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Comparison of different selection methods in Indian mustard (*Brassica juncea* (L.) Czern & Coss)

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Abstract

In any crop improvement programme, when ever individual plant selection for a particular characters are made in the segregating generations, it is usually accompanied with changes in the related characters. Therefore, it is imperative to know the role of component characters in the selection experiments aimed to increase seed yield.

The breeding methods viz., unselected bulk, bulk S.S.D. (Single siliqua per plant) and pedigree were compared for five characters, viz., number of primary branches, number of secondary branches, seeds/siliqua, 1000 seed weight and seed yield (plant in four crosses viz. Narendra Rai × NDR 8220, Narendra Rai × NDR 8208, Narendra Rai × NDRE 4 and Vardan × Kranti of Indian mustard (*Brassica juncea* L. Czern & Coss). was compared. All the crosses showed significant differences among their progenies under all the methods for the five characters studies. Progenies from pedigree were found to have better mean, range, heritability and genetic advance for majority of characters. Pedigree and SSD proved to be better method in identification of early progenies in different population.

Keywords: Comparison, mustard, Rai × NDR, *Brassica juncea* L.

Introduction

Oilseed production assumes great important in India because of the gap in demand and supply of edible oils, which forced our country to import vegetable oils to the tune of crores of rupees, causing a heavy drain of the foreign exchange in past years, In India, the major oilseed crop are groundnut, rapeseed-mustard, sesame, linseed, castor, sunflower, safflower, soybean and niger. In terms of area and production, India ranks first in the world for sesame, niger, and castor; second for groundnut and third for rapeseed-mustard next only to China and Canada. Among oilseed crops, rapeseed-mustard occupied a prominent position in the country and stands next to groundnut. In the *Brassica* group, *Brassica campestris* var. toria, var. yellow sarson, var. brown sarson, *B. juncea*, *B. napus*, *Eruca sativa* are grown under diverse situations and have considerable contribution in area and production. Botanically oilseed *Brassicacae* constitute different crops comprising two-distinct forms from their breeding point of view. One is self compatible and self pollinated form, comprising yellow sarson, tora type brown sarson (*Brassica campestris* L.), Indian mustard (*Brassica juncea* L. Czern & Coss) and gobhi sarson (*Brassica napus* L.) while other group consists of self incompatible and highly cross pollinated crops viz. lotni type brown sarson and toria (*Brassica campestris* L.) and taramira (*Eruca sativa* L.). All these crops are grown under wide range of agroclimatic conditions. However, mustard occupies largest acreage and accounts for more than 75 per cent of the area under oilseed *Brassicacae*. This is primarily because Indian mustard has higher biomass production, better yielding potential, drought hardiness, better built in genetic tolerance to leaf blight and aphid infestation and responds well to the given dose of fertilizer and irrigation than other cultivated oleiferous *Brassicacae*. So it has an edge over other oleiferous *Brassicacae* under irrigated as well as under rainfed conditions.

Materials and Methods

comparison of different selection methods in early segregating generations of Indian mustard consisted of four crosses namely cross I (Narendra Rai × NDR 8220), Cross II (Narendra Rai × NDR 8208), cross III (Narendra Rai × NDRE 4) and cross IV (Vardan × NDR8208) in F₃ and F₄ generations. Each of the base population was grown and divided in four sub plots to exercise the four different selection methods viz. unselected bulk, bulk, S.S.D. and pedigree method during rabi.

The different selection methods were applied in F₃ generation of all four crosses. All the

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treatments (F_4 generations \times 4 methods + parents) were grown in Randomized Block Design in three replications consisting 3 row of parents and 5 row of each segregating generation per replication. Full package of practices was followed during the crop period to raise the good crop.

Five plants in parental lines and five plants from each segregating population were randomly taken from each treatment for recording the observations of five metric traits in each replication as number of primary branches per plant, number of secondary branches per plant, number of seeds/siliqua, 1000 seed weight (g), seed yield/ plant (g).

The data collected from the experiment was analysed on individual plant basis for response to different methods of selection. Following statistical analysis was estimated.

Analysis of variance: The data for each of the character studies was subjected to analysis of variance as prescribed for Randomized Block Design (Panse & Sukhatme, 1978)

Coefficient of variability: The genotypic and phenotypic variance and their coefficients of variability were calculated according to method given by Burton and de-Vane (1953) [1].

Heritability: It was estimated as per formula used by Hanson *et al.* (1956) [2].

Expected genetic advance: It was computed as per formula of Johson *et al.* (1955).

Result and Discussion

Analysis of variance of design of experiment was done in all the 4 crosses for each method separately. The methods were M I (Random Bulk), M II (Bulk), M III (SSD) & M IV (Pedigree). The significance of treatments variation in different methods were as given Table 1. perusal of table showed significant variation for all the pre and post harvest traits in F_4 generation for all the 4 crosses for all the 4 methods. The material developed from selected in F_3 through different breeding methods exhibited significant variation for all the pre and post harvest traits in all the crosses. More ever there was significant variation among the treatments in all the crosses developed though the application of different methods. Means and range for five characters in four F_4 population advance by unselected bulk, bulk, SSD and pedigree methods in 4 crosses are presented in Table 2, 3, 4 and 5. A perusal of tables showed that there was role of different selection methods applied in F_3 for changing the

mean and range of quantitative character under all the 4 crossing F_4 population. All the character showed significantly higher mean in pedigree method over rest of the methods followed by SSD, bulk and unselected bulk in all the four crosses. Unselected bulk method for all the traits in 4 crosses was observed inferior in comparison to remaining three methods. There was marked differences in the range under different populations in all the 4 crosses. Pedigree method showed maximum variability followed by SSD, bulk and unselected bulk in remaining three crosses. The coefficient of variability was estimated at both phenotypic (PCV) and genotypic (GCV) levels for all the metric traits under different F_4 populations advanced by four different selection methods. The heritability in broad sense (h^2b) and genetic advance in per cent of mean (Ga%) for five quantitative traits in F_4 population advanced by 4 selection methods in four crosses has been worked out and are given in Table 1.2, 1.3, 1.4 and 1.5. In order to facilitate the description the heritability (h^2b) and genetic advance (Ga%) were grouped into high (>75%, >4% respectively), moderately higher (50 to 75% and 30 to 40%) moderately low (30 to 50% and 20 to 30%) and low (<30% and <20%) categories.

In F_4 generation, pedigree method exhibited significantly higher mean for yield and other attributes over other methods (SSD, bulk & unselected bulk) in all the four crosses. Experimentally pedigree method in segregating population has also been found to be comparable to or better than SSD, bulk and unselected bulk (Mitra & Mehra, 1999) in grasspea. A perusal of relative magnitude of range of variability in F_4 generation pedigree method had wider range for seed yield in comparison to rest of the methods in all the crosses. Based on finding, it was apparent that none of the selection methods was consistent in enhancement of pCV for all the characters under study because estimates of PCV in different selection methods were variable in both the crosses of each generation for yield and its component traits. Very inconsistent and contracting results have been reported by Rai & Murty (1979) [4], Singh *et al.* (1980) [5] and Husain *et al.* (1984) [3].

it seems that selection for yield and its components traits through above mentioned methods would be worth attempting as these characters have been found to be under additive gene action. Further more, on the basis of absolute values of heritability and genetic advance. The same character had variable magnitude of these two parameters over different methods and crosses. Indicating thereby, significant role of various selection methods.

Table 1: Analysis of variance (Mean squares) for different methods in four crosses of Indian mustard

Cross	Methods	Source of variation	d.f.	Number of primary branches/plant	Number of secondary branches/plant	seeds/siliqua	1000-seed weight (g)	Seed yield/plant (g)
CI (Narendra Rai \times NDR 8220)	M I	Replications	2	0.033	0.256	0.915*	0.135	0.491
		Treatments	4	1.313**	11.769**	2.181*	0.181*	4.119**
		Error	8	0.085	0.663	0.203	0.031	0.250
	M II	Replications	2	0.010	0.773	0.450	0.068	0.844*
		Treatments	4	1.528**	12.433**	2.381**	0.198**	4.416**
		Error	8	0.119	0.869	0.129	0.019	0.157
	M III	Replications	2	0.037	0.290	0.157	0.005	0.101
		Treatments	4	1.528**	13.236**	2.612**	0.230**	4.716
		Error	8	0.050	0.391	0.386	0.040	0.319
	M IV	Replications	2	0.010	0.068	0.165	0.005	0.419
		Treatments	4	1.591**	14.022**	2.698**	0.212**	4.873**
		Error	8	0.070	0.546	0.291	0.026	0.416

CII (Narendra Rai × NDR 8208)	M I	Replications	2	0.097	0.564	0.128	0.021	0.407
		Treatments	4	1.564**	12.856**	2.395**	0.220**	4.326**
		Error	8	0.124	0.656	0.211	0.036	0.114
	M II	Replications	2	0.009	0.070	0.588	0.027	0.719
		Treatments	4	1.693**	14.300**	2.606**	0.254**	4.892**
		Error	8	0.169	1.207	0.415	0.012	0.367
	M III	Replications	2	0.036	0.640	0.420	0.007	0.123
		Treatments	4	1.83	14.972**	2.735**	0.245**	4.996**
		Error	8	0.094	0.756	0.321	0.033	0.345
	M IV	Replications	2	0.323	0.471	0.855**	0.146**	0.473
		Treatments	4	1.925	15.272**	2.841**	0.273**	5.347**
		Error	8	0.117	0.981	0.030	0.005	0.130

Cross	Methods	Source of variation	d.f	Number of primary branches/plant	Number of secondary branches/plant	Seeds/siliqua	1000-seed weight (g)	Seed yield/plant (g)
CIII (Narendra Rai × NDR E4)	M I	Replications	2	0.016	0.068	0.616	0.110**	0.904*
		Treatments	4	1.790**	18.354**	2.409**	0.222**	4.500**
		Error	8	0.186	0.865	0.303	0.012	0.187
	M II	Replications	2	0.129	0.930	1.106*	0.086	0.455
		Treatments	4	2.415**	15.201**	2.809**	0.269**	5.270**
		Error	8	0.056	1.037	0.199	0.025	0.133
	M III	Replications	2	0.026	0.310	0.134	0.039	0.163
		Treatments	4	2.145**	15.354**	2.841**	0.275**	5.237**
		Error	8	0.048	0.544	0.427	0.036	0.382
	M IV	Replications	2	0.035	0.337	0.537	0.0003	0.217
		Treatments	4	2.169**	16.492**	2.923*	0.2757**	5.516**
		Error	8	0.070	0.312	0.528	0.0306	0.369
CIV (Vardan × NDR 8208)	M I	Replications	2	0.131	0.809	0.473	0.004	0.130
		Treatments	4	2.339**	14.046**	2.596**	0.239	4.889**
		Error	8	0.171	0.969	0.147	0.031	0.201
	M II	Replications	2	0.040	0.209	0.880	0.096	0.563
		Treatments	4	2.646**	15.538**	2.777*	0.339**	5.154**
		Error	8	0.168	0.963	0.431	0.28	0.394
	M III	Replications	2	0.024	0.141	0.140	0.18	0.398
		Treatments	4	2.687**	16.022**	2.723*	0.308**	5.468**
		Error	8	0.229	1.283	0.415	0.027	0.307
	M IV	Replications	2	0.316	1.770	0.564	0.078	0.496
		Treatments	4	2.875**	16.621**	2.849**	0.322**	5.965**
		Error	8	0.114	0.652	0.161	0.034	0.324

Where, M I= Unselected bulk method, M II= Bulk method, M III = SSD method, M IV= Pedigree method

Table 2: Genetic parameters of yield and its component characters in F₄ population of cross I (Narendra Rai × NDR-8220) under different selection methods in Indian mustard

Selection methods	Parameters	Characters				
		Number of primary branches/plant	Number of secondary branches/plant	Seeds/siliqua	1000-seed weight (g)	Seed yield/plant (g)
M I	Mean	3.66	10.16	10.42	4.060	9.74
	Range	2.69-4.40	7.30-12.00	9.10-11.30	3.72-4.40	7.80-10.86
	PCV (%)	19.23	20.56	8.91	7.02	12.74
	GCV (%)	17.49	18.94	7.79	5.49	11.66
	H ² b (%)	82.74	89.00	76.45	61.25	83.75
	Ga (%) of mean	22.89	75.14	12.92	2.47	27.35
M II	Mean	3.89	10.54	10.84	4.22	10.12
	Range	2.85-4.70	7.60-12.45	9.46-11.75	3.90-4.58	8.10-11.20
	PCV (%)	19.73	20.62	8.65	6.65	12.41
	GCV (%)	17.61	18.63	7.99	5.77	11.77
	H ² b (%)	79.75	81.61	85.36	75.31	90.04
	Ga (%) of mean	24.99	75.65	14.21	2.56	28.94
M III	Mean	3.94	10.78	11.12	4.31	10.32
	Range	2.90-4.75	7.75-12.75	9.65-12.00	3.96-4.70	8.25-11.45
	PCV (%)	18.70	20.05	9.55	7.84	12.95
	GCV (%)	17.81	19.20	7.75	5.84	11.73
	H ² b (%)	90.71	91.64	65.78	61.14	82.11
	Ga (%) of mean	25.69	82.10	13.69	2.91	29.13
M IV	Mean	4.03	11.09	11.36	4.43	10.61
	Range	2.96-4.85	7.96-13.10	9.90-12.35	4.10-4.80	8.50-11.75

	PCV (%)	18.85	20.24	9.20	6.71	12.99
	GCV (%)	17.66	19.11	7.88	5.63	11.49
	H ² b (%)	87.80	89.15	73.38	70.29	78-16
	Ga (%) of mean	26.08	83.32	14.42	2.60	28.77

Where, M I= Unselected bulk method, M II= Bulk method, M III = SSD method, M IV= Pedigree method

Table 3: Genetic parameters of yield and its component characters in F₄ population of cross II (Narendra Rai × NDR-8208) under different selection methods in Indian mustard.

Selection methods	Parameters	Characters				
		Number of primary branches/plant	Number of secondary branches/plant	Seeds/siliqua	1000-seed weight (g)	Seed yield/plant (g)
M I	Mean	3.95	10.55	10.73	4.42	10.03
	Range	2.904-7.5	7.56-12.50	9.35-11.65	4.08-4.80	8.03-11.10
	PCV (%)	19.68	20.59	9.03	7.05	12.29
	GCV (%)	15.54	19.11	7.95	5.59	11.82
	H ² b (%)	79.44	86.11	77.51	62.74	92.47
	Ga (%) of mean	24.72	79.26	14.07	2.64	28.72
M II	Mean	4.20	11.21	11.38	4.67	10.63
	Range	3.10-5.04	8.05-13.25	9.94-12.35	4.30-5.08	8.52-11.80
	PCV (%)	19.61	21.06	9.41	6.51	12.88
	GCV (%)	16.98	18.64	7.51	6.09	11.55
	H ² b (%)	75.01	78.34	63.76	87.46	80.44
	Ga (%) of mean	24.64	79.83	13.11	3.45	29.14
M III	Mean	4.25	11.31	11.49	4.75	10.74
	Range	3.10-5.10	8.10-13.36	10.00-12.45	4.40-5.15	8.60-11.90
	PCV (%)	19.46	20.69	9.23	6.81	12.82
	GCV (%)	17.81	19.21	7.81	5.63	11.60
	H ² b (%)	83.73	86.20	71.52	68.45	81.82
	Ga (%) of mean	27.93	85.83	14.58	2.94	29.88
M IV	Mean	4.36	11.62	11.82	4.88	11.04
	Range	3.20-5.25	8.35-13.70	10.30-12.80	4.50-5.30	8.83-12.25
	PCV (%)	19.46	20.63	9.17	6.30	12.40
	GCV (%)	17.81	18.78	7.66	6.13	11.93
	H ² b (%)	83.73	82.93	69.82	94.63	92.63
	Ga (%) of mean	28.57	84.46	19.10	3.60	32.45

Where, M I= Unselected bulk method, M II= Bulk method, M III = SSD method, M IV= Pedigree method

Table 4: Genetic parameters of yield and its component characters in F₄ population of cross III (Narendra Rai × NDRE-4) under different selection methods in Indian mustard

Selection methods	Parameters	Characters				
		Number of primary branches/plant	Number of secondary branches/plant	Seeds/siliqua	1000-seed weight (g)	Seed yield/plant (g)
M I	Mean	4.29	10.86	10.93	4.50	10.23
	Range	3.15-5.15	7.30-12.80	9.55-11.86	4.16-4.88	8.20-11.35
	PCV (%)	19.79	20.66	9.17	6.36	12.46
	GCV (%)	17.05	18.80	7.66	5.89	11.73
	H ² b (%)	74.19	82.79	69.82	85.63	88.49
	Ga (%) of mean	25.58	79.03	12.79	3.14	28.70
M II	Mean	4.55	11.53	11.60	4.77	10.84
	Range	3.30-5.50	8.28-13.60	10.10-12.60	4.40-5.20	8.62-12.05
	PCV (%)	19.07	20.81	8.91	6.83	12.53
	GCV (%)	18.34	18.85	8.04	5.97	12.07
	H ² b (%)	92.44	81.99	81.38	76.45	92.77
	Ga (%) of mean	31.23	84.38	15.24	3.28	32.69
M III	Mean	4.60	11.63	11.72	4.84	10.74
	Range	3.35-5.55	8.36-13.70	10.20-12.70	4.45-5.25	8.76-12.15
	PCV (%)	18.79	20.13	9.47	7.02	12.93
	GCV (%)	18.7	19.10	7.65	5.84	11.63
	H ² b (%)	93.53	90.08	65.35	69.12	80.90
	Ga (%) of mean	31.57	87.35	14.05	3.23	30.12
M IV	Mean	4.74	11.95	12.04	4.98	11.25
	Range	3.51-5.70	8.55-14.10	10.50-13.05	4.60-5.40	9.00-12.45
	PCV (%)	18.51	19.98	9.57	6.73	12.84
	GCV (%)	17.65	19.43	7.42	5.74	11.64
	H ² b (%)	90.86	94.53	60.18	72.76	82.28
	Ga (%) of mean	30.45	92.52	13.65	3.32	31.23

Where, M I= Unselected bulk method, M II= Bulk method, M III = SSD method, M IV= Pedigree method

Table 5: Genetic parameters of yield and its component characters in F₄ population of cross IV (Vardan × NDR-8208) under different selection methods in Indian mustard

Selection methods	Parameters	Characters				
		Number of primary branches/plant	Number of secondary branches/plant	Seeds/siliqua	1000-seed weight (g)	Seed yield/plant (g)
M I	Mean	4.63	11.07	11.14	4.86	10.51
	Range	3.30-5.60	7.95-13.10	9.70-12.10	4.50-5.25	8.40-11.66
	PCV (%)	20.42	20.85	8.81	6.52	12.64
	GCV (%)	18.36	18.86	8.11	5.42	11.89
	H ² b (%)	80.85	81.81	84.71	69.34	88.60
	Ga (%) of mean	32.07	81.33	15.08	2.92	30.35
M II	Mean	4.91	11.64	11.69	5.04	10.94
	Range	3.50-5.95	8.35-13.70	10.20-12.65	4.60-5.50	8.76-12.10
	PCV (%)	20.29	20.73	9.42	7.20	12.87
	GCV (%)	18.50	18.94	7.56	6.39	11.52
	H ² b (%)	83.13	83.45	64.44	78.77	80.13
	Ga (%) of mean	34.47	85.49	13.64	4.19	29.82
M III	Mean	4.97	11.74	11.83	5.15	11.14
	Range	3.35-6.0	8.40-13.90	10.35-12.80	4.75-5.60	8.90-12.36
	PCV (%)	20.60	21.20	9.21	6.74	12.78
	GCV (%)	18.21	18.87	7.42	5.94	11.77
	H ² b (%)	78.15	79.30	65.03	77.73	84.86
	Ga (%) of mean	33.94	85.80	13.35	3.69	31.90
M IV	Mean	5.12	12.09	12.13	5.32	11.45
	Range	3.65-6.20	8.70-14.30	10.60-13.10	4.90-5.76	9.10-12.70
	PCV (%)	19.86	20.22	8.47	6.79	12.97
	GCV (%)	18.74	19.08	7.80	5.83	11.98
	H ² b (%)	89.00	89.09	84.79	73.61	85.32
	Ga (%) of mean	37.24	90.53	15.30	5.67	33.64

Where, M I= Unselected bulk method, M II= Bulk method, M III = SSD method, M IV= Pedigree method

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