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Correlation study of yield and yield contributing traits in advanced generation lines of Indian mustard (*Brassica juncea* L.)

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Abstract

A study was undertaken with forty four Indian mustard advanced generation lines along with checks to analyze the correlation analysis of eleven yield contributing characters. The experiment was conducted at Oilseed Breeding Block of Norman E. Borlaug Crop Research Centre and the laboratory, Department of Genetics and Plant Breeding at Govind Ballabh Pant University of Agriculture and Technology, Pantnagar for two seasons viz. *rabi* 2019 and *rabi* 2020. Correlation analysis revealed that seed yield is positively and significantly correlated with number of primary branch at both genotypic and phenotypic level in both the seasons while plant height, length on main raceme, siliquae on main raceme had significant positive association at genotypic level in both the seasons. These traits may be considered for selection and yield improvement of Indian mustard genotypes.

Keywords: *Brassica juncea*, correlation, Indian mustard

1. Introduction

Indian mustard (*Brassica juncea* L.) is a crucial oilseed crop farmed widely as a rainfed crop in India during the Rabi season. One-third of the nation's demands for edible oil are met by mustard oil, and to satisfy these needs, the nation heavily relies on vegetable oil imports. With the present level of production and productivity, the demand supply gap of edible oils in future is anticipated to increase further due to expected increase in population and better living standard. By 2030, the demand for edible oils is predicted to rise to 11.12 million tonnes^[1]. This is equivalent to producing 32.35 million tonnes of edible oilseeds in 2030. By increasing the area planted with oil seed crops, it will be possible to reduce the import of vegetable oils. By enhancing the existing lines, it is crucial to raise the yields of mustard crops. To do this, it is necessary to understand the numerous traits that contribute to seed yield as well as their relationships with one another. In this experiment, we looked at how various yield-contributing traits correlated or were mutually associated. The interaction of yield components will aid a breeder in determining the type, degree, and direction of selection pressure on traits.

2. Material and Methods

Experiment was conducted at Oilseed Breeding Block of Norman E. Borlaug Crop Research Centre and the laboratory study was done in the Oilseed Quality Laboratory of Department of Genetics and Plant Breeding at Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand, India during Rabi season of 2019-20, 2020-21. The experimental material employed in the present study consists of a set of 44 diverse advanced generation Indian mustard lines along with three checks. The material was planted in randomized block design with three replications at Oilseed Breeding Block of Norman E. Borlaug Crop Research Centre, Pantnagar. The plot size consisted of 5 rows of 3m length with row to row and plant to plant spacing of 30 cm and 15 cm, respectively. The standard package of practices for mustard cultivation was followed. The observations were recorded for eleven yield contributing characters viz., days to maturity, plant height (cm), length of main raceme (cm), silique on main raceme, number of primary branch, number of secondary branch, siliqua length(cm), number of seeds/siliqua, 1000 seed weight(g), oil content (%) and seed yield (kg/ha). Data was recorded for five randomly selected plants of each genotype in each replication.

The data was subjected to correlation analysis using R studio. Correlation coefficients were calculated as per the formulae suggested by Falconer (1981)^[4].

3. Results and Discussion

Correlation analysis gives us an estimate of degree of association among two or more variables or characters. The dependence of yield on different yield attributing characters can be known by correlation coefficients. The results of genotypic and phenotypic correlation coefficients were presented in table 1 and table 2. In *rabi*. 2019, Seed yield had significant positive correlation with plant height ($r_p = 0.308$, $r_g = 0.444$), length of main raceme ($r_p = 0.208$, $r_g = 0.254$), siliquae on main raceme ($r_p = 0.195$, $r_g = 0.198$), number of primary branches ($r_p = 0.303$, $r_g = 0.411$) at both phenotypic level and genotypic level. siliqua length ($r_p = 0.125$, $r_g = 0.219$) having significant positive correlation with seed yield at genotypic level whereas for all other characters it was found to be non significant.

During *rabi*. 2020 seed yield had significant positive correlation with number of primary branches ($r_p = 0.305, 0.623$) and 1000 seed weight ($r_p = 0.276$, $r_g = 0.387$) at both genotypic and phenotypic level while there is significant positive correlation with plant height ($r_p = 0.096$, $r_g = 0.268$), length on main raceme ($r_p = 0.102$, $r_g = 0.334$), siliquae on main raceme ($r_p = 0.098$, $r_g = 0.237$) and oil content ($r_p = 0.101$,

$r_g = 0.263$) at genotypic level.

In *rabi*. 2019, number of seeds per siliqua had significant positive association with 1000 seed weight ($r_p = 0.218$, $r_g = 0.254$) while significant negative association with days to maturity ($r_p = -0.424$, $r_g = -0.523$), and plant height ($r_p = -0.282$, $r_g = -0.350$) at both phenotypic level and genotypic level. Oil content ($r_p = 0.152$, $r_g = 0.252$) having significant positive association at genotypic level. Number of seeds per siliqua had significant positive association with siliqua length ($r_p = 0.449$, $r_g = 0.561$), 1000 seed weight ($r_p = 0.200$, $r_g = 0.308$) and oil content ($r_p = 0.195$, $r_g = 0.323$) while significant negative association with days to maturity ($r_p = -0.350$, $r_g = -0.542$) and plant height ($r_p = -0.263$, $r_g = -0.359$) at both phenotypic level and genotypic level in *rabi*. 2019.

Similar results were obtained by several researchers like Dawar *et al.* (2018) [2], Ankit Kumar *et al.* (2018) [1], Kumar *et al.* (2017) [6], Lakra *et al.* (2020) [8], Rout *et al.* (2019) [14], Kumar *et al.* (2018) [7], Roy *et al.* (2017) [15], Saleem *et al.* (2017) [16], Yadav *et al.* (2017) [17], Gupta (2018) [5], Devi (2018) [3], Lodhi *et al.* (2014) [9], Rathod *et al.* (2013) [12], Rauf and Rahim (2018) [13], Pal *et al.* (2019) [10].

Table 1: Phenotypic and genotypic correlation among yield and its contributing traits in *Brassica juncea* L. advanced generation lines along with checks (*rabi*, 2019)

Characters		Days to maturity	Plant height (cm)	Length of main raceme	Siliqua on main raceme	No. of primary branch	No. of secondary branch	Siliqua length (cm)	No. of seeds/siliqua	1000 seed weight(g)	Oil content (%)	Seed yield(kg/ha)
Days to maturity	P	1.000										
	G	1.000										
Plant height (cm)	P	0.388**	1.000									
	G	0.453**	1.000									
Length of main raceme	P	-0.042 ^{NS}	0.257**	1.000								
	G	-0.025 ^{NS}	0.380**	1.000								
Siliqua on main raceme	P	-0.124 ^{NS}	0.270**	0.223*	1.000							
	G	-0.142 ^{NS}	0.332**	0.293**	1.000							
No. of primary branch	P	0.265**	0.225**	0.196*	-0.162 ^{NS}	1.000						
	G	0.290**	0.259**	0.242**	-0.158 ^{NS}	1.000						
No. of secondary branch	P	0.101 ^{NS}	0.185*	0.098 ^{NS}	-0.158 ^{NS}	0.137 ^{NS}	1.000					
	G	0.116 ^{NS}	0.226**	0.146 ^{NS}	-0.195*	0.179*	1.000					
Siliqua length (cm)	P	-0.151 ^{NS}	-0.038 ^{NS}	-0.084 ^{NS}	-0.195*	-0.146 ^{NS}	0.018 ^{NS}	1.000				
	G	-0.200*	-0.002 ^{NS}	-0.129 ^{NS}	-0.248**	-0.204*	0.095 ^{NS}	1.000				
No. of seeds/siliqua	P	-0.424**	-0.282**	0.011 ^{NS}	-0.051 ^{NS}	0.128 ^{NS}	-0.131 ^{NS}	-0.044 ^{NS}	1.000			
	G	-0.523**	-0.350**	0.027 ^{NS}	-0.073 ^{NS}	0.153 ^{NS}	-0.181*	-0.062 ^{NS}	1.000			
1000 seed weight(g)	P	-0.105 ^{NS}	-0.138 ^{NS}	0.238**	-0.004 ^{NS}	-0.119 ^{NS}	-0.099 ^{NS}	0.119 ^{NS}	0.218*	1.000		
	G	-0.111 ^{NS}	-0.157 ^{NS}	0.266**	-0.009 ^{NS}	-0.125 ^{NS}	-0.125 ^{NS}	0.161 ^{NS}	0.254**	1.000		
Oil content (%)	P	-0.309**	-0.055 ^{NS}	0.116 ^{NS}	-0.133 ^{NS}	-0.117 ^{NS}	0.092 ^{NS}	-0.106 ^{NS}	0.152 ^{NS}	0.066 ^{NS}	1.000	
	G	-0.363**	-0.113 ^{NS}	0.198*	-0.176*	-0.131 ^{NS}	0.131 ^{NS}	-0.130 ^{NS}	0.252**	0.082 ^{NS}	1.000	
Seed yield(kg/ha)	P	0.034 ^{NS}	0.308**	0.208*	0.195*	0.303**	-0.064 ^{NS}	0.125 ^{NS}	-0.091 ^{NS}	0.105 ^{NS}	-0.089 ^{NS}	1.000
	G	0.056 ^{NS}	0.444**	0.254**	0.198*	0.411**	-0.082 ^{NS}	0.219*	-0.155 ^{NS}	0.124 ^{NS}	-0.155 ^{NS}	1.000

Table 2: Phenotypic and genotypic correlation among yield and its contributing traits in *Brassica juncea* L. advanced generation lines along with checks (*rabi*, 2020)

Characters		Days to maturity	Plant height (cm)	Length of main raceme	Siliqua on main raceme	No. of primary branch	No. of secondary branch	Siliqua length (cm)	No. of seeds/siliqua	1000 seed weight (g)	Oil content (%)	Seed yield (kg/ha)
Days to maturity	P	1.000										
	G	1.000										
Plant height (cm)	P	0.317**	1.000									
	G	0.401**	1.000									
Length of main raceme	P	-0.081 ^{NS}	0.463**	1.000								
	G	-0.167 ^{NS}	0.653**	1.000								
Siliqua on main raceme	P	-0.022 ^{NS}	0.560**	0.625**	1.000							
	G	-0.011 ^{NS}	0.685**	0.716**	1.000							
No. of primary	P	0.084 ^{NS}	0.281**	0.250**	0.313**	1.000						

branch	G	0.151 ^{NS}	0.438 ^{**}	0.195 [*]	0.275 ^{**}	1.000						
No. of secondary branch	P	0.055 ^{NS}	0.036 ^{NS}	0.089 ^{NS}	0.139 ^{NS}	0.185 [*]	1.000					
	G	0.111 ^{NS}	0.018 ^{NS}	0.007 ^{NS}	0.080 ^{NS}	0.154 ^{NS}	1.000					
Siliqua length (cm)	P	-0.188 [*]	-0.140 ^{NS}	0.027 ^{NS}	0.057 ^{NS}	0.245 ^{**}	0.157 ^{NS}	1.000				
	G	-0.221 [*]	-0.193 [*]	0.036 ^{NS}	-0.009 ^{NS}	0.214 [*]	0.228 ^{**}	1.000				
No. of seeds/siliqua	P	-0.350 ^{**}	-0.263 ^{**}	0.214 [*]	0.033 ^{NS}	-0.043 ^{NS}	0.005 ^{NS}	0.449 ^{**}	1.000			
	G	-0.542 ^{**}	-0.359 ^{**}	0.171 ^{NS}	-0.234 ^{**}	-0.230 ^{**}	-0.023 ^{NS}	0.561 ^{**}	1.000			
1000 seed weight(g)	P	-0.323 ^{**}	0.007 ^{NS}	0.236 ^{**}	0.169 ^{NS}	0.095 ^{NS}	-0.096 ^{NS}	0.344 ^{**}	0.200 [*]	1.000		
	G	-0.364 ^{**}	-0.008 ^{NS}	0.329 ^{**}	0.206 [*]	0.086 ^{NS}	-0.148 ^{NS}	0.494 ^{**}	0.308 ^{**}	1.000		
Oil content (%)	P	-0.334 ^{**}	-0.168 ^{NS}	0.030 ^{NS}	-0.010 ^{NS}	-0.098 ^{NS}	0.081 ^{NS}	0.215 [*]	0.195 [*]	0.279 ^{**}	1.000	
	G	-0.482 ^{**}	-0.333 ^{**}	0.140 ^{NS}	0.010 ^{NS}	-0.033 ^{NS}	0.155 ^{NS}	0.343 ^{**}	0.323 ^{**}	0.357 ^{**}	1.000	
Seed yield(kg/ha)	P	-0.008 ^{NS}	0.096 ^{NS}	0.102 ^{NS}	0.098 ^{NS}	0.305 ^{**}	-0.133 ^{NS}	0.098 ^{NS}	-0.095 ^{NS}	0.276 ^{**}	0.101 ^{NS}	1.000
	G	-0.042 ^{NS}	0.268 ^{**}	0.334 ^{**}	0.237 ^{**}	0.623 ^{**}	-0.166 ^{NS}	0.136 ^{NS}	-0.270 ^{**}	0.387 ^{**}	0.263 ^{**}	1.000

4. Conclusion

The results in the present study revealed that characters like number of primary branch having significant positive correlation with seed yield at both genotypic and phenotypic level in both the seasons while plant height), length on main raceme, siliquae on main raceme had significant positive association at genotypic level in both the seasons. Hence, the direct selection for these traits through simple breeding procedures can be helpful in improving the yield of the mustard genotypes.

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