



Genetic component analysis for seed yield and component traits in Indian mustard (*Brassica juncea* L.)

Sneha Adhikari*, Sanjana Pathak, Deepak Joshi, Usha Pant, AK Singh and Ram Bhajan

Department of Genetics and Plant Breeding, GBPUA & T, Pantnagar 263145, U. S. Nagar, Uttarakhand, India

*Corresponding author: snehaadhikari24@gmail.com

(Received: 31 August 2017; Revised: 16 March 2018; Accepted: 17 May 2018)

Abstract

Ten diverse Indian mustard genotypes/parents suitable for different sowing condition were mated in half diallele design to know the nature of gene action for inheritance of seed yield and its components traits. The results showed the presence of sufficient amount of variability among the experimental material used for the study. The estimates of σ_s^2 were found to be higher than the σ_g^2 for all characters under study that indicated preponderance of non-additive gene action for inheritance of characters thereby suggesting heterosis breeding as the best method of improvement. The genetic advance (G_A) ranged from 0.043 for siliqua density on main raceme to 4.929 for plant height. Higher heritability accompanied by higher genetic advance under selection was found in case of glucosinolate content, seed yield/ plant, number of siliquae on main raceme, number of secondary branches/plant and days to maturity. For all the traits under study the value of predictability ratio was lower than unity. It represented the involvement of non-fixable type of variance. Degree of dominance ranged from 3.38 to 1.55. Therefore based on the results it can be concluded that all the characters under study were governed by non-additive gene action so heterosis breeding can be utilized for further improvement.

Key words: Degree of dominance, genetic advance, heritability, Indian mustard

Introduction

Oilseed brassicas belong to family Brassicaceae and genus *Brassica* and are important source of edible oil with the lowest amount of saturated fats and leafy vegetables rich in minerals and antioxidative property. These crops commonly known as rapeseed-mustard are an important group of oilseed crop accounting about one-fourth of the total oilseeds production in the country. Indian mustard [*Brassica juncea* (L) Czern & Coss] is a natural amphidiploids ($2n=36$) of *B. rapa* ($2n=20$) and *B. nigra* ($2n=16$) and is a largely self pollinated with 2 – 15 per cent of cross pollination that may take place due to honeybees. Among the crops under the group Indian mustard accounts for more than 80 per cent of the area under rapeseed-mustard, followed by Toria, Yellow Sarson and Brown Sarson. In India, the area, production and productivity of rapeseed-mustard was 5.79 mha, 6.31 mt and 1089 kg/ha respectively during 2014-15 (Agriculture Statistics at a Glance, 2015).

In past, some improvements in the genetic potential of the varieties have been obtained with the use of conventional breeding methods like mass selection, pure line selection, disruptive selection and inter-varietal hybridization. But the selection and reselection were extensively followed in the low yielding local land races, and progenies of hybrids. As a result the rate of increase

in yield per unit area has been slow. The yield level has almost reached a plateau in these crops. Therefore, a precise genetic understanding of inheritance of yield and of physiological characters that determine the potential yield could be helpful in developing future high yielding varieties/hybrids of these crops. It has also been realized that reassessment of traditional breeding methods, based on valid genetic information of crop yield would be necessary for obtaining visible gains in their production (Thurling, 1974).

Survey and study of genetic variability is a logical way to initiate any breeding programme. Variation is the secret of success in plant breeding programme because it widens the scope of selection. The genetic facts are inferred from observations on phenotypes. Since phenotype is an artifact of the joint effect of genotype and environment, non-genetic part exerts large influence on genetic variability. The exploitable variability is, therefore, required to be judged through various genetic parameters like heritability, genetic advance and others. Such a study appears to be extremely necessary for planning genetic improvement in Indian mustard.

Materials and Methods

The experimental material for present study comprised of 10 diverse genotypes of Indian mustard (*Brassica juncea* L.)

Table 1: List of genotypes along with the pedigree

Name of the line	Pedigree	Features
PRL-2012-13	BBM-06-02×Ashirwad	Late sown
NRC-HB-101	BL-4×Pusa Bold	Late sown
Divya-55	Divya-22×Laxmi	Timely sown
DRMR-675-39	PCR-20×Sej	Timely sown
PRE-2011-15	(PRB-2004-6×PR-2002-20)×NDRE-4	Early sown
RRN-778	Protogynous Varuna × RRN 601	Timely sown
RB-57	Laxmi×CS-52	Timely sown
RMM-09-04	Rohini×Maya	Timely sown
Maya	Varuna×KRV-11	Timely sown
PM-25	Sej-8×Pusa Jaganath	Early sown

involving two genotypes suitable for early sown (PRE-2011-15, PM-2), six for timely sown (Divya-55, Maya, DRMR-675-39, RRN-778, RB-57 and RMM-09-4) and two for late sown (PRL-2012-13, NRC-HB-101) situations. The parents were crossed in diallel mating design excluding reciprocals (half diallel) during *Rabi* season 2014-15. The list of genotypes along with the pedigree is given in table.1. Experiment material consisting of 10 parents and 45 F_1 's was evaluated in a randomized block design with three replications during *Rabi* 2015-16.

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 flowering, Days to maturity, Plant height (cm), Length of main raceme (cm), Number of siliquae on main raceme, Siliqua density, Number of primary branches per plant, Number of secondary branches per plant, Siliqua length (cm), Number of Seeds per siliqua, Seed yield per plant (g), Test weight (g), Oil content (%), Glucosinolate content (μ mole/g fat free meal). The plot means used for statistical analyses were obtained on the basis of mean of randomly selected plants for each plot in all replication except 1000-seed weight and oil content which were based on whole plot basis. Statistical analysis was carried out as suggested by using method 2 and model I (fixed effect model) of Griffing (1956a).

Estimation of genetic components and other genetic parameters for method 2 model I

$$A. \quad \sigma^2 g = (MS_g - MS_e)/(p+2)$$

$$B. \quad \sigma^2 s = MS_s - MS_e$$

$$C. \quad \sigma^2 e = MS_e$$

$$D. \quad \sigma^2 A = 2\sigma^2 g$$

$$E. \quad \sigma^2 D = \sigma^2 s$$

Heritability narrow sense

Heritability in narrow sense (h^2_n) was calculated as per formula given by Burton and De Vane (1953) and Allard (1960).

$$h^2(n) = \text{Additive genetic variance} / \text{Phenotypic variance}$$

$$\text{Predictability ratio} = \sigma^2 A / \sigma^2 D$$

$$\text{Degree of dominance (dominance ratio)} = (\sigma^2 D / \sigma^2 A)^{1/2}$$

Expected genetic advance under selection (GA) was computed according to the formula given by Johnson et al. (1955) expressed as :

$$GA = (\sigma^2 g / \sigma p) \times K$$

Results and Discussion

The results of analysis of variance for various characters are presented in table 2. There were highly significant differences between treatments for all the characters studied. This showed the presence of sufficient amount of variability among the experimental material used for the study. The estimates of σ^2_g , σ^2_s , σ^2_A , σ^2_D , h^2_b , G_A , h^2_n , predictability ratio, and degree of dominance for various characters have are presented in table 2. The highest heritability in broad sense (h^2_b) was observed for glucosinolate content (98.8 %) followed by seed yield/plant (93.2%), number of siliquae on main raceme (90.0%), days to maturity (85.7%), number of secondary branches/plant (77.4%), number of primary branches/plant (73.6%), siliqua density on main raceme (69.3%), oil content (67.0%), test weight (54.9%). Moderate estimates of heritability were reported for plant height (47.8%), length of main raceme (45.8%), length of siliqua (42.7%), days to flowering (32.7%) and number of seeds / siliqua (29.0%) (Meena et al. 2016 and Singh et al. 2016). Classification of broad sense heritability into high (>0.50), medium (between 0.25-0.50) and low (<0.25) followed by Stanfield (1969).

Table 2: Estimation 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_b (%)	Genetic Advance	h^2_n (%)	PR	DR
Days to flowering	3.21	57.71	6.59	6.41	57.71	32.7	1.024	9.1	0.111	3.00
Days to maturity	20.03	240.98	3.34	40.06	240.98	85.7	4.143	14.1	0.166	2.45
Plant height	50.79	999.00	55.40	101.59	999.00	47.8	4.929	8.8	0.102	3.14
Length of main raceme	12.53	117.13	14.84	25.06	59.87	45.8	2.395	25.1	0.419	1.55
No. of siliquae on main raceme	20.86	370.14	2.31	41.72	370.14	90.0	4.333	10.1	0.113	2.98
Siliqua density	0.003	0.07	0.00	0.01	0.06	69.3	0.043	7.9	0.087	3.38
No. of Primary branches/plant	0.15	2.10	0.06	0.31	2.10	73.6	0.336	12.5	0.146	2.62
No. of Secondary branches/plant	2.33	44.62	0.68	4.66	44.93	77.4	1.343	9.3	0.104	3.11
siliqua length	0.02	0.27	0.03	0.04	0.27	42.7	0.092	11.9	0.149	2.59
No. of Seeds / siliqua	0.19	3.81	0.46	0.37	3.81	29.0	0.232	8.0	0.098	3.20
Seed yield/ plant (g)	3.02	15.07	0.22	6.03	15.07	93.2	1.676	28.3	0.400	1.58
Test weight (g)	0.04	0.60	0.03	0.08	0.43	54.9	0.151	15.3	0.195	2.26
Oil content (%)	1.22	17.70	0.60	2.44	14.28	67.0	0.903	14.1	0.171	2.42
Glucosinolate	720.18	5830.37	8.96	1440.36	5645.79	98.8	26.671	20.3	0.255	1.98

The genetic advance (G_A) ranged from 0.043 for siliqua density on main raceme to 4.929 for plant height. Heritability alone does not always ensure an increased gain through selection. Normally estimates of heritability and genetic advance together accounts for predicting the gain through selection. In the present investigation, higher heritability accompanied by higher genetic advance under selection was found in case of glucosinolate content, seed yield/ plant , number of siliquae on main raceme, number of secondary branches/ plant and days to maturity (Singh *et al.*, 2016). The estimates of σ^2_s were found to be higher than the σ^2_g for all characters under study that indicate importance of specific combining ability in the inheritance of characters. Reference to the estimates of σ^2_A and σ^2_D for various characters exhibited that the relative magnitude of later was high for all the traits which indicated preponderance of non-additive gene action in governing the characters (Tahir *et al.*, 2007).

The moderate to low range of narrow sense further confirmed this view. Moderate heritability was observed for seed yield/ plant (28.3%), length of main raceme (25.1%), glucosinolate content (20.3%), test weight (15.3%), oil content (14.1%), days to maturity (14.1%), number of primary branches/plant (12.5%), length of siliqua (11.9%) and number of siliquae on main raceme (10.1%) and low for number of Secondary branches/plant (9.3%), days to flowering (9.1%), plant height (8.8%), number of seeds / siliqua (8.0%) and siliqua density on main raceme (7.9%). As results showed presence of high magnitude of non-additive action, thus, maintenance and exploitation of heterozygosity is the best option. Since this type of gene action is non-fixable, simple selection method would be ineffective. Under such situation the exploitation of heterosis or alternatively biparental mating with recurrent selection or diallel selective mating may be the most appropriate methodology to hasten the pace of genetic improvement of these traits.

For all the traits under study the value of predictability ratio was lower than unity. It represented the involvement of non-fixable type of variance. Degree of dominance ranged from 3.38 to 1.55. The range indicated the highest estimate of degree of dominance was found in siliqua density on main raceme (3.38) followed by number of seeds per siliqua (3.20), plant height (3.14), number of secondary branches per plant (3.11), days to flowering (3.00), number of siliquae on main raceme (2.98), number of primary branches per plant (2.62), siliqua length (2.59), days to maturity (2.45), oil content (2.42), test weight (g) (2.26), Glucosinolate content (1.98), seed yield per plant (1.58) and length of main raceme (1.55), The high estimate

of degree of dominance represents involvement of over dominance so maintenance of heterozygosity in the base population must be preferred. Over dominance is the condition where the development of hybrid over pure line and inbred development can be justified.

References

- Allard RW. 1960. Principles of plant breeding. *John Wiley and Sons*, New York, 138-142.
- Burton GW and De Vane EH. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron J* **45**: 478-481.
- Government of India. Ministry of agriculture, Department of agriculture, cooperation & farmers welfare. Directorate of Economics & Statistics. 2016. Agriculture statistics at a glance 2015. YMCA Library building 1 Jai Singh Road, New Delhi. *Oxford Univ. Press*, 221.
- Griffing B. 1956b. A generalized treatment of use of diallel crosses in quantitative inheritance. *Heredity* **10**: 31-50.
- Johnson RW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in soybeans. *Agron J* **47**: 314-318.
- Meena Jitendra; Harsha and Pant U. 2016. Analysis of genetic components and other genetic parameters for seed yield and its contributing traits in Indian mustard [*B. juncea* L. Czern & Coss.] *Intl J Farm Sci* **6**: 31-36.
- Singh V, Ram Bhajan and Pant U. 2016. Molecular Diversity Analysis of Indian-Mustard Genotypes Through SSR Marker. *Environ Eco* **34**: 1212-1217.
- Stansfield WD. 1969. Theory and problems of Genetics. Schaum's Outline series, Mc Graw-Hill Book Co., New Delhi, 281.
- Tahir TA, Singh SP, Vikash and Gangwar LK. 2007. Inheritance of yield contributing characters and oil content in Indian mustard (*B. juncea*). *J Oilseeds Res* **24**: 244-247.
- Thurling N. 1974. Morphological determinants of yield in rape seed (*B. campestris* and *B. napus*) II. yield components, *Aust J Agric Res* **25**: 711-721.