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Diversity studies among basmati and non-basmati type aromatic rice (*Oryza sativa*L.) genotypes for grain yield and its attributing characters

Kalmeshwer Gouda Patil[1,3], Nagesh[1,4], Veeresh Gouda Patil[1,4], Kulkarni, R. S[1] and Shashidhar, H. E[2]

[1]*Department of Genetics and Plant Breeding, University of Agricultural Sciences, GKVK, Bangaluru, Karnataka, India*
[2]*Department of Biotechnology, University of Agricultural Sciences, GKVK, Bangaluru, Karnataka, India*
[3]*Monsanto, Bangaluru, Karnataka, India*
[4]*International Crop Research Institute for the Semi-Arid Tropics, Patancheru, Hyderabad, Andhra Pradesh, India*

ABSTRACT

Twenty four aromatic rice genotypes were evaluated for grain yield, its attributing characters andmicronutrients viz., iron and zinc content in grains. Charactersbased on the estimated D^2values as thesquare of the generalized distance 24 genotypes were grouped into six clusters by treating the. Maximumdivergence was observed between cluster III and cluster VI (D^2=944.68) while, minimum divergence wasobserved between cluster I and cluster III (D^2= 88.42). Cluster IV was the biggest cluster consisting ofeight genotypes viz., IET 19227, IET 19234, IET 19391, IET 19491, IET 19492, Taraori basmati, Basmati370 and Mattalaga followed by cluster III, comprised of five genotypes viz., IET 18973, IET 18981, IET18990, IET 18993 and IET 19294. The clusters I and VI contained only two genotypes viz., IET 19441 andPusa basmati; Gandhasali and Jeerigesanna respectively.

INTRODUCTION

Rice (*Oryzasativa*L.) has a renowned relationship with the humans since ages.Presently, more than half of the world's population depends on rice as a staple food. Asiacan be considered as 'Rice Basket' of the world, as more than 90 per cent of the rice isproduced and consumed in Asia, a region with high population density. India producessome of the best quality rice in the world. Though a high-volume commodity, a class ofaromatic, superfine premium rice has evolved its own market niches, making rice trade acommercial success internationally. A class of premium rice with specific graincharacteristics, traditionally grown on either side of the Indus River, is popularly knownas the basmati rice and these varieties are also known as "Queen of fragrance". Thesuperiority of basmati cultivars over other premium rice varieties is its superfine grainswhich have a distinct aroma, excellent elongation ability and the soft, flaky texture of thecooked rice [1].

Besides the much sought after basmati types which get high price in internationalmarkets, the country also abounds with hundreds of indigenous short grain aromaticcultivars and landraces grown in pockets of different states. Almost every state has its own collection of aromatic rice that performs well in native areas [2]. These aromatic ricelines also possess exemplary quality traits like aroma,fluffiness and taste. However, the improvement of these ricevarietiesvery much neglected asthey lack export value *per se*. The short and medium grained aromatic rice varietiesare generally low yielders, susceptible to lodging, pest and diseases. Due to quest for highyielding varieties, a large number of these aromatic rice varieties slowly vanished from thefarmer's field. There are very few reports available on evaluation and genetics of somequality traits of these types. Limited organized efforts have been made till now for theirimprovement or to check the rapid erosion of germplasm base by formulating andconservation programs [3]. Hence, this study has been undertaken tofind out the amount of variability present in the Basmati as well as non-Basmati aromaticgenotypes.

MATERIALS AND METHODS

The material used in the study comprised of twenty four aromatic rice genotypesgrown in different agro-ecological zones of India. These genotypes were evaluated forgrain yield and its attributing characters following randomized complete block designwith three replications during *Kharif*2007 at Ramagondanahalli village, outskirts ofBangalore, Karnataka, India. Spacing from row to row and from plant to plant was 30 cm and15 cm respectively and the crop was raised as per the recommended package of practices.Observations on days to 50 per cent flowering, plant height, number of tillers per plant,number of productive tillers per plant, panicle length, grain length, grain breadth, L/Bratio, test weight and grain yield per plant were studied on five random plants in eachgenotype. The zinc and iron content of seed samples was estimated by AtomicAbsorption Spectrophotometer as suggested by Lindsay and Novell (1978).

RESULTS AND DISCUSSION

Improvement in grain yield is normally attained through involvement of thegenetically diverse parents in breeding programmes. For identifying such diverse parentsfor crossing, by means of Mahalanobis's D^2 statistic has been used in several crops. It is apowerful tool used to quantify the genetic divergence between the genotypes and to relateclustering pattern with the geographical origin. D^2 statistic has been employed widely toresolve divergence at intervarietal, species and subspecies levels in classifying problemsin crop plants. In the present investigation, 24 genotypes of rice were considered forassessment of nature of genetic diversity by adopting Mahalanobis's (1936) concept ofgeneralized distance (D^2) considering twelve characters.

Twenty four aromatic rice genotypes were grouped into six clusters by treating the estimated D^2 values as the square of the generalized distance. Maximumdivergence was observed between cluster III and cluster VI (D^2 =944.68) while,minimum divergence was observed between cluster I and cluster III (D^2 = 88.42). ClusterIV was the biggest cluster consisting of eight genotypes *viz*., IET 19227, IET 19234, IET19391, IET 19491, IET 19492, Taraori basmati, Basmati 370 and Mattalaga followed bycluster III, comprised of five genotypes *viz.*, IET 18973, IET 18981, IET 18990, IET18993 and IET 19294. The clusters I and VI contained only two genotypes *viz*., IET19441 and Pusa basmati; Gandhasali and Jeerigesanna respectively. The patterns ofdistribution of genotypes into various clusters are given in the Table 1.It was observed that, 23 genotypes from different parts of the country and anexotic genotype (Azucena) representing diverse agro-climatic conditions were distributedat random among the clusters formed, based on their genetic distance. The inter-clusterdistance was not consistent with the geographic distribution of varieties. The varietiesbelonging to diverse ecological regions clustered together whereas, genotypes of thesame region have entered widely into separate groups. Similarly, Biswas and Sasmal(1990), Mukharjee*et al.* (1999), and Roy *et al.* (2004), have reported that, geographicaldiversity is not related with genetic diversity in rice.

The intra and inter-cluster D^2 and D values among the six clusters are given in theTable 2 and represented in Fig. 1. The intra-cluster D^2 and D exhibited that, cluster VI(D^2 = 346.45, D= 18.61) had the maximum genetic diversity followed by cluster IV (D^2 =309.73, D=17.59) and cluster V (D^2=180.47, D=13.43). The inter-cluster D^2 values of thesix clusters revealed that highest inter-cluster generalized distance (D^2 = 944.68) wasbetween cluster III and cluster VI while, the lowest (D^2 = 88.42) was between cluster Iand cluster III. The intra-cluster and inter-cluster distances indicated that, cluster VI hadthe maximum intra-cluster distance followed by cluster IV. From the above, it could beconcluded that, considerable diversity existed among 24 genotypes included in thepresent study. This could be the result of selection in different direction by nature andhuman forces.

The nearest and distant clusters from each of the cluster based on D values are presented in Table 3. Cluster I was nearest to cluster III (9.40) and distant from cluster VI (30.05). Cluster II exhibited close proximity with cluster IV (18.09) and maximum divergence with cluster V (29.57). Cluster III was nearest to cluster I (9.40) while, it was farthest from cluster VI (30.73). Cluster IV showed close proximity with cluster III (17.87) and maximum divergence with cluster V (27.33). Cluster V exhibited intimate relation with cluster I (24.54) and wide diversity with cluster II (29.57). Nearest and farthest clusters for cluster VI were II (19.46) and III (30.73) clusters respectively.

Table 1. Grouping of rice genotypes based on D^2 analysis

Cluster	No. of genotypes	Genotypes	Pedigree	Source
I	2	IET 19441	HKR 240/ Taraori basmati	Haryana
		Pusa basmati	Pusa 150 X Karnal local	Haryana
II	4	IET 18193	IR 68/ IR 3270-1-38-2-1-1	IRRI, Philippines
		IET 18675	Selection from Basmati	Himachal Pradesh
		IET 19228	IR 720114-8-NDR-28-1-4-1-B-115	IRRI, Philippines
		IET 19236	IR 72713-2-NDR-1-1-1-B-115	IRRI, Philippines
III	5	IET 18973,	Basmati 386/ Super basmati	Haryana
		IET 18981	Pusa basmati 1/ HDC 19	Haryana
		IET 18990	Pusa basmati 1/ IR BB 55	Haryana
		IET 18993	Kasturi/ IET 11345	Uttar Pradesh
		IET 19294	N 22/ Manoharsali	-
IV	8	IET 19227	Selection from ParbhaniChinnur	Maharashtra
		IET 19234	Selection from Krishnabhog	Chattisgarh
		IET 19391	Mutant of Dehradun basmati	Uttaranchal
		IET 19491	P1121/ Type 3	Uttar Pradesh
		IET 19492	P1121/ Type 3	Uttar Pradesh
		Taraori basmati	Selection from Basmati 370	Haryana
		Basmati 370	Selection from Dehradun basmati	Himachal Pradesh
		Mattalaga	Local line	Karnataka
V	3	Kalanamak	Local line	Uttaranchal
		Azucena	Exotic line	Philippines
		K 44-1	Local line	Karnataka
VI	2	Gandhasali	Local line	Karnataka
		Jeerigesanna	Local line	Karnataka

Table 2. Average intra and intercluster D^2 values

Cluster	I	II	III	IV	V	VI
I	**19.01** **(4.360)**	469.99 (21.679)	88.42 (9.403)	394.21 (19.855)	602.63 (24.549)	903.37 (30.056)
II		**123.83** **(11.128)**	442.47 (21.035)	327.32 (18.092)	874.79 (29.577)	378.93 (19.466)
III			**61.81** **(7.862)**	319.54 (17.876)	749.47 (27.376)	944.67 (30.736)
IV				**309.73** **(17.599)**	747.25 (27.336)	692.79 (26.321)
V					**180.47** **(13.434)**	798.95 (28.266)
VI						**346.45** **(18.613)**

** Values in the parenthesis indicate Average intra and intercluster Dvalues*

Table3. The nearest and farthest clusters from each cluster based on D^2 values in twenty four aromatic rice genotypes

Cluster No.	Nearest cluster with D^2 value	Farthest cluster with D^2 value
I	III	VI
II	IV	V
III	I	VI
IV	III	V
V	I	II
VI	II	III

Genotypes grouped into the same cluster presumably diverge little from oneanother as the aggregates of characters measured. Theoretically, crossing of genotypesbelonging to the same cluster is not expected to yield superior hybrids or desirablesegregants. However, theoretically a general notion exists that larger the divergencebetween genotypes, higher will be the heterosis (Falconer, 1981). Therefore, it would bedesirable to attempt crosses between genotypes belonging to distant clusters for gettinghighly heterotic crosses. In this context, inter-cluster distance were worked outconsidering the twelve characters and the inter-cluster distance varied from 9.40 (betweencluster I and III) to 30.05 (between cluster I and VI). These values suggest wide diversitybetween these clusters. Therefore, genotypes from these clusters can be selected forhybridization programme to get desirable segregants.

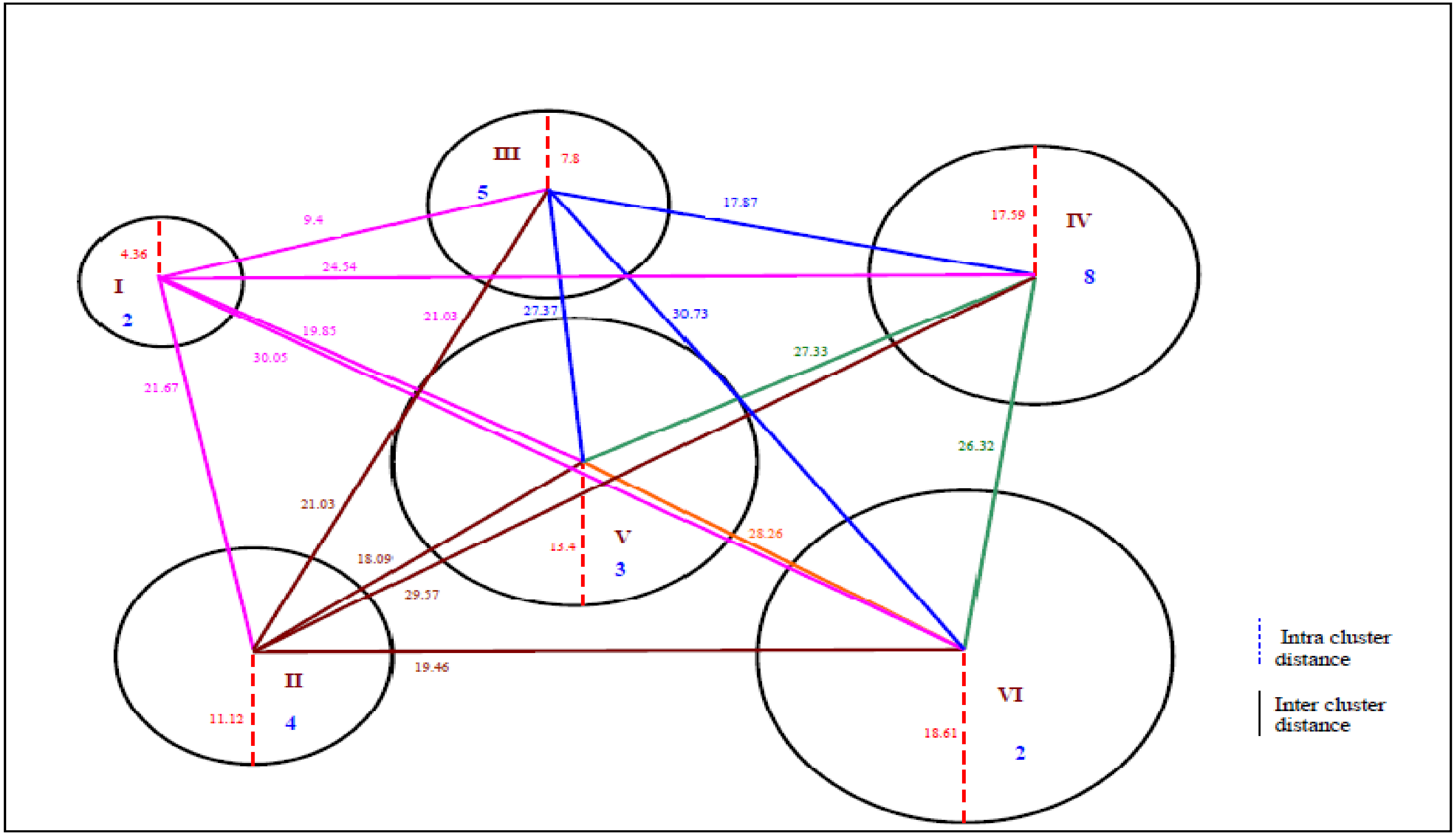

Fig. 1 Diagrammatic representation of the clustering pattern of the 24 aromatic rice genotypes based on D valves

The per cent contribution of each character towards divergence is presented inTable 4. It was observed that grain yield per plant was the single largest contributor(52.53%) towards divergence followed by grain length (26.44%), zinc content (7.60%),grain breadth (5.07%), test weight (4.71%), panicle length and iron content (0.72%). Theremaining characters *viz.*, days to 50 per cent flowering, number of tillers per plant,number of productive tillers per plant and L/B ratio did not contribute significantly to thetotal divergence. Contribution of each character towards genetic divergence has beenestimated from the number of times that each character appeared in the first rank. It hasbeen observed that grain yield per plant contributed the maximum towards the geneticdivergence followed by grain length, zinc content and test weight, indicating the majorrole of these characters in differentiating of inter-cluster levels. Similar observations havebeen recorded by Das *et al.* (2004) and Roy *et al.* (2004) while Zaman*et al.* (2005)reported grain yield as the least contributing character towards genetic diversity in rice.The above results imply that, in order to select genetically diverse genotypes forhybridization, the material should be screened for the important traits like, grain yield,grain length, zinc content and test weight.

Table 4. Per cent contribution of twelve characters towards diversityintwenty four aromatic rice genotypes

Sl. No.	Character	Per cent contribution
1.	Days to 50 % flowering	Trace
2.	Plant height (cm)	0.72
3.	Number of tillers per plant	Trace
4.	Number of productive tillers per plant	Trace
5.	Panicle length (cm)	2.17
6.	Grain length (mm)	26.44
7.	Grain breadth (mm)	5.07
8.	L/B ratio	Trace
9.	Test weight (g)	4.71
10.	Iron content (mg kg^{-1})	0.72
11.	Zinc content (mg kg^{-1})	7.60
12.	Grain yield per plant (g)	52.53
	Total	**100**

Table5. The mean values of clusters for twelve characters in twenty four aromatic rice genotypes

Cluster	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}
I	115.33	85.50	21.67	17.83	21.28	10.93	1.72	6.36	20.75	7.58	21.00	11.12
II	113.58	92.92	24.75	19.75	19.43	7.83	1.75	4.47	17.23	7.89	17.34	13.30
III	112.13	86.07	23.73	19.40	21.10	10.80	1.68	6.45	21.65	7.23	18.22	12.69
IV	118.92	82.46	23.17	18.75	19.41	9.17	1.80	5.12	20.31	9.29	19.05	12.72
V	118.56	117.33	21.78	18.00	22.71	8.70	1.89	4.61	23.24	16.18	35.40	13.53
VI	109.33	109.50	21.17	16.83	21.58	6.40	1.72	3.72	12.78	11.19	24.85	14.26

X_1-*Days to 50 % flowering* X_2-*Plant height (cm)* X_3-*Number of tillers per plant*
X_4-*Number of productive tillers per plant* X_5-*Panicle length (cm)* X_6-*Grain length (mm)*
X_7-*Grain breadth (mm)* X_8- *L/B ratio* X_9-*Test weight (g)*
X_{10}- *Iron content (mg kg^{-1})* X_{11}- *Zinc content (mg kg)$^{-1}$)* X_{12}-*Grain yield per plant (g)*

The mean values of twelve characters studied in 24 rice genotypes for six clustersare presented in Table 5. The cluster VI (109.33 days) had the early flowering genotypeswhereas, cluster IV (118.92 days) had the late flowering genotypes. The genotypes of cluster IV (82.46 cm) were dwarfest while, genotypes of cluster V (117.33 cm) weretallest compared to other clusters. Cluster I had the genotypes with lowest number oftillers per plant (21.17) and productive tillers per plant (16.83) on contrary, the cluster IIhad the genotypes with highest number of tillers per plant (24.75) and productive tillersper plant (19.75). The genotypes lying in the cluster IV had shortest panicle length of19.41 cm while, the genotypes in cluster V had longest panicle length of 22.71 cm.

The mean grain length was lowest in cluster VI (6.40 mm) and highest in cluster I(10.93 mm). The genotypes of cluster III had slender grains of 1.68 mm while, cluster Vhad bolder grains of 1.89 mm. The L/B ratio was lowest in cluster VI (3.72) and highestin cluster III (6.45). The genotypes in the cluster V had highest iron (16.18 mg kg-1) andzinc (35.40 mg kg-1) content whereas, the genotypes in the cluster III and II had lowestiron (7.23 mg kg-1) and zinc (17.34 mg kg-1) content respectively. Cluster I had thelowest yielding genotypes with a mean of 11.12 g per plant and the cluster VI had thehighest yielding genotypes with a mean of 14.26 g per plant.

CONCLUSION

Hence, it is worthy to notethat in calculating cluster means, the superiority of particular genotype in respect to agiven character get diluted by other genotype that are related and grouped in the samecluster but which are inferior or intermediary for that character in question. Hence, apartfrom selecting genotypes from the clusters which have high inter-cluster distance forhybridization, one can also think of selecting genotypes based on extent of

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geneticdivergence in respect to a particular character of interest. This is to mean that, if breeder'sintention is to improve grain yield, he can select genotypes which are highly divergentwith respect to these characters.

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