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Genetic divergence studies among rice genotypes

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Abstract

This study aim to estimate genetic diversity among the 30 rice genotypes using Mahalanobis D². The clustering pattern grouped 30 rice genotypes into six non-overlapping clusters under drought condition. Cluster number V having highest genotype (8) followed by Cluster VI having six rice genotypes and Cluster II having 5 genotypes. The clustering pattern grouped 30 rice genotypes into six non-overlapping clusters under controlled condition in which Cluster I having six genotypes followed by cluster V grouped with six genotypes and cluster VI also having six genotypes. Barani deep, Nagina-22, Shusk samrat, Nagobanyo Red Cover associated with drought tolerance and high yield. Therefore, these lines may be used as donor parent in breeding programme to develop the drought tolerant rice cultivar having high yield under drought and control conditions or may be released as variety for its cultivation in drought prone environment.

Keywords: Genetic diversity, drought tolerant, rice genotypes

Introduction

Rice (*Oryza sativa* L.) is the staple food of more than three billion people in the world. Recent estimates on climate change predict that because of water deficiency, the intensity and frequency of drought are becoming a serious problem for crop production, especially in rice cultivation. Rice is highly sensitive to water stress. Due to irregular rain, rice plants can be damaged by drought during seedling, flowering, and maturity stages. The injuries normally occur on leaves at the seedling stage and on sterile spikelets at the reproductive stage. Particularly, at the reproductive stage, floral fertility in rice is extremely sensitive to water deficiency. Identifying rice varieties and breeding lines with high levels of drought tolerance for use as donors in breeding and gene discovery is one of the main challenges for rice research (Serraj and Atlin, 2008) [9].

Materials and Methods

The experiment was carried out in the field of Student Instructional Farm of N.D. University of Agriculture and Technology, Kumarganj, Faizabad during *Kharif* season of 2015-2016. Observations were recorded on randomly selected five plants from each entry line in each replication at maturity. These plants were harvested and threshed separately. Taken Data on Seedling Vigour, Days to 50% flowering, Plant height (cm), Leaf relative water content (RWC), Panicle bearing tillers per plant, Number of Spikelets per panicle, Number of grains per panicle, Spikelet fertility (%), Test weight/plant (g), Biological yield/plant (g), Harvest index were recorded. Based on genetic distances (D₂ values), the genotypes were grouped into clusters of genetically closer related groups following the Tocher's method (Rao, 1952) [7]

Results and Discussion

The selection of suitable diverse parents for hybridization is an important feature of any crop breeding programmes because parental diversity in optimum magnitude is required to obtain superior genotypes in segregating generations (Moll *et al.*, 1962) [6]. The importance of genetic divergence in plant breeding has been emphasized by several scientists (Griffing and Lindstrom, 1954; Moll *et al.* 1962; Arunachalam 1981; Hawkes 1981) [2, 6, 1, 3].

In the present study, the thirty genotypes of rice were grouped into six non-overlapping clusters under both drought and control conditions (Table 1a and 1b). Jha *et al.*, 1999 [4] also reported that genotypes in different clusters are genetically variable, which may provide basis for consideration in hybridization programmes.

Cluster number V having highest genotype (8) namely, IR-91167-31-3-1-33, IR-92960-75-1-3, Taramoon, Sarjoo-52, IR-64, Sirarakhong Ashang Maa, Saponyo and Gopal Bhok. The cluster I having six genotypes *i.e.* NDR-97, NDR-118, Shusk Samrat, NDR-1, Nagina-22 and R-RHZ-2. Cluster VI also have six rice genotypes, namely, Pusa Basmati, I R-68144-2B-2-2-3-1-120, IR-91167-133-1-1-2-3, Teineni Rrvisheng MAA, Nedu and DZULBORHE. Cluster II having 5 genotypes these are NDR-359, Amker, IR-68144-2B-2-2-3-1-127, Ngobanyo Red cover and Barani Deep. Cluster IV having four genotypes namely, Khusoi-ri-sareku, Ayaar, Maigothi and Kelhrie cha and Cluster III having only one genotype *i.e.*, IR-83668-35-2-2-2. while in The clustering pattern grouped 30 rice genotypes into six non-overlapping

clusters under controlled condition (Table 1 b). Cluster I having six genotypes, *i.e.*, Pusa basmati, Amker, Sarjoo-52, Baranideep, Teineni Rrvisheng Maa and Nedu; cluster IV having six genotypes namely, Khusoi-ri-sareku, IR-92960-75-1-3, Taramoon, Maigothi, IR-64 and Saponyo; cluster V grouped with six genotypes namely, IR-68144-2B-2-2-3-1-20, Ayaar, Nagobanyo Red Cover, IR-91167-133-1-1-2-3, Sirarakhong Ashng Maa and Kelhrie Chha and cluster VI also having six genotypes *i.e.*, NDR-118, NDR-359, NDR-1, IR-68144-2B-2-2-3-1-27, Gopal Bhok and DZULBORHE. Cluster II having five genotypes namely, NDR-97, Shusk Samrat, Nagina-22, IR-91167-31-3-1-33 and R-RHZ-2. Cluster III having only one genotype *i.e.*, IR-83668-35-2-2-2.

Table 1(a): Clustering pattern of rice genotype on the basis on D² analysis for 10 character in drought condition

Cluster	No. genotypes	Name of varieties
Cluster I	6	NDR-97, NDR-118, Shusk Samrat, NDR-1, Nagina-22, R-RHZ-2
Cluster II	5	NDR-359, Amker, IR-68144-2B-2-2-3-1-127, Ngobanyo Red cover, Barani Deep
Cluster III	1	IR-83668-35-2-2-2
Cluster IV	4	Khusoi-ri-sareku, Ayaar, Maigothi, kelhrie cha
Cluster V	8	IR-91167-31-3-1-33, IR-92960-75-1-3, Taramoon, Sarjoo-52, IR-64, Sirarakhong Ashang Maa, Saponyo, Gopal Bhok
Cluster VI	6	Pusa Basmati, IR-68144-2B-2-2-3-1-120, IR-91167-133-1-1-2-3, Teineni Rrvisheng MAA, Nedu, DZULBORHE

Table 1(b): Clustering pattern of rice genotype on the basis on D² analysis for 12 character in controlled condition

Cluster	No. genotypes	Name of varieties
Cluster I	6	Pusa basmati, Amker, Sarjoo-52, Baranideep, Teineni Rrvisheng Maa
Cluster II	5	NDR-97, Shusk Samrat, Nagina-22, IR-91167-31-3-1-33, R-RHZ-2
Cluster III	1	IR-83668-35-2-2-2
Cluster IV	6	Khusoi-ri-sareku, IR-92960-75-1-3, Taramoon, Maigothi, IR-64, Saponyo
Cluster V	6	IR-68144-2B-2-2-3-1-20, Ayaar, Nagobanyo Red Cover, IR-91167-133-1-1-2-3, Sirarakhong Ashng Maa, Kelhrie Chha
Cluster VI	6	NDR-118, NDR-359, NDR-1, IR-68144-2B-2-2-3-1-27, Gopal Bhok, DZULBORHE

The intra cluster distance under drought condition as shown in Table 2(a) ranged from 0.00 (cluster V) to 221.18 (cluster IV). The highest inter cluster distance was recorded between cluster I and cluster VI (1407.13) followed by cluster IV and cluster VI (889.81), cluster I and cluster V (879.06), cluster V and cluster VI (737.32) and cluster II and cluster V (534.05) while under controlled condition (Table 2 b) ranged from 0.00 (cluster III, IV, V and VI) to 534.74 (cluster II). The highest inter cluster distance was recorded between cluster III and cluster VI (5966.22) followed by between cluster IV and cluster VI (4913.83), cluster I and cluster VI (4325.81), cluster V and cluster VI (4275.51) and cluster III and cluster VI (2180.59). It revealed that wider diversity among them and crossing among the genotypes would yield the maximum heterosis. These results are supported by Saini and Kaicke (1987) [8].

Under drought condition, highest grain yield per plant were recorded by genotypes of cluster III (5.89) followed by cluster I (5.25) and cluster II (4.75) (Table 3a) while in controlled

condition, Cluster mean for grain yield per plant ranged from 12.72 (cluster VI) to 19.12 gm (cluster III). Highest grain yield per plant were recorded by genotypes of cluster III (19.12) followed by cluster I (18.06) and cluster IV (17.14). (Table 3b)

Conclusion

Genetically distant parents are usually able to produce higher heterosis and the clustering pattern could be utilized in choosing parents for cross combinations which are likely to generate the highest possible variability for effective selection of various economic traits. The findings of this study indicate that Barani deep, Nagina-22, Shusk samrat, Nagobanyo Red Cover associated with drought tolerance and high yield. Therefore, these lines may be used as donor parent in breeding programme to develop the drought tolerant rice cultivar having high yield under drought and control conditions.

Table 2(a): Estimation of average inter cluster D² value under drought condition

Characters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	56.44	238.04	396.33	313.56	879.06	1407.13
Cluster 2		102.65	208.90	237.20	507.03	764.62
Cluster 3			153.55	414.33	534.05	609.99
Cluster 4				221.18	532.85	889.81
Cluster 5					0.00	737.32
Cluster 6						130.00

Table 2 (b): Estimation of average inter cluster D²value under control condition

Characters	Cluster 1	Cluster 2	Cluster3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	415.43	800.78	629.21	588.20	1728.68	4325.81
Cluster 2		534.74	1419.64	1037.19	1520.79	2429.40
Cluster 3			0.00	676.25	2180.59	5966.22
Cluster 4				0.00	1297.21	4913.83
Cluster 5					0.00	4275.51
Cluster 6						0.00

Table 3(a): Cluster mean of 30 rice germplasm under drought condition

Characters	Days to 50 % flowering	Plant height (cm)	Panicle tillers/ plant	Spikelets/ panicle	Grains/ panicle	Spikelet fertility (%)	Test weight (g)	Biological yield (g)	Harvest index (%)	Grain Yield / Plant
Cluster I	91.27	75.48	2.55	70.22	60.72	86.89	18.84	12.80	40.67	5.25
Cluster II	106.26	95.96	1.93	81.53	76.46	93.69	21.93	12.01	38.49	4.75
Cluster III	150.66	148.54	2.66	172.66	164.33	95.16	24.13	14.26	41.32	5.89
Cluster IV	118.16	141.83	1.75	133.25	109.33	83.59	17.16	11.12	31.37	3.48
Cluster V	113.41	102.47	1.70	126.50	110.12	87.04	17.90	11.00	32.08	3.60
Cluster VI	112.50	90.63	1.66	95.38	85.88	89.70	17.16	11.25	33.50	3.80

Table 3 (b): Cluster mean of 30rice germplasm under controlled condition

Characters	Seedling vigour	Days to 50 % flowering	Plant height (cm)	R.W.C	Panicle tillers/ plant	Test weight (g)	Spikelets/ panicle	Grains/ panicle	Spikelet fertility (%)	Biological yield (g)	Harvest index (%)	Grain Yield/Plant
Cluster I	34.17	102.77	111.34	53.53	8.27	22.93	124.22	110.33	89.12	42.85	41.68	18.06
Cluster II	38.76	89.80	86.85	37.88	6.53	21.99	103.40	88.66	86.92	40.03	36.74	14.72
Cluster III	57.93	145.66	156.16	53.31	5.66	26.01	188.00	181.66	96.66	48.61	40.28	19.12
Cluster IV	41.47	104.50	125.58	64.29	8.55	21.12	151.55	135.38	89.39	41.98	41.27	17.14
Cluster V	41.78	104.44	130.45	57.23	6.44	21.48	133.33	123.94	92.90	43.11	38.07	16.55
Cluster VI	30.12	95.11	86.75	51.85	6.94	22.11	98.33	90.16	91.69	33.43	37.91	12.72

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