SHORT COMMUNICATION

Study of genetic diversity for agro-morphological and quality characters in diverse aromatic rice germplasm

Rita Chopkar* and AK Sarawgi

College of Agriculture, Indira Gandhi Agriculture University, Raipur-492012, Chhattisgarh, India
*Corresponding author e-mail: ritachopkar@gmail.com

ABSTRACT

Grain quality has always been an important consideration in rice variety selection and development. Fine grained aromatic rice fetch higher demand than the normal variety in national as well as international market. Indian sub continent has rich diversity of short grain aromatic rice grown in various parts of country while long grain basmati types are confined to the north-western region. Knowledge of genetics of aroma would help in deciding the breeding procedure to evolve the scented varieties. In the present study 81 aromatic rice germplasm, collected from different locations of Chhattisgarh were evaluated for divergence analysis. Observations were recorded on five randomly selected plants for 16 agro-morphological and quality characters. Based on relative magnitude of D^2 estimates 81 genotypes which were grouped into nine clusters. A wide range of variation was observed in cluster means for all the characters studied. The genotypes from cluster II having desired mean value for quality characters like hulling, milling and head rice recovery percentage and panicle length; cluster VII having high value for kernel length and length breadth ratio and cluster V for earliness and high yield could be incorporated in hybridization for developing high yielding, early maturing with good quality aromatic rice variety.

Key words: Germplasm, morphological characters, aromatic rice, genetic diversity

Asian cultivated rice (*Oryza sativa* L.) is one of the most important crops in the world. Rice not only serves as a primary food source for more than half of the world's population, but also provides an excellent model system for studying a wide range of biological questions (Wang et al., 2014). Grain quality has always been an important consideration in rice variety selection and development. Fine grained aromatic rice fetch higher demand than the normal variety in national as well as international market. Indian sub continent has rich diversity of short grain aromatic rice grown in various parts of country, while long grain basmati types are confined to the north-western region. Knowledge of genetics of aroma would help in deciding the breeding procedure to evolve the scented varieties. Rice the dietary staple food for more than three million people is grown worldwide in diverse agro-climatic zones. Grain quality in rice has been assuming an increasingly important issue particularly since last decade due to

change in the consumer preference for better quality rice as a result of changed life style of the consumers in the country and India's emergence as one of the major exporters of rice in the international markets. Aromatic/quality rice is a special class of rice with high market value due to its superior grain qualities and pleasant aroma (Roy et al., 2015). The demand for special purpose aromatic rice has dramatically increased over the past two decades and the success of any breeding programme depends upon the selection of the parents for hybridization. Genetic divergence among the genotypes play an important role in the selection of parents having wider variability for different agronomical and quality characters (Nayak et al., 2004; Pradhan and Mani, 2005).

The experimental material consisted of 81 aromatic rice germplasm including check Nagri Dubraj. The diversified accessions collected from different parts

Table 1. Clustering pattern of 81 aromatic rice germplasm

Cluster No.	No. of genotypes	Genotypes
I	4	NDR IRRI69,NDR IRRI-75,NDR IRRI 347,Sabarmati
II	11	Kalajauvan, Lectimachi-A,Lectimachi-B,Karpurkranti,Basmati-B,Kalanamak 1,Kalanamak 2,ASGPC-19,Biloni, Urai Butta,Chebdra Chhal
III	4	KGSR-3-1-1,IGSR-3-1-5,IGSR-2-1-6,Latera
IV	12	Lajkuli badan,Kanika bhog,Heera Kani,Basni, Parijat,Jalaka,Kalajeevan, Pimpudibasa,Takkuranana, IGSR-3-1-2A,IGSR-3-1-40,ASGPC-12,ASGPC-14
V	4	Hankesh,Lalmati, Lal kahwa,Ramdhuri
VI	22	Malasia,Bayasa Bhog,Muni Bhog, Chitar bhog, Duban Mua,Dudga,Dudgi,Dudh Nag, Dudhraj, Ganjo, Garrakat,Jhilli Safri,Jhulari, Karunji pghool.Rajin 7,Rajin 12,Ram Kli,Tulsi Bhog,Mohan Bhog,Raja Bhog,Kubrimohar
VII	7	NDR IRRi 2004,Duleraj,Dulharia,Yamini, Tarori Basmati,Pusa Basmati-1,Vasmati
VIII	11	Chhabiswa, Kheerasai,NDR IRRi 67,NDR IRRI 3131,Katari bhog, Badshapasand, Kalanamak 3, ASGPC-34, ASGPC-38,ASGPC-39,N.Dubraj.
IX	6	Chhatri Bhog,LoktiMusi,Tenduphool,Sonth,Type-3,Basmati 370

of country under ICAR network project in Aromatic Short Grain 1 trial (ASG1). The trial was sown in randomized block design with two replications. The analysis of genetic divergence using Mahalanobis D^2 (1936) statistics was done as described by Spark (1973) and grouping the genotypes were done into different clusters. Twenty five days old seedlings were transplanted with a spacing of 20cm and 15 cm between rows and between plant, respectively. Observations were recorded on five randomly selected plants for 16 agro-morphological and quality characters.

Based on relative magnitude of D^2 estimates, 81 genotypes were grouped into nine clusters. Among the different clusters (Table 1), cluster VI contains maximum 22 genotypes and Cluster I, III and V contains a minimum of 4 genotypes each. The cluster II and VIII possessed 11 genotypes each; Cluster IV 12; cluster VII 7 and Cluster IV contain 6 genotypes. A wide range of variation was observed in cluster means for all the character studied. The clustering pattern of genotypes revealed that the genotypes originated in

different states were clustered together or genotypes originated from the same states were distributed in different clusters. It indicated that there was no parallism between clustering pattern and geographical distribution of genotypes (UshaKumari and Rangaswami, 1997). The cluster V and VI having highest and lowest value for character, days to 50% flowering, cluster VIII and IX characterized by highest and lowest value for character total tiller per hill and effective tillers per hill respectively. The cluster VII characterized lowest mean value for characters spikelet fertility percentage, hulling percentage, milling percentage, head rice recovery percentage, kernel breadth and highest value for kernel length and L/B ratio. The cluster V characterized highest mean value for grain yield (Kg/ha) and lowest value by cluster IX (Table 2). The highest mean value for hulling percentage, milling percentage and head rice recovery characterized by cluster II. The genotypes kubrimohar, Mohan bhog, Malaysia, Duban Mau from cluster II and

Table. 3 Average intra (bold) and inter cluster distance values

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX
I	**2.169**	6.114	3.631	5.851	2.916	4.721	3.773	5.223	4.520
II		**2.224**	5.478	3.256	5.443	3.214	7.323	3.004	5.313
III			**2.433**	4.100	4.861	5.210	4.843	4.677	4.862
IV				**2.431**	5.523	4.119	7.054	3.197	6.099
V					**2.822**	4.588	4.563	4.862	5.792
VI						**1.803**	5.827	3.552	4.604
VII							**2.323**	5.575	5.156
VIII								**2.725**	5.321
IX									**3.319**

Table 2. Cluster mean values for 16 agro-morphological and quality characters of 81 aromatic rice germplasm

Characters/ cluster	DF(50%)	PH(cm)	PL(cm)	TT/hill	ET/hill	FG/p	UFG/p	SF%	TW(g)	Hull%	Mill%	HRR%	KL(mm)	KB(mm)	L/Bratio	GY(Kg/ha)
I	87.62	110.75	25.38	8.82	7.38	119.97	26.94	82.12	23.90	78.76	77.14	38.58	6.86	2.09	3.30	4864.00
II	113.18	173.27	27.85	9.45	8.13	173.16	19.89	89.60	13.67	83.22	81.20	67.11	4.55	2.10	2.18	4255.09
III	93.12	142.73	27.12	9.10	7.35	156.11	54.96	73.88	18.41	79.18	75.07	31.05	5.25	2.08	2.54	4062.50
IV	112.38	149.69	25.32	10.47	9.17	192.40	48.84	79.89	11.99	80.17	78.37	66.26	4.20	2.10	2.00	4571.75
V	78.25	119.83	26.12	9.27	8.42	120.35	20.98	84.65	17.76	80.35	78.46	64.54	6.54	1.84	3.59	5165.25
VI	116.07	147.65	21.36	9.12	7.81	172.93	16.18	91.27	16.96	81.53	80.35	56.25	5.77	2.00	2.90	3352.34
VII	94.50	138.64	26.57	11.36	8.31	79.39	21.56	77.33	21.78	76.96	74.97	30.01	7.40	1.83	4.06	2321.43
VIII	111.68	174.66	26.76	12.13	10.43	153.40	23.77	86.81	15.62	80.38	77.82	55.44	5.40	2.06	2.64	4646.50
IX	108.33	166.58	25.92	8.72	6.07	86.13	25.85	76.58	25.85	81.73	80.54	42.60	6.64	2.31	2.94	2013.75

DF(50%)- Days to 50% flowering, PH(cm)- Plant height, PL(cm)-Panicle length, TT/hill-Total tillers/hill, ET/hill-Effective tillers/hill, FG/p-Fertile grains/panicle, UFG/p-Unfertile grain/panicle, SF%- Spikelet fertility%, TW(g)-Test weight, Hull%-Hulling %, Mill%-Milling %, HRR%-Head rice recovery%, KL(mm)-Kernel length, KB(mm)-Kernel breadth, L/B ratio-Length/Breadth ratio GY(Kg/ha), Grain yield (Kg/ha)

Lokti Musi and Tenduphool from cluster IX can be utilized for hybridization programme due to highest genetic variation differences. The inter-cluster distance (Table 3) ranged from 2.916 to 7.323 between cluster I and V and II and VII, respectively. The lowest and highest intra-cluster distance was observed in cluster VI and IX, respectively. The selection will be desirable when selection of parents should be done from two cluster having wider inter-cluster distance to get more variability and high heterotic effect (Mishra et al., 2003; Chaturvedi and Maurya, 2005; Shekhawat et al., 2015). The genotypes from cluster II (Kalajavan, Lectimachi-B, Karpurkranti, ASGPC-19) having desired mean value for quality characters like hulling percentage, milling percentage and head rice recovery and panicle length, cluster VII (Dulharia, Yamini ,Taroari Basmati, Vasmati) having high value for kernel length and L/B ration and cluster V(Hankesh) low value for days to 50 percentage flowering but highest value for grain yield (Kg/ha). This may be used in hybridization programme to achieve desired segregants for good grain quality with higher yield. In order to successfully meet future food requirement, it is necessary to manage the continuing genetic erosion and address the issues of genetic conservation and optimum utilization of what remains of the genetic diversity of important rice crop plants.

REFERENCES

Chaturvedi HP and Maurya DM (2005). Genetic divergence analysis in rice (*Oryza sativa* L.) Ad. Plant Sci. 18(1): 349-353

Mahalanobis PC (1936). On the generalized distance in statistics. Proc. Natl. Inst. Sce. India 2: 49-55

Mishra LK, Sarawgi AK and Mishra RK (2003). Genetic diversity for morphological and quality traits in rice (*Oryza sativa* L.) Ad. Plant Sci. 16(1): 287-293

Nayak AR, Chaudhury D and Reddy JN (2004). Genetic divergence in scented rice. Oryza 41(3&4): 79-82

Pradhan SK and Mani SC (2005). Genetic diversity in basmati rice. Oryza 42(2): 150-152

Somnath R, Amrita B, Mawkhlieng B, Misra AK, Pattanayak A, Harish GD, Ngachan SK, Bansal KC (2015). Genetic diversity and population structure in aromatic and quality rice (*Oryza sativa* L.) landraces from North-Eastern India. PLoS ONE 10(6): e0129607

Shekhawat HVS, Singh RP, Agrawal RK, Singh SP and Prasad R (2015). Study of genetic variability and diversity in germplasm lines of rice. Oryza 52(2): 87-92

Spark DN (1973). Algorithm as 58 applications. Statistics 22(1): 19-25

Ushakumari R and Rangaswamy P (1997). Studies on genetic diversity in international early rice genotypes. Ann. Agric. Res. 18(1): 29-33

Wang CH, Zheng XM , Xu Q , Yuan XP , Huang L, Zhou HF , Wei XH and Ge S (2014). Genetic diversity and classification of *Oryza sativa* with emphasis on Chinese rice germplasm. Heredity 112: 489-496