

Correlations and Factor Wise Contributions of Various Traits Related to Yield in Rapeseed (*Brassica napus* L.)

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Abstract: Twenty *Brassica napus* L. genotypes including a check cultivar Abasin-95 was evaluated to study correlation and path co-efficient analysis to partition the cause and effect relationship into direct and indirect components. The experiment was laid out in randomized complete block design with three replications at Khyber Pakhtunkhwa Agricultural University, Peshawar, Pakistan during 2010-11. Correlation analysis revealed that seed yield plant⁻¹ had significant positive genetic (r_G) and phenotypic (r_P) correlation with flowering (0.44, 0.34), maturity (0.68, 0.51), plant height (0.55, 0.46), primary branches plant⁻¹ (0.83, 0.68), main raceme length (0.71, 0.49), pods main raceme⁻¹ (0.74, 0.60) and pods plant⁻¹ (0.87, 0.79), whereas significant positive phenotypic association with seeds pod⁻¹ (0.39). Path coefficient analysis indicated that primary branches plant⁻¹ had maximum positive direct effect on seed yield plant⁻¹ followed by pods main raceme⁻¹, seeds pod⁻¹ and 1000-seed weight, whereas, pods plant⁻¹, main raceme length, maturity, flowering and plant height had positive indirect effect on seed yield. The most prominent characters which influence seed yield in rapeseed were primary branches plant⁻¹, pods main raceme⁻¹, seeds pod⁻¹, pods plant⁻¹, main raceme length and 1000-seed weight. Strong association of these yield components with seed yield suggested good selection criteria for improving seed yield in rapeseed.

Key words: Rapeseed • Correlation • Path coefficient analysis • yield component

INTRODUCTION

The genus *Brassica* is an important member of the cruciferae family. It comprises of several economically important species which yield edible roots, stems, leaves, buds, flowers and seed as condiment. Most of the species are used as oilseed crop and some as forage [1]. The oilseed *Brassica* species (*B. napus*, *B. rapa*, *B. campestris* and *B. jancea*) are now the third most important source of edible oil in the world after palm and soybean oil [2]. Yield is a complex trait characterized by low heritability and affected by genotype x environment interactions. The genetic background of any pair of characters, whether yield, height, or maturity characters is unlikely to be under totally separate control, mainly due to linkage or pleiotropy [3]. The improvement through breeding could be made successfully by selecting the genetic material after determining the exact contribution of various components towards yield [4]. Therefore, information on the association of plant characters with seed yield is of great importance to a breeder in selecting a desirable genotype. In many cases

the reported correlations are highly dependent on the environment and on the material. Basing decisions solely on correlation coefficients may not always be effective because they provide only limited information, disregarding interrelations among traits. Thus, information obtained from correlation coefficient can be enhanced by partitioning them into direct and indirect effects for a set of prior cause and interrelationship. The path coefficient analysis helps the breeder(s) to explain direct and indirect effects and hence has extensively been used in breeding work in different crop species by various researchers [5, 6]. The objective of this study was to determine the interrelationships between yield and some yield components and to identify characters with significant effects on yield for potential use as selection criteria.

MATERIALS AND METHODS

Field experiment was conducted at experimental field of Khyber Pukthoonkhwa Agricultural University, Peshawar-Pakistan during 2010-11. The experimental

material comprised of twenty *Brassica napus* L. genotypes including a check cultivar Abasin-95 was laid out in randomized complete block design with three replications. The entries were sown in three rows each of 4 m length with spacing of 60 cm between rows and 20 cm between the plants. All cultural practices like land preparation, sowing, fertilizer application, hoeing and pest control were applied as recommended. Data were recorded for twelve different traits at appropriate time on 10 randomly selected plants in each genotype from and replication.

Correlation Coefficient: Genetic (r_G) and phenotypic (r_P) correlations was computed using the procedure of Singh and Choudhery [7].

Path Coefficient Analysis: Path coefficient analysis was performed according to the method prescribed by Dewey and Lu [8] by solving the following equations using genetic correlations. Seed yield plant⁻¹ were kept as resultant variables (effect) while yield contributing and quality traits as casual variables (causes). Equations to calculate direct and indirect effects as indicated by the path diagram are as under:

The following set of simultaneous equations were formed and solved for estimating the direct and indirect effects.

$$r_{1y} = a + r_{12}b + r_{13}c + \dots + r_{12i}$$

$$r_{2y} = r_{21}ab + r_{23}c + \dots + r_{21i}$$

$$r_{ny} = r_{n1}ab + r_{n2}c + \dots + i$$

where r_{1y} to r_{ny} = coefficients of correlation between causal factors 1 to n and dependent character y.

$r_{12}, r_{21}, r_{31} \dots r_{ni}$ = genetic correlation among the causal factors 1 to n.

a, b, c, i = direct effects of characters a to i on the dependent character y

Residual effect (R) = $1 - (a^2 + b^2 + c^2 \dots + i^2 + 2abr_{12} + 2acr_{13} + \dots)$

RESULTS AND DISCUSSIONS

The results of genetic and phenotypic correlation between the traits studied are given in Table 1. Seed yield plant⁻¹ showed significant positive genetic correlation with days to flowering, days to maturity, plant height, primary branches plant⁻¹, main raceme length, pods main raceme and pods plant⁻¹, whereas correlation of seeds pod⁻¹ with seed yield was only significant and positive at phenotypic level. Positive association of these yield components have frequently been cited with seed yield [9-11].

The maximum significant positive genetic and phenotypic correlations were observed for pods main raceme⁻¹ and pods plant⁻¹, followed by primary branches and pods plant⁻¹ and their coefficient were (0.98, 0.79) and (0.93, 0.85), respectively. Significant positive association of pods plant⁻¹ with other traits had also been reported earlier by Meena *et al.* [12], Sadat *et al.* [10], Azadgoleh *et al.* [13] and Gangapur *et al.* [1]. In addition, the maximum negative and significant genetic and phenotypic correlations existed between 1000-seed weight

Table 1: Genetic correlation (above diagonal) and phenotypic correlation (below diagonal) between various traits of 20 *Brassica napus* genotypes evaluated at Agricultural University, Peshawar during 2010-11

Traits	DF	DM	PH	PB	MRL	PMR	PPP	PL	SPP	TSW	OIL	SY
DF	1	0.75**	0.73**	0.42 ^{NS}	0.47*	0.56**	0.46*	0.12 ^{NS}	-0.01 ^{NS}	-0.45*	0.30 ^{NS}	0.44*
DM	0.60**	1	0.55*	0.53*	0.54*	0.31 ^{NS}	0.45*	0.53*	0.34 ^{NS}	-0.03 ^{NS}	0.17 ^{NS}	0.68**
PH	0.49**	0.37**	1	0.72**	0.88**	0.87**	0.76**	-0.30 ^{NS}	-0.44*	-0.35 ^{NS}	-0.01 ^{NS}	0.55*
PB	0.28*	0.36**	0.42**	1	0.85**	0.89**	0.93**	-0.21 ^{NS}	-0.25 ^{NS}	-0.13 ^{NS}	0.04 ^{NS}	0.83**
MRL	0.27*	0.47**	0.70**	0.45**	1	0.73**	0.86**	-0.03 ^{NS}	-0.15 ^{NS}	-0.20 ^{NS}	0.02 ^{NS}	0.71**
PMR	0.43**	0.34**	0.72**	0.48**	0.68**	1	0.98**	-0.47*	-0.25 ^{NS}	-0.36 ^{NS}	0.19 ^{NS}	0.74**
PPP	0.36**	0.38**	0.59**	0.85**	0.64**	0.79**	1	-0.27 ^{NS}	-0.10 ^{NS}	-0.24 ^{NS}	0.15 ^{NS}	0.87**
PL	0.06 ^{NS}	0.26*	-0.10 ^{NS}	-0.13 ^{NS}	-0.06 ^{NS}	-0.33**	-0.17 ^{NS}	1	0.60**	0.44*	-0.15 ^{NS}	0.11 ^{NS}
SPP	0.03 ^{NS}	0.21 ^{NS}	-0.24 ^{NS}	-0.17 ^{NS}	-0.19 ^{NS}	-0.18 ^{NS}	-0.06 ^{NS}	0.55**	1	0.30 ^{NS}	0.53*	0.30 ^{NS}
TSW	-0.24 ^{NS}	-0.01 ^{NS}	-0.10 ^{NS}	-0.05 ^{NS}	-0.05 ^{NS}	-0.17 ^{NS}	-0.11 ^{NS}	0.34**	0.14 ^{NS}	1	-0.58**	0.22 ^{NS}
OIL	0.22 ^{NS}	0.15 ^{NS}	0.01 ^{NS}	-0.02 ^{NS}	0.01 ^{NS}	0.11 ^{NS}	0.07 ^{NS}	-0.10 ^{NS}	0.28*	-0.25*	1	0.27 ^{NS}
SY	0.34**	0.51**	0.46**	0.68**	0.49**	0.60**	0.79**	0.20 ^{NS}	0.39**	0.14 ^{NS}	0.15 ^{NS}	1

*, ** = Significant at 5 and 1% probability, respectively whereas NS = Non-significant

DF= Days to flowering, DM= Days to maturity, PH= Plant height, PB= Primary branches plant⁻¹, MRL= Main raceme length, PMR= Pods main raceme⁻¹, PPP= Pods plant⁻¹, PL= Pod length, SPP= Seeds pod⁻¹, TSW= 1000-seed weight, Oil= Oil content, SY= Seed yield plant⁻¹

Table 2: Path coefficient analysis showing direct, indirect and total effects of various traits with seed yield plant⁻¹ of 20 *Brassica napus* genotypes evaluated at Agricultural University, Peshawar during 2010-11

Traits	Direct effect	Indirect effects											Total indirect effect	Total effect
		DF	DM	PH	PB	MRL	PMR	PPP	PL	SPP	TSW	OIL		
DF	-0.07 ^{NS}	-	0.041	0.089	0.259	-0.040	0.247	-0.019	0.014	-0.005	-0.114	0.042	0.51*	0.44
DM	0.06 ^{NS}	-0.055	-	0.067	0.325	-0.046	0.137	-0.018	0.065	0.134	-0.008	0.024	0.63**	0.68
PH	0.12 ^{NS}	-0.053	0.044	-	0.460	-0.076	0.385	-0.032	-0.036	-0.175	-0.088	-0.002	0.43 ^{NS}	0.55
PB	0.62**	-0.031	0.029	0.087	-	-0.073	0.393	-0.038	-0.026	-0.098	-0.032	0.006	0.22 ^{NS}	0.83
MRL	-0.09 ^{NS}	-0.034	0.030	0.107	0.521	-	0.325	-0.035	-0.004	-0.060	-0.051	0.003	0.80**	0.71
PMR	0.44*	-0.041	0.017	0.105	0.546	-0.063	-	-0.040	-0.057	-0.099	-0.092	0.026	0.30 ^{NS}	0.74
PPP	-0.04 ^{NS}	-0.034	0.025	0.093	0.574	-0.073	0.434	-	-0.033	-0.038	-0.061	0.021	0.91**	0.87
PL	0.12 ^{NS}	-0.008	0.029	-0.036	-0.132	0.003	-0.207	0.011	-	0.239	0.112	-0.021	-0.01 ^{NS}	0.11
SPP	0.40 ^{NS}	0.001	0.019	-0.054	-0.152	0.013	-0.111	0.004	0.034	-	0.077	0.073	-0.10 ^{NS}	0.30
TSW	0.25 ^{NS}	0.033	-0.002	-0.042	-0.079	0.017	-0.161	0.010	0.065	0.220	-	-0.097	-0.04 ^{NS}	0.22
OIL	0.14 ^{NS}	-0.022	0.009	-0.001	0.027	-0.002	0.082	-0.006	-0.019	0.208	-0.147	-	0.13 ^{NS}	0.27

Residual effect = 0.101 and R² = 0.99

*,** = Significant at 5 and 1% probability, respectively whereas NS = Non-significant

DF= Days to flowering, DM= Days to maturity, PH= Plant height, PB= Primary branches plant⁻¹, MRL= Main raceme length, PMR= Pods main raceme⁻¹, PPP= Pods plant⁻¹,PL= Pod length, SPP= Seeds pod⁻¹, TSW= 1000-seed weight, Oil= Oil content.

and oil content (-0.58, -0.25), followed by pods main raceme⁻¹ and pod length (-0.47, -0.25). These present findings are in contrast with the earlier findings of Sadat *et al.* [10] and Khan *et al.* [14], who reported positive association of these traits with seed yield plant⁻¹.

Days to flowering, maturity, plant height, primary branches, main raceme length, pods main raceme⁻¹, pods plant⁻¹ and seed yield plant⁻¹ showed significant association with each other at both genetic and phenotypic level. Furthermore, pod length, seeds pod⁻¹, 1000-seed weight and oil content exhibited non significant correlation with most of studied traits at both genetic and phenotypic level. Similar observations are also reported by Aytac and Kinaci [11], Khan *et al.* [15] and Mena *et al.* [12].

As simple correlation coefficient did not give clear information about interrelationship between casual and resultant variables, the genetic correlation coefficient were partitioned into direct and indirect effects to establish the intensity of effects on independent variable on dependent one through path coefficient analysis (Table 2).

Path coefficient analysis revealed that maximum direct effect was recorded by primary branches plant⁻¹, followed by pods main raceme⁻¹ on seed yield plant⁻¹. The direct effect and genetic correlation between these traits is positive thus indicating the true relationship and signifies the direct selection through this traits in breeding program. These results are in accordance with the previous findings of Sadat *et al.* [10], Gangapur *et al.* [1] and Khan *et al.* [16].

Days to flowering, maturity and main raceme length exhibited non-significant direct and significant total indirect effects on seed yield plant⁻¹. Although, the direct effects are low and the genetic correlation are positive, but the indirect effect of days to flowering, maturity and main raceme length via other traits is high, therefore selection should be made on the basis of traits which influenced seed yield indirectly. Similar observations were also reported by Sadat *et al.* [10], Jeromela *et al.* [17] and Baradaran *et al.* [18].

Furthermore, plant height, pod length, seeds pod, 1000-seed weight and oil content had non significant direct and total indirect effects on seed yield plant⁻¹. The direct effect and genetic association of these traits are positive thus indicating the true relationship of these traits with seed yield plant⁻¹. Positive associations of yield component with seed yield have frequently been cited [16, 19].

CONCLUSION

The maximum positive direct effect was observed by primary branches plant⁻¹, followed by pods main raceme⁻¹, seeds pod⁻¹, 1000-seed weight, oil content, plant height, pods main raceme⁻¹ and days to maturity on seed yield plant⁻¹. Furthermore, maximum positive indirect effect of pods plant⁻¹ via primary branches plant⁻¹, followed by pods main raceme⁻¹ via primary branches plant⁻¹, main raceme length via primary branches plant⁻¹, plant height via primary branches plant⁻¹ and pods plant⁻¹ via pods main raceme⁻¹. Therefore, it has clearly

indicated the need for giving due weightage for primary branches plant⁻¹, pods main raceme⁻¹, seeds pod⁻¹, 1000-seed weight and pods plant⁻¹ for improving seed yield in Brassica.

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