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ASSESSMENT OF GENETIC DIVERSITY IN GENE POOL OF INDIAN MUSTARD [*BRASSICA JUNCEA* (L.) CZERN & COSS.]

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Abstract

A better understanding on the genetic diversity of Indian mustard is essential for the proper utilization of genotypes in crop improvement. Present study was carried out to determine the genetic diversity among 88 diverse genotypes of Indian mustard procured from CCS HAU Hisar, PAU Ludhiana, ICAR-IARI New Delhi and ICAR-DRMR Bharatpur which were grown in paired rows of 4 m length with a spacing of 45 x 15 cm (row × plant). Data were recorded on 11 different agronomic traits. Wide range of variation in agronomic parameters was observed such as seed yield per plant, number of secondary branches per plant, 1000-seed weight and number of primary branches per plant. Based on Manhattan dissimilarity coefficients, all the 88 genotypes were grouped into six distinct clusters. Among the six clusters, cluster VI and IV had the maximum number of genotypes (30 and 28 genotypes, respectively) and cluster II and cluster V with least number of genotypes (two genotypes in each cluster). The Manhattan dissimilarity coefficients ranged from 1.63 to 14.05. Based on the genetic dissimilarity matrix, the maximum dissimilarity (14.05) was observed between the genotypes, RH-0502 and M-7. Genotypes of cluster V had maximum mean values for seed yield per plant and 1000-seed weight. Cluster II recorded for medium maturity with maximum mean values for most of the agronomic traits. In the present endeavor, high genetic diversity among the genotypes were observed, which can be used in future breeding programmes for developing mustard cultivars and germplasm management purposes.

Key words: Indian mustard, descriptive analysis, genetic diversity and agronomic traits.

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is a natural amphidiploid (2n = 36) and third most important oilseed crop of the world after soybean and palm. It is grown in both tropical and subtropical countries, occupying large area among the oilseeds *Brassica* group. Naturally it is autogamous species, yet in this crop frequent out-crossing occurs which varies from 5-30% depending upon the environmental conditions and random variation of pollinating insects (Rakow and Woods, 1987). Oilseeds *brassica* occupied second position (25%) after soybean (38%) in share of total oilseeds production, however, stand first (23%) in edible oil production in the country (Jat *et al.,* 2019). Indian mustard is one of the important sources of edible oil in India and it contributes a major share in mustard production globally. India, predominantly import the refined edible oil from other nations with slight export. The condition will be more challenging with rising consumption up to 2030 with the projected population (Jat *et al.*, 2019). Therefore, to deal with the increased oil demand, there is an urgent need to boost the oil yield along with yield potential of rapeseed and mustard. To initiate a breeding programme primary emphasis is on diversity/variability present in existing gene pool. Genetic divergence evaluation for understanding breeding materials has substantial implications for the advancement of crop plants. In Indian mustard, information on genetic diversity could assist breeders and geneticists to understand the germplasm structure, predict right combinations to produce the best progenies (Vaishnava *et al.*, 2006; Hu *et al.*, 2007; Alie *et al.*, 2009; Singh *et al.*, 2010) and permit them to extend the genetic basis of breeding material (Qi *et al.*, 2008). The objective of present study was to assess the genetic diversity in Indian mustard to identify the extreme divergent parents, which may further be used for hybridization programme and ultimately to produce more divergent segregants. Heterosis may likely be produced by divergent parents making them suitable for hybrid development.

Materials and Methods

The present investigation was carried out on 88 Indian mustard genotypes developed/maintained by four different centers of India (CCS HAU Hisar, PAU Ludhiana, IARI New Delhi and DRMR Bharatpur) for this experiment. All 88 genotypes of Indian mustard were grown in paired rows of 4 m length with a spacing of 45 x 15 cm (row × plant) at Research Area of Oilseeds Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar during *rabi*, 2018-19. The description of genotypes has been given in Table 1. All the recommended package and practices were followed to raise the healthy crop. Observations were recorded on five random and competitive plants for eleven agronomic traits *viz;* days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliqua on main shoot, main shoot length (cm), siliqua length (cm), number of seeds per siliqua, seed yield per plant (g) and 1000-seed weight (g). Based on dissimilarity coefficients, a dendrogram was constructed on

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the basis of Manhattan dissimilarity coefficients using the unweighted pair group method with arithmetic mean with the help of DARwin 6.0 programme (Perrier and Jacquemoud-Collet, 2006). Principal Coordinate Analysis was performed to depict the dissimilarity among groups or individual genotypes using DARwin 6.0 programme.

Results and Discussion

Descriptive analysis indicates the presence of significant variation among the studied traits. Mean, range and coefficient of variation (CV) for all the 11 traits are presented in Table 2. Wide range of variation was observed for most of the traits like seed yield per plant (22.61%), number of secondary branches per plant (22.48%), 1000-seed weight (21.23%) and number of primary branches per plant (20.24%). Thus it indicates ample scope for mustard improvement through simple selection for different agronomic traits. The variability for days to 50% flowering and days to maturity was very low, it ranged from 33-60 and 131-150 days with an average of 41.55 and 141.88 days, respectively. EC-30-1, EJ-20, Heera, EC-29-9-1 and DRMRB-6 were recognized as medium early maturing genotypes (≤135days). Plant height ranged from 156.50 cm to 234 cm with an average value of 193.67 cm. Low plant height is desirable in mustard due to ease in agronomic practices hence genotypes RH-0502, M-187, DRMRB-12, M-3 and EJ-20 may be used as donor parents for this trait. Number of primary branches per plant varied from 3.0 to 9.75 with an average of 5.36 while, number of secondary branches per plant ranged from 5.0 to 17.75 with an average value of 11.44. The genotypes *viz;* EC-61-67-1, M-108 and RH-1512 can be used as source lines for both traits *i.e.* number of primary branches per plant as well as number of secondary branches per plant. Main shoot length is recognized as the most important fruiting zone in Indian mustard. Hence, its length and number of siliqua on main shoot are desirable traits for enhancing seed potential. In this study, main shoot length varied from 51.50 to 89.75 cm, while number of siliqua on main shoot ranged from 32.00 to 68.50.

Four genotypes *viz.* DRMRB-14, RH-401 B, DRMRB-10 and EC-308575 had more than 85 cm long main shoot along with maximum number of siliqua (>55) on main shoot. Number of seeds per siliqua ranged from 7.80 to 16.80. The variability for seed yield per plant was high; it varied from 8.50 g to 31.75 g with an average of 19.93 g. Six genotypes *viz.,* M-183, RH-406, RH-1512, EC-30-1, RH-749 and DRMRB-19 had more than 26.00 g seed yield per plant, on other hand 13 genotypes had 1000-seed weight more than 6.0 g. Such results are in concurrence with the results of Singh *et al.,* 2013. None of the genotypes was found to be most promising collectively for all the agronomic traits. However, some genotypes could be recognized as promising for different traits (Table 3). Based upon multiple trait superiority, four ideal genotypes identified in this study were DRMRB-8 (medium maturity, more number of primary branches per plant, long main shoot length, more siliqua on main shoot and more seeds/ siliqua), EC-29-9-1 (medium maturity, medium dwarf plant stature and more number of secondary branches per plant), RH-401 B (long main shoot length, more number of siliqua on main shoot, siliqua length and higher seed yield) and DRMRB-14 (medium maturity, long main shoot length, more number of siliqua on main shoot and higher seed yield).

Degree of relatedness among individuals in a population can be measured by genetic distance (Garcia *et al.,* 2004) and genetic improved by breeding method can be achieved by this (Liu *et al.,* 2019). In 88 genotypes of Indian mustard genetic divergence analysis was performed using Manhattan dissimilarity coefficients for all 11 agronomic traits. Genetic diversity results showed sufficient dissimilarity characteristics and reflected significant genetic diversity among Indian mustard genotypes. Such significant genetic variation has also been reported by Alie *et al.* (2009); Singh *et al.* (2010) on metric traits in Indian mustard. All the 88 genotypes of Indian mustard were grouped into six diverse clusters based on Manhattan dissimilarity coefficients and categorized these genotypes on the basis of 11 agronomic characters (Figure 1). Genetic diversity was estimated among 44 genotypes of Indian mustard using Manhattan methods resulting four clusters (Vinu *et al.*, 2013; Sheikh, 2011). Mahmud *et al*. (2008) and Nath *et al*. (2003) reported four & five clusters in *Brassica* species, respectively. Mean value of different clusters for 11 agronomic traits is presented in Table 4. The cluster I includes 17 genotypes developed/maintained by all four centre *viz.,* ICAR-DRMR, Bharatpur (Rajasthan), PAU, Ludhiana (Punjab), HAU, Hisar (Haryana) and ICAR-IARI (New Delhi). The genotypes of this cluster were considered as long main shoots (83.79 cm) and more number of siliqua on main shoot (53.24). In mustard, main shoot length is measured as the most important fruiting zone. Hence, its length and number of siliquae on main shoot are desirable traits for increasing seed yield. The genotypes of this cluster may be used as donor parents for these traits. The second cluster had only 2 genotypes developed/maintained at ICAR-DRMR, Bharatpur and ICAR-IARI, New Delhi.

These genotypes were good performer for most of the traits possessing medium maturity (134 days), more number of primary branches per plant (5.75), more number of secondary branches per plant (13.38), long siliqua length (4.58 cm), more number of seeds per siliqua (15.23) along with higher seed yield per plant (22.90 g) and 1000-seed weight (5.08 g). Nine genotypes were grouped in cluster III. Genotypes of this cluster belong mainly to three centers *viz*., ICAR-DRMR, Bharatpur, ICAR-IARI, New Delhi and HAU Hisar. These genotypes were average performer for most of the characters possessing average seed yield, average 1000-seed weight and average number of seeds per siliqua etc. The fourth cluster comprised of 28 genotypes from all the four centers. The genotypes of this cluster were considered for medium maturity (139 days) and medium dwarf plant height stature. Dwarf plant stature is considered as desirable trait due to ease in carrying out agronomic practices; hence genotypes of cluster IV may be used as donor for this trait. Such results are in concurrence with the results of Singh *et al.* (2013). The cluster V had only two genotypes developed at HAU, Hisar and PAU, Ludhiana. These genotypes had more number of secondary branches per plant (12.63), long main shoots (75.50 cm) along with higher seed yield per plant (23.63 g) and 1000-seed weight (5.12 g). Thirty genotypes were grouped in cluster VI which randomly belonged to all four

centers. These genotypes had poor to moderate estimates for most of the traits with more number of primary branches per plant (5.64). In earlier study, Gohel and Mehta (2014); Anushree and Pandey (2017); Chandra *et al.* (2018) reported similar trend of genetic diversity in some oilseed rape genotypes. None of the cluster/genotypes was found to be most promising collectively for all the agronomic traits.

The Manhattan dissimilarity coefficients ranged from 1.63 to 14.05 indicating the diverse nature of genotypes under study. Based on the genetic dissimilarity matrix, the maximum dissimilarity (14.05) was observed between the genotypes, M-7 & RH -0502. On the other hand, a minimum dissimilarity value of 1.63 was found between genotypes, M-167 & DRMRB-2 which was followed by 1.65, between DRMRB-15 & Pusa Mehak; DRMRB-5 & M-167 and 1.67, between RH-222 & EC-61-6-1; DRMRB-1 & Pusha Bahar. The genotype, M-7 was found to be the most diverse as it exhibited the highest dissimilarity coefficient values with most of the genotypes *viz*. RH-0502 (14.05); M-3 (13.66); EJ-20 (13.53); M-187 (13.39) and DRMRB-12 (13.12) etc. These diverse genotypes can be used efficiently in the mustard breeding programme for selection of some desirable recombinants. So, the obtained results confirmed that the use of diversity analysis is a good tool to determine the phenotypic differences among the genotypes, which agrees with the results of Crossa & Cornelius (1997); Marijanovic-Jeromela *et al.* (2009). Similar results concerning the genetic diversity for yield and its component traits have also been reported by Singh *et al.* (2013); Vinu *et al.* (2013); Chandra *et al.* (2018).

Principal Coordinate Analysis (PCoA) was drawn up for comparison to the dendrogram. The two-dimensional PCoA can be divided into four quadrants (Q), as indicated in Figure 2. There is a strong tendency for the PCoA to show the same trends with clustering of genotypes as in the dendrogram. The following similarities were observed between the dendrogram and the PCoA: Most of the genotypes which found in cluster-I could be found in Q-II and Q-III near to axis. Genotypes of cluster II were set up near to center in Q-II. All the genotypes which found in cluster III were set up near to center in Q-I with some in the Q-IV. Genotypes of cluster IV were found closely together in Q-I and Q-II, near to end point of axis. RH-725 and M-178 were found near to center in Q-III. All the genotypes which found in cluster VI were found in Q-III and Q-IV. It is important to note that majority of genotypes were grouped closely together at center in quadrant. Vinu *et al.* (2013) also used PCoA to delineate and visualize 44 Indian mustard genotypes into four clusters.

Conclusion

To conclude the results, genetic diversity of Indian mustard genotypes has been studied on the basis of 11 different agronomic traits. Wide range of genetic variation has been observed for different traits based upon this analysis. The genotypes of cluster II and V may be used as donor parents for main shoot length, number of siliqua on main shoot, number of primary branches per plant, seed yield per plant and 1000-seed weight. M-7 was found to be the most diverse genotype as it showed the highest dissimilarity coefficient values with most of the genotypes. This outcome will form a major criterion for selection of genetic materials with great diversity for breeding programs, particularly to increase the germplasm base of the mustard improvement programme.

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Table 2: Mean, range and coefficient of variation (CV %) for 11 different traits in Indian mustard

Characters	Minimum	Maximum	Mean	CV (%)
Days to 50% flowering	33.00	60.00	41.55	14.07
Days to maturity	131.00	150.00	141.88	3.15
Plant height (cm)	156.50	234.00	193.67	8.81
Number of primary branches	3.00	9.75	5.36	20.24
Number of secondary branches	5.00	17.75	11.44	22.48
Main shoot length (cm)	51.50	89.75	72.35	12.22
Number of siliqua on main shoot	32.00	68.50	46.33	15.89
Siliqua length (cm)	3.10	5.30	4.08	12.80
Seeds per siliqua	7.80	16.80	12.41	15.49
Seed yield (g)	8.50	31.75	19.93	22.61
1000-seed weight (g)	2.44	6.68	4.74	21.23

Table 1: List of 88 genotypes of Indian mustard used in present study

S. No.	Genotypes	Source Centre	S. No.	Genotypes	Source Centre	S. No.	Genotypes	Source Centre	S. No.	Genotypes	Source Centre
1	DRMRB 1	DRMR	**23**	NPJ 124	IARI	**45**	EC 62-67-1	IARI	**67**	RH-1515	HAU
2	DRMRB 2	DRMR	**24**	NPJ 113	IARI	**46**	RH-115	HAU	**68**	RH-1509	HAU
3	DRMRB 3	DRMR	**25**	NRCDR -02	IARI	**47**	RH-0121	HAU	**69**	M 7	PAU
4	DRMRB 4	DRMR	**26**	EJ 20	IARI	**48**	RH-222	HAU	**70**	M 12	PAU
5	DRMRB 5	DRMR	**27**	NPJ 156	IARI	**49**	RH-401B	HAU	**71**	M 10	PAU
6	DRMRB 6	DRMR	**28**	MST- II-14-32	IARI	**50**	RH-406	HAU	**72**	M 3	PAU
7	DRMRB 7	DRMR	**29**	Bio YSR	IARI	**51**	RH-502	HAU	**73**	M 179	PAU
8	DRMRB 8	DRMR	**30**	Heera	IARI	**52**	RH-8701	HAU	**74**	M 156	PAU
9	DRMRB 9	DRMR	**31**	NON waxy Mutant	IARI	**53**	RH-119	HAU	**75**	M 167	PAU
10	DRMRB 10	DRMR	**32**	EC 308575	IARI	**54**	RH-749	HAU	**76**	M 82	PAU
11	DRMRB 11	DRMR	**33**	EC 27-21	IARI	**55**	CS-52	HAU	**77**	M 183	PAU
12	DRMRB 12	DRMR	**34**	EC 27-9	IARI	**56**	RB-50	HAU	**78**	M 40	PAU
13	DRMRB 13	DRMR	**35**	EC 28-1	IARI	**57**	RH-305-1	HAU	**79**	M 198	PAU
14	DRMRB 14	DRMR	**36**	EC 28-18	IARI	**58**	RH-555	HAU	**80**	M 4	PAU
15	DRMRB 15	DRMR	**37**	EC 29-9-1	IARI	**59**	RH-630	HAU	**81**	M 27	PAU
16	DRMRB 16	DRMR	**38**	EC 29-5-4-2	IARI	**60**	RH-832	HAU	**82**	M 187	PAU
17	DRMRB 17	DRMR	**39**	EC 30-1	IARI	**61**	RH-923	HAU	**83**	M 178	PAU
18	DRMRB 18	DRMR	**40**	EC 61-6-1	IARI	**62**	RH-1475	HAU	**84**	M 21	PAU
19	DRMRB 19	DRMR	**41**	EC 61-42-1	IARI	**63**	RH-1490	HAU	**85**	M 17	PAU
20	DRMRB 20	DRMR	**42**	CE 61-52-1	IARI	**64**	RH-725	HAU	**86**	M 108	PAU
21	Pusa Bahar	IARI	**43**	EC 61-67-1	IARI	**65**	RH-501	HAU	**87**	M 146	PAU
22	Pusa Mehak	IARI	**44**	EC 62-46-1	IARI	**66**	RH-1512	HAU	**88**	M 160	PAU

Table 3: List of promising genotypes of Indian mustard for different traits

Characters	No. of genotypes	Name of genotypes
Days to 50% flowering (≤36 days)	14	EC-61-67-1, EC-62-42-1, DRMRB-12, M-187, EC-29-9-1 DRMRB-5, EC-28-1, DRMRB-2, NPJ-124, DRMRB-8, EC-61-6-1, DRMRB-18, DRMRB-14 and M-183
Days to maturity (≤136 days)	10	EC-30-1, EJ-20, Heera, EC-29-9-1, DRMRB-6, RH-222, Pusa Mehak, NPJ-124, NPJ-156 and EC-29-5-4-2
Plant height (<175 cm)	12	RH -0502, M-187, DRMRB-12, M-3, EJ-20, EC-61-67-1, DRMRB-16, EC-29-9-1, DRMRB-7, DRMRB-2, EC-62-42-1 and M-4
Number of primary branches (>7)	7	M-7, DRMRB-8, EC-62-67-1, RH-832, M-108, M-12 and RB-50
Number of secondary branches (>15)	10	EC-29-9-1, EC-61-67-1, EJ-20, M-10, M-108, EC-30-1, M-82, RH-1512, RH-1509 and EC-62-42-1
Main shoot length (>85 cm)	8	M-82, DRMRB-14, RH-401 B, DRMRB-8, DRMRB-10, EC-308575, DRMRB-18 and RH-8701
Number of siliqua on main shoot (>55)	13	DRMRB-10, DRMRB-8, EC-308575, DRMRB-19, DRMRB-14, RH -1490, DRMRB-3, RH-501, MST-11-14-32, M-146, RH-401 B, M-21 and CS-52
Siliqua length (≥5 cm)	7	RH-0305-1, RH-749, NPJ-124, DRMRB-2, RH-501, DRMRB-4 and MST-11-14-32
Seeds per siliqua (>15)	7	DRMRB-15, DRMRB-19, RH-1512, DRMRB-4, M-187, EC-28-18 and DRMRB-8
Seed yield (>25.50 g)	10	M-183, RH-406, RH-1512, EC-30-1, RH-749, DRMRB-19, DRMRB-14, MST-11-14-32, RH-401 B and EC-29-5-4-2
1000-seed weight (>6.0 g)	13	RH-1515, RH-0305-1, RH-1509, DRMRB-5, RH-501, M-146, M-156, M-198, RH-725, M-167, RH-555, DRMRB-12 and EC-30-1

Table 4: Mean performance of different clusters based upon eleven agronomic traits

Genotype	No. of genotypes	DF	DM	PH	PBr	SBr	MSL	SqMs	SqL	S/Sq	SY	TW
C-I	17	39.06	141.35	193.31	5.07	11.44	83.79	53.24	3.98	12.09	20.74	4.41
C-II	2	38.50	134.00	197.25	5.75	13.38	68.53	48.38	4.58	15.23	22.90	5.08
C-III	9	38.56	141.33	195.03	5.39	11.98	62.86	38.78	4.25	13.48	21.92	4.76
C-IV	28	38.46	139.75	174.83	5.20	11.43	70.44	44.38	3.95	12.08	19.56	4.70
C_V	2	45.00	145.00	190.25	5.13	12.63	76.50	44.88	4.28	12.68	23.63	5.12
C VI	30	46.70	144.63	211.05	5.64	11.09	70.46	46.45	4.16	12.38	18.79	4.89

Note: DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), PBr = Primary branches per plant, SBr = Secondary branches per plant, MSL = Main shoot length (cm), SqMs = Siliqua on main shoot, SqL = Siliqua length (cm), S/Sq = Seeds per siliqua, SY = Seed yield (g) and TW = 1000-seed weight (g).

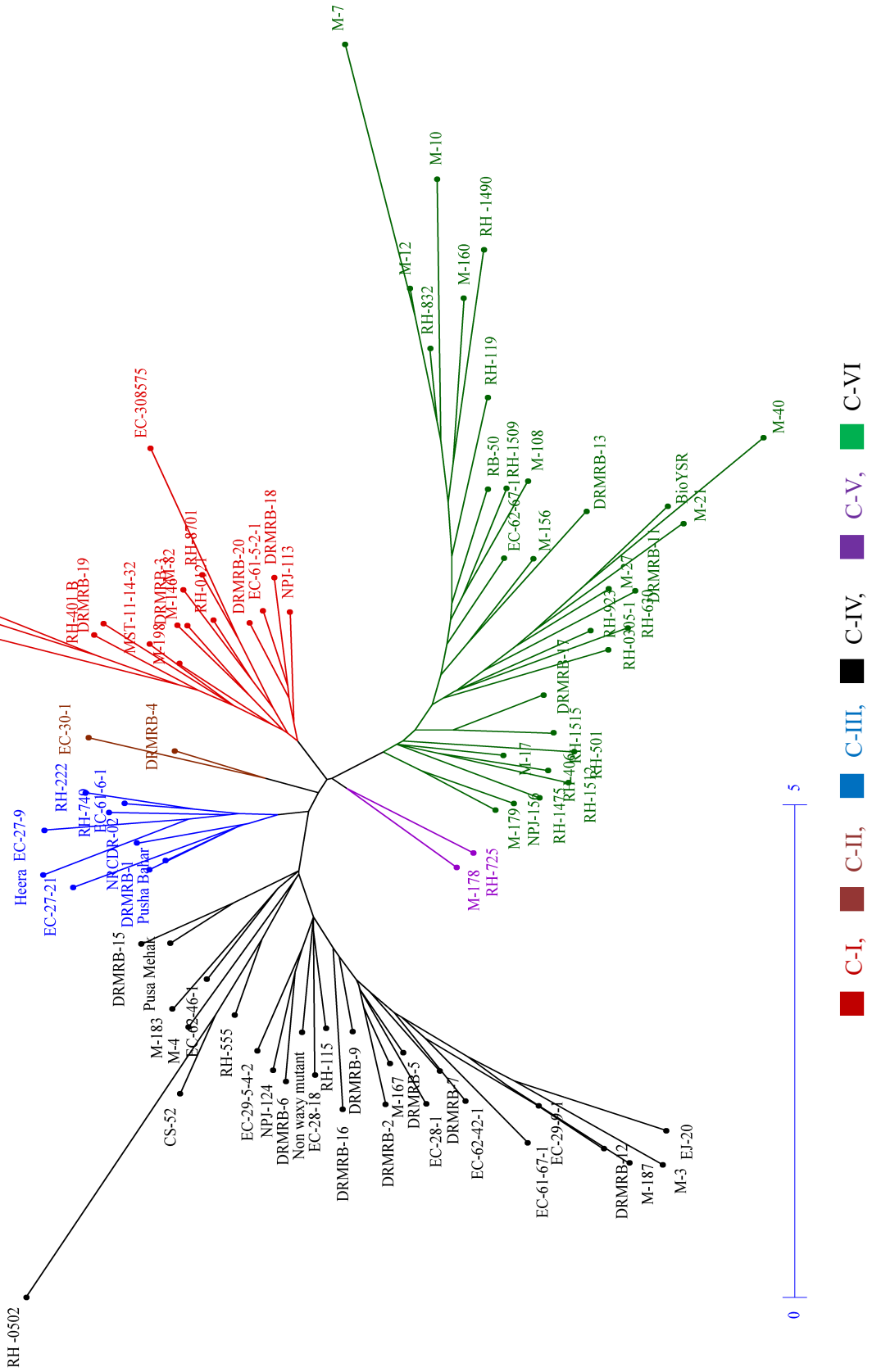

Figure 1: Dendrogram based on Manhattan dissimilarity coefficients representing relationship among 88 genotypes of Indian mustard

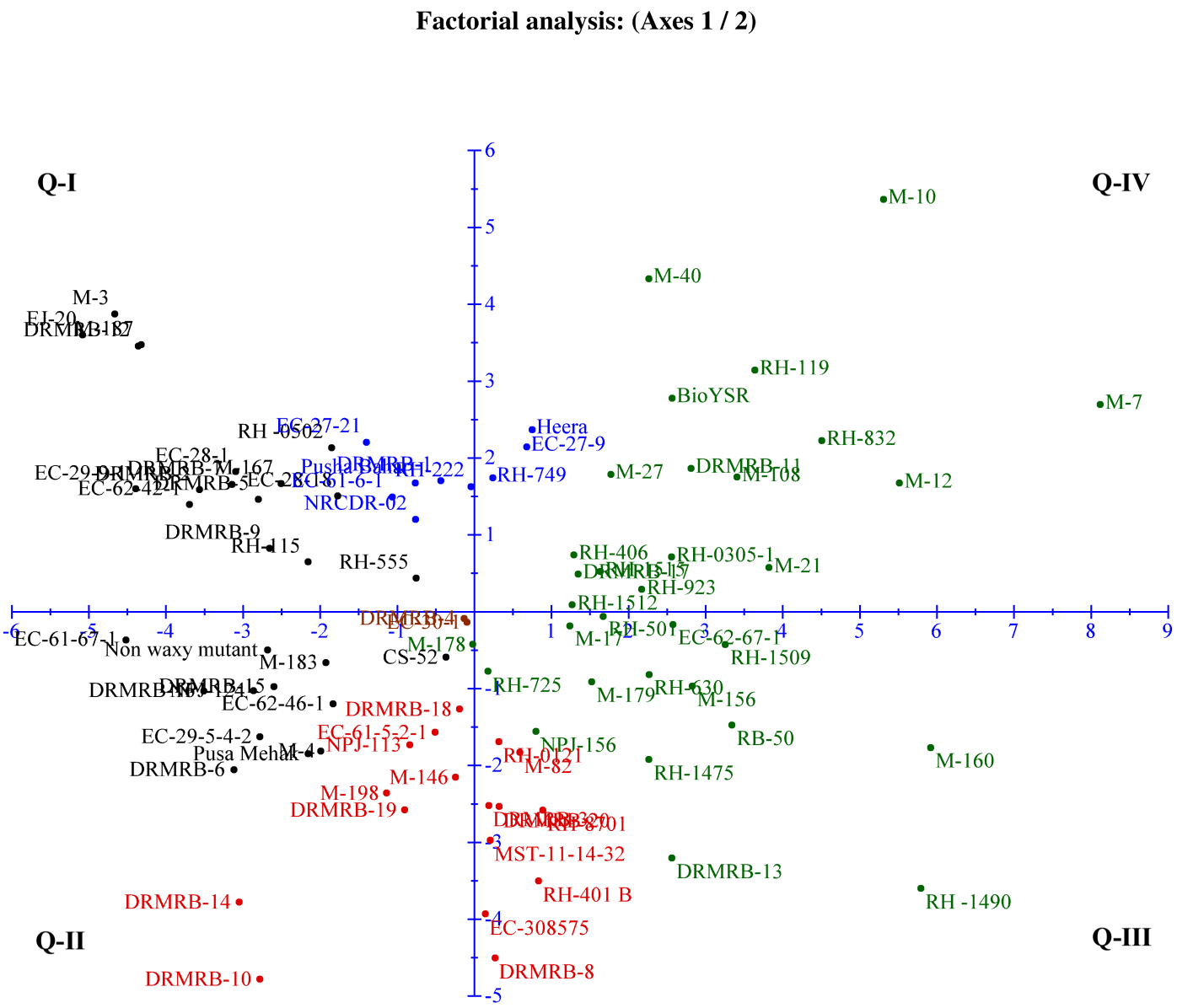

Figure 2: Scatter diagram of 88 genotypes of Indian mustard based on principal coordinates analysis superimposed with clustering