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ASSESMENT OF GENETIC COMPONENTS IN INDIAN MUSTARD (*Brassica juncea .L*)

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ABSTRACT

Genetic variability variationBrassica juncea.Lwas studied during 2017-2018. Analysis of data showed existence of significant difference among the cultivars for seed and agronomic traits. The coefficient of variation (genotypic/phenotypic) wasrelatively higher for number of branches (secondary),siliquae length, Harvest index and seed yield per plant. Whereas moderate variation was observed for main shoot length followed by 1k seed weight, no. of primary branches and siliquae on main shoot. Significant heritability (bs) was observed for seed and agronomic traits namely HI, secondary branches,Days to 50% and 100% flowering,siliquae length and number on main shoot. Highest GA was recorded for seed per siliquae, secondary branches, yield/plant and siliquae length. The maximum intra-cluster distance was recorded within cluster II followed by I, IV and III clusters. Maximum inter-cluster distance is observed between II &IV. These results suggest maximum divergence between cluster II, IV and III, IV and maximum divergence observed among cluster II and IV.

INTRODUCTION

Mustard (*B. junceaL.czern* and coss.) accounts for nearly one third of the total edible oil produced and one fourth of consumed in India. Total acreage, production and productivity of mustard crop was 6.70 million hectare (7.96) mt and 1188 kg/ha, respectively in 2018-19. The yield productivity is low as compared to other countries as 34% area is sown under rain fed conditions. In India, mustard and rape seed was largely grown on dry lands without assured irrigations mostly in Uttar Pradesh, Rajasthan, Gujarat, West Bengal and Madhya Pradesh.

This genus comprises a diverse group of genera (338) and species (3709). It includes all importantvegetables and oilseed crops (Mithila*et al.*, 2005). Among edible oils used for human consumption, rapeseed/ mustard oil has lowest amount of saturated (C_{12}, C_{14} and C_{16})fatty acids. The oil content of different forms ranges from 38-43 per cent. The yield per acre in India is substantially lower due to cultivation on rainfed regions as compared to developed nations where cultivated in regions with assured irrigation.

Development of new cultivars is largely depends upon study of genetic parameters viz. variability(genetic/ phenotypic), heritability (broad and narrow sense) and genetic advance (GA). In addition, path coefficient analysis provides more realistic picture of complex gene combination. The estimation of genetic variation would be of prime importance for any breeder to develop better cultivars (Islam*et al*., 2015). The improvement of genetics for better yield and quality of mustard cultivars can help to provide quality edible oil and protein meal for human consumption as well as feeding animals and development of non-edible industrial products. The development of genetically superior rapeseed, variety/hybrids having desirable parameters and better adaptability to rainfed conditions is required.

Material and Methods

The present was conducted during the rabiseason of 2017-2018, at Plant breeding, School of Agriculture, LPU research farm (31.25N and 75.70Elatitude and longitude). Twenty eight (Table 1) genotypes were space planted in 5m row length with row to row and plant to plant spacing of 50x15cm respectively. The trial was planted in RCBD design with three replications. The material used during this experimental trial was listed in Table 1.

Results and Discussion

The ANOVA revealed that significant mean sum of square due to genotypes (Table 2) for all traits. Thereby, indicating substantial amount of genetic variability among genotypes as well as little influence of the environment (non-significant) on the expression of character. High genotypic/phenotypic coefficient of variation (Table 2) was recorded for Harvest index (HI) followed by seed yield, seeds per siliquae, number of secondary branches and siliquae length. These results were in agreement with Alireza*et.al*. (2011) andDevmani*et.al*.,(2014). Highest heritability (bs) was indicated by HI followed by secondary branches,days to50% and 100% flowering, number of siliquae on main shoot, 1000 seed weight and oil content. These results were also consistent with the findings of Kumar*et al*., (2017), Akabari*et al*., (2015) etc. Genetic advance(GA) as percentage of mean was highest for most of studied traits i.e. harvest index, seeds per siliquae, siliquae length, number of secondary branches, seed yield per plant, 1000 seed weight, and number of primary branches. Lodhi*et al*.,(2013), Amit*et al*.(2013), Sutariya*et al*.(2011), and Kumar*et al*.(2017)were also reported similar results for seed yield per plant. In addition, positive correlations were reported for the plant height, silique on main shoot, seed yield per plant, primary branches and secondary branches byRai*et al*.(2016) and

Basalma (2008). Genotypic path coefficient analysis (Table 3, 4) revealed highest positive direct effect on seed yield/plant

Path coefficient analysis indicated showed negative direct effect of yield/plant with days to 50% flowering (-2.4) followed by plant height (0.556), days to 100% flowering(0.658) and silique length (-0.214). However, the study showed positive direct effect of yield/plant with days to flowering (1.958), silique on main shoot(0.224) seeds per silique (0.218) and harvest index(0.904). Clustering of genotypes under study in figure Based on the d2 values all the genotypes were grouped into 4 clusters (Table 5) signaling presence of diversity for different traits. Cluster II (9 genotypes) has highest number of genotypes followed cluster I (8) and cluster IV (6) and cluster III(5). The seed yield per plant was recorded highest for cluster I(55.32). The days flowering was recorded minimum for cluster III(61.4).The days to 50% flowering was recorded for cluster III(76.5) (and days to 100% flowering was recorded minimum for cluster III.(123.06) The plant height was high for cluster II(186.30), number of primary branches was high was for cluster II(7.5), number of secondary branches was highest for cluster II (17.30) length of main shoot was highest for cluster II(76.28) and siliquae on main shoot was highest for cluster II(68.39) and seeds per siliquae was highest for cluster IV(17.65) and siliquae length was highest for cluster IV(6.97)and harvest index was highest for cluster I(32.89)1000 seed weight was highest for cluster I(11.20),oil content is highest for cluster IV(38.99). These results are in continuity with studies reported by Khushboo*et al.*(2018), Singh *et al.*(2011), Chauhan*et.al*(2008), Binod*et al.*(2000).

Table1. List of genotypes and source

r. No.	Genotypes	Source	r. No.	Genotypes	Source
1	GS-2	Bharathpur, Rajasthan	15	GUJARATMUSTARD-3	Bharathpur, Rajasthan
2	PBR-97	PAU, Ludhiana	16	JUMKA	Bharathpur, Rajasthan
3	DMH-1	Bharathpur, Rajasthan	17	RH-30	Bharathpur, Rajasthan
4	RGN-73	Bharathpur, Rajasthan	18	PUSASAAG-1	Bharathpur, Rajasthan
5	PUSA JAIKISAN	IARI,Newdelhi	19	NRLHB-101	Bharathpur, Rajasthan
6	SMR-9	Bharathpur, Rajasthan	20	PB-50	Bharathpur, Rajasthan
7	PUSA MUSTARD-28	IARI,Newdelhi	21	TM-4	Bharathpur, Rajasthan
8	PUSA MUSTARD-24	IARI,Newdelhi	22	KRANTHI	Bharathpur, Rajasthan
9	JD-6	Bharathpur, Rajasthan	23	DRMR-1	Bharathpur, Rajasthan
10	RCC-4	Bharathpur, Rajasthan	24	TM-204	Bharathpur, Rajasthan
11	ONK-1	Bharathpur, Rajasthan	25	ZEM-1	Bharathpur, Rajasthan
12	GSC-7	Bharathpur, Rajasthan	26	KBS-3	Bharathpur, Rajasthan
13	HPBS-1	Bharathpur, Rajasthan	27	TM-215	Bharathpur, Rajasthan
14	NEELAM	Bharathpur, Rajasthan	28	JYANT	Bharathpur, Rajasthan

Table 2. Estimation of various genetic parameters of Mustard genotypes

Characters	**General mean**	**Range**		**Coefficient of variation**		**Heritability (%)**	**Genetic advance (5%)**	**G.A. as - percentage of mean**
		Mini.	**Max.**	**Genotypic**	**Phenotypic**			
Days to flowering	67.643	56.333	77.333	7.17	8.102	78.32	8.842	13.072
Days to 50% flowering	82.917	71.333	92.333	6.239	6.471	92.945	10.274	12.39
Days to 100% flowering	82.917	120.333	137.66	3.93	4.077	92.898	10.097	7.803
Plant height	175.17	153.417	199.933	7.634	9.483	64.814	22.178	12.661
Number of primary branches of plant	6.807	4.6	9.867	15	18.739	64.08	1.684	24.736
Number of secondary branches of plant	15.041	11.3	19.567	21.6	22.244	94.294	6.499	43.208
Length of main shoot	66.742	52.333	89.217	17.343	20.031	74.969	20.246	30.935
Seed yield per plant	43.423	24.7	56.667	21.273	24.318	76.525	16.646	38.336
Seeds per silique	14.877	3.823	23.333	23.094	23.99	76.524	6.813	45.798
Silique on main shoot	60.882	43.6	73.133	14.044	15.046	87.123	16.441	27.004
Silique length	5.937	4.8	8.367	20.987	21.97	91.214	2.451	41.297
1000 seed weight	10.635	7.3	13.167	16.817	16.857	79.545	3.675	34.561
Harvest index	79.545	15.733	38.433	24.222	27.159	99.527	11.489	44.503
Oil content	38.293	35.667	40.483	4.428	4.552	94.616	3.398	8.872

Table 3. Phenotypic path coefficient analysis showing direct and indirect effects of oil yield traits.

Traits	**Direct effect on seed yield per plant**	**Indirect effect**					
		Siliquae on main shoot	**Seeds per siliquae**	**Siliquae length**	**Harvest index**	**1000 seed weight**	**Oil content**
Siliquae on main shoot	**0.224**		-0.06471	0.09749	0.09238	0.00028	-0.00193
Seeds per siliquae	**0.218**	-0.06653		-0.1768	-0.14756	0.00034	-0.00006
Siliquae length	**-0.215**	-0.10139	0.17885		0.01141	0.00056	0.00045
Harvest index	**0.904**	-0.02287	-0.03554	-0.00272		0.00141	-0.00114
1000 seed weight	**0.005**	0.01326	0.01657	-0.02512	0.26532		-0.00073
Oil content	**0.008**	-0.05343	-0.00159	-0.0119	-0.12703	-0.00044	

Table 4. Phenotypic path coefficient analysis showing direct and indirect effects of agronomic traits.

Traits	Direct effect On seed Yield plant	Indirect effect via					
		Days to flowering	**Days to 50% flowering**	**Days to 100% flowering**	**Plant height**	**Number of primary branches of plant**	**Number of secondary branches of plant**
Days to flowering	**1.958**		-2.46627	0.48869	0.13628	-0.02008	-0.00296
Days to 50% flowering	**-2.458**	1.96469		0.047058	0.11291	-0.0179	-0.00231
Days to 100% flowering	**0.658**	1.45474	-1.75847		-0.05465	0.0281	0.0126
Plant height	**0.556**	0.4801	-0.4993	-0.06468		0.02857	-0.02888
Number of primary branches of plant	**0.075**	-0.52208	0.5843	-0.24554	0.21086		-0.0337
Secondary branches	**-0.047**	0.1227	-0.12036	-0.17555	0.33995	0.05388	

Table6. Distribution of 28 genotypes of mustard by d2 statistics

Cluster	Number of genotypes	Name of genotypes
1	8	PBR-97,DMH-1,PUSAMUSTARD -24,TM-4,KRANTHI,DRMR-1,TM-204,TM-215
2	9	RGN-73,SMR-9,PUSAMUSTARD-28,JD-6,GUJARAT MUSTARD-3,RH-30,PB-50,PUSA SAAG-1 ,ZEM-1
3	5	PUSA JAIKISAN,ONK-1,JUMKA,NRCHB-1,KBS-3
	6	GS-2,RCC-4,GSC-7,NEELAM,JYANT

Table7. Intra and inter cluster distance (D2, D values) in mustard genotypes

Cluster number	I	II	III	IV
I	**20.54**	30.87	38.94	39.30
II		**23.44**	45.216	47.67
III			**13.36**	24.34
Iv				**17.26**

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