index.php/Journal/about
Volume 3,Issue 5 (2025)