

Analysis of genetic components and other genetic parameters for seed yield and its contributing traits in Indian mustard, *Brassica Juncea* (L) Czern and Coss

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ABSTRACT

An experiment was conducted to know the inheritance pattern of seed yield and its components in a 15 × 15 half diallel cross set of Indian mustard, *Brassica juncea* (L) Czern and Coss. The estimates of components of variance were significant for all the characters. The additive gene action was predominant for the expression of characters viz days to 50 per cent flowering, number of seeds per siliqua and oil content whereas non-additive gene action was more significant for expression of remaining characters. Predictability ratio was highest for oil content (25.622) followed by number of seeds per siliqua (2.471) and days to 50 per cent flowering (1.591). Average degree of dominance showed partial dominance for days to flowering (0.793), number of seeds per siliqua (0.636) and oil content (0.197) and over dominance for remaining traits. The complete degree of dominance was not shown by any character. The genetic component studies revealed that both additive and non-additive gene action play their role in inheritance of various characters in Indian mustard.

Keywords: *Brassica juncea*; seed yield; gene action; predictability ratio; degree of dominance

INTRODUCTION

Indian mustard, *Brassica juncea* (L) Czern and Coss is an important oilseed crop of the world. It plays a major role in catering to the edible oil demand of the country. Rapeseed and mustard crops are being cultivated in 53 countries spreading over six continents across the globe. India (14.8%) is having third largest share in

rapeseed-mustard production in the world next only to China and Canada. Among annual oilseeds, rapeseed and mustard contributed about 23 per cent acreage and over 25 per cent production over the last five years in India. The area, production and productivity of rapeseed and mustard was 6.34 million ha, 7.82 MT and 1234 kg/ha respectively during year 2012-13 (Anon 2013). The major rapeseed and

mustard growing states are Rajasthan, Uttar Pradesh, Madhya Pradesh, Gujarat, Haryana and Punjab. The jump in the production of these crops is largely accounted by Indian mustard (*Brassica juncea* L.) which occupies 80 per cent of the total area under them. The drastic increase in production and productivity is achieved by immense potential of high yielding varieties. The exploitable variability is therefore required to be judged through various genetic parameters like heritability, genetic advance and others (Singh et al 2011). Such a study appears to be extremely necessary for planning genetic improvement in Indian mustard. The present study was undertaken to know the gene action for seed yield and other contributing characters in Indian mustard.

MATERIAL and METHODS

The experimental material for present study comprised a set of 15 diverse genotypes of Indian mustard, *Brassica juncea* L. involving four early maturing genotypes (NDRE-4, PRE-2007-6, PR-2006-1 and PRE-2009-9), six agronomically superior genotypes (NDYR-8, Kranti, Maya, Bhaghirathi, RGN-74 and RGN-145), two late maturing genotypes (Vardan and Ashirwad) and three bold seeded genotypes (PRB-2006-5, PRB-2008-5 and PRB-2004-3-4) (Table 1). The parents were crossed in all possible combinations excluding reciprocals during Rabi season 2011-12. Experimental material consisting of 15 parents and 105 F_1 s was

evaluated in a randomized block design with three replications during Rabi season 2012-13. Each plot comprised 1 row of 3 meter long. The crop was sown at a distance of 30 cm and plant to plant distance of 10 cm was maintained by thinning after 20-25 days of sowing. Single row of Indian mustard cultivar NDRE-4 was sown on either side of each block as guard row. Five competitive plants from parents and F_1 s were randomly selected from each plot and tagged at the time of vegetative stage for recording of data on days to 50 per cent flowering, days to maturity, chlorophyll content (SPAD value), plant height (cm), length of main raceme (cm), siliqua length (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae on main raceme, number of seeds per siliqua, siliqua density, seed yield per plant (g), test weight (g), oil content (%) and glucosinolate content (μ mole/g fat free meal). Statistical analysis was carried out as suggested by Jinks and Hayman (1953) and Hayman (1954).

RESULTS and DISCUSSION

Analysis of variance revealed that there were significant differences between treatments for all the characters under study. This showed the presence of sufficient amount of variability among the experimental material (Table 2). Estimation of genetic components and other genetic parameters indicated that (Table 3) estimates of σ^2_{sca} were found to be higher

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Table 1. List of genotypes along with the pedigree

Genotype	Pedigree	Feature
PRB-2006-5	-	Bold seeded
Maya	Varuna × KRB-11	High yielding
Bhaghirathi	Varuna × Appressed mutant	High yielding
Vardan	Varuna, Keshari, CSU-10, IB 1775, IB 1786, IB1866	Late maturity
RGN-145	-	High yielding
PRB-2008-5	(Varuna × Pusa Bold) × BSIPS-23	Bold seeded
PRB-2004-3-4	BSIPS-72 × BSIPS-13	Bold seeded
PRE-2009-9	(Kanti × NDRE-02-01) × (Varuna × NDRE-02-01)	Early maturity
Ashirvad	Krishna × Vardan	Late maturity
PR-2006-1	Krishna-2-1 × HS-027-1	Early maturity
RGN-74	-	High yielding
Kranti	Selection from Varuna	High yielding
PRE-2007-6	RK 02-2 × NPJ 90-10	Early maturity
NDRE-4	TM 9 × Seeta	Early maturity
NDYR-8	-	Yellow seeded

than the σ^2_{gca} for all characters except number of seeds per siliqua and oil content. Perusal of table revealed that the additive gene action was pre-dominant for the expression of characters viz days to 50 per cent flowering, number of seeds per siliqua and oil content whereas non-additive gene action was more significant for expression of characters viz days to maturity, chlorophyll content, plant height, length of main raceme, length of siliqua, number of primary branches, number of secondary branches, number of siliqua on main raceme, siliqua density, seed yield per plant, test weight and glucosinolate content. These findings are in agreement with earlier reports by Singh and Lallu (2004) and Tahir et al (2007). Predictability ratio was highest for oil content (25.622) followed by number of seeds per siliqua (2.471) and days to 50 per cent flowering (1.591). It indicated that

for the predominance of fixable variance any selection methodology can be utilized for improvement of such characters. For rest of the traits the value of predictability ratio was lower than one. It represented the involvement of non-fixable type of variance. Average degree of dominance showed partial dominance for days to flowering (0.793), number of seeds per siliqua (0.636) and oil content (0.197) and over dominance for primary branches/plant (7.971), glucosinolate content (4.607), chlorophyll content (4.36), siliqua length (3.874), length of main raceme (3.728), test weight (3.23), siliquae on main raceme (2.038), secondary branches/plant (1.745), seed yield per plant (1.593), plant height (1.407), days to maturity (1.103) and siliqua density (1.026). The complete degree of dominance was not shown by any character. The findings are in close association with the reports of

Table 2a. Analysis of variance for different characters

Source of variation	df	Mean square						
		Days to 50% flowering	Days to maturity	Chlorophyll content	Plant height	Length of main raceme	Siliqua length	Primary branches/plant
Replication	2	131.954	19.55	0.950	145.900	42.566	0.019	2.531
Treatment	119	79.871*	44.315*	16.957*	473.799*	95.815*	0.233*	0.989*
Error	238	12.104	3.723	0.227	55.311	24.113	0.084	0.302
SEm±		2.008	1.114	0.275	4.293	2.835	0.167	0.317
CD _{0.01}		7.376	4.091	1.011	15.769	10.411	0.614	1.164
CD _{0.05}		5.596	3.103	0.767	11.962	7.898	0.466	0.883
CV (%)		7.193	1.873	1.164	4.716	8.070	6.699	11.578

*Significant at 1 per cent level

Table 2b. Analysis of variance for different characters

Source of variation	df	Mean square							
		Secondary branches /plant	# siliquae on main raceme	# seeds /siliqua	Siliqua density	Seed yield /plant	Test weight	Oil content	Glucosinolate content
Replication	2	2.424	5.5025	3.162	0.055	5.682	0.017	1.8245	247.233
Treatment	119	6.356*	72.268*	1.991*	0.197*	22.093*	1.296*	2.055*	324.54*
Error	238	2.711	12.228	1.395	0.035	2.650	0.032	0.561	6.404
SEm±		0.950	2.018	0.622	0.107	0.939	0.1039	0.432	1.461
CD _{0.01}		3.491	7.414	2.286	0.396	3.451	0.3816	1.586	5.365
CD _{0.05}		2.648	5.624	1.734	0.301	2.618	0.2895	1.203	4.070
CV (%)		15.078	9.933	1.734	10.621	18.633	5.122	1.877	1.407

*Significant at 1 per cent level

Table 3. Estimation of genetic components and other genetic parameters

Character	σ^2_{gca}	σ^2_{sca}	2e	2A	2D	$h^2(n)$	Predictability ratio	Degree of dominance
Days to 50% flowering	20.806	26.156	12.104	41.612	26.156	0.704	1.591	0.793
Days to maturity	9.108	22.375	3.723	18.216	22.375	0.517	0.814	1.108
Chlorophyll content (SPAD value)	0.421	16.01	0.228	0.842	16.01	0.051	0.053	4.36
Plant height (cm)	70.210	278.112	55.298	140.420	278.112	0.348	0.505	1.407
Length of main raceme (cm)	0.023	0.641	0.302	0.046	0.641	0.048	0.072	3.728
Silique length (cm)	0.130	3.906	2.711	0.260	3.906	0.038	0.067	3.874
Primary branches/plant	0.555	70.587	24.113	1.111	70.587	0.012	0.016	7.971
Secondary branches/plant	7.424	45.191	12.228	14.848	45.191	0.229	0.329	1.745
# siliquae on main raceme	0.016	0.13	0.035	0.031	0.13	0.173	0.241	2.038
# seeds/silique	0.053	0.043	0.084	0.106	0.043	0.590	2.471	0.636
Silique density on main raceme	0.145	0.306	1.395	0.291	0.306	0.157	0.950	1.026
Seed yield/plant (g)	0.179	0.907	0.032	0.357	0.907	0.320	0.394	1.593
Test weight (g)	0.850	17.743	2.65	1.700	17.743	0.080	0.096	3.23
Oil content (%)	0.781	0.061	0.561	1.563	0.061	0.715	25.622	0.197
Glucosinolate (%)	7.157	303.864	6.406	14.3141	303.864	0.045	0.047	4.607

Chaudhary et al (1988) and Singh et al (2011). The dominance component was relatively larger than the additive component for all the characters except 50 per cent flowering, number of seeds per siliqua and oil content for which additive component was found to be more important. Heritability in narrow sense was high for oil content, 50 per cent flowering, number of seeds per siliqua and maturity; moderate for plant height, seed yield per plant, secondary branches per plant, siliqua on main raceme and siliqua density and low for rest of the characters. Since this type of gene action is not fixable in nature, simple breeding methods would be ineffective. Under such a situation the appropriate methodology will be heterosis breeding, alternatively biparental mating followed by recurrent selection or diallel selective mating to hasten the pace of genetic improvement of these characters. The success of any breeding programme depends to a great extent on the knowledge of genetic architecture of the population being handled. Reliable information about the nature and magnitude of gene action involved in the expression of quantitatively inherited traits of economic importance may be considered as the most desirable prerequisite for any crop improvement programme. Foregoing results and inferences revealed the presence

of wide spectrum of exploitable variability in the material studied with respect to various quantitative and quality traits projecting thereby immense scope for genetic upgradation in Indian mustard.

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