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Genetic variability and heritability studies for yield and attributes in Indian mustard

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Abstract

Indian mustard is an important oilseed crop. In the backdrop of introducing suitable Indian mustard varieties to south India, the present investigation was carried out to evaluate the genotypes for two *Rabi* seasons. The observations recorded on 16 characters were analyzed using combined ANOVA. The genotypic coefficient of variance was high for secondary branches per plant, racemes per plant, economical yield, biological yield, harvest index, seed yield and oil yield. The traits, plant height, secondary branches per plant, racemes per plant, siliqua length, test weight, economical yield, biological yield, seed yield and oil yield registered high heritability indicating less influence of the environment. Genetic advance as percent mean was high for secondary plants per plant, racemes per plant, economical yield, biological yield, harvest index, seed yield and oil yield indicating possibility of rapid improvement. The genotypes DRMR 4005, TPM-1, TM-136, TM-217 and 6IJ0401 were top yielders for seed yield.

Keywords: Indian mustard, variability, heritability (broad sense), oil yield

1. Introduction

The genera brassica belongs to family Cruciferae comprises of economically important species yielding edible roots, stems, leaves, buds, flowers and seed condiments. The genus consists of more than 3200 species with diverse morphology and pollination types. Among them, most of the species are cultivated for oil purpose and some as forage. Oilseed *Brassica* is commonly known as rapeseed mustard which occupies an important position in the rain fed agriculture of the country. The species such as *B. campestris*, *B. napus* and *B. juncea* are the allotetraploids from which edible oil is extracted. Their diploid progenitors are *B. nigra*, *B. napus* and *B. carinata* (Nagaharu, 1935) [11].

Indian mustard is a prime oilseed crop of north India. The state, Rajasthan contributes maximum chunk of national production. In recent years, acreage in South India is picking up. In Karnataka, it is grown in an area of 0.02 lakh hectares with a production of 0.01 lakh tons. Productivity of the crop is considerably low in the state (500 kg ha⁻¹) than the average yield in the country (Indiastat, 2016) [12]. In order to exploit and explore consumer demand, introduction of high grain and oil yielding varieties suitable for Southern India is indispensable. In this connection, primary step in breeding research is to collect available genetic resources in mustard, evaluation of genetic material for their yield potential and pest-disease resistance. Later, through screening procedure best performing genetic material may be used for further breeding programme with the sole interest of improving productivity to national average and imparting of pest and disease resistance.

Breeding program for development of high yielding and pest-disease resistant varieties requires partitioning of phenotypic variability into genotypic (heritable) and environmental (non-heritable) components. Breeder expects the influence of environmental factors in total variation among genetic materials to be minimal. Influence of environment is captured through heritability. Seed yield, the trait of interest to breeders is complex in its appearance. It not only depends on number of morphological characters governed by genes but also on extraneous environmental factors. Therefore, it is necessary to partition the overall variability into heritable and non-heritable components which enables the breeders to adapt suitable breeding procedure for further improvement of genetic stocks. Generally, the estimates of heritability alone will not provide idea about expected gains in the desired trait over successive generations. Hence, in addition to heritability, estimates of genetic advance should also be considered. Genetic advance refers to the change in mean value of the trait among successive generations (Shukla *et al.*, 2006) [14].

Thus, in the present investigation, a set of 38 Indian mustard genotypes were used for estimating phenotypic and genotypic coefficient of variance, heritability in broad sense and genetic advance as percent mean.

2. Materials and Methods

The present investigation was conducted to evaluate the 38 Indian mustard genotypes for yield and attributing characters. Among the genotypes, 18 were collected from DRMR, Bharatpur and 17 from BARC, Trombay. The performance of these genotypes was compared with national check NRCHB-101 and two local checks *viz.*, Sannasaasive and Doddasaasive collected locally. The present experiment was conducted at Botanical garden, Agriculture College, Dharwad, Karnataka. The experiment was laid out in RCB in two seasons of *Rabi* 2016 and *Rabi* 2017 in a plot size of 4.5 m × 5 m in both the seasons along with recommended agronomical practices. A spacing of 45 cm × 10 cm was maintained in the field, along with chemical control of white rust.

The observations were recorded for 16 yield and attributing traits. From each plot five competent plants were randomly selected and observations were recorded. The average values for each genotype was used in statistical analysis. The data was recorded for the characters *viz.*, Days to 50 percent flowering, Days to maturity, Plant height (cm), Number of primary branches per plant, Number of secondary branches per plant, Number of racemes per plant, Number of siliqua per plant, Number of seeds per silique, Siliqua length, 1000 seed weigh, Oil content (%), Economical yield (g), Biological yield per plant (g), Harvest Index (%), Seed yield (kg/ha) and Oil yield (kg ha⁻¹).

Statistical analysis of the data was carried out in Indostat (version 9.1) statistical package using combined analysis procedures as described by Gomez and Gomez (2010) [7]. From the combined ANOVA, various components of variances were derived. The coefficients of variability were estimated by procedures given by Burton and Devane (1953) [4] and classified according to Sivasubramanian and Menon (1973) [16]. The heritability broad sense was computed as per the procedures by Hanson *et al.* (1956) [8] and classified according to Robinson (1951) [12]. Similarly, genetic advance as percent mean was calculated following methodology by Johnson *et al.* (1955) [10].

3. Results and Discussion

The experimental data of two seasons was analyzed using combined analysis technique in Indostat (9.1) to infer on the influence of year as random variable on the performance of the genotypes. The combined ANOVA technique was used to assess the statistical significance of varietal variances with respect to selected 16 characters/traits. Prior to the combined ANOVA, Bartlett's test was performed to verify the homogeneity of error variances for two seasons. The Bartlett's test was found non-significant with 'F max' value less than three for all the characters. This indicated the existence of homogeneity of error variances of two seasons. Thus, under homogeneity of error variances, unweighted combined ANOVA was used to assess significance of genotype means across characters. The results of combined ANOVA with genotypes as a source of variation for all the characters was found statistically significant which reflected the existence of sufficient variability among the genotypes (Table 1). This variability can be attributed to differences in their place of collection. The influence of season indicated by year as source of variation was found statistically significant for number of primary branches, number of secondary branches, number of racemes per plant, number of siliqua per plant and economical yield. The interaction between year and genotypes was found non-significant for all the characters except oil content. This indicated ranking of genotypes across seasons remained constant (Gomez and Gomez, 2010) [7] for all the characters except oil content.

Among the genotypes, yield realized per hectare was highest in TM 136 (817.93 kg ha⁻¹) and lowest in RH 1573 (257.56 kg ha⁻¹). The genotypes registered an average 526.71 kg ha⁻¹ of seed yield (Table 2). The phenotypic coefficient of variance for the trait was 37.50 percent (high) and genotypic coefficient of variance was 28.38 percent (high). The heritability in broad sense was 57.30 percent and genetic advance as percent mean was 44.24 percent. Similar results were reported by Sheikh *et al.* (2009) [13], Tahira *et al.* (2018) [21]. Since, Indian mustard is an oil seed crop, oil yield was also considered as economic trait which is the product of seed yield and oil yield. The genotypes exhibited average oil yield of 208.91 kg ha⁻¹. Among the genotypes, RH 1573 recorded low oil yield (102.56 kg ha⁻¹) while, genotype TM-136 (322.77 kg ha⁻¹) had highest oil yield.

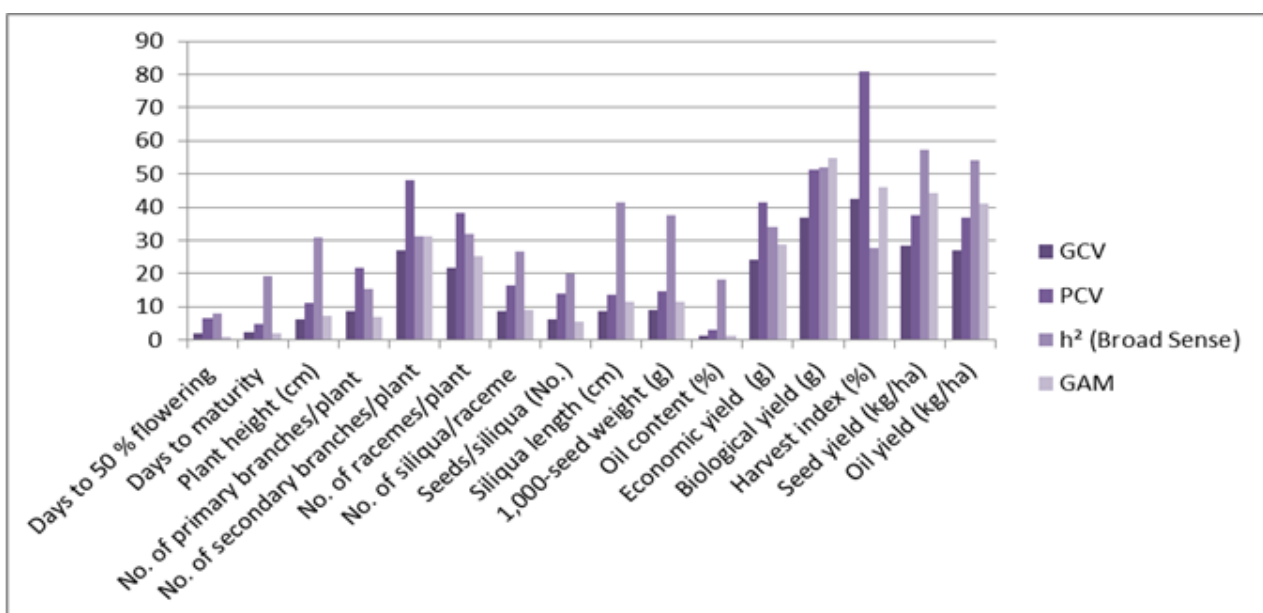


Fig 1: Comparison between PCV, GCV, Heritability (BS) and GAM across characters in Indian mustard.

Table 1: Combined/pooled ANOVA of two season for 16 characters in Indian mustard.

Source of variations	d.f.	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	No. of racemes/plant	No. of siliqua/raceme	Seeds/siliqua (No.)	Siliqua length (cm)	1,000-seed weight (g)	Oil content (%)	Economic yield (g)	Biological yield (g)	Harvest index (%)	Seed yield (kg/ha)	Oil yield (kg/ha)
Replications within year	2	9.96	9.70	226.42	3.75*	0.24	0.25	23.08	0.33	0.15	0.29	4.77*	2.07	366.13	175.89	24768.11	3268.90
Years	1	13.27	6.67	93.27	0.63**	32.12*	35.11**	72.48**	4.22	0.34	0.01	9.36**	47.57**	38.24	24.91	1608.03	1282.55
Year X genotypes	2	6.00	4.79	138.04	0.09	5.98	3.40	4.91	2.92	0.10	0.04	0.26	2.86	13.25	47.97	4748.44	924.58
Overall Sum	5	9.04	7.13	164.44	1.66	8.91	8.48	25.69	2.15	0.17	0.14	3.88*	11.48	159.40	94.53	12128.22	1933.90
Genotypes	37	7.64*	32.98**	677.26**	1.89**	32.72**	79.88**	40.40**	7.23**	1.81**	1.05**	3.09**	22.88**	1445.69**	901.53**	150721.97**	21925.44**
Pooled Error	185	5.07	13.52	184.13	0.90	8.79	21.00	12.73	2.92	0.34	0.23	1.32	5.61	193.45	273.48	16669.87	2709.50
Mean		36.33	84.06	145.95	4.76	7.41	14.46	25.22	13.83	5.64	4.09	39.81	7.05	39.23	24.07	526.71	208.91
Sem		0.91	1.48	5.47	0.38	1.19	1.85	1.44	0.69	0.24	0.19	0.46	0.95	5.60	6.66	52.01	20.97
CD at 1%		2.57	4.19	15.46	1.08	3.38	5.22	4.06	1.95	0.67	0.54	1.31	2.70	15.84	18.84	147.06	59.29
CD at 5%		1.79	2.92	10.78	0.76	2.36	3.64	2.84	1.36	0.47	0.38	0.91	1.88	11.05	13.14	102.61	41.37

Table 2: Variability, heritability and genetic advance for yield and attributes in Indian mustard.

	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	No. of racemes/plant	No. of siliqua/raceme	Seeds/siliqua (No.)	Siliqua length (cm)	1,000-seed weight (g)	Oil content (%)	Economic yield (g)	Biological yield (g)	Harvest index (%)	Seed yield (kg/ha)	Oil yield (kg/ha)
GCV	1.80	2.14	6.21	8.52	26.96	21.67	8.51	6.13	8.75	9.07	1.36	24.06	36.83	42.51	28.38	27.09
PCV	6.46	4.87	11.18	21.74	48.25	38.39	16.51	13.79	13.59	14.78	3.19	41.33	51.12	80.80	37.50	36.81
Range Lowest	33.33	77.17	130.67	3.86	3.30	8.63	20.51	11.13	4.63	3.18	38.85	3.64	14.50	10.47	257.56	102.56
Range Highest	37.83	88.17	178.81	6.17	14.79	22.62	32.43	16.30	6.53	4.83	41.40	10.69	64.63	71.17	817.93	322.77
h ² (Broad Sense)	7.80	19.40	30.90	15.30	31.20	31.80	26.60	19.80	41.50	37.70	18.30	33.90	51.90	27.70	57.30	54.20
GAM	1.04	1.94	7.11	6.87	31.04	25.19	9.05	5.62	11.61	11.47	1.20	28.85	54.65	46.08	44.24	41.07
General Mean	36.33	84.06	145.95	4.76	7.41	14.46	25.22	13.83	5.64	4.09	39.81	7.05	39.23	24.07	526.71	208.91
Genotypic variance	0.43	3.24	82.19	0.16	3.99	9.81	4.61	0.72	0.24	0.14	0.30	2.88	208.71	104.67	22342.02	3202.66
Phenotypic variance	5.50	16.76	266.32	1.07	12.78	30.81	17.34	3.64	0.59	0.37	1.61	8.49	402.16	378.16	39011.89	5912.16

The phenotypic coefficient of variance was 36.81 percent and genotypic coefficient of variance was 27.09 percent. The heritability in broad sense was 54.20 percent and genetic advance as percent mean was 41.07 percent. These results were in accordance with Zebarjadi *et al.* (2011) [22].

3.1 Coefficients of Variability

The traits number of secondary branches per plant, number of racemes per plant, economical yield, biological yield, harvest index, seed yield and oil yield registered high coefficients of variance both at genotypic and phenotypic levels. These results indicated presence selection can be practiced for these traits among the genotypes. Similar results were reported by Swamy (1993) [17], Jaylala (2001) [19], Gangapur (2008) [6], and Synrem *et al.* (2014) [19]. Similarly, traits like days to 50 percent flowering, days to maturity and oil content registered low variation both at genotypic and phenotypic level indicating absence of considerable variability for maturity and oil content. These results were in accordance with those by Dawar *et al.* (2018) [5] and Tahira *et al.* (2014) [20].

The traits *viz.*, plant height, number of primary branches per plant, number of siliqua per raceme, number of seeds per siliqua, siliqua length and test weight registered low GCV with either low or moderate PCV. These results indicated the presence of environmental coefficient of variance (ECV) on the traits to considerable extent.

3.2 Heritability in Broad Sense

The influence of environment can be further validated by heritability in broad sense. The character days to 50 percent

flowering had low heritability which indicated profound influence of the environment on the trait. The heritability in broad sense was moderate for days to maturity, number of primary branches per plant, number of siliqua per raceme, number of seeds per siliqua, oil content and harvest index. It can be inferred that these traits are moderately influenced by environment. These results are in agreement with Gangapur (2008) [6] while in contrast to Belete *et al.* (2012) [3], Tahira *et al.* (2018) [21], Alam (2010) [11] and Dawar *et al.* (2018) [5]. The traits *viz.*, plant height, number of secondary branches per plant, number of racemes per plant, siliqua length, 1000 seed weight, economical yield, biological yield, seed yield and oil yield registered high heritability indicating less influence of the environment. Thus, selection is effective for these traits (Zebarjadi *et al.*, 2011, Synrem *et al.*, 2014; Dawar *et al.*, 2018 and Tahira *et al.*, 2018) [21, 19, 5, 21].

3.3 Genetic Advance as percent Mean

The heritability estimates in broad sense alone is not a true indicator of effectiveness of selection for the trait since their scope is restricted by their interaction with the environment (Johnson *et al.*, 1955) [10]. Generally, in a set of genotypes, only broad sense heritability can be estimated. Hence, broad sense heritability values are considered for estimation of predicted response to selection. Thus, genetic advance over mean is the reliable tool for estimating the gain for the character over the generations. The genetic advance over percent mean was found high for traits such as number of secondary branches per plant, number of racemes per plant, economical yield, biological yield, harvest index, seed yield

and oil yield. Thus, there is possibility of rapid improvement for these traits. Similar results were observed by Swamy (1993)^[17], Synrem *et al.* (2014)^[19], Dawar *et al.* (2018)^[5] while these results were in contrast to the findings of Swarnkar *et al.* (2002)^[18] and Singh *et al.* (2011)^[15].

Thus, the present findings provide scope for selection for the traits with high genetic advance as percent mean among the genotypes used in the study. It was evident that seed yield and oil yield have higher response to selection (GAM) which can be exploited for improvements. The genotypes DRMR 4005, TPM-1, TM-136, TM-217 and 6IJ0401 were the top yielders from the performance of two *rabi* seasons for seed yield and oil content. These lines could be recommended for Multi Location Trials for the stability of the genotypes with regard to the seed yield and oil yield.

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