

Research Article

Determination of Gene Action and Some Genetic Parameters for Yield and its Contributing Characters in *Brassica Juncea* L.

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Abstract

The estimates of σ_s^2 were found to be higher than the σ_e^2 for all characters except days to initial flowering, length of main raceme and 1000-seed weight indicating greater importance of specific combining ability in the inheritance of characters. Reference to the estimates of σ_A^2 and σ_D^2 for various characters revealed that the additive gene action was predominant for the expression of seven characters viz., days to initial flowering, days to maturity, plant height, length of main raceme, siliqua density, siliqua length and 1000-seed weight exhibiting greater importance of additive gene action for these traits whereas, non-additive gene action was preponderant for the expression of 8 characters viz., number of siliquae on main raceme, number of primary branches/plant, number of secondary branches/plant, number of seeds/siliqua, seed yield/plant, protein content, oil content and glucosinolate content. Predictability ratio was high (>1) for days to initial flowering followed by 1000-seed weight, length of main raceme, days to maturity, siliqua density, siliqua length, and plant height indicating the predominance of fixable variability for these traits. For rest of the characters the value of predictability ratio was lower than one indicating the preponderance of non-fixable type of variance. Further the degree of dominance less than one for all these traits indicating partial dominance. The estimates of narrow sense heritability (h^2_n) were high (>0.30) for 10 characters including seed yield.

This indicated the availability of additive genetic variance in substantial amount, thereby suggesting the increased possibility of improvement through selection. Moderate estimates of h^2_n (0.10 to 0.30) were found for number of primary branches/plant, protein content, siliquae on main raceme and glucosinolate content. Thus, there exist limited scopes of improvement through selection for these traits. However, for oil content the h^2_n was low indicating the near absence of additive genetic variability in the material studied, hence no scope of improvement for oil content.

Keywords: Narrow sense heritability, Degree of dominance, Predictability ratio, σ_A^2 , and σ_D^2

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Introduction

Brassica juncea L. is one of the most important oilseed crops by accounting 15% of world's total oilseed crop production. It is self pollinated crop with considerable amount of cross pollination. Improvement in yield of any crop needs suitable breeding programme which can enhance yield. The choice of breeding strategy to be used depends upon type of genetic variance present in the population. The genotypes which were showed good *per se* performance, sometimes, may not necessarily produce desirable progenies when used in breeding programme. In last century, many scientists reported considerable extent of heterosis in *Brassica juncea* L. Again, the genetic variation is single most factor that helps to select a good parent. Therefore, understanding of nature of gene action and inheritance of seed yield and its associated traits in *Brassica juncea* L. is going to be beneficial in long run. Among the various mating designs developed for determination of the genetic architecture of quantitative characters, the diallel cross method, outline by Jinks [1], [2] and Hayman [3], [4] has received considerable attention of Breeders and Scientists alike.

Material and Method

The experimental material for the present study comprised of 10 diverse genotypes viz. PWR 15-8, PRHC 17-1, FS-14-24, PWR 15-8-1, RGN73, Maya, PRHC 12-14, Kranti, PM 25 and PRHC 13-14 of Indian mustard (*Brassica juncea* L.). The parents were crossed in *diallel* mating design excluding reciprocals (half *diallel*) during *rabi* season 2014-15. Experimental material consisting of 10 parents and 45 F₁'s was evaluated in a randomized block design with

three replications during *rabi* 2014-15 for 15 characters which includes yield and its associated traits alongwith two quality traits viz. protein content (%) and glucosinolate ($\mu\text{mol/g}$). Each plot comprised of single row of 3 meter length with inter row spacing of 30 cm. Plant to plant distance of 15 cm was maintained by thinning densely grown plants after 15-20 DAS. A single row of Divya was sown on each side of the block as guard row. Five competitive plants from parents and F_1 's (half *diallel*) were randomly selected from each plot and tagged at vegetative stage for recording of observations. All the observations on various characters were recorded on them. The plot means used for statistical analysis were obtained on the basis of mean of randomly selected plants for each plot in all replications except 1000-seed weight and oil content which were based on bulk sample of selected 5 plants.

Statistical Analysis

Fifteen characters under study were analyzed through the technique of analysis of variance to test whether treatments are differing significantly among themselves or not. [5] The mathematical model utilized in the Randomized Complete Block Design is as follows:

$$Y_{ij} = \mu + t_i + r_j + e_{ij}$$

Where,

Y_{ij} = Mean performance of i^{th} treatment in the j^{th} block;

μ = General mean;

t_i = Effect of i^{th} treatment ;

r_j = Effect of j^{th} replication ;

e_{ij} = Random error associated with y_{ij} ;

Estimation of genetic components and other genetic parameters for method 2 model I of Griffings [6].

The genetic variance parameters were estimated as given below:

- $\sigma^2_g = (\text{MS}_g - \text{MSe}) / (p+2)$
- $\sigma^2_s = \text{MS}_s - \text{MSe}$
- $\sigma^2_e = \text{MSe}$
- $\sigma^2_A = 2\sigma^2_g$
- $\sigma^2_D = \sigma^2_s$

Heritability narrow sense

Heritability in narrow sense h^2_n (%) was calculated as per formula given by Burton and De Vane [7] and Allard [8].

$$h^2_n = 2\sigma^2_g / 2\sigma^2_g + \sigma^2_s + \sigma^2_e$$

Predictability ratio

The additive ('D') and dominance ('H') genetic variance were used to estimate predictability ratio.

$$\text{Predictability ratio} = \sigma^2_A / \sigma^2_D$$

If predictability ratio

<1; show more non fixable variance

>1; show more fixable variance

Degree of dominance

The additive ('D') and dominance ('H') genetic variance were used to estimate dominance ratio.

$$\text{Degree of dominance (dominance ratio)} = \sqrt{(\sigma^2_D / \sigma^2_A)}$$

If dominance ratio is = 1 show complete dominance

a. >1 show over dominance

b. <1 show partial dominance

Results and Discussion

The data recorded for different characters under study were analyzed for Randomized Complete Block Design. The results of analysis of variance for various quantitative characters showed highly significant mean squares due to treatments for all the characters except for oil content (**Table 1**). Thus, the results showed the presence of considerable variability in the experimental materials used for the study. The result of analyses of variance for general combining ability and specific combining ability showed that mean squares due to GCA and SCA were highly significant for all the characters except for oil content (**Table 2**). This showed that both additive and non-additive gene action were important for expression of characters studied. Relative magnitude of mean squares due to GCA was higher than the mean squares due to SCA for all the characters, barring oil content and glucosinolate content. This indicated predominance of additive gene action for the expression of these characters. Higher magnitude of mean squares due to SCA indicated the predominance of non-additive gene action for oil content and glucosinolate content as also reported earlier [9-14]

Table 1 Analysis of variance for different characters in parents and their F1 hybrids in Indian mustard

S.V.	d.f.	Mean squares							
		DF	DM	PH	LMR	SMR	SD	PB	SB
Replication	2	10.52	12.21	45.27	6.72	52.17	0.01	0.78	14.62
Treatment	54	241.18**	223.39**	1236.62**	381.81**	151.20**	0.10**	2.10**	48.21**
Error	108	5.79	6.28	34.21	11.12	6.89	0.003	0.69	3.59
		SL	S/S	TW	Y/P	OC	PC	GC	
Replication	2	0.13	0.31	0.15	0.54	10.50	2.88	0.39	
Treatment	54	0.60**	4.72**	1.02**	23.78**	7.12	4.31**	51.25**	
Error	108	0.12	0.69	0.09	0.89	5.28	0.91	0.74	

Table 2 Analysis of variance for combining ability for different characters in mustard genotypes

S.V.	d.f.	Mean squares							
		DF	DM	PH	LMR	SMR	SD	PB	SB
GCA	9	361.61**	307.70**	1515.22**	528.88**	53.74**	0.13**	1.07**	36.04**
SCA	45	24.15**	27.81**	191.58**	46.94**	49.73**	0.01**	0.63**	12.08**
Error	108	1.93	2.09	11.41	3.71	2.30	0.001	0.23	1.20
		SL	S/S	TW	Y/P	OC	PC	GC	
GCA	9	0.67**	4.46**	1.40**	25.05**	2.18	1.73**	13.86**	
SCA	45	0.11**	1.00**	0.13**	4.50**	2.41	1.38**	17.72**	
Error	108	0.04	0.23	0.03	0.30	1.76	0.30	0.25	

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 of any crop improvement programme. Hence, the *diallel* analysis was carried out to discern information on gene action governing yield, oil content and their component characters.

The estimates of σ_g^2 , σ_s^2 , σ_A^2 , σ_D^2 , h_n^2 , predictability ratio, and degree of dominance for various characters are presented in **Table 3**. The heritability measures as an index of transmissibility. This infers as to how much emphasis should be placed for selection for a case of particular trait. Narrow sense heritability h_n^2 is the ratio of additive genetic variance and total phenotypic variance [15]. The knowledge of heritability for a trait will help in deciding the scope of improvement of that particular trait through selection [16].

The estimates of σ_s^2 were found to be higher than the σ_g^2 for all characters except days to initial flowering, length of main raceme and 1000-seed weight indicating greater importance of specific combining ability in the inheritance of characters. Reference to the estimates of σ_A^2 and σ_D^2 for various characters revealed that the additive gene action was predominant for the expression of seven characters viz., days to initial flowering, days to maturity, plant height, length of main raceme, siliqua density, siliqua length and 1000-seed weight exhibiting greater importance of additive gene action for these traits whereas, non-additive gene action was preponderant for the expression of 8 characters viz., number of siliquae on main raceme, number of primary branches/plant, number of secondary branches/plant, number of seeds/siliqua, seed yield/plant, protein content, oil content and glucosinolate content.

Table 3 Estimates of genetic components and other genetic parameters for different characters in Indian mustard

Characters	σ^2_g	σ^2_s	σ^2_e	σ^2_A	σ^2_D	h^2_n	PR	DD
Days to initial flowering	29.97	22.22	1.93	59.95	22.22	71.28	2.70	0.61
Days to maturity	25.47	25.72	2.09	50.94	25.72	64.68	1.98	0.71
Plant height	125.32	180.17	11.41	250.64	180.17	56.68	1.39	0.85
Length of main raceme	43.76	43.24	3.71	87.53	43.24	65.09	2.02	0.70
No. of siliquae on main raceme	4.29	47.43	2.30	8.57	47.43	14.71	0.18	2.35
Silique density	0.01	0.01	0.00	0.02	0.01	60.61	1.67	0.77
No. of Primary branches/ plant	0.07	0.40	0.23	0.14	0.40	18.26	0.35	1.68
No. of Secondary branches/ plant	2.90	10.88	1.20	5.81	10.88	32.48	0.53	1.37
silique length	0.05	0.07	0.04	0.10	0.07	49.06	1.53	0.81
No. of seeds / silique	0.35	0.77	0.23	0.71	0.77	41.46	0.92	1.04
1000-seed weight (g)	0.11	0.09	0.03	0.23	0.09	64.65	2.43	0.64
Seed yield/ plant (g)	2.06	4.21	0.30	4.13	4.21	47.81	0.98	1.01
Oil content (%)	0.04	0.65	1.76	0.07	0.65	2.82	0.11	3.05
Protein Content (%)	0.12	1.08	0.30	0.24	1.08	14.72	0.22	2.13
Glucosinolate	1.14	17.48	0.25	2.27	17.48	11.35	0.13	2.77

Classification of narrow sense heritability into high (>0.30), medium ($0.30-0.10$) and low (<0.10) following Robinson (1966) showed that estimates of h^2_n were low to high for days to initial flowering (71.28%), days to maturity (64.68%), plant height (56.68%), length of main raceme (65.09%), silique density (60.61%), 1000-seed weight (64.65%), silique length (49.06%), seed yield/plant (47.81%), number of seeds/silique (41.46%) and number of secondary branches/plant (32.48%); and moderate estimates were recorded for number of primary branches/plant (18.26%), protein content (14.72%), siliquae on main raceme (14.71%) and glucosinolate content (11.35%) and low for oil content (2.82%).

Predictability ratio was high (>1) for days to initial flowering (2.70) followed by 1000-seed weight (2.43), length of main raceme (2.02), days to maturity (1.98), silique density (1.67), silique length (1.53), and plant height (1.39) indicating the predominance of fixable variability for these traits. For rest of the characters the value of predictability ratio was lower than one indicating the preponderance of non-fixable type of variance. Further the degree of dominance less than one for all these traits indicating partial dominance. Degree of dominance higher than one showed over dominance for siliquae on main raceme (2.35), number of seeds/silique (1.04), seed yield/plant (1.01), number of primary branches/plant (1.68), number of secondary branches/plant (1.37), protein content (2.13), oil content (3.05) and glucosinolate content (2.77).

The estimates of narrow sense heritability (h^2_n) were high (>0.30) for 10 characters including seed yield. This indicated the availability of additive genetic variance in substantial amount, thereby suggesting the increased possibility of improvement through selection. Moderate estimates of h^2_n (0.10 to 0.30) were found for number of primary branches/plant, protein content, siliquae on main raceme and glucosinolate content. Thus, there exist limited scopes of improvement through selection for these traits. However, for oil content the h^2_n was low indicating the near absence of additive genetic variability in the material studied, hence no scope of improvement for oil content. Based on these results it can be inferred that large portion of variability for five traits including oil content is of non-fixable type. Similar observations were also reported earlier [17-19]. This type of genetic variability stems from heterozygosity, therefore, maintenance of heterozygosity or its restoration at the end of breeding programme will be necessary for desired expression of these traits. As this type of gene action is non-fixable in nature, simple selection methods may not be effective. Therefore, the appropriate breeding methodologies could be suggested as heterosis breeding or biparental mating followed by recurrent selection as these are likely to be more rewarding [20, 21].

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Publication History

Received	18 th Dec 2018
Revised	14 th Jan 2019
Accepted	20 th Jan 2019
Online	30 th Jan 2019

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