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EVALUATION OF F_1 HYBRID DEVELOPED THOUGHT SELF-INCOMPATIBILITY MECHANISM IN RADISH

Abstract: Research was conductedwith 57 (20 Parents and 37 F_1s) radish genotypes to study the horticultural characteristics, the genetic diversity of these genotypes and to investigate the heterotic effects of the F_1 hybrids which is developed thought self-incompatibility mechanism and to know the relationship between the diversity among the parents and high heterosis expressed in the selected hybrids.Multivariate techniques were used to classify 57 radish genotypes. All the genotypes were grouped into five clusters. The highest inter–cluster distance was observed between cluster II and III and the lowest between II and V. The maximum values of inter-cluster distance indicated that the genotypes belonging to cluster II and cluster V were far diverged from those of cluster III. The relationship study between genetic diversity and heterosis revealed that genetic distance between cluster II and cluster V was lowest (1.823) but the cross between the parental genotypes showed better heterotic performance among 37 crosses. Significant positive correlation between genetic distance and heterosis was found in pod length.Considering heterotic performance and self-incompatibility status the crosses P_7Xp_8 (SIXSI), $P_{31}XP_{26}$ (SIXSI), P_4XP_{22} (SCXSI), $P_{24}XP_{26}$ (SIXSI), P_4XP_{31} (SCXSI), $P_{11}XP_{31}$ (SCXSI), and P22XP23(SIXSI) appeared to be promising.

Key words: Radish, F_1 hybrid, Self-incompatibility and Heterosis

Introduction

Radish (*Raphanus sativus* L, 2n = 2x = 18) is one of the popular and widely consumed winter vegetable of Bangladesh belonging to the family cruciferae (Brassicaceae) or the mustard family. In terms of area radish is the second major vegetable crop and first major winter vegetable crop in Bangladesh in terms of production (Ivy, 2008). It is widely cultivated in the cool season of BD covering an area of 25.5 thousand hectors and producing 235 thousand M. tons. Its yield rate is 3.73 M.tons per acres (Anonymous, 2008).

Radish is highly cross-pollinated quick growing vegetable crop, helps in increasing cropping intensity. Its fleshy edible roots are rich in Ca, P and Vit-C (Srinivas and Naik, 1990). Tender leaf is a good source of protein and vitamin C and supplies a variety of minerals (Shadu, 1986).Radishes are useful for liver and gallbladder and liver troubles.

Although radish is one of the most widely grown winter vegetables in Bangladesh, the production of vegetables seeds in Bangladesh is below the national requirements. Hybrid varieties give higher yield and better quality than open-pollinated varieties. Both the hybrid and biennial types do not produce seeds under Bangladesh condition. So, huge quantities of seeds are being imported every year at the cost of valuable foreign currency. Again the imported seeds are not always available in time for sowing. Moreover, the seeds produced by hybrid varieties are not suitable for getting better production. In this situation, it is very important to develop hybrids with high yield potential with consistent performance over diverse environments.

Recently hybrid seed production using self-incompatibility (SI) in many vegetable has drawn attention of breeders. SI system is widely used to produce hybrid seeds in radish (Kalloo, 1988). Level of SI varied considerably within the same species and even within a self-incompatible population and there are gradations in individual plants (Doloi and Rai, 1982). Discovery of self-incompatibility as an alternative source of male sterility in radish has opened up an avenue in the production of hybrid seed on commercial scale. Utilization of SI for hybrid seed production is considered better than the use of CMS. As because in the former hybrid seeds can be obtained from both the parents (Hinata and Nishio, 1980).Therefore, research work on various aspects of self-incompatibility system needs to be explored for its utilization in breeding.For production of hybrids, selection of parent is very important. Genetic diversity can be used as a major tool in parent selection for efficient hybridization program (Falconar, 1960; Bhatt, 1970)if it is positively correlated with heterosis. So for efficient exploitation of heterosis in radish, genetic diversity and its relationship with the heterosis need to be known.

Successful exploitation of heterosis through economic production of hybrid seed in a large scale is dependent on various essential prerequisites and information in this regard has not yet been fully

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explored on radish in Bangladesh. Therefore, conceiving the above idea the present investigation was undertaken with the following objectives:

- To study the horticultural characteristics of parents and F_1 hybrids of Radish.
- To know the genetic diversity among the genotypes (parents and hybrids).
- To investigate the heterotic effects of the F_1 hybrids for some desirable yield contributing characters.
- To study the relationship between the diversity among the parents and high heterosis expressed in the selected hybrids.

MATERIALS AND METHODS

The experiment was conducted at the Bangladesh Agricultural University, Mymensingh, Bangladesh, during the winter season of 2008-2009. The location of the site is 24.00 N latitude and 90.00 E longitudes with an elevation of 8.4 m above sea level.

Design and layout:The experiment with 37 hybrids and 20 parents were grown in tri-replicated Randomized Complete Block (RCB) design. Two rows of each constituted the experimental unite. The row spacing was 60 cm having plant spacing of 30 cm within the row.

Collection of data:Data were recorded at edible root stage and seed maturing stages. At both the time ten randomly selected competitive plants from each plot were taken for recording the following characters:

1.Plant height2.No of leaf /plant 3. Leaf length 4. Leaf breadth
5.Root length 6.Root breadth 7.Root weight 8.Booting stage
9.1st flowering stage 10.No of primary branches /plant 11.No of secondary branches/plat
12.Pod /plant 13.pod length 14.Pod breadth 15.Seed /pod
16.100 seed weight

Statistical Analysis:All the collected data of the present study were statistically analyzed. The statistical analyses for various characters under investigation were done and the analysis of variance for each of the characters was performed by F test and mean values were separated by DMRT (Steel and Torrie, 1980). The analysis of variance was done according to Goulden's methods (1959). Simple correlation coefficient for all the possible pairs of characters at phenotypic and genotypic levels were analyzed following Hayes *et al.* (1955) and Singh and Chowdhury (1985). Correlation coefficients were further partitioned into components of direct and indirect effects by path coefficient analysis originally described by Dewey and Lu (1959).

Multivariate Analysis:

Principal Coordinate Analysis (PCO):Principal coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Through the use of all dimensions of it gives the minimum distance between each pair of n points using similarity matrix (Digby *et al.*, 1989). Inter-distance between genotypes was studied by PCO

Clustering Analysis (CLSA):Genotypes were divided into groups on the basis of data set into some number of mutually exclusive groups. The clustering was done using hierarchical classification. In Genstat, the algorithm is used for searching. The optimal values of the criteria followed by some initial classification of the genotypes into required number of groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swopping two genotypes of different classes, and so on.

Canonical Vector Analysis (CVA):The canonical vector analysis is based upon the roots and vectors of W-1B, where w is the pooled with in groups covariance matrix and B is the among groups covariance matrix. It provides two-dimensional plots, which helped in separating different populations involved.

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Computation of Average Intra-cluster Distances: Once the clusters were formed, the average intra-cluster distance for each cluster was calculated by taking all possible D^2 values within the numbers of cluster obtained from PCO. The formula used was D^2/n, where D^2 is the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the average D^2 values, represent the distances (D^2) with in cluster.

Cluster Diagram:

Using the values of intra-and inter-cluster distance diagram. It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

RESULTS AND DISCUSSION

The results on the basis of horticultural characteristics, analysis of variance, diversity and heterosis and the relationship between diversity and heterosis based on different characters of 57 radish genotypes (20 parents and 37 F_1s) are presented in Table 1 to Table 6 .

2. Analysis of variance: Analysis of variance revealed significant differences for all the characters among the genotypes (Table 4), indicating considerable genetic variability in the material.

Table 1: Total variation among the 16 characters describing 57 lines of radish

Principal component axis	Eigen values	% of total variation accounted for	Cumulative percent
Plant height	41.914	61.69	61.69
Root length	10.723	15.78	77.47
Root breath	4.705	6.93	84.4
Root weight	3.245	4.78	89.18
No of leaf	1.796	2.64	91.82
Leaf length	1.253	1.84	93.66
Leaf breath	1.075	1.58	95.24
Booting stage	0.895	1.32	96.56
1st flowering	0.778	1.14	97.7
No of P B/plant	0.536	0.79	98.49
No of S B/plant	0.413	0.61	99.1
Pod per plant	0.297	0.44	99.54
Pod length	0.195	0.29	99.83
Pod breath	0.074	0.11	99.94
Seed per pod	0.034	0.05	99.99
100 seed wt	0.007	0.01	100

3. Diversity of radish genotypes: Genetic diversity of the radish genotypes were analyzed by three multivariate techniques, results of which are discussed as follows:

Principal component analysis: The principal component analysis yielded Eigen values of each principal component axes of ordination of genotypes with the first axes totally accounted for the variation among the genotypes, while five of these with Eigen values above unity accounted for 91.82 %. (Table 1) The first ten principal axes accounted for 98.49 % of the total variation among the 16 characters describing 57 lines of radish .

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Construction of scatter diagram

Based on the values of principal component scores 1 and 2 obtained from the principal component analysis, a two- dimensional scatter diagram (Z_1–Z_2) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in Fig- 1. The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that there exists considerable diversity among the genotypes of radish. The scattered diagram for the genotypes of five clusters revealed that the cluster-II and cluster-IV were distantly located which suggesting more diverged from rest of the clusters.

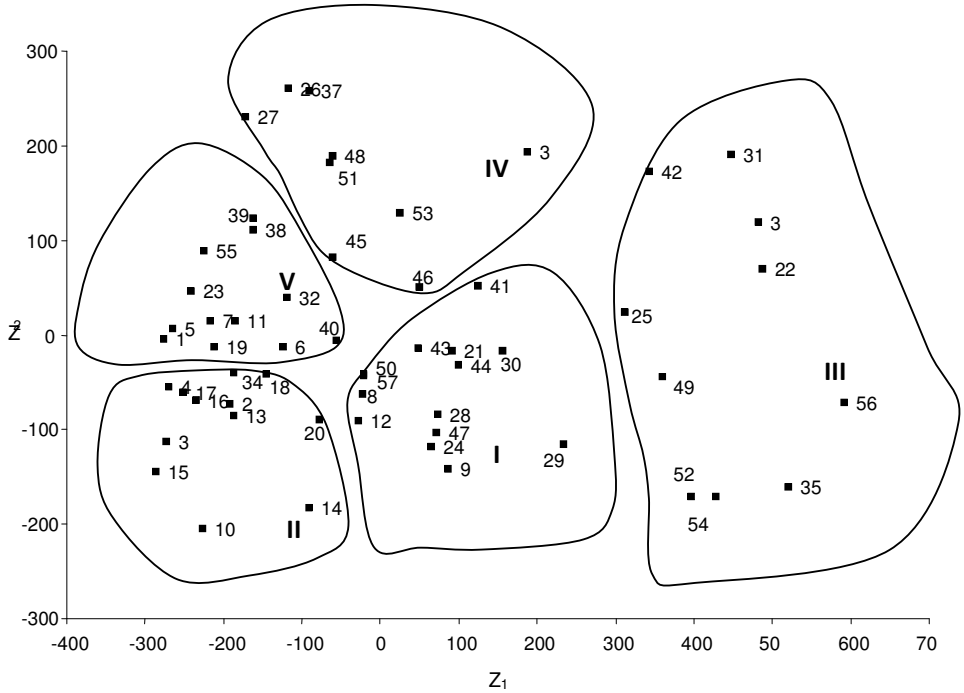

Figure 1: Relative position of 57 genotypes of radish in Z_1-Z_2 graph using their principal component score based on quantitative characters superimposed with clustering.

(i) Non-hierarchical clustering:

Non- hierarchical clustering using co-variance matrix grouped 57 genotypes of radish into five different clusters. These results confirmed the clustering pattern of the genotypes obtained through principal component analysis.The pattern of distribution of genotypes into five clusters is described in Table 2.

Table 2: Distribution of 57 genotypes of radish in five clusters

Cluster no.	Member number	Genotypes
I	15	P_{13}, P_{15}, P_{22}, P_4XP_{16}, P_4XP_{26}, P_5XP_{26}, P_7XP_8, P_8XP_7, $P_{17}XP_{12}$, $P_{17}XP_{15}$, $P_{22}XP_4$, $P_{22}XP_{23}$, $P_{26}XP_4$, $P_{31}XP_4$, $P_{35}XP_{31}$
II	12	P_5, P_7, P_8, P_{16}, P_{23}, P_{24}, P_{26}, P_{31}, P_{32}, P_{33}, P_{35}, $P_{12}XP_7$,
III	10	P_4XP_{22}, P_4XP_{31}, $P_{10}XP_{26}$, $P_{13}XP_5$, $P_{13}XP_{35}$, $P_{17}XP_{32}$, $P_{26}XP_{10}$, $P_{31}XP_{26}$, $P_{32}XP_{33}$, $P_{35}XP_{13}$

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IV	9	P_5XP_{11}, P_5XP_{24}, $P_{11}XP_{31}$, $P_{15}XP_{17}$, $P_{23}XP_{22}$, $P_{24}XP_{26}$, $P_{26}XP_5$, $P_{31}XP_{11}$, P_31XP_{35}
V	11	P_4, P_{10}, P_{11}, P_{12}, P_{17}, P_{34}, P_4XP_{24}, $P_{11}XP_5$, $P_{16}XP_5$, $P_{16}XP_{24}$, $P_{32}XP_{34,}$

(ii) Canonical Vector Analysis (CVA):

Canonical vector analysis was performed to obtain the inter-cluster distances (Mahalnobis's D^2 values). The intra-cluster distances were computed by the values of inter- genotypic distance matrix of PCO according to Singh and Choudhary (1985). These values of inter-cluster distance (D^2) are presented in Table 3. Statistical distances represent the index of genetic diversity among the clusters.

Table 3: Average intra and inter cluster distances (D^2) for 57 lines of radish

	Cluster- I	Cluster- II	Cluster- III	Cluster- IV	Cluster- V
Cluster-I	**1.013**				
Cluster-II	3.776	**0.947**			
Cluster-III	4.468	8.240	**1.471**		
Cluster- IV	3.845	4.487	6.561	**1.241**	
Cluster- V	3.795	1.823	7.950	2.879	**0.852**

The inter-cluster distance was maximum between cluster II and III (8.240).The inter-cluster distance was minimum between cluster II and V (1.823). The maximum values of inter-cluster distance indicated that the genotypes belonging to cluster II were far diverged from those of cluster III and cluster V. The genotypes belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among the segregates. Similar reports were also made by Bansal et al. (1999), Mokate et al. (1998), Kumar and Rangasamy (1997) and Singh et al. (1996).

4. Heterosis

The mean sum of square from analysis of variance for different leaf and root characters are presented in the Table 6. The analysis of variance revealed highly significant differences for all the characters among the entries. The mean sum of square due to parent differed significantly, indicating great deal of diversity among them. The estimates of heterosis over better parent are presented in **Table 6**.

Table 4: Inter parental distance

	P_2	P_3	P_4	P_5	P_6	P_7	P_8	P_9	P_{10}	P_{11}	P_{12}	P_{13}	P_{14}	P_{15}	P_{16}	P_{17}	P_{18}	P_{19}	P_{20}
P_1	1.65	1.54	1.10	0.49	1.78	1.54	2.00	2.39	2.11	1.53	2.18	1.68	2.25	1.86	1.75	0.89	2.05	1.42	2.19
P_2		0.75	1.16	1.46	0.69	0.87	0.86	1.58	1.01	0.64	1.05	0.63	0.99	1.17	0.91	1.26	0.82	0.75	0.83
P_3			1.09	1.33	1.20	0.80	1.46	2.12	0.91	0.86	1.61	1.00	1.30	0.81	0.77	1.31	1.08	1.02	1.29
P_4				1.05	1.56	1.20	1.75	2.05	1.50	1.13	1.60	1.17	1.67	1.45	1.55	0.94	1.69	1.07	1.64
P_5					1.57	1.27	1.82	2.19	1.95	1.28	1.99	1.52	2.02	1.78	1.50	0.80	1.77	1.23	2.02
P_6						1.05	0.51	1.40	1.39	0.74	1.04	0.74	1.10	1.48	0.98	1.28	0.88	0.89	0.99
P_7							1.41	2.04	1.30	0.41	1.49	1.07	1.37	1.06	0.70	1.24	0.81	0.88	1.25

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P_8								1.08	1.46	1.07	0.86	0.93	1.03	1.77	1.36	1.48	1.03	0.99	0.88
P_9									1.94	1.70	0.83	1.44	1.24	2.46	2.14	1.72	1.76	1.41	1.43
P_{10}										1.26	1.43	1.19	0.92	1.02	1.25	1.69	1.27	1.17	1.00
P_{11}											1.15	0.77	1.18	1.19	0.81	1.09	0.70	0.70	1.04
P_{12}												0.91	0.80	1.85	1.68	1.52	1.24	0.95	0.83
P_{13}													0.99	1.26	1.16	1.11	1.10	0.84	1.07
P_{14}														1.48	1.35	1.62	1.12	0.97	0.76
P_{15}															0.91	1.61	1.37	1.31	1.48
P_{16}																1.43	0.91	1.13	1.35
P_{17}																	1.61	0.97	1.71
P_{18}																		1.02	0.93
P_{19}																			0.88

Table 5. Analysis of variance for different characters in radish

Source of variation	d.f.	Plant height	No of leaf	Leaf length	Leaf breadth	Root length	Root breadth	Root volume	Root weight	Booting stage
Replication	2	0.012	0.995	1.524	4.472	2.545	0.893	348.108	2163.667	8.515
Genotypes	56	0.027**	39.732**	70.266**	12.175**	392.654**	87.784**	139158.008**	49302.627**	2.667**
Parents	19	0.024**	20.534**	83.933**	19.53**	47.363**	91.256**	19933.343**	10939.931**	2.312**
Hybrid	36	0.029**	46.555**	61.089**	8.234**	207.148**	80.706**	157321.728**	29554.726**	1.200**
Error	112	0.008	0.873	1.79	1.458	7.967	2.956	2628.418	1737.178	1.271

*P=O.O5, *P=0.01

Source of variation	d.f.	1st flowering	50% flowering	No of primary b/plant	No of secondary b/plant	Pod/plant	Pod length	Pod breadth	Seed/pod	100 seed weight
Replication	2	7.702	2.041	3.388	85.901	2814.988	4.543	0.162	0.292	0.004
Genotypes	56	24.714**	2.440**	19.551**	2117.417**	286886.16**	212.135**	1.964**	4.377**	0.164**

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Parents	19	4.929**	2.330**	36.446**	1954.150**	30364.632**	149.391**	1.779**	2.414**	0.125**
Hybrid	36	8.045**	1.538**	9.989**	1717.312**	358579.515**	249.528**	2.074**	5.504**	0.172**
Error	112	2.833	2.874	1.273	29.252	1377.441	4.599	0.689	0.394	0.006

*P=O.O5, *P=0.01

6. Correlation between genetic divergence and heterosis

Correlation coefficient between inter-genotypic distances and their heterotic effects in 37 hybrids were computed to quantify the relationship between them. Significant and positive relationship was found for pod length and negatively significant correlation coefficient was found for root breath, No. of leaf/plant, leaf breath, No of S.B/plant against better parents (Table 6). Only No. of S B/plant produced negatively correlation against both mid parent and better parent.

Table 6. Correlation coefficients (r) between parental distances and heterosis of 37 F_1's for 16 characters in radish

Characters	Correlations	
	MP	BP
Plant height	0.049	0.046
Root length	-0.035	0.029
Root breath	-0.112	-0.394*
Root weight	0.019	-0.029
No of leaf	-0.290	-0.340*
Leaf length	0.102	-0.006
Leaf breath	-0.068	-0.316*
Booting stage	0.037	-0.118
1st flowering	0.260	0.301
No of P B / plant	0.159	0.110
No of S B / plant	-0.415*	-0.566**
Pod per plant	0.254	0.180
Pod length	0.384*	0.422**
Pod breadth	0.016	-0.012
Seed per pod	0.075	0.037
100 seed wt	-0.200	-0.244

CONCLUSIONS

- Analysis of variance revealed significant differences among the genotypes for all the characters indicating considerable genetic variability in the materials.
- All the genotypes were grouped into five clusters.

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- The scattered diagram for the genotypes of five clusters revealed that the cluster-II and cluster-III were distantly located which suggesting there are more divergence from rest of the clusters.
- The highest inter–cluster distance was observed between cluster II and III (8.240) and the lowest between II and V (1.823).
- The inter-genotypic distances of parents using all the dimensions. It was observed that P_1 and P_9 both produced considerable distances with other genotypes
- Considering heterotic performance and self-incompatibility status the crosses P_7Xp_8(SIXSI), $P_{31}XP_{26}$(SIXSI), P_4XP_{22}(SCXSI), $P_{24}XP_{26}$(SIXSI), P_4XP_{31}(SCXSI), $P_{11}XP_{31}$(SCXSI), $P_{22X}P_{23}$ (SIXSI) appeared to be promising.
- Significant positive correlation between genetic distance and heterosis was found in pod length but positive non significant correlation was observed in plant height, 1st flowering , no of p b/plant, pod/plant, seed/pod against both for mid parent and better parent.
- The crosses between the genotypes P_7, P_8, P_{23}, P_{24}, P_{26}, and P_{31} of cluster II and P_4, P_{11} of cluster V produced higher heterosis.

RECOMMENDATIONS

- Further refinement of self-incompatible lines and their performances in hybrid development.

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