Correlation and Path Analysis of Yield-Attributing Traits in Indian Mustard (*Brassica juncea* L. Czern & Coss.) Mutants and Non-Mutants

Abstract

Twenty-nine genotypes of Indian mustard comprising of twenty-one M_{4-5} mutants of the parent varieties TM-2 and PM-27, five newly developed F_{6-7} lines and three check varieties (TM-2, NRCHB-101 and PM-27) were evaluated in a randomized block design during Rabi 2019-20 and Rabi 2020-21 to assess the correlation and path coefficients for seed yield and related traits. The genotypes were evaluated for fourteen quantitative characters. Seed yield per plant was positively correlated with number of siliquae on main shoot at the genotypic level. Number of siliquae on main shoot was positively correlated with plant height, main shoot length, siliqua density and 1000-seed weight. Path analysis based on genotypic correlations showed positive direct effects of number of siliquae on main shoot, number of primary branches and secondary branches per plant and seed yield per plant.

Keywords: Indian mustard, seed yield, correlation, path coefficient analysis

Introduction

Oilseeds play an important role in the human diet and known for their application in industrial use. India is the fifth largest vegetable oil economy in the world, produces 7.4 % oilseeds, 5.8 % oils, 6.1 % oil meal and 9.3 % of edible oils (Jat *et al.*, 2019). Of the total oilseed production, *Brassica* accounts for 24 % of the oilseeds acreage and occupies second rank after soybean. Indian mustard (2n=36) is a Rabi oilseed crop grown during October to February-March under diverse agro-climatic conditions. It is used for its oil, oil meal and as green leafy vegetables. According to the DRMR, Bharatpur, in the global scenario, rapeseed-mustard crops are cultivated in 35.95 million hectares with a production of 71.49 million tonnes and productivity of 1990 kg/ha as in 2019-20. India holds the position in second after Canada in acreage (19.81%) and fourth in production (10.37%) behind Canada, European Union and China (Jat *et al.*, 2019). In India, rapeseed-mustard crops occupy 6.86 million hectares, produce 9.12 million tonnes of oilseeds with average productivity of 1331 kg/ha as in 2019-20. The state of Assam is among the six major rapeseed-mustard crop producing states in the country. Assam contributes about 4.5 per cent of area and 2.05 percent of production of total rapeseed-mustard in India. Rapeseed-mustard is grown in substantial area in Assam with a productivity of 647 kg/ha (DRMR, 2022). In India, growing of rapeseed mustard serves as an important source of income for small and marginal farmers. However, owing to the low availability of edible oils and their continuous import in the country, it is important to increase the yield and production of these crops. As mustard is a long duration crop, toria is more popular in Assam but produces lesser yield than mustard. Therefore, it is important to develop short-duration superior Indian mustard varieties and to increase the average oilseed production in the state. However, yield is a complex polygenic trait and therefore it is important to analyse the relationship between yield and component characters. The association between the yield contributing characters can be determined with the help of correlation analysis. Path analysis helps to identify the direct and indirect effects of different components on seed yield which is required in the selection of high yielding genotypes. With this view, the present investigation was conducted based on correlation and path analysis to study the inter-relationships between the characters.

Materials and methods

During *Rabi* 2019-20 and *Rabi* 2020-21, twenty-one M_4 mutant lines (developed by gamma irradiation of the parent lines TM-2 and PM-27), five newly developed F_6 lines (2019-20) and three check varieties (TM-2, PM-27 and NRCHB-101) of Indian mustard (Table 1) were used for this experiment. The materials were collected from Department of Plant Breeding and Genetics, AAU, Jorhat. The experimental farm was located at the Department of Plant Breeding & Genetics, Assam Agricultural University, Jorhat, Assam at a latitude of 26º 45´ North and a longitude of 94º 12´ East with an elevation of 87 m above mean sea level. The layout was followed in randomized block design with three replications. The agronomic practices were followed according to the standard package and practices of the crop during the cultivation.

Table 1: List of genotypes used in the study

Sl. No.	Line No.	Designation	Sl. No.	Line No.	Designation
	Mutant lines of TM-2			**Mutant lines of TM-2**	

1	15	JMM-TM2-15	**18**	10	JMM-TM2-10
2	17	JMM-TM2-17	**19**	2	JMM-TM2-2
3	38	JMM-TM2-38	**Mutant lines of PM-27**		
4	34	JMM-TM2-34	**20**	1	JMM-PM27-1
5	20	JMM-TM2-20	**21**	11	JMM-PM27-11
6	47	JMM-TM2-47	**Newly-developed lines**		
7	160	JMM-TM2-160	**22**		JM13-2
8	1	JMM-TM2-1	**23**		JM13-3
9	4	JMM-TM2-4	**24**		JM13-4
10	51	JMM-TM2-51	**25**		JM13-5
11	22	JMM-TM2-22	**26**		JM13-6
12	73	JMM-TM2-73	**Check varieties**		
13	208	JMM-TM2-208	**27**		TM-2
14	28	JMM-TM2-28	**28**		NRCHB-101
15	14	JMM-TM2-14	**29**		PM-27
16	23	JMM-TM2-23			
17	27	JMM-TM2-27			

Morpho-phenological observations

Fourteen quantitative characters viz., days to 50% flowering (DF), days to maturity (DM), plant height in cm (PH), number of primary branches (PBN) and secondary branches per plant (SBN), main shoot length in cm (MSL), number of siliquae on main shoot (SMS), siliqua density on main shoot in no./cm (SD), number of seeds per siliqua (SPS), number of flowers on terminal main shoot (TF), number of siliqua on terminal main shoot (TS), 1000-seed weight in g (TSW), oil content in % (OC) and seed yield per plant in g (SYP) were recorded according to the standard procedure.

The genotypic and phenotypic correlation coefficients between two characters were calculated by analysis of covariance following the standard procedures by Dabholkar, 1999. Path coefficient analysis was carried out using the genotypic correlation coefficients to by following Dewey and Lu (1959) and Dabholkar (1999). The statistical methods were computed using Microsoft Excel 2007.

Results and discussion

As yield is a complex quantitative trait, it is influenced by various yield attributing characters both at genotypic and phenotypic levels. Correlation studies determine the degree and direction of association between different yield component traits (Mondal and Khajuria, 2009; Shalini *et al.*, 2000). The genotypic correlations between the characters were studied year-wise, which were presented in Table 2 (2019-20) and Table 3 (2020-2021).

In the first year, SYP was positively correlated with PH, SMS, SD, 1000-seed weight and PBN at the genotypic level. Swetha *et al.* (2019) and Singh *et al.* (2013) reported positive correlation of seed yield with PH, SMS and 1000-seed weight. Similarly, positive correlation of seed yield with PBN were reported by Nandi *et al.* (2021), Ray *et al.* (2019), Tantuway *et al.* (2018) and Kumari and Kumari (2018).

In the second year, positive correlation was observed between SYP, SPS, TF, TS and SMS. These findings were similar to the results reported by Pandey *et al.* (2020), Tiwari *et al.* (2018), Kumar *et al.* (2018) for SPS; by Swetha *et al.* (2019), Yadav and Pandey (2018), and Singh *et al*. (2013) for SMS. However, SYP was negatively correlated with DF, which indicates early flowering genotypes might also be higher yielder. Similar results were observed by Saiyad*et al.* (2020) and Kumar *et al*. (2016).

Considering both the years, it was observed that SYP was positively correlated with SMS and negatively correlated with DF at the genotypic level. Similarly, TS was positively correlated with PH and 1000-seed weight at genotypic level, while it was correlated with MSL and SD at both phenotypic and genotypic levels in both the years. PH showed high

Table 2: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients between different characters in Indian mustard during 2019-20

	DF	DM	PH	PBN	SBN	MSL	SMS	SD	SPS	TF	TS	TSW	OC	SYP
DF	1	0.820**	0.604**	-0.108	-0.159	0.053	0.270	0.340	0.383*	0.021	-0.141	0.805**	0.176	0.199
DM	0.165	1	0.713**	-0.016	-0.324	0.465*	0.670**	0.436*	-0.267	0.257	-0.029	0.157	0.711**	0.241
PH	0.233	0.469*	1	0.181	-0.093	0.680**	0.806**	0.356	-0.186	0.360	0.093	0.510**	0.337	0.562**
PBN	-0.042	-0.012	0.157	1	0.463*	0.274	0.318	0.121	-0.109	0.292	0.215	-0.037	-0.475**	0.418*
SBN	-0.059	-0.100	-0.047	0.508**	1	0.260	0.141	-0.162	-0.282	0.192	0.485**	-0.289	-0.693**	-0.079
MSL	0.054	0.397*	0.587**	0.206	0.227	1	0.750**	-0.141	-0.261	0.347	0.139	0.407	-0.027	0.105
SMS	0.118	0.412*	0.711**	0.296	0.186	0.624**	1	0.548**	-0.335	-0.002	0.408*	0.463*	0.118	0.525**
SD	0.083	0.080	0.218	0.157	-0.036	-0.333	0.520**	1	-0.145	0.135	0.461*	0.179	0.230	0.574**
SPS	0.138	-0.167	-0.108	-0.058	-0.190	-0.184	-0.213	-0.047	1	-0.126	-0.296	0.116	0.214	-0.266
TF	0.129	0.303	0.287	0.166	0.142	0.189	0.069	0.219	-0.075	1	0.328	-0.260	-0.110	-0.200
TS	0.021	-0.063	0.084	0.204	0.300	0.017	0.261	0.290	-0.111	0.291	1	0.191	-0.539**	0.183
TSW	0.185	-0.006	0.363	-0.034	-0.218	0.260	0.348	0.129	0.066	-0.087	0.279	1	0.132	0.450*
OC	0.135	0.257	0.220	-0.311	-0.371	-0.007	0.030	0.030	0.109	-0.114	-0.380*	0.037	1	0.291
SYP	0.164	0.263	0.440*	0.260	0.002	0.176	0.451*	0.332	-0.065	0.039	0.049	0.170	0.162	1

* Significant at 5 % probability, ** Significant at 1% probability

Table 3: Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients between different characters in Indian mustard during 2020-21

	DF	DM	PH	PBN	SBN	MSL	SMS	SD	SPS	TF	TS	TSW	OC	SYP
DF	1	0.243	0.072	-0.047	-0.030	-0.219	-0.019	0.273	-0.339	-0.186	-0.343	-0.167	0.402*	-0.399*
DM	0.338	1	0.100	-0.146	0.035	-0.007	0.186	0.219	-0.208	-0.268	-0.221	-0.151	-0.017	-0.278
PH	0.078	0.036	1	0.230	0.276	0.450*	0.743**	0.284	0.075	-0.051	0.041	0.265	-0.083	0.263
PBN	-0.112	-0.128	0.238	1	0.114	0.286	0.373*	0.121	-0.291	0.006	0.153	0.358	-0.301	-0.012
SBN	0.009	0.015	0.283	0.141	1	0.147	0.163	-0.006	-0.007	0.397	0.288	-0.123	-0.194	0.236
MSL	-0.225	-0.138	0.430*	0.160	0.179	1	0.513**	-0.482**	0.314	-0.002	0.101	0.342	0.160	0.366
SMS	-0.018	0.089	0.648**	0.318	0.205	0.471**	1	0.500**	0.029	-0.002	0.277	0.441*	-0.218	0.367*
SD	0.241	0.223	0.164	0.157	0.003	-0.538**	0.481**	1	-0.302	0.296	0.232	0.096	-0.451*	0.030
SPS	-0.124	-0.082	0.069	-0.122	0.137	0.156	0.129	-0.058	1	0.414*	0.303	0.339	0.043	0.499**
TF	-0.091	-0.132	0.014	0.036	0.305	0.069	0.069	0.221	0.250	1	1.020	0.225	-0.403*	0.431*
TS	-0.227	-0.085	0.031	0.051	0.220	0.189	0.198	0.017	0.138	0.801**	1	0.157	-0.432*	0.425*
TSW	-0.102	-0.053	0.199	0.260	-0.065	0.247	0.394*	0.120	0.195	0.260	0.110	1	0.069	0.225
OC	0.195	0.068	-0.054	-0.260	-0.099	0.017	-0.125	-0.141	0.000	-0.254	-0.302	0.062	1	0.022
SYP	-0.384*	-0.238	0.277	0.108	0.240	0.259	0.309	0.041	0.414*	0.315	0.228	0.134	-0.089	1

* Significant at 5 % probability, ** Significant at 1% probability

Table 4: Direct and indirect effects of different component characters on seed yield per plant in Indian mustard during 2019-20 (based on genotypic correlation)

	DM	PH	PBN	SBN	MSL	SMS	SPS	TS	TSW	Genotypic correlation with SYP
DM	**-0.482**	0.463	-0.006	0.026	-0.453	0.538	0.097	0.009	0.048	0.241
PH	-0.344	**0.649**	0.068	0.008	-0.663	0.647	0.067	-0.027	0.157	0.562**
PBN	0.008	0.117	**0.377**	-0.038	-0.267	0.255	0.040	-0.063	-0.011	0.418*
SBN	0.156	-0.061	0.174	**-0.082**	-0.254	0.114	0.102	-0.141	-0.089	-0.079
MSL	-0.224	-0.041	0.103	-0.021	**-0.975**	0.602	0.095	-0.040	0.125	0.105
SMS	-0.323	0.523	0.120	-0.012	-0.731	**0.803**	0.122	-0.119	0.142	0.525**
SPS	0.129	-0.121	-0.041	0.023	0.254	-0.269	**-0.363**	0.086	0.036	-0.266
TS	0.014	0.060	0.081	-0.040	-0.136	0.328	0.107	**-0.291**	0.059	0.183
TSW	-0.076	0.331	-0.014	0.024	-0.397	0.372	-0.042	-0.056	**0.307**	0.450*

Residual = 0.295 Direct effect (path coefficient) in bold face on the leading diagonal

Table 5: Direct and indirect effects of different component characters on seed yield per plant in Indian mustard during 2020-21 (based on genotypic correlation)

	DM	PH	PBN	SBN	MSL	SMS	SPS	TS	TSW	Genotypic correlation with SYP
DM	**-0.308**	-0.017	0.016	0.006	-0.001	0.104	-0.083	-0.015	0.020	-0.278
PH	-0.031	**-0.173**	-0.026	0.048	0.034	0.413	0.030	0.003	-0.035	0.263
PBN	0.045	-0.040	**-0.112**	0.020	0.022	0.207	-0.117	0.011	-0.047	-0.012
SBN	-0.011	-0.048	-0.013	**0.173**	0.011	0.090	-0.003	0.020	0.016	0.236
MSL	0.002	-0.078	-0.032	0.025	**0.075**	0.285	0.126	0.007	-0.045	0.366
SMS	-0.057	-0.129	-0.042	0.028	0.039	**0.556**	0.012	0.019	-0.058	0.367*
SPS	0.064	-0.013	0.033	-0.001	0.024	0.016	**0.401**	0.021	-0.045	0.499**
TS	0.068	-0.007	-0.017	0.050	0.008	0.154	0.121	**0.069**	-0.021	0.425*
TSW	0.046	-0.046	-0.040	-0.021	0.026	0.245	0.136	0.011	**-0.132**	0.225

Residual effect = 0.697 Direct effect (path coefficient) in bold face on the leading diagonal positive phenotypic correlation with MSL and SMS while DF showed negative correlation with SYP. Kumar *et al.* (2018) also reported negative phenotypic correlation between SYP and DF.

Path coefficient analysis is used to partition the observed correlation coefficient between yield and component traits into direct and indirect effects (Wright, 1921). It helps in identifying the component traits in selection criteria for yield improvement. The path analysis was carried out year-wise as presented in Table 4 and Table 5. Path analysis based on genotypic correlations in both the years revealed that SMS and PBN were important yield attributing traits contributing highest positive direct effects on yield. Considering both the years, DM showed highest negative direct effect towards SYP. SBN also contributed positively towards seed yield to some extent. In a study conducted by Tripathi *et al.* (2019), PBN was observed to have positive direct effect while DF showed negative direct effect towards SYP.

Conclusion

Interrelationship among the yield attributing traits is very much important for effective selection in a crop improvement programme. In the present investigation**,** correlation and path analysis indicated that the number of siliqua on main shoot (SMS), number of primary branches (PBN) and number of secondary branches (SBN) were the major yield attributing characters. Considering these traits, selection would be effective for enhancing seed yield in Indian mustard.

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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