

Correlation and path analysis in rapeseed (*Brassica napus* L.) genotypes under heat stress condition

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Abstract

This investigation assessed the genetic potential of 20 rapeseed genotypes under heat stress during the Rabi season 2020–21 at Sindh Agriculture University, Tandojam, using a randomized complete block design with three replications. Seven agronomic traits were evaluated: plant height, branches per plant, siliques per plant, silique length, yield per plant, seed index, and oil content. All traits exhibited significant variation, indicating broad genetic diversity. Punjab Sarson outperformed others in multiple traits, while PARC Canola, Hbo-555, and Faisal Canola showed high seed yields under stress. Significant positive correlations with seed yield per plant were found for plant height (0.349**), siliques per plant (0.610**), silique length (0.319*), seed index (0.313*), and oil content (0.266*). Path analysis revealed that siliques per plant (1.792) and oil content (2.379) had the strongest direct effects on seed yield, making them effective targets for selection. However, heritability for all traits was low under heat stress, suggesting that selection should be delayed until later segregating generations for better genetic gain.

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Received 04/06/2025
Accepted 16/07/2025

Keywords: Correlation, rapeseed, path analysis, heat stress, heritability

INTRODUCTION

One significant species that is primarily cultivated as an oilseed crop in tropical and subtropical regions is rapeseed (*Brassica napus* 2n = 4x = 36) (Solanki *et al.*, 2017). *Brassica nigra* and *Brassica campestris* were inter-specifically crossed to produce rapeseed (2n=36), an amphidiploid species having chromosome numbers of 2n=16 and 2n=20, respectively, according to cytological investigations (Rout *et al.*, 2018). It has grown extensively in several nations due to its high oil content. Along with its oil content, it also has a respectable quantity of protein, about 18–22%. Cottonseed, which is not a conventional oilseed crop, is the primary source of local oil in Pakistan. Some plants, including sunflower and maize, are also grown for their oil. However, of the traditional oilseed crops, Brassica is the main contributor (Ali and Mirza, 2005).

Extreme climatic occurrences in Pakistan include high temperatures, floods, water shortages, droughts, and increased disease and insect attacks. Pakistan's climate change susceptibility status is poor, with the Global Climate Change Vulnerability Index (CCVI) placing it 29th on the list of most susceptible countries in 2009–2010 and 16th in 2010–2011 (Ali *et al.*, 2017). Given the importance of rapeseed, environmental pressures that reduce yield or cause quality loss will have a detrimental influence on the economic return and worldwide supply of rapeseed oilseed (Koscielny *et al.*, 2018).

The study of agricultural species for enhanced traits that can help the crops withstand harsher climatic conditions is the core of trait-based breeding efforts worldwide (Singh *et al.*, 2007). Physiological processes like photosynthesis and chlorophyll, as well as the electrolyte leak-

age of plant tissue exposed to a range of temperatures, have been used to select for heat tolerance in whole plants (Fracheboud *et al.*, 1999). A major problem in many agricultural areas worldwide is the disruption of normal plant growth and development caused by high temperatures, particularly during the early stages of development. Many plant species' typical agronomical, morphological, biochemical, and physiological processes are slowed by excessive heat stress, resulting in substantial yield loss. Many *Brassica* plants, notably the essential rapeseed oilseed crop, are also affected (Ismail and Hall, 1999). This complex feature, yield, is controlled by several other traits, most of which are quantitatively inherited. It is essential to evaluate the contribution of each characteristic to give more attention to those that have the biggest effects on seed yield (Tuncturk and Ciftci, 2007).

Heritability, character association, and genotypic and phenotypic diversity have all been shown to be important for future genetic development by numerous scientists (Saini and Sharma, 1995; Lekh *et al.*, 1998; Ali *et al.*, 2002). Gosh and Gulati (2001) further demonstrated that traits with high heritability can be utilized to effectively select plants based on phenotypic performance because they are regulated by additive genes.

Since plant breeders rarely focus on just one characteristic, it's critical to examine the connections between them, especially those between seed yield and other characteristics. As the number of independent factors influencing a single dependent variable increases, a certain degree of interdependence is expected. In these situations, correlations might not be enough to adequately characterize the interactions so that breeders can decide between direct and indirect selection (Ofori, 1996).

A critical statistical procedure for assessing high-yield breeding programs and looking at both direct and indirect contributions to yield factors is the computation of correlation coefficients (Mohammad *et al.*, 2002). A statistical method for quantifying each trait's contribution to seed production is path coefficient analysis, which splits correlation coefficients into direct and indirect effects (Duarte and Adams, 1972). Each component's relative importance is shown by the path coefficient (Dewey and Lu, 1959). To thoroughly ascertain the impact of a single independent variable on the dependent variable, path coefficient analysis may be employed. Consequently, both direct and indirect influences are easily understood by path analysis (Tahira *et al.*, 2017). This conclusion was supported by Sabaghnia *et al.* (2010) and Rameeh (2011), who added that the path-coefficient approach, which separates correlation coefficients into direct and indirect effects, might help develop an effective selection strategy.

In the field of plant breeding, heritability is crucial since it allows for the prediction of the performance of a population's future generation in terms of decision-making. In a population with higher heritability, selection is easier and the response to selection is higher, which leads to a different genotypic variance, which in turn affects the population's phenotypic variance (Saleem *et al.*, 2016). Breeders can estimate the selection response based on the performance of the next generation (Larik *et al.*, 1989) by knowing a trait's heritability.

Therefore, the current study sought to evaluate heritability in rapeseed as well as the coefficients of correlation among observable characteristics and their direct and indirect impacts on seed production and oil content under heat stress conditions.

MATERIALS AND METHODS

The experiment was conducted at the Botanical Garden, Sindh Agriculture University, Tandojam, during Rabi Season, 2020-21. The experiment was laid out in RCBD with three replications.

The heat stress was imposed under field condition by sowing rapeseed genotypes after the recommended date of sowing. The date of sowing was 10th December 2020. Twenty genotypes, such as Punjab Sarson, Rabi Sarson, NARC Sarson, PARC canola hybrid, Faisal canola, Hyola-401, Rainbow, Pakola, Con-I, Con-II, Con-III, Westar, Dunkeld, Abasin-95, Hyola-42, Hbo-555, Mun-I, Kungola, Hbo-63, Kn-277 were included for this study. The seven important characters, i.e., Plant height (cm), Branches plant⁻¹, Siliques plant⁻¹, Silique length (cm), Seed yield plant⁻¹, Seed index (1000 seeds weight), and Oil content%, were recorded.

Table 1: Analysis of Variance mean squares

SOV	D.F	PH	BPP	SPP	SL	SYPP	SI	OC
Replications	02	789.1	2.28	219.8	0.35	0.76	0.01	0.13
Genotypes	19	468.6**	0.95*	868.4*	1.01**	9.07*	0.12**	14.9**
Error	38	151.0	0.35	220.8	0.28	4.44	0.04	4.01

Note: ** = Significant at 1% level; * = Significant at 5% level, SOV= Source of variation, D.F=Degrees of freedom PH=Plant height, BPP=Branches per plant, SPP=Siliques per plant, SL=Silique length, SYPP=Seed yield per plant, SI=Seed index, OC=Oil content

Statistical analysis

Computer software Statistix 8.1 was used for ANOVA and the LSD test. The correlation and path were analyzed as suggested by Dewey and Lu (1959). Heritability in the broad sense was computed according to Allard (1960).

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance was performed for seven characters recorded from twenty rapeseed genotypes Table 1. The results revealed that mean squares for plant height, silique length, seed index, and oil content were found highly significant at P<0.01 probability level, while the mean squares were significant at P<0.05 probability level for branches plant⁻¹, siliques plant⁻¹, and seed yield plant⁻¹.

Many previous studies have validated our findings, such as Rameeh (2016), who found considerable genetic variation for various seed yield contributing features using analysis of variance. According to Pal *et al.* (2019), analysis of variance found that the treatments were highly significant for all thirteen features, implying that the chosen genotypes were genetically diverse and that there was a great degree of variability among them.

Correlation coefficient

The correlations of PH with BPP (0.301), SL (0.269), SYPP (0.349), SI (0.289), and OC (0.275) were noted as positive and significant, while the relation of PH with SPP (0.227) was also positive, but non-significant (Table 2). The relationship between the number of BPP with SPP (0.375) was positive and significant, while the relationship between BPP with SYPP (0.223), SI (0.072), and OC (0.153) was also positive but non-significant. The relationship of BPP with SL (-0.044) was negative and non-significant. The correlation of SPP with SL (-0.019) and OC (-0.065) was negative and non-significant, while the correlation of SPP with SYPP (0.610) was positive and significant, SI (0.072) was positive and non-significant in correlation with SPP. Association of seed index with oil content was positive and significant.

Table 2: Correlation coefficient of various traits in rapeseed genotypes

Characters	PH	BPP	SPP	SL	SYPP	SI
BPP	0.301*					
SPP	0.227 ^{NS}	0.375**				
SL	0.269*	-0.044 ^{NS}	-0.019 ^{NS}			
SYPP	0.349**	0.223 ^{NS}	0.610**	0.319*		
SI	0.289*	0.072 ^{NS}	0.072 ^{NS}	0.054 ^{NS}	0.313*	
OC	0.275*	0.153 ^{NS}	-0.065 ^{NS}	0.022 ^{NS}	0.266*	0.310*

Note: **, * = Significant at 1% level & 5% probability level; NS = Non-significant

Our findings are further confirmed by many past researchers, such as Majidi *et al.* (2015) who reported a positive correlation between SYPP with BPP and SPP. Sabaghnia *et al.* (2015) assessed 49 *Brassica napus* L. genotypes under normal and water stress conditions to determine the association between 20 agronomic traits; under water stress conditions, seed yield was significantly positively inter-related with most of the characters. Hasan *et al.* (2016) calculated correlation at the genotypic and phenotypic level in eight rapeseed genotypes; a variety of characters, such as days to flowering and maturity, plant height, silique length, and silique plant⁻¹, demonstrated a significant positive correlation with seed yield plot⁻¹. Rout *et al.* (2018) and Radic *et al.* (2021) also corroborated the findings.

Path coefficient analysis

The relation between yield and important yield components is partitioned by path analysis, which is associated with correlation into direct and indirect effects. SYPP is a dependable variable while PH, BPP, SPP, SL, SI, and OC are independent variables (Table 3). The path investigation showed that the direct influence of plant height on yield was negative (-1.3053). The indirect effect on yield through BPP, SPP, SL, SI, and OC was 0.0058, 0.8165, -0.1991, -0.2842, and 1.892, respectively. The total effect on yield was 0.9258. The direct influence of BPP over yield was negative (-2.1066). Through PH, SPP, SL, SI, and OC, the corresponding indirect effects were 0.0036, 0.5675, 0.2647, 0.0076, and 0.5833. The yield was negatively impacted overall (-0.6799). SPP had a favorable direct impact on seed yield (1.7919). Through PH, BPP, SL, SI, and OC, the corresponding indirect effects were -0.5948, -0.6672, 0.016, and -0.081. Overall, the yield was positively impacted (0.5523). SL had a negative direct impact on seed yield (-0.3522). PH, BPP, SL, SI, and OC all had indirect effects that were, respectively, -0.7381, 1.5833, -0.4445, 0.0406, and 0.4857. Overall, the yield was positively impacted (0.5748). The direct influence of SI on seed yield was negative (-0.3278). While the indirect effects through PH, BPP, SL, SI, and OC were -1.1316, 0.0489, -0.7399, 0.0436, and 1.5385, respectively. The total effect on yield was positive (0.0842). The direct influence

of OC on seed yield was positive (2.3792). PH, BPP, SL, SI, and OC, on the other hand, had indirect effects of -1.038, -0.5165, -0.061, -0.0719, and -0.212, respectively. Overall, the yield was positively impacted (0.4798). Saqib (2011), Ara *et al.* (2013), Rout *et al.* (2018), and Radic *et al.* (2021) all observed similar results.

Heritability estimation

Heritability estimates are very important to know whether genotypes are affected by environmental factors, to use the material for further breeding objectives. Plant height showed lesser genetic variance ($\sigma^2g = 105.8$) and higher phenotypic variance ($\sigma^2p = 256.9$), which caused moderate heritability (41.2%) (Table 4). Moderate broad-sense heritability indicated some environmental effect on plant height. BPP had lower genetic variance ($\sigma^2g = 0.2$) than phenotypic variance ($\sigma^2p = 0.55$), therefore, a low heritability estimate (36.4%) was observed for this trait, which shows that the environment had more influence on this character. For SPP, there was also more difference in genotypic variance ($\sigma^2g = 215.8$) and phenotypic variance ($\sigma^2p = 436.7$) and resulting in moderate heritability (49.4%). For SL, the genetic variance was ($\sigma^2g = 0.24$) lower than phenotypic variance ($\sigma^2p = 0.52$), which resulted in moderate broad-sense heritability (46.1%). For yield plant⁻¹, there was smaller genetic variance ($\sigma^2g = 1.54$) than phenotypic variance ($\sigma^2p = 5.98$), that in result produced low broad sense heritability (25.7%), which means that the environment affected this character. For SI, there was a slight difference between genetic variance ($\sigma^2g = 0.03$) and phenotypic variance ($\sigma^2p = 0.07$), which resulted in moderate broad-sense heritability (42.9%). For oil content, the genetic variance ($\sigma^2g = 3.62$) was comparatively lower than phenotypic variance ($\sigma^2p = 7.63$), and it caused moderate broad-sense heritability (47.4%). Naheed *et al.* (2017) found similar results, observing moderate heritability values for seed weight and seed yield plant⁻¹. From 0.146 (seeds pod⁻¹) to 0.488 (seed yield), the broad sense heritability varied. Given the rapid genetic advancement and moderate heritability of seed weight and yield, mass selection for these traits could lead to improvement (Ali *et al.*, 2002).

Table 3: Direct (bold) and indirect (unbold) effect of different traits on seed yield plant⁻¹

Traits	Plant height	Branches plant ⁻¹	Siliques plant ⁻¹	Seed yield plant ⁻¹	Seed index	Oil content %	Seed yield plant ⁻¹
Plant height	-1.3053	0.0058	0.8165	-0.1991	-0.2842	1.892	0.9258
Branches plant⁻¹	0.0036	-2.1066	0.5675	0.2647	0.0076	0.5833	-0.6799
Siliques plant⁻¹	-0.5948	-0.6672	1.7919	0.739	0.016	-0.081	0.5523
Silique length	-0.7381	1.5833	-0.4445	-0.3522	0.0406	0.4857	0.5748
Seed index	-1.1316	0.0489	0.739	0.0436	-0.3278	1.5385	0.0842
Oil content %	-1.038	-0.5165	-0.061	-0.0719	-0.212	2.3792	0.4798

Table 4: Heritability estimation for different traits in rapeseed genotypes

Traits	Genotypic variance (σ^2g)	Phenotypic variance (σ^2p)	Heritability % (Broad sense)
Plant height	105.8	256.9	41.2
Branches plant⁻¹	0.20	0.55	36.4
Siliques plant⁻¹	215.8	436.7	49.4
Silique length	0.24	0.52	46.1
Seed yield plant⁻¹	1.54	5.98	25.7
Seed index	0.03	0.07	42.9
Oil content %	3.62	7.63	47.4

CONCLUSION

All the traits, such as plant height, branches plant⁻¹, number of siliques plant⁻¹, silique length, yield plant⁻¹, seed index, and oil content, were highly significant, indicating a greater amount of genetic variation is present in this germplasm of rapeseed crop. Under heat stress conditions, the per se performance remained high for the genotype Punjab Sarson with respect to many characteristics. However, three other genotypes, including PARC Canola, Hbo-555, and Faisal Canola, were also found to be high in seed production. Five characters, including PH, SPP, SL, SI, and OC, revealed significant and positive associations with seed yield plant⁻¹; hence, selection of these traits during segregating populations will help to evolve high-yielding rapeseed genotypes for heat stress. According to path coefficient analysis, silique plant⁻¹ and oil content had the most direct beneficial impact on seed yield plant⁻¹. Therefore, using these variables to directly select genotypes for seed yield may be beneficial. Notably, none of the traits exhibited strong heritability in heat stress situations; as a result, it is hypothesized that these qualities might be selected for later in the segregating generations.

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