Crop Improvement Programme Making Essential to Know the Spectrum of Diversity in any Crop System

Oil seed *Brassicas*, with predominantly cultivated Indian mustard (*B. juncea* L. Czern and Coss) have major share in edible oil economy of Bihar, offering potential option for diversifying the predominant Rice-Wheat system (*Khachatourians et al., 2004*) and grown mainly as rainfed / irrigated situations under early, timely and late sown agro-ecologies. The extent of variability and diversity available decides the success of crop improvement programme making essential to know the spectrum of diversity in any crop system.
species and parents based on genetic divergence (Ashana and Pandey, 1980; Ananda and Rawat, 1984). Genetic variability in respect to genetic diversity is the prerequisite for the crop improvement through selection of high yielding progenies. The quantification of genetic diversity by biometrical approaches can help choose diverse parents for a successful hybridization programme, as hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains (Singh, 1986) and also provides opportunity to obtain the desirable recombinations in the segregating generations (Uddin and Chowdhury, 1994) and could be utilized in transgressive breeding. Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991).

Therefore, the present investigation was carried out to determine the divergence among 50 different genotypes of rapeseed mustard.

**Materials and Methods**

The experiment consisting of 50 Indian mustard genotypes, including four checks namely, Pusa Mahak (Zonal Check), Varuna (National Check), Pusa Bold (National Check) and Rajendra Suphlam (Local Check) for divergence study, received from different All India Co-ordinated Research Project Project-Rapeseed and Mustard centres: DRMR, Bharatpur, Rajasthan, CCSHAU, Hisar, Haryana, BARC, Trombay, Maharashtra, GBPUAT, Pantnagar, Uttarkhand, CSAUAT, Kanpur, U. P, IARI, NewDelhi, ARS, RAU, Sriganganagar, Rajasthan, DR. RPCAU, Dholi, Bihar, NDUAT, Faizabad, U. P and BAU, Kanke, Ranchi, Jharkhand, was laid out in Randomized Complete Block Design (RCBD) with three replications during **Rabi** season (2015-16) and was planted on 10th October 2015 under rainfed condition providing only basal dose of fertilizers i. e. N: P₂O₅: K₂O: S:: 40: 40: 40 kg/ha under residual moisture conditions after the harvest of preceding medium early (110-115 days) paddy cv., Rajendra Bhagwati. At the research farm of Tirhut College of Agriculture, Dholi, Muzaffarpur (Dr. Rajendra Prasad Central Agricultural University, Pusa), Bihar (25. 5° N, 85. 4°E and 52. 12 m MSL) in Loam soil (8. 4 pH). Each plot was consisted four rows of 5. 0 m length keeping row to row and plant to plant distance 30cm and 10cm, respectively. The spacing between plants was maintained at 10cm by thinning at 14 DAS.

Meteorological data (**Kharif** and **Rabi** 2015-16) reflected that the experiment was sown, on residual moisture condition, as the preceding **Kharif** crop rice has received 697. 20 mm rainfall distributed in 25 rainy days between June to September (23rd to 38th meteorological weeks 2015). After that experiment at all its phenological stages of Indian mustard crop has not received any rainfall.

The observations were recorded for days to first flower open, days to 50% flowering, days to physiological maturity, primary branches plant⁻¹, secondary branches plant⁻¹, number of siliqua plant⁻¹, length of siliqua, stem girth, internode length, height of the plant, number of siliqua on primary mother axis, height of first primary branch, height of first siliqua, angle of branch, angle of siliqua, number of seeds siliqua⁻¹, root volume, root length, root girth, 1000 seed weight, biological yield, harvest index, oil content and dry matter efficiency and grain yield /plant. The data were recorded on five randomly selected plants from each genotype in each replication leaving the border rows to avoid the sampling error. The observations were recorded using standard methodology. Readings from five plants were averaged replication-wise and the mean data was subjected statistical analyse for yield and its attributing traits.
Amongst various classificatory analyses, utilized to understand workable variability, $D^2$ statistic (Mahalonobis, 1928, 1935) using Tocher method (Tocher Rao, 1952) and Euclidean method (Rao, 1952) based on wards’ minimum variance dendogram are successfully utilized by various crop breeders for clustering and quantitative measurement of divergence among the genotypes (varieties, strains, mutants, ECs, ICs, etc.) Mahalanobis (1936) $D^2$ statistic was used for assessing genetic divergence among the test entries. The clustering of $D^2$ values was formed by using generalized distance based- Tocher’s method as described by Rao (1952) and also by using Non- hierarchical Euclidean cluster analysis (Beale, 1969; Katyal et al., 1985) was conducted using computer package (Windostat version 8.5) whereas the formula given by Singh and Choudhary (1977) was utilized for the calculation of intra and inter – cluster distances.

**Results and Discussion**

The analysis of variance revealed highly significant differences among the genotypes for all the 25 traits under study, reflecting presence of considerable variability and genetic worth of the genotypes. Thus, providing adequate scope for selection of superior genotypes aimed at utilizing exploitable variability for enhancing genetic yield potential under rainfed condition of *Brassica juncea*.

50 Indian mustard genotypes, based on tocher method were grouped in eight different clusters (Table 1). Highest number of genotypes (24) were accommodated in cluster I followed by cluster III (11), cluster II (8), cluster III (3) whereas clusters IV, VI, VII and VIII were oligo-genotypic. Such grouping of genotypes into clusters by Tochers method are based on generalized distance which is statistic related to the coefficient of racial likeliness developed by Mahalanobis (1936) and Rao (1952). More precise clustering method is non-hierarchical Euclidean method (based on Wards minimum variance dendogram) which more critically identifies sub clusters of the main groups at different levels, thus offering additional opportunity to crop breeders, in more critically planning the hybridization programme, using diverse parents aimed at genetic enhancement of any crop species, including crop *Brassicas*. Euclidean method also accommodated these genotypes in eight different clusters (Table 2) but the genotypes in the clusters, instead of generalized distance used in Tocher method the relative association among the different genotypes is presented in the form of wards minimum variance dendogram, which was prepared using rescaled distance in Euclidean method.

Brassica scientists have utilized these approaches based on generalized distance (Tocher method) and more precisely on rescaled distance (Euclidean method) for selecting diverse potential lines and subsequent utilization, there off, in hybridization – selection breeding program. Highest number of genotypes were in cluster II (14) followed by cluster III (9), cluster V (8), cluster I (6), cluster VI (5), cluster IV (4), cluster VII (3) and cluster VIII which was oligo-genotypic. From both the methods of clustering only rewardive genotype in oligo-genotypic cluster was Rajendra Suphlam (VIII in both Euclidean and Tocher method). Among 50 studied, the only dissimilar genotype, namely Rajendra Suphlam have exhibited diversity might be due to geographical uniqueness of this genotype than others.

It is very clear from the perusal of clustering pattern of 50 genotypes by Euclidean and Tocher method that three genotypes, namely Varuna (in mono-genotypic cluster VI) and
Pusa Bold (V) by Tocher method (fence-sitter genotypes) accommodated in one cluster (VII) in Euclidean method with Pusa Mahak forming sub cluster (among Pusa Bold and Varuna) with main group of three genotypes. This is also noteworthy that cluster VII (Euclidean method) exhibited maximum intra-cluster distance. Similarly fence-sitter genotypes RGN-13, Divya, TM-2 (III by Tocher method) accommodated with oligo-genotype (RH-0116 by Tocher method) in cluster IV (all four genotypes) by Euclidean method. Largest cluster I with 24 genotypes in Tocher method whereas 14 genotypes in cluster II of Euclidean method. Cluster I of Tocher method rescaled and placed 6, 14 and 4 fence-sitter genotypes wholly in Euclidean cluster I and II and partly in III cluster, respectively. The two sub-clusters exhibited similarity between RH-0406 and RGN-13; and between Divya and TM-2 thus more precisely explaining the diversity of the genotypes studied using Euclidean method which could be utilized for diverse parents selection process.

Maximum inter-cluster distance between cluster V and VIII (5970.024) followed by IV and VIII (5742.101) and II and VIII (4549.622) from Euclidean method exhibiting 7, 3 and 14, altogether 24 crosses (Table 3) respectively. Whereas, between cluster III and VIII (1985.184) followed by IV and VIII (1739.174), I and VIII (1411.921), III and VIII (1182.809) and IV and VIII (1079.075) with 6, 1, 5, 6 and 1, altogether 19 divergent crosses (Table 4) respectively from Tocher method reflected that crosses involving genotypes from these cluster will be beneficial from Tocher method, in general whereas Euclidean method, in particular. Thus, hybridization programme, shall be formulated in such a way that the parents belonging to clusters with maximum divergence could be utilized in heterosis breeding and could throw transgressive segregants in F₂ generation. Such genotypes may be chosen from widely separated clusters (Fig. 1 and 2), for crossing programme to get benefits in desirable directions as per breeding objectives. There was no parallelism between genetic diversity and their geographic distributions as the genotypes from one or other geographical regions were grouped together in same cluster and developed from same organization were placed in different clusters might be due to free exchange of genetic materials between clusters and regions and also the number of studied traits and parentage/methodology (For Example induced mutagenesis) involved highly influenced group constellation of 50 genotypes Similar results were observed by Khan (2000), Kumar et al., (2000 a) and Kumar et al., (2000 b).

On comparing generalized distance based Tocher method and precise rescaled sub-cluster forming Euclidean method (Table 6) 19 promising divergent crosses suggested. Among these crosses as one of the parent the only common oligo-genotypic cluster VIII with Rajendra Suflam proved its uniqueness whereas Pusa Mahak (oligognotypic in cluster VII Tocher method) and cluster VII (along with two other genotypes Varuna and PusaBold in Euclidean method) were most divergent and the crosses based on inter-cluster distance involving these genotypes could give heterotic combination for enhancement of yield; and in F₂ generations could throw usefully desirable transgressive segregants for rainfed Indian mustard genetic enhancement. Three diverse genotypes, RH0406, Pusa Mahak and Rajendra Suflam superior based on both method can be utilized as testers and crossed with 7 divergent genotypes as lines (Divya, TM-2, RH0116, PM-25, Kanti, Rohini and RGN-13) based on both Tocher and Euclidean method which can be further utilized in hybridization selection breeding programme to get most useful segregants.
Table 1 Clustering pattern of 50 genotypes of Indian mustard genotypes on the basis of Tocher method

| Cluster No. | Intra cluster distance | No. of Genotypes within cluster | Genotypes in cluster |
|------------|------------------------|--------------------------------|----------------------|
| I          | 21.469                 | 24                             | NDRE-7, PKRS-28, PM-28 (NPJ-124), KMR10-2, PusaTarak (EJ9913), TM-215, RAURD-212, PM-27, RH-8812, RAURD (E)-1001, PantRai, PusaBahar, TPM-1, RH-30, Kranti, PusaAgrani (SEJ-2), NDRE-4, NRC-DR-2, Krishna, TM-4, Basanti, Shivani, RAURD-78, BAUM08-57, |
| II         | 25.408                 | 8                              | DRMRLEJ902, RH-8814, TPM-128, Maya, TM-151, KMR10-1, BAUM08-56, DRMR150-35 |
| III        | 37.321                 | 11                             | RGN-13, Divya, TM-2, RH-0116, PM-25, Kanti, Rohini, RAURD (E)-1002, RH-0701, RAURD-214, RGN-48 |
| IV         | 0.000                  | 1                              | RH-0406 |
| V          | 32.277                 | 3                              | RH-8701, RH-0819, Pusa Bold |
| VI         | 0.000                  | 1                              | Varuna |
| VII        | 0.000                  | 1                              | Pusa Mahak (JD-6) |
| VIII       | 0.000                  | 1                              | Rajendra Suphlam |

Table 2 Clustering pattern of 50 genotypes of Indian mustard genotypes on the basis of non–hierarchical Euclidean method

| Cluster No. | Intra cluster distance | No. of Genotypes within cluster | Genotypes in cluster |
|------------|------------------------|--------------------------------|----------------------|
| I          | 31.609                 | 6                              | NDRE-7, PKRS-28, PM-28 (NPJ-124), KMR10-2, PusaTarak (EJ9913), TM215 |
| II         | 26.671                 | 14                             | RAURD-212, PM-27, RH-8812, RAURD (E)-1001, PantRai, PusaBahar, TPM-1, RH-30, Kranti, PusaAgrani (SEJ-2), NDRE-4, NRC-DR-2, Krishna, TM-4 |
| III        | 48.775                 | 9                              | DRMRLEJ902, RH-8814, KMR10-1, BAUM08-56, TPM-128, Basanti, Shivani, RAURD-78, BAUM08-57 |
| IV         | 56.081                 | 4                              | RH-0406, RGN-13, DIVYA, TM-2 |
| V          | 53.913                 | 8                              | RH-0116, PM25, Kanti, Rohini, RAURD (E)-1002, RH-0701, RAURD-214, RGN-48 |
| VI         | 80.649                 | 5                              | TM-151, Maya, DRMR150-35, RH-8701, RH-0819 |
| VII        | 219.294                | 3                              | Varuna, PusaBold, Pusa Mahak (JD-6) |
| VIII       | 0.000                  | 1                              | Rajendra Suphlam |

Table 3 Suitable divergent genotypes based on inter cluster distances in Tochers method

| SNO. | INTER CLUSTER DISTANCE | CLUSTERS | DIVERGENT GENOTYPES | NUMBER OF CROSSES |
|------|------------------------|----------|---------------------|-------------------|
| 1    | 1985.184               | III      | Divya, TM-2, RH-0116, PM-25, Kanti, Rohini | 6 |
|      |                        | VIII     | Rajendra Suphlam    |                   |
| 2    | 1739.174               | IV (O)   | RH-0406             | 1                 |
|      |                        | VIII     | Rajendra Suphlam    |                   |
| 3    | 1411.921               | I        | RAURD-212, PM-27, RH-8812, RH-30, Kranti | 5 |
|      |                        | VIII     | Rajendra Suphlam    |                   |
| 4    | 1182.809               | III      | Divya, TM-2, RH-0116, PM-25, Kanti, Rohini | 6 |
|      |                        | VII      | Pusa Mahak          |                   |
| 5    | 1079.075               | IV (O)   | RH-0406             | 1                 |
|      |                        | VII      | Pusa Mahak          |                   |
| TOTAL|                        |          |                     | 19                |
### Table 4: Suitable divergent genotypes based on inter cluster distances in Euclidean method

| SNO. | INTER CLUSTER DISTANCE | CLUSTERS | DIVERGENT GENOTYPES | NUMBER OF CROSSES |
|------|-------------------------|----------|---------------------|------------------|
| 1    | 5970. 024               | V        | RH-0116, PM-25, RGN-48, RH-0701, RAURD (E) -1002, Kanti, Rohini | 7                |
|      | VIII (O)                |          | Rajendra Suphlam    |                  |
| 2    | 5742. 101               | IV       | RHB4056, RGN-13, Divya, TM-2 | 4                |
|      | VIII (O)                |          | Rajendra Suphlam    |                  |
| 3    | 4549. 622               | II       | RAURD-212, PM-27, RH-8812, RAURD (E) -1001, Punt Rai, Pusa Bahar, TPM-1, RH-30, Kanti, Pusa Agrani (SU-2), NDRE-4, NRC-DR-2, Krishna, TM-4 | 14               |
|      | VIII (O)                |          | Rajendra Suphlam    |                  |
| 4    | 3981. 891               | I        | NDRE-7, PKRS-28, PM-28 (NPJ-124), KM R10-2, Pusa Tarak (E59913), TM-215 | 6                |
|      | VIII (O)                |          | Rajendra Suphlam    |                  |
| 5    | 3270. 975               | III      | DRMRL3J0902, RH-8814, KMR10-1, BAUM08-56, TPM-128, Basanti, Shivani, RAURD-78, BAUM08-57 | 9                |
|      | VIII (O)                |          | Rajendra Suphlam    |                  |
| 6    | 2768. 430               | IV       | RH-0406, RGN-13, Divya, TM-2 | 9                |
|      | VIII                   |          | Varuna, Pusa Bold, Pusa Mahak |                  |
| 7    | 2764. 117               | V        | RH-0116, PM-25, RGN-48, RH-0701, RAURD (E) -1002, Kanti, Rohini | 24               |
|      | VII                    |          | Varuna, Pusa Bold, Pusa Mahak |                  |

**TOTAL**

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### Table 5: Comparisons of Diverse *Brassica juncea* genotypes based on genetic distance, cluster mean and superior *per se* performance for earliness, oil content and seed yield component traits. (Tocher's and Euclidean method)

| S. N. | Characters | Cluster | Suitable Parents | Cluster | Suitable Parents | Common Parents | *per se* Performance |
|-------|------------|---------|------------------|---------|------------------|----------------|----------------------|
| 1     | Days to First Flower Open | Early VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (35. 67**) |
| 2     | Days to 50% flowering | Early VIII | Pusa Mahak, Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (95. 00**) |
| 3     | Days to physiological maturity | Early VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (123. 33**) |
| 4     | Primary branches plant | VII | Pusa Mahak | VIII | Rajendra suphlam | - |
| 5     | Secondary branches plant | VII | Pusa Mahak | VIII | Rajendra suphlam | - |
| 6     | Number of siliqua plant | VII | Pusa Mahak | VIII | Rajendra suphlam | - |
| 7     | Length of siliqua | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (6. 33**) |
| 8     | Stem girth | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (8. 40**) |
| 9     | Internode length | Low | Divya, Kanti, PM-25, Rohini, TM-2 | V | RH-0116, PM-25, Kanti, RGN-48, RAURD (E) -1002 | Kanti (7. 73) |
| 10    | Height of the plant | Tall | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (243. 73**) |
| 11    | Number of siliqua on primary mother axis | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (65. 67**) |
| 12    | Height of first primary branch Non-basal branching | VII | Pusa Mahak | V | RH-0116, PM-25, Kanti, RGN-48, RAURD (E) -1002 | Kanti (93. 60) |
| 13    | Height of first siliqua High position | VII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (9. 93**) |
| 14    | Angle of branch Compact | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (35. 67) |
| 15    | Angle of siliqua Semi-apressed | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (13. 33) |
| 16    | Number of seeds siliqua | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (12. 67**) |
| 17    | Root volume | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (35. 23**) |
| 18    | Root length | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (24. 56**) |
| 19    | Root girth | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (3. 97**) |
| 20    | 1000 Seed weight | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (7. 69**) |
| 21    | Biological yield | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (2416. 67) |
| 22    | Harvest index | VII | Pusa Mahak | VII | Varuna, Pusa Bold, Pusa Mahak | Pusa Mahak (23. 85**) |
| 23    | Oil content | VII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam | All are at par |
| 24    | Dry matter efficiency | VII | Pusa Mahak | VII | Varuna, Pusa Bold, Pusa Mahak | Pusa Mahak (19. 34**) |
| 25    | Grain yield/plant | VIII | Rajendra suphlam | VIII | Rajendra suphlam | Rajendra suphlam (29. 33**) |
Table 6 Suitable common divergent and less divergent crosses based on inter cluster distances in Tocher and Euclidean method

| Clusters | Cross | Clusters | Cross | Common Crosses | Clusters (Tocher) | Clusters (Euclidean) |
|----------|-------|----------|-------|---------------|------------------|---------------------|
| Crosses between cluster III (6 genotypes) and VIII (O) | IV×VIII (O) | 1. 1 Divya× Rajendra suphlam | 1. 1 Divya× Rajendra suphlam | IIIxVIII (O) | IV×VIII (O) |
| III×VIII (O) | 1. 2 TM-2× Rajendra suphlam | IV×VIII (O) | 1. 3 RH-0406× Rajendra suphlam | 3. RH-0116× Rajendra suphlam | IIIxVIII (O) | V×VIII (O) |
| III×VIII (O) | 1. 4 PM-2× Rajendra suphlam | V×VIII (O) | 2. 1 RH-0116× Rajendra suphlam | 5. Kanti× Rajendra suphlam | IIIxVIII (O) | V×VIII (O) |
| III×VIII (O) | 1. 5 Kanti× Rajendra suphlam | V×VIII (O) | 2. 2 PM-25× Rajendra suphlam | 6. Rohini× Rajendra suphlam | IIIxVIII (O) | V×VIII (O) |
| III×VIII (O) | 1. 6 Rohini× Rajendra suphlam | V×VIII (O) | 2. 3 RGN-48× Rajendra suphlam | 7. RH-0406× Rajendra suphlam | IV (O) ×VIII (O) | IV×VIII (O) |
| IV (O) ×VIII (O) | 2. 1 RH-0406× Rajendra suphlam | V×VIII (O) | 2. 5 RAURD (E) -1002× Rajendra suphlam | 9. PM-27× Rajendra suphlam | IIIxVIII (O) | IIxVIII (O) |
| Crosses between cluster I (5 genotypes) and VIII (O) | V×VIII (O) | 2. 6 Kanti× Rajendra suphlam | 10. RH-8812× Rajendra suphlam | IIIxVIII (O) | IIxVIII (O) |
| I×VIII (O) | 3. 1 RAURD-212× Rajendra suphlam | V×VIII (O) | 2. 7 Rohini× Rajendra suphlam | 11. RH-30× Rajendra suphlam | IIIxVIII (O) | IIxVIII (O) |
| I×VIII (O) | 3. 2 PM-27× Rajendra suphlam | I×VIII (O) | 3. 1 RAURD-212× Rajendra suphlam | 12. Kanti× Rajendra suphlam | IIIxVIII (O) | IIxVIII (O) |
| I×VIII (O) | 3. 3 RH-8812× Rajendra suphlam | I×VIII (O) | 3. 2 PM-27× Rajendra suphlam | | | |
| I×VIII (O) | 3. 4 RH-30× Rajendra suphlam | I×VIII (O) | 3. 3 RH-8812× Rajendra suphlam | | | |
| I×VIII (O) | 3. 5 Kanti× Rajendra suphlam | I×VIII (O) | 3. 4 RH-30× Rajendra suphlam | | | |
| Crosses between cluster III (6 genotypes) and VIII (O) | I×VIII (O) | 3. 5 Kanti× Rajendra suphlam | | | | |
| III×VIII (O) | 4. 1 Divya× Pusa Mahak | I×VIII (O) | 3. 6 RAURD (E) 1001× Rajendra suphlam | | | |
| III×VIII (O) | 4. 2 TM-2× Pusa Mahak | I×VIII (O) | 3. 7 Pant Rai× Rajendra suphlam | | | |
| III×VIII (O) | 4. 3 RH-0116× Pusa Mahak | I×VIII (O) | 3. 8 Pusa Bahar× Rajendra suphlam | | | |
| III×VIII (O) | 4. 4 PM-25× Pusa Mahak | I×VIII (O) | 3. 9 TPM-1× Rajendra suphlam | | | |
| III×VIII (O) | 4. 5 Kanti× Pusa Mahak | I×VIII (O) | 3. 10 Pusa Agrani× Rajendra suphlam | | | |
| III×VIII (O) | 4. 6 Rohini× Pusa Mahak | I×VIII (O) | 3. 11 NDRE-4× Rajendra suphlam | | | |
| Crosses between cluster IV (O) and VII (O) | I×VIII (O) | 3. 12 NRC-DR-2× Rajendra suphlam | | | | |
| IV (O) ×VII (O) | 5. 1 RH-0406× Pusa Mahak | I×VIII (O) | 3. 13 Krishna× Rajendra suphlam | | | |
| Total | 19 Crosses | Total | 25 Crosses | | | |

Sub Total (a) most divergent crosses: 12

Sub Total (b) divergent crosses: 7

Total divergent crosses: 19

These crosses are divergent in Tocher method but in Euclidean method although they are common in V×VIII but less divergent than I×VIII, III×VIII, IV×VII and V×VIII in Euclidean method.
Fig. 1 Clustering of 50 Indian mustard genotypes based on Tocher’s method
Fig. 2 Clustering pattern of 50 Indian mustard genotypes by wards minimum variance dendogram (Euclidean method)
Fig. 3 Cluster diagram depicting intra and inter-cluster distances. Fig. 4 Cluster diagram depicting intra and inter-cluster distances based on Tocher’s method based on Euclidean method.

Fig. 5 Maximum contribution towards Total divergence

Amongst 19 crosses suggested, 12 crosses involved Divya, TM-2, RH0406 (Euclidean cluster IV) whereas RH-0116, PM-25, Kanti, Rohini, (Euclidean cluster V), RAURD-212, PM-27, RH8812, RH-30 and Kranti (Euclidean cluster II) with Rajendra Supham were more divergent common from both Euclidean and Tocher methods. These crosses on the basis of days to first open, days to 50% flowering and days to physiological maturity further identified as parents involving Late × Early (RH-0116/Rajendra Supham, PM-25/Rajendra Supham, Kanti/ Rajendra Supham). On the basis of height of first siliqua (i.e. productive height of the genotype), four crosses involved cross...
between High × Low position of siliqua (Divya/ Rajendra Suphlam, RH-0116/ Rajendra Suphlam, PM-25/ Rajendra Suphlam and Kanti/ Rajendra Suphlam). Interestingly all 12 except three crosses involved Basal/Non-Basal (based on height of first primary branch < 30 cm and >30 cm as non-basal branching type) whereas three crosses, namely Divya/ Rajendra Suphlam, TM-2/ Rajendra Suphlam and RH-0116/ Rajendra Suphlam involved both basal branching parents in hybridization. Most important but difficult components, namely harvest- index and dry matter efficiency, all these crosses involved Low/High parents as Rajendra Suphlam and Pusa Mahak are only two genotypes with high harvest- index and dry matter efficiency. Out of the studied, 50 genotypes under rainfed (only residual rainfall, no rainfall during different phenological crop growth from seeding to siliqua pre- maturity stage i. e. October-February). Overall three crosses namely RH-0116/ Rajendra Suphlam, PM-25/ Rajendra Suphlam, Kanti/ Rajendra Suphlam were most promising as they involved Late × Early (days to first open, days to 50% flowering and days to physiological maturity), Basal/Non-Basal, High × Low placed siliqua and Low×High (harvest- index and dry matter efficiency) parents, and could have possibility to exhibit heterosis and could throw transgressive segregants. Additionally, only one cross between Pusa Mahak and Rajendra Suphlam involved, along with superiority in one many other traits, high harvest – index and dry matter efficiency, could be a better option for heterosis breeding for mustard improvement under rainfed condition.

In Tocchers method (Table 5) primary branches plant$^{-1}$, secondary branches plant$^{-1}$, number of siliqua plant$^{-1}$, height of first primary branch, harvest index dry matter efficiency highest cluster means fall in cluster VII which is oligo-genotypic accommodating Pusa Mahak; whereas for length of siliqua, stem girth, internode length, height of the plant, number of siliqua in primary mother axis, angle of branch, angle of siliqua, number of seeds siliqua$^{-1}$, root volume, root length, root girth, 1000 seed weight, biological yield,, oil content and grain yield /plant highest cluster means recorded in cluster VIII which is also oligo-genotypic accommodating Rajendra suphlam. On basis of highest cluster mean for four traits viz., days to first flower open, days to 50%flowering, days to physiological maturity and height of first siliqua for cluster III was noticed which comprises of 11 genotypes (Table 1). But in terms of lowest mean values i. e. for earliness for days to first flower open, days to 50%flowering and days to physiological maturity and lower placement of first primary branch and first siliqua along with lower angle of branch and also lower angle of siliqua for cluster VIII unique genotype Rajendra Suphlam exhibited its worth. In Euclidean method (Table 5) on basis of highest cluster mean harvest index and dry matter efficiency falls in cluster VII (PusaMahak) and for rest of important component traits i. e. primary branches plant$^{-1}$, secondary branches plant$^{-1}$, number of siliqua plant$^{-1}$, length of siliqua, stem girth, internode length, height of the plant, number of siliqua in primary mother axis, angle of branch, angle of siliqua, number of seeds siliqua$^{-1}$, root volume, root length, root girth, 1000 seed weight, biological yield,, oil content and grain yield /plant it falls in cluster VIII (Rajendra Suphlam) the oligo-genotypic cluster (Fig. 3 and 4).

On comparison between both methods based on cluster mean values and on per se performance lowest mean values for days to first flower open, days to 50% flowering, days to physiological maturity, angle of branch and angle of siliqua Pusa Mahak was superior genotype; whereas maximum mean values for
length of siliqua, stem girth, internode length, height of the plant, number of siliqua in primary mother axis, height of first primary branch, height of first siliqua, number of seeds siliqua\(^{-1}\), root volume, root length, root girth, 1000 seed weight, biological yield, oil content and grain yield/plant cluster VIII genotype Rajendra suphlam was superior. This suggests that overall, on cluster mean basis, Rajendra suphlam is an early maturing genotypes shows compact and semi–appressed angle of branch and siliqua respectively and also characters like deep and voluminous root system which makes suitable for drought condition. Rajendra suphlam also shows maximum cluster mean values for most of the characters like stem girth, internode length, height of the plant, number of seeds siliqua\(^{-1}\), 1000 seed weight, biological yield, oil content and grain yield/plant which suggested usefulness of material for hybridization. Similar results were observed by Patel and Patel (2006), Singh et al., (2007), Zaman et al., (2010), Mahmud et al., (2012), Binod Kumar and Anil Pandey (2012).

Root length (45. 47%) followed by height of first primary branch (25. 71) and root volume (14. 29) characters covered 85. 39 % contribution (Fig. 5) and were found maximum contributing characters towards total divergence. Similar observation by Zaman et al., (2010) and Doddabhimappa et al., (2010). This suggests, under rainfed condition, genotypes with superiority in root traits like deep tap rooted with more volume can provide more capacity to absorb water under moisture stress conditions in rainfed situation. Rajendra suphlam proved its worth as the genotype best suited with deep tap rooted along with more root volume, having spreaded capillary system advantage and least height of primary branch initiation providing more productive area from bottom to top for rainfed agro- ecologies of Bihar.

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