

ASSESSMENT OF GENETIC PARAMETERS IN RAPESEED GENOTYPES

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ABSTRACT

The current study was carried out to estimate correlation, heritability, and genetic distance in ten (Punjab sarson, Hyola-401, Rainbow, Waster, Abasion-95, Hyola-42, Hbo-555, Mun-1, Kangola and Kn-277) rapeseed genotypes at Botanical Garden, SAU, Tandojam during the crop season 2018-19. The data were collected of seven different traits plant height (cm), branches plant⁻¹, silique plant⁻¹, seeds silique⁻¹, silique length (cm), seed yield plant⁻¹ and seed index) for further genetic analysis. Mean squares displayed that all studied characters were differed significantly, showing that exploited rapeseed genotypes retain valuable genetic resources hence may be used in future breeding programs. Of the total traits, four traits such as silique plant⁻¹ ($r = 0.33^*$), seeds silique⁻¹ ($r = 0.34^*$), silique length ($r = 0.35^*$) and seed index ($r = 0.31^*$) showed positive and significant associations with seed yield plant⁻¹, demonstrating that utilization of these traits will enhance seed yield in rapeseed genotypes; however, these characters may be set as selection criteria for evolving high yield rapeseed genotypes. The maximum (179.23) genetic distance was found between Hyola-42 and Mun-1, followed by Hyola-42 and Hbo-555 (166.10), Mun-1 and Kn-277 (162.38), Abasin-95 and Mun-1 (156.79), Hyola-401 and Mun-1 (148.79), Hbo-555 and Kn-277 (148.52), Westar and Mun-1 (146.36) and Abasin-95 and Hbo-555 (143.61). These pairs of genotypes may be given priority in the hybridization program because they carry different genetic recombination and will lead to a great amount of heterosis in hybrids. High heritability was estimated for plant height ($h^2 = 95.54\%$), branches plant⁻¹ ($h^2 = 80.92\%$), silique plant⁻¹ ($h^2 = 84.26\%$), seeds silique⁻¹ ($h^2 = 90.20\%$), silique length ($h^2 = 82.60\%$), seed yield plant⁻¹ ($h^2 = 79.12\%$) and seed index ($h^2 = 66.66\%$), signifying that these traits were under genetic control.

Keywords: correlation, genetic diversity, heritability, rapeseed, seed yield

INTRODUCTION

Several oilseed crops are being cultivated in Pakistan, whereas rapeseed and mustard crops possess special place. Rapeseed is placed on 3rd and 2nd important oil seed crop of Pakistan and the world in the marker as vegetable oil, respectively (Hasan *et al.*, 2006). The seeds of *Brassica napus* tend to have 40-46% oil in its seeds in comparison with other oil crops, including cotton (25%), soya (20%), maize (15%), while in oil properties, it is very close to sunflower (40%). It is widely grown in many countries because of its high percentage of oil (Ali and Mirza, 2005). From total consumption (2.325 million tons), Pakistan only produces about 34% of edible oil (0.606 million tons), and the remaining 66% of its total is being imported from other countries. However, 0.068 million tons (approximately 11.22%) are contributed only by rapeseed in the local market (Ullah *et al.*, 2016). Diversity analysis significantly assists the plant breeder in the documentation of proper parents for definite breeding purposes. To comprehend hybrid vigor, genetically different parents are generally suitable. From those parents, vast variability could be anticipated in obtaining vigorous progenies (Joseph *et al.*, 1999). The information about the genetic variability for the characters among propulsions is quite necessary for crop improvement program, since the plant selection is based on genetic variability, which has been proved a successful strategy in numerous crop species (Dubey, 2006). The amount of genetic diversity is considered a commanding tool for hybridization in respect to generate new high yielding potential varieties (Khan *et al.*, 2005). The utilization of available genetic variations in the breeding materials is a key step to evolving new high yielding and early maturing varieties. Rapeseed production can be improved commercially with the use of using hybrid seeds efficiently. Effective use of variations at the genetic level is possible in the breeding program if the necessary information about the genetic effects is accessible (Singh *et al.*, 2013). Variability analysis among the genotypes for different traits association with certain characters relative to other yield-related characteristics would be of utmost importance in designing the effective breeding strategy (Mary and Gopalan, 2006). The breeding strategies have always been carried out to introduce genotypes, showing high yield and better-quality so as release new varieties to farmers for commercial cultivation. The essential requirement for achieving this objective, there

should be enough variability; consequently, useful genotypes may be evolved for further investigation to complete the breeding goal (Joya *et al.*, 2016).

Correlation analysis is an effective tool to determine the relationship among different traits in genetically diverse population for enhancement of crop improvement process (Dhimi *et al.*, 2018; Kandel *et al.*, 2018). In plant breeding, the correlations are very important because of its reflection on the degree of dependence between two or more traits. Correlation analysis shows the intensity of dependence (correlation) between studied traits. In crop breeding, the breeders mostly elucidate the relationship between agronomic and morphological traits using simple correlation (Kharel *et al.*, 2018). The knowledge of heritability and selection response helps in many crop improvements programs. Plant breeders are keen to explore and create genetic variability in the existing genetic material (Sohail *et al.*, 2018). The heritability estimation is easy and takes less time in the selection procedure, resulting in more significant genetic progress. Heritability determines the extent to which a character is passing from generation to generation. It is the most valuable tool when used in correspondence with other traits in calculating genetic advance that follows the selection for those traits (Khan *et al.*, 2016). Therefore, the current study was planned to estimate genetic in parameters rapeseed genotypes.

MATERIALS AND METHODS

This research was laid out at Botanical Garden, Sindh Agriculture University, Tandojam during the rabi season 2018-19. In this study, a set of ten rapeseed genotypes of (*Brassica napus*) were sown in a Randomized Complete Block Design having four replications. The genotypes were Punjab-sarson, Hyola-401, Rainbow, Waster, Abasion-95, Hyola-42, Hbo-555, Mun-1, Kangola and Kn-277. A total of seven traits were recorded, including plant height (cm), branches plant⁻¹, silique plant⁻¹, seeds silique⁻¹, silique length (cm), seed yield plant⁻¹ and seed index (1000-seed weight, g). The plant to plant and row to row distance was kept at 30 and 75 cm, respectively. All cultural practices were applied accordingly. According to Gomez and Gomez (1984), the data was statistically analyzed, while Least Significant Differences test was used for comparing the mean differences. Heritability (Broad sense) was calculated by Allard (1960), whereas the genetic distance between different genotypes of rapeseed and correlation analysis was calculated by SPSS (Ver. 21) computer package.

RESULTS AND DISCUSSION

The current study was carried out to estimate correlation, heritability and genetic distance in rapeseed genotypes. The ANOVA was carried out for seven parameters recorded for yield contributing traits (Table 1). Mean squares displayed that the majority of the characters, including plant height, branches plant⁻¹, seeds silique⁻¹, silique length, seed yield plant⁻¹, and seed index were highly significant differences ($P \leq 0.01$) among the tested genotypes, showing that exploited rapeseed genotypes retain valuable genetic resources hence may be used in future breeding programs. Bilal *et al.*, (2015) also reported significant differences ($P \leq 0.05$) among the evaluated genotypes for days to maturity, plant height, pods plant⁻¹ and yield plant⁻¹, which confirmed the occurrence of genetic differentiation. At the molecular level, Chen *et al.*, (2017) stated a significant genetic difference between Japanese and exotic lines

Table-1: Mean squares of different traits of rapeseed genotypes.

Source of variances	D.F.	Plant height	Branch plant ⁻¹	Silique plant ⁻¹	Seeds silique ⁻¹	Silique length	Seed yield plant ⁻¹	Seed index
Replication	3	1.68	0.24	43.30	2.68	0.31	31.36	0.27
Genotypes	9	792.22**	5.96**	2201.09**	58.66**	2.42**	6.16**	0.12**
Error	27	9.12	0.33	98.14	1.55	0.12	0.38	0.01

** indicates significant level at 1% of probability level.

.Considering the mean performance of rapeseed genotypes (Table 2), the maximum plant height (172.25 cm) was attained by Rainbow, maximum branches were recorded in Westar (7.25), and maximum silique plant⁻¹ (253.05) were set in Mun-1. Concerning parameter seeds silique⁻¹, the top seeds silique⁻¹ was counted in Hyola-401 (28.38), while, maximum silique length (cm) was recorded by the genotype Punjab Sarson (8.43 cm). Regarding seed yield plant⁻¹, Punjab Sarson (12.39 g) produced the greater seed yield, whereas higher seed index was obtained in Westar (3.85 g). These genotypes tend to have promising genetic potential hence preference should be given in upcoming breeding programs.

Similarly, Ali *et al.*, (2013) also referred that Carinata-83 were superior for seed yield and yield contributing traits, whereas Carinata-70 was the best for oil quality traits. Overall, carinata-70 and carinata-83 were the best performing genotypes/accessions hence could be used in breeding programs.

Table-2: Mean performance of rapeseed genotypes for various traits.

Genotypes	Plant height (cm)	Branches plant ⁻¹	Silique plant ⁻¹	Seeds silique ⁻¹	Silique length (cm)	Seed yield plant ⁻¹ (g)	Seed index (1000-grain weight, g)
Punjab Sarson	17.40	4.75	220.90	24.08	8.43	12.39	3.53
Hyola-401	126.95	4.32	179.30	28.38	8.22	11.40	3.79
Rianbow	172.25	5.10	221.10	23.01	7.83	10.27	3.83
Westar	145.25	7.25	237.40	16.60	6.24	9.33	3.85
Abasin-95	146.45	7.00	223.30	16.70	6.54	9.63	3.61
Hyola-42	145.80	6.65	231.25	15.91	6.53	9.71	3.41
Hbo-555	166.50	4.65	243.95	20.81	7.43	10.16	3.71
Mun-1	162.85	5.00	253.05	20.80	7.98	9.35	3.57
Kungola	158.70	4.30	236.15	21.10	7.29	9.31	3.35
Kn-277	155.85	3.85	187.70	21.50	8.01	7.87	3.75
LSD (5%)	4.38	0.84	71.05	1.80	0.52	3.03	0.41

Seed yield is the indirect product of various characters, which are not controlled by a single gene. Therefore, the improvement in related character increases the subsequent enhancement in the yield. Hence, the understanding of cause and effect relationship is quite necessary in association studies, which provides the basis to establish the appropriate selection principles for breeding program based on yield-related characters for attaining usual enhancement of yield (Wang *et al.*, 2012). The correlation coefficient was determined between seven characters (Table 3). Of the total traits, four traits such as silique plant⁻¹ ($r = 0.33^*$), seeds silique ($r = 0.34^*$), silique length (0.35^*) and seed index ($r = 0.31^*$) disclosed positive and significant relationships with seed yield plant⁻¹, demonstrating that utilization of aforesaid traits will enhance seed yield in rapeseed genotypes, however, the traits including silique plant⁻¹, seeds silique, silique length and seed index may be set as choice characters for developing high yield rapeseed genotypes. A significantly positive phenotypic correlation of plant height and branches plant⁻¹ with seed yield plant⁻¹ was observed (Ali *et al.*, 2013). A positive correlation was also noticed for days to flowering, days to ripening, branches plant⁻¹, and pods plant⁻¹ with seed yield (Sharafi *et al.*, 2015). For seed yield improvement in rapeseed, the genotypic and phenotypic correlations analysis revealed that the number of pods plant⁻¹ had highly significant positive correlation with seed yield (Tahira *et al.*, 2017). Rauf and Rahim (2018) also reported positively significant associations of various traits (silique length, seeds plant⁻¹, seeds silique⁻¹ and 1000-seed weight) with seed yield.

Table-3: Correlation coefficient (r) between various traits of rapeseed genotypes.

Traits	Plant height	Branches plant ⁻¹	Silique plant ⁻¹	Seeds silique ⁻¹	Silique length	Seed yield plant ⁻¹
Branches plant ⁻¹	-0.29					
Silique plant ⁻¹	0.25	0.22				
Seeds silique ⁻¹	0.01	-0.71**	-0.32*			
Silique length	0.27	0.72**	-0.15	0.73**		
Seed yield plant ⁻¹	0.25	0.24	0.33*	0.34*	0.35*	
Seed index	-0.08	0.21	-0.05	0.25	0.15	0.31*

*, ** indicates significant level at 5 and 1% of probability level, respectively.

The matrix data from attributes was developed based on Euclidean genetic distance calculations. All 45 pair wise comparisons of the 10 rapeseed breeding materials are given in Table 4. The highest genetic distance (179.23) was noted between Hyola-42 and Mun-1, followed by Hyola-42 and Hbo-555 (166.10), Mun-1 and Kn-277 (162.38), Abasin-95 and Mun-1 (156.79), Hyola-401 and Mun-1 (148.79), Hbo-555 and Kn-277 (148.52), Westar and Mun-1 (146.36) and Abasin-95 and Hbo-555 (143.61). These genotypes may be given priority in the hybridization program because they carry different genetic recombination's and lead to a great amount of heterosis in hybrids. Cluster analysis (Rameeh, 2015)

revealed that rapeseed genotypes grouped into three categories, while greater seed yield had maximum mean values of days to maturity, plant height and pods plant⁻¹.

Table-4: Estimation of genetic distance between different rapeseed genotypes.

Genotypes	Punjab Sarson	Hyola-401	Rainbow	Westar	Abasin-95	Hyola-42	Hbo-555	Mun-1	Kungola
Hyola-401	56.59								
Rainbow	22.75	48.46							
Westar	48.14	19.11	35.98						
Abasian-95	56.46	22.16	40.87	11.22					
Hyola-42	78.60	38.55	60.96	33.00	22.87				
Hbo-555	90.95	136.41	113.21	133.34	143.61	166.10			
Mun-1	104.94	148.79	127.39	146.36	156.79	179.23	15.36		
Kungola	12.27	47.32	19.97	38.59	47.34	69.55	98.22	112.19	
Kn-277	58.69	36.24	38.65	24.55	16.72	25.27	148.52	162.38	50.33

The selection procedure may be practiced at ease if the high heritability of the character is achieved (Barnard *et al.*, 2002). The characters, such as plant height ($h^2=95.54\%$), branches plant⁻¹ ($h^2=80.92\%$), silique plant⁻¹ ($h^2=84.26\%$), seeds silique⁻¹ ($h^2=90.20\%$), silique length ($h^2=82.60\%$), seed yield plant⁻¹ ($h^2=79.12\%$) and seed index ($h^2=66.66\%$) showed high estimation of heritability in Broad sense (Table 5). High heritability of above-mentioned traits indicated that the variations were mainly controlled genetically despite environmentally, indicating the influence of additive gene action. Shaukat *et al.*, (2014) reported high heritability estimates (b.s.) of 0.90 for erucic acid content, moderate for glucosinolate content (0.53), and low for protein content (0.45) and oil content (0.16). The inclination of heritability from moderate to high refers that genetic control was more and selection would lead to rapid enhancement. Sohail *et al.*, (2018) assessed heritability for morph-yield traits in brassica. Pods on main raceme and pod length exhibited high heritability (0.87) followed by seeds pod⁻¹ (0.86), main raceme length (0.83), primary branches plant⁻¹ (0.80), pod width (0.79), seed yield plant⁻¹ (0.77), 100 seeds weight (0.71) and plant height (0.66).

Table-5: Estimation of heritability in broad sense for different traits of rapeseed genotypes.

Traits	Genotypic variance (δ^2g)	Phenotypic variance (δ^2p)	Heritability % (Broad sense)
Plant height	195.77	204.89	95.54
Branch plant ⁻¹	1.40	1.73	80.92
Silique plant ⁻¹	525.73	623.87	84.26
Seeds silique ⁻¹	14.27	15.82	90.20
Silique length	0.57	0.69	82.60
Seed yield plant ⁻¹	1.44	1.82	79.12
Seed index	0.02	0.03	66.66

CONCLUSIONS

It is concluded that silique plant⁻¹, seeds silique⁻¹, silique length and seed index showed positive and significant associations with seed yield plant⁻¹, demonstrating that utilization of these traits will enhance seed yield in rapeseed genotypes. The greater genetic distance was found between Hyola-42 and Mun-1, followed by Hyola-42 and Hbo-555, Mun-1 and Kn-277, Abasin-95 and Mun-1, Hyola-401 and Mun-1, Hbo-555 and Kn-277, Westar and Mun-1 and Abasin-95 and Hbo-555. These genotypes may be given priority in the hybridization program because they carry different genetic recombinations and lead to a great amount of heterosis in hybrids.

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