

# Parental diversity to realize maximum heterosis in Indian mustard (Brassica juncea (L.) Czern & Coss)

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#### Abstract

In the present investigation, divergence classification - a method devised by Arunachalam and Bandopadhyay (1984) were used to classify the 36 mustard genotypes to draw a limit of parental diversity in expressing maximum heterosis. Mahalanobis D<sup>2</sup> statistic was used to estimate genetic diversity (D<sup>2</sup> values) and then the genotypes were classified into four divergence classes based on mean and standard deviation of all D<sup>2</sup> values. According to divergence classification, DCI involved most distantly and DCIV the most closely related parents where as, DC II and DC III involved the medium divergent parents. A scoring system was adopted to work out the relative order of importance of the divergence classes. The overall scores for each divergence classes based on significant and desirable heterosis (q) and mean (y) of such crosses for all characters were carried out to rank the divergence classes. According to the scoring system, the most desirable class would be with the lowest total score. Results clearly showed the superiority of classes DC III followed by DC II, as both the classes received low overall score and maximum number of heterotic cross combinations. In conclusion it can be said that divergence classification appears to be effective in clubbing the genotypes for parental diversity and suggested that parents with intermediate diversity would be used to produce heterotic cross combination.

Key words : *Brassica juncea*, Indian mustard, D<sup>2</sup> statistic, parental diversity, divergence classification

#### Introduction

Indian mustard is one of the most important sources of vegetable oil grown during *Rabi* season. The productivity level in India is low (1001 kg/ha) compared to that of world average (1333 kg/ha). However, there is considerable scope for improving the yield potential of this crop. Further, the projected consumption of rapeseed-mustard in 2020 in India will be around 14 million tonnes, which is almost double that of the present production. To meet the demand of the growing population and for achieving the target, research efforts would have to be intensified.

In Indian mustard the increase in productivity has been continuous but not striking. Improvement through selection is an important criterion to increase the productivity in this crop. Genetic improvement for quantitative traits depends upon the nature and amount of genetic diversity present in the base material as well as the extent to which the desirable traits are heritable. The concept of genetic divergence provides an idea about the genetic diversity among the parents and has always been of vital utility in determining diversity among the parents. However, it is a major point of interest to the breeders, to examine the extent of increase in the expression of heterosis for economic traits. The quantification of genetic diversity through biometrical procedures has made it possible to choose genetically diverse parents for their use in a successful breeding programming.

Heterosis breeding could be an added advantage for obtaining quantum jumps in the production and productivity of Indian mustard. The exploitation of heterosis to raise the yield levels has been tried by several workers. The level of heterosis as well as selection advance in segregating generations depend upon the genetic diversity among the parents rather than geographical diversity. Therefore, the choice of diverse parents with good combining ability is the prerequisite for efficient hybridization programme. In the present investigation, the multivariate analysis methods such as Mahalanobis  $D^2$  statistic [1] and divergence classification [2] were used to classify the genotypes and to draw the limits of parental divergence in expressing maximum heterosis.

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#### Materials and methods

Experimental material consisted of 29 lines and 7 testers, which were selected from different geographic regions such as, eight from IARI, New Delhi; five from NBPGR. New Delhi; three each from Pusa, Bihar and Kangra; two each from PAU, Ludhiana and S. K. Nagar; one each from HAU, Hisar, Pantnagar, Faizabad and BARC, Bombay; seven commercial varieties and two male sterile lines (Table 1). 203 possible cross combinations were made in a Line × Tester mating design of Kempthorne [3]. The parents and F<sub>1</sub>'s were grown in a randomized blocks design with three replications at the Indian Agricultural Research Institute. New Delhi during rabi season 1996-97. Experimental plot consisted of four-meter long rows spaced 40 cm apart and plants within rows were spaced 15 cm apart. Two rows each of experimental entry were grown for recording of observations. The observations were recorded on 12 quantitative characters from five competitive plants selected randomly from each plot. Recommended package of practices for mustard cultivation was adopted for growing the experimental material.

The divergence analysis among the parents was carried out using Mahalanobis  $D^2$  statistic [1]. Divergence classification of the genotypes were done based on mean and standard deviation of all  $D^2$  values, as given by Arunachalam and Bandyopadhyay [2]. The method was devised to delineate the parental divergence into four divergence classes (DC I, DC II, DC III and DC IV). The mean (m) and standard deviation (s) of the  $D^2$  values were calculated and then divergence classes were are defined as follows,

 $\begin{array}{rll} \text{CD I} & : D^2 \text{ values } > \text{ or } (m + s) \\ \text{DC II} & : D^2 \text{ values } < (m + s) \text{ and } > \text{ or } = m \\ \text{DC III} & : D^2 \text{ values } > \text{ or } = (m - s) \text{ and } < m \\ \text{DC IV} & : D^2 \text{ values } < (m - s) \end{array}$ 

	Table	1.	Experimental	material	used	in	this	study	
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Lines	Genotype	Source
L1	PSR-18	PUSA, Bihar
L2	SKM-93-28	S.K. Nagar
L3	VSL-5	IARI, New Delhi
L4	NPJ-30	IARI, New Delhi
L5	RH-9303	HAU, Hissar
L <sub>6</sub>	NDR-8208	Faizabad
L7	TM-38	BARC, Bombay
L <sub>8</sub>	YSRL-10	PAU, Ludhiana
L9	NPJ-35	IARI, New Delhi
L10	DLM-55	IARI, New Delhi
L11	Strain-26	IARI, New Delhi
L12	AD-2041	IARI, New Delhi
L13	PSMT-40	PUSA, Bihar
L14	RL-1359	PAU, Ludhiana

L16         NKG-207         NBPGR, New Delhi           L17         IB-618         NBPGR, New Delhi           L18         NIC-11703         NBPGR, New Delhi           L19         BEC-201AB         NBPGR, New Delhi           L20         SKM-92-66         S.K. Nagar		500 (00	
L17         IB-618         NBPGR, New Delhi           L18         NIC-11703         NBPGR, New Delhi           L19         BEC-201AB         NBPGR, New Delhi           L20         SKM-92-66         S.K. Nagar	L15	RCC-462	Kangra
L18         NIC-11703         NBPGR, New Delhi           L19         BEC-201AB         NBPGR, New Delhi           L20         SKM-92-66         S.K. Nagar	L16	NKG-207	NBPGR, New Delhi
L19         BEC-201AB         NBPGR, New Delhi           L20         SKM-92-66         S.K. Nagar	L <sub>17</sub>	IB-618	NBPGR, New Delhi
L <sub>20</sub> SKM-92-66 S.K. Nagar	L18	NIC-11703	NBPGR, New Delhi
	L19	BEC-201AB	NBPGR, New Delhi
	L20	SKM-92-66	S.K. Nagar
L <sub>21</sub> PSMI-34 PUSA, Bihar	L <sub>21</sub>	PSMT-34	PUSA, Bihar
L <sub>22</sub> Strain-23 IARI, New Delhi	L22	Strain-23	IARI, New Delhi
L <sub>23</sub> IB-642 NBPGR, New Delhi	L <sub>23</sub>	IB-642	NBPGR, New Delhi
L <sub>24</sub> PRG-904 GBPUA&T, Pantnagar	L24	PRG-904	GBPUA&T, Pantnagar
L <sub>25</sub> RCC-5 Kangra	L25	RCC-5	Kangra
L <sub>26</sub> DBS-10 IARI, New Delhi	L <sub>26</sub>	DBS-10	IARI, New Delhi
L <sub>27</sub> KBJ-3 Kangra	L27	KBJ-3	Kangra
L <sub>28</sub> B. oxyrrhina A IARI, New Delhi	L <sub>28</sub>	B. oxyrrhina A	IARI, New Delhi
L <sub>29</sub> Prakash A ( <i>B. tornefortii</i> ) IARI, New Delhi	L <sub>29</sub>	Prakash A (B. tornefortii)	IARI, New Delhi
Testers	Testers		
T <sub>1</sub> Varuna	T1	Varuna	
T <sub>2</sub> Kranti	T <sub>2</sub>	Kranti	
T <sub>3</sub> Pusa Bold	T <sub>3</sub>	Pusa Bold	
T <sub>4</sub> Bio-722	T <sub>4</sub>	Bio-722	
T₅ RH-30	T <sub>5</sub>	RH-30	
T <sub>6</sub> PR-45	T <sub>6</sub>	PR-45	
T7 Prakash	<u>T7</u>	Prakash	

It may be noted that in this classification, DC I and DC IV were the extreme divergent classes in either direction. According to this classification the DC I involved the most distantly and DC IV the most closely related parents. On the other hand, the class DC II and DC III involved the medium divergent parents.

After establishment of the divergence class, the number of crosses (n) falling in each divergence class, the proportion of crosses (q) showing significant heterosis (heterosis over better parent) in desired direction and the mean (y) for each character over such crosses were worked out. In case of characters, such as days to 50% flowering, days to maturity and plant height the negative direction was considered as desired direction, whereas, for all others characters the positive direction was considered as desired one.

Divergence classes were ranked for their relative order of importance on the basis of values of q and y separately. In order to come to a final decision jointly on the ranking based on q and y, a scoring procedure was adopted. The divergence class which gave the highest value of q was allotted a score 1, the next best a score of 2 and so on. In case of tie the classes received the same score. The same scoring procedure followed for y. The scores over q and y were added over all characters to obtain a final score for each divergence class.

### Results and discussion

The  $D^2$  values were used to constitute the divergence classes based on the mean and standard deviation of the  $D^2$ -values (Table 2). The mean of  $D^2$  values (42.33)

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Divergence classes	Range of D <sup>2</sup> values	Number of crosses	Line x Tester pairs
DCI	69.8-150.05	26	L8T1, L23T1, L25T1, L29T1, L29T2, L23T3, L29T3, L29T4, L1T7, L2T7, L4T7, L5T7, L6T7, L9T7, L10T7, L11T7, L12T7, L13T7, L16T7, L18T7, L19T7, L20T7, L21T7, L22T7, L26T7, L28T7
DC II	42.25-64.59	54	L3T1, L7T1, L10T1, L12T1, L14T1, L15T1, L17T1, L21T1, L24T1, L27T1, L5T2, L10T2, L19T2, L3T3, L6T3, L7T3, L8T3, L10T3, L17T3, L19T3, L21T3, L25T3, L1T4, L4T4, L8T4, L12T4, L18T4, L21T4, L23T4, L24T4, L25T4, L27T4, L28T4, L1T5, L5T5, L12T5, L20T5, L21T5, L23T5, L27T5, L5T6, L8T6, L12T6, L13T6, L21T6, L23T6, L25T6, L29T6, L3T7, L15T7, L14T7, L23T7, L24T7, L27T7
DC III	17.07-42.05	105	$ \begin{array}{l} L_2T_1, \ L_4^{-1}, \ L_6T_1, \ L_9T_1, \ L_{11}T_1, \ L_{13}T_1, \ L_{16}T_1, \ L_{18}T_1, \ L_{19}T_1, \ L_{22}T_1, \ L_{26}T_1, \ L_{28}T_1, \\ L_6T_2, \ L_7T_2, \ \ L_8T_2, \ L_9T_2, \ L_{14}T_2, \ L_{15}T_2, \ L_{16}T_2, \ L_{17}T_2, \ L_{20}T_2, \ L_{21}T_2, \ L_{22}T_2, \ L_{23}T_2, \\ L_{24}T_2, \ L_{25}T_2, \ L_{26}T_2, \ L_{27}T_2, \ L_{28}T_2, \ L_{17}T_3, \ L_{27}T_3, \ L_{12}T_3, \ L_{13}T_3, \ L_{14}T_3, \ L_{15}T_3, \\ L_{16}T_3, \ L_{18}T_3, \ L_{20}T_3, \ L_{22}T_3, \ L_{24}T_3, \ L_{26}T_3, \ L_{27}T_3, \ L_{27}T_4, \ L_{3}T_4, \ L_{5}T_4, \ L_{5}T_5, \ L_{7}T_4, \ L_{9}T_4, \\ L_{10}T_4, \ L_{11}T_4, \ L_{13}T_4, \ L_{14}T_4, \ L_{15}T_4, \ L_{16}T_4, \ L_{17}T_4, \ L_{19}T_4, \ L_{20}T_4, \ L_{20}T_4, \ L_{26}T_4, \ L_{27}T_5, \\ L_{3}T_5, \ L_{4}T_5, \ L_{6}T_5, \ L_{8}T_5, \ L_{9}T_5, \ L_{10}T_5, \ L_{11}T_5, \ L_{13}T_5, \ L_{14}T_5, \ L_{16}T_5, \ L_{17}T_5, \ L_{18}T_5, \\ L_{19}T_5, \ L_{22}T_5, \ L_{24}T_5, \ L_{25}T_5, \ L_{26}T_5, \ L_{28}T_5, \ L_{29}T_5, \ L_{17}T_6, \ L_{27}T_6, \ L_{22}T_6, \ L_{24}T_6, \ L_{26}T_6, \\ L_{27}T_6, \ L_{28}T_6, \ L_{7}T_7, \ L_{8}T_7, \ L_{17}T_7, \ L_{25}T_7, \ L_{29}T_7, \\ \end{array}$
DC IV	8.94-16.78	18	L1T1, L5T1, L20T1, L2T2, L3T2, L4T2, L11T2, L12T2, L13T2, L18T2, L4T3, L9T3, L11T3, L28T3, L6T4, L7T5, L15T5, L6T6

Table 2. Divergence classification of Indian mustard genotypes based on mean and standard deviation of D<sup>2</sup> values

and standard deviation (25.7) were used to form the four divergence classes. So, the four divergence classes were then defined by four intervals as follows :

DCIV containing 26 and 18  $F_1$  cross combinations, respectively. In this experiment 203  $F_1$  cross combinations were dealt with to get precise result.

DC-I :  $D^2 > or = 67.21$ 

DC-II :  $D^2 < 67.21$  and > or = 42.33 DC-III :  $D^2$  > or 17.05 and < 42.33 DC-IV  $D^2 < 17.05$ 

Based on the divergence classification, DCIII contained the maximum number of 105  $F_1$  cross combinations, whose D<sup>2</sup> values ranged between 17.07-42.05. Divergence class, DCII contained 54 number of  $F_1$  cross combinations followed by DCI and

The overall scores based on the significant and desirable heterosis (q) and mean (y) of such crosses for all the characters were given in Table 3. DCIII received an overall score of 34 followed by DCII (46), DCI (54) and DCIV (63). According to scoring system, the most desirable class would be with the lowest total score. The results clearly showed the superiority of classes DCIII and DCII.

Among the divergence classes, DCIII contained the maximum number of heterotic crosses (Table 2)

Table 3. Proportion of crosses showing significant desirable heterosis for different characters and overall score for each divergence

DC	n		DF			DM			PH			MSL			PB			SB	
		q	у	a+b	q	У	a+b	q	у	a+b	q	у	a+b	q	У	a+b	q	у	a+b
DCI	26	0	0	0+0	2	139.83	3+3	1	142.33	1+2	2	77.04	4+3	3	7.33	2+1	7	22.33	2+1
DC II	54	0	0	0+0	3	140.67	2+2	0	0	0+0	16	82.23	2+2	2	7.33	1+1	8	20.08	1+2
DC III	105	6	80.22	1+1	14	141.43	1+1	1	145.00	1+1	36	85.03	1+1	2	6.5	1+2	6	19.99	3+3
DC IV	18	2	77.17	2+2	1	139.67	4+4	0	0	0+0	5	80.64	3+4	0	0.0	0+0	4	19.25	4+4

DC	n		S/SQ			HI	_		SY			OC		Total score (all a + b values added)
		q	Y	a+b	q	У	a+b	q	у	a+b	q	у	a+b_	-
DCI	26	1	16.66	2+1	4	0.27	3+3	0	0.00	0+0	0	0.00	0+0	54
DC II	54	0	0.00	0+0	6	0.34	2+1	4	36.69	1+2	1	43.63	2+1	46
DC III	105	5	16.19	1+2	7	0.29	1+2	4	28.30	1+3	4	40.03	1+2	34
DC IV	18	5	16.19	1+2	0	0.00	0+0	2	42.25	2+1	1	30.34	2+3	63

n = Number of crosses falling in each divergence class; q = the proportion of crosses showing significant heterosis in desired direction y = the mean for each character over such crosses: a = score on q; b = score on y

NB : No crosses have shown significant heterosis in desired direction for the characters siliqua on main shoot and seed weight.

and received the lowest overall score (Table 3) suggesting that this class was the most desirable class followed by DCII. These results agree with those of Arunachalam and Bandyopadhyay [2]. The cross VSL  $5 \times$  Kranti (Table 4) according to divergence classification (as came under DC IV) should not have high heterosis but showed high heterosis for seed yield (41.00%) and two yield components (DF, SB) as an exception.

 Table 4.
 Relationship of top 22 crosses heterotic for yield with their divergence classification

Crosses	Heterosis	DC	Significant
	for seed		heterosis for
	yield		other characters
$PSR18 \times Prakash$	25.35	Ι	SB, HI
SKM 93-28 × Kranti	31.35*	IV	MSL
VSL 5 × Kranti	41.00*	IV	DF,SB
VSL 5 × RH 30	34.06	Ш	н
VSL 5 $\times$ Prakash	45.23 <sup>*</sup>	H	
NPJ 30 × PR 45	46.12*	111	
RH 9303 $ imes$ Prakash	36.49	1	PB,SB,OC
YSRL 10 × Pusa Bold	73.75**	11	MSL,SB
YSRL 10 × RH 30	34.48	HI	
NPJ 35 × RH 30	49.14 <sup>*</sup>	III	
Strain 26 $\times$ BIO 772	30.95*	111	MSL
AD 2041 $\times$ Pusa Bold	61.64	111	
AD2041 × RH 30	39.12	11	
AD2041 × PR 45	29.41	H	MSL
AD2041 $\times$ Prakash	34.54	11	
PSMT 34 $\times$ Pusa Bold	46.41*	II	MSL,SB
PSMT 34 $\times$ Prakash	35.36	I	
DBS 10 $\times$ Pusa Bold	53.31*	111	PB,SB,S/SQ
DBS 10 $\times$ Prakash	38.12	1	MSL,SB
KBJ 3 × RH 30	37.50	П	MSL,SB
KBJ 3 × PR 45	30.59	111	MSL,SB
KBJ 3 × Prakash	50.42 <sup>*</sup>	Ш	PB,SB

\* and \*\* Significant at 5% and 1% level of significance

DC = Divergence classification, Heterosis = Better parent heterosis

According to this divergence classification the intermediate type of parental divergence (class DC II and DC III) are expected to yield maximum number of highly heterotic crosses. Out of total 22 top heterotic

crosses (Table 4) examined, 16 of these belonged to DC II and DC III. Similarly, Arunachalam and Bandyopadhyay [2] in rapeseed and groundnut, Anand and Rawat [4] in mustard, Prasad and Singh [5] in maize, Pal and Ghosh [6] and Ali *et al.* [7] in *B. napus,* reported that the magnitude of heterosis was higher with intermediate parental divergence.

Furthermore, Chauhan and Singh [8] also found that with increase of genetic divergence between parents, there was an increase in heterosis up to certain level, beyond which the heterosis for yield was partly cancelled due to negative heterosis for certain components. Therefore, this method of divergence classification appears to be effective in clubbing the genotypes for parental diversity and suggested that the magnitude of heterosis was higher with intermediate parental divergence.

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