Prerna Chouhan
Department of Genetics and
Plant Breeding, College of
Agriculture, Indira Gandhi
Krishi Vishwavidyalaya, Raipur,
Chhattisgarh, India

Madhuri Singh
Department of Genetics and
Plant Breeding, College of
Agriculture, Indira Gandhi
Krishi Vishwavidyalaya, Raipur,
Chhattisgarh, India

Sunil Kumar Nair
Department of Genetics and
Plant Breeding, College of
Agriculture, Indira Gandhi
Krishi Vishwavidyalaya, Raipur,
Chhattisgarh, India

Sandeep Bhandarkar
Department of Genetics and
Plant Breeding, College of
Agriculture, Indira Gandhi
Krishi Vishwavidyalaya, Raipur,
Chhattisgarh, India

Study of genetic diversity for yield and yield contributing traits in rice (*Oryza sativa* L.)

Prerna Chouhan, Madhuri Singh, Sunil Kumar Nair and Sandeep Bhandarkar

DOI: https://doi.org/10.22271/chemi.2021.v9.i2g.11863

Abstract
Genetic diversity analysis through cluster were performed in selected 96 aromatic rice genotypes inclusive six checks and were distributed into 15 clusters for 16 quantitative yield related characters. In this, there were 2 genotypes in cluster I, 11 in cluster II, 8 in cluster III, 5 in cluster IV, 7 in cluster V, 12 in cluster VI, 5 in cluster VII, 8 in cluster VIII, 8 in cluster IX, 6 in cluster X, 2 in cluster XI, 3 in cluster XII, 6 in cluster XIII, 7 in cluster XIV, 6 in cluster XV. Cluster XIII showed highest mean performance for grain yield per plant i.e 18.42 followed by cluster VII i.e 12.47. Hence, the genotypes showing high mean performance should be inter-crossed from diverse cluster which will be helpful to produce better recombinations whose genetic variability is high.

Keywords: Aromatic rice, genetic diversity, cluster analysis, mean

Introduction

Aromatic rice considered as an important part among the sub-group of rice having best quality with much higher price than high quality non-aromatic rice in international market. It is known for its nut like aroma and taste caused by the chemical compound 2-acetyl-1-pyrroline. Generally in India, the aromatic rice Basmati known as 'Queen of Fragrance' is famous for its fragrance and delicate flavour.

In recent years, in both traditional and non-traditional rice-growing countries the demand for aromatic rice is arousing at a faster rate. Since aromatic rice has been very appetizing and flavoursome, it is highly preferred.

Among the civilians aromatic rice has led to large scale of popularity owing to its globalization, culinary changes and health benefits. Intensive breeding efforts was the main reason in the reduction of genetic diversity of modern rice cultivars (Cuevas-Perez *et al.* 1992; Dilday 1990) [2, 3]. Genetic uniformity could become a problem for the selection of germplasm to develop improved varieties.

A more diverse germplasm would enhance the selection efficiency of desirable varieties in the rice breeding programs. However, this method has some demerits with respect to time, space, and labour cost along with the accurate level of genetic diversity among the germplasms also remain unknown.

Study of genetic divergence among the plant materials is a vital tool to the plant breeder for an efficient choice of parents for crop improvement. Genetically diverse parents are likely to contribute desirable segregants and/or high heterotic crosses. Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them.

In the present investigation, an attempt was made to classify the extent of genetic diversity for certain yield and quality traits in scented rice genotypes for ultimate use in hybridization programme.

Material and Methods

The experiment was carried out at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidalaya, Raipur, (C.G.), India. Ninty six germplasm lines inclusive six checks (Table 1) available at Rice germplasm, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) were used during kharif,

Corresponding Author:
Prerna Chouhan
Department of Genetics and
Plant Breeding, College of
Agriculture, Indira Gandhi
Krishi Vishwavidyalaya, Raipur,
Chhattisgarh, India

2018 for the analysis of genetic diversity. Observations were recorded for 16 yield related characters such as Days to 50 per cent flowering, Plant height (cm), Stem thickness (cm), Number of productive tillers per plant, Productive tilers, Panicle length of main axis (cm), Panicle number per plant, Panicle weight per plant (g), Number of spikelets per panicle, Number of filled & unfilled spikelets per panicle, Grain length (mm), Grain width (mm), Biological yield per plant (g), Harvest index (%), Grain weight of 1000 fully developed grains (g), Grain yield per plant (g).

Genetic diversity analysis

Estimated through cluster analysis in which all the 96 genotypes were grouped into fifteen clusters as shown in (Table 2), gives an idea about the significant amount of genetic diversity in the material with the help of two methods namely, Tocher and Euclidean method (Rao, 1952) [4] have been used along with cluster distribution in dendogram form shown in (Fig.1) using Agglomerative Clustering Method.

Cluster mean

Cluster means were calculated for all the physiological and agronomic characters which showed significant differences among the clusters. Out of 96 genotypes studied, with the help of cluster mean performance (Table 3), we can select genetically diverse and agronomically superior genotypes.

Result and Discussion

The cluster-VI had maximum number of genotypes (12) followed by cluster-II (11), cluster-III,VIII, IX (8), cluster-V,XIV (7), cluster-X, XIII, XV (6), cluster-IV,VII (5), cluster-XII (3), cluster-I, XI (2). The cluster-I consists of genotypes *viz.*, Anterved and Jou Phool. The genotypes of cluster-II consists of Elaychi, Lokti Machhi, Shri Kamal, Chinnor, Bisni, Laxmi Bhog, K. Phool (K:1209), K. Phool (K:2209), K. Phool (K:2283), K. Phool (K:2382) And K. Phool (K:25II). Cluster–III having the genotypes *viz.*, Tulsi Manjari, Shyam Jira-2, Lohandi, Jai Gundi, Fundri, Tilkasturi, Dhaniyaphool And Bansmati. Cluster-Iv Consists Of Genotypeskera Ghul, Samund Chini, Ganga Baru, Katarni Bhog And Jou Phool-2. Cluster-V Consists Of Kubri Mohar, Bans Patri, Bhanta Phool-2, Samudra Fan Safed Jira, Tulsi Mala And B. Bhog (B:973). Cluster-VI Consist of Sham Jira, Shyam Jira-1, Ganga Prasad, Badshah Bhog-2, Vishnu Bhog, Shital Bhog, Kari Gillas, Chhatri-2, Jira Dhan, Bhanta Phool-1, Vishnu Bhog S-1 And Badshah Bhog S-1. Cluster-VII consists of Muni Bog, Badshah Bhog-1, Amrit Bhog, Jeera Phool and Tulsi Mongra. Cluster-VIII consists of Kapoor Sar, Kali Kamod, Sukala Phool, Dhawara Sawa, Lahsun Bhog, B.Bhog (B:381), B. Bhog (B:667) and B. Bhog (B:799II). Cluster-IX consists of Jata Shankar, Tedesi, Chini Kapoor, Tulsi Prasad, Ichchawati, Jonja Phool and Nangodar Barhasal. Cluster-X consist of Dubraj Dubraj (D:26), Dubraj (D:33A), Dubraj (D:35), Dubraj (D:80) and Indira Sugandhit Dhan-1. Cluster-XI consist of Thakur Bhog and Tarun Bhog S-1. Cluster-XII consists of Raja Bhog, Bhainsa Punchhi and Kala Jira. Cluster-XIII consists of Bag Muchh, Chhatri-1, Mai Dubraj, Tulsi Manjar, B. Bhog (B:2297) And Dubraj (D:33BI). Cluster-XIV consists of Atma Shital, Nawab Bhog, Dujai, Loung Phool, B. Bhog (B:323I), B. Bhog (B:1010) and B. Bhog (B:2354). Cluster-XV consists of Dubraj (D:18II), Dubraj (D:19I), Dubraj (D:22I), Dubraj (D:76I), Dubraj S-1 and C.G. Sugandhit Bhog. The clustering pattern of genotypes indicated existence of significant amount of variability, which was in conformation with the findings of Soni *et al.* (1999) [5] and Ahmed *et al.* (2010) [1].

Table 1: List of 96 genotypes of aromatic rice used in the study

S.N.	Accession Name	S.N.	Accession Name	S.N.	Accession Name
1	Anterved	33	Chini Kapoor	65	Tulsi Manjar
2	Elaychi	34	Bag Muchh	66	Jou Phool-2
3	Tulsi Manjari	35	Chhatri-1	67	Jeera Phool
4	Kera Ghul	36	Chhatri-2	68	Tulsi Mongra
5	Kubri Mohar	37	Bisni	69	Kadam Phool(K:1209)
6	Sham Jira	38	Lohandi	70	Kadam Phool(K:2209)
7	Shyam Jira-1	39	Atma Shital	71	Kadam Phool(K:2283)
8	Shyam Jira-2	40	Jira Dhan	72	Kadam Phool(K:2382)
9	Lokti Machhi	41	Dhawara Sawa	73	Kadam Phool(K:25ii)
10	Bans Patri	42	Jai Gundi	74	B.Bhog(B:323i)
11	Ganga Prasad	43	Tulsi Prasad	75	B.Bhog(B:381)
12	Muni Bog	44	Bhainsa Punchhi	76	B.Bhog(B:667)
13	Badshah Bhog-1	45	Bhanta Phool-1	77	B.Bhog(B:799ii)
14	Badshah Bhog-2	46	Bhanta Phool-2	78	B.Bhog(B:973)
15	Vishnu Bhog	47	Samudra Fan	79	B.Bhog(B:1010)
16	Shri Kamal	48	Fundri	80	B.Bhog(B:2297)
17	Shital Bhog	49	Lahsun Bhog	81	B.Bhog(B:2354)
18	Samud Chini	50	Nawab Bhog	82	Dubraj (D:18ii)
19	Kapoor Sar	51	Tilkasturi	83	Dubraj (D:19i)
20	Kali Kamod	52	Ichchwati	84	Dubraj (D:22i)
21	Sukala Phool	53	Mai Dubraj	85	Dubraj (D:26)
22	Chinnor	54	Dujai	86	Dubraj (D:33a)
23	Jou Phool	55	Jonja Phool	87	Dubraj (D:33bi)
24	Jata Shankar	56	Kala Jira	88	Dubraj (D:35)
25	Dubraj	57	Laxmi Bhog	89	Dubraj (D:76i)
26	Ganga Baru	58	Nangodar	90	Dubraj (D:80)
27	Amrit Bhog	59	Barhasal	91	Tarun Bhog Selection-1 (Check)
28	Thakur Bhog	60	Dhaniya Phool	92	Dubraj Selection-1 (Check)
29	Raja Bhog	61	Loung Phool	93	Vishnu Bhog Selection-1 (Check)
30	Kari Gilas	62	Bansmati	94	Indira Sugandhit Dhan-1 (Check)

| 31 | Tedesi | 63 | Safed Jira | 95 | C.G. Sugandhit Bhog (Check) |
| 32 | Katarni Bhog | 64 | Tulsi Mala | 96 | Bhadsha Bhog Selection-1 (Check) |

Table 2: Distribution pattern of 90 genotypes inclusive six checks under different clusters

| Clusters	No. of Genotypes	Genotypes
Cluster-I	2	ANTERVED, JOU PHOOL
Cluster-II	11	Elaychi, Lokti Machhi, Shri Kamal, Chinnor, Bisni, Laxmi Bhog, K. Phool(K:1209),K.Phoolk:2209), K. Phool(K:2283), K.Phool(K:2382),K.Phool(K:25ii)
Cluster-III	8	Tulsi Manjari, Shyam Jira-2, Lohandi, Jai Gundi, Fundri, Tilkasturi, Dhaniyaphool, Bansmati
Cluster-IV	5	Kera Ghul, Samund Chini, Ganga Baru, Katarni Bhog, Jou Phool-2
Cluster-V	7	Kubri Mohar, Bans Patri, Bhanta Phool-2, Samudra Fan, Safed Jira, Tulsi Mala, B.Bhog(B:973)
Cluster-VI	12	Sham Jira, Shyam Jira-1, Ganga Prasad, Badshah Bhog-2,Vishnu Bhog, Shital Bhog, Kari Gillas, Chhatri-2, Jira Dhan Bhanta Phool-1, Vishnu Bhog S-1, Badshah Bhog S-1
Cluster-VII	5	Muni Bog, Badshah Bhog-1, Amrit Bhog, Jeera Phool, Tulsi Mongra
Cluster-VIII	8	Kapoor Sar, Kali Kamod, Sukala Phool, Dhawara Sawa, Lahsun Bhog, B.Bhog(B:381), B.Bhog(B:667), B.Bhog(B:799ii)
Cluster-IX	8	Jata Shankar, Tedesi, Chini Kapoor, Tulsi Prasad, Ichchawati, Jonja Phool, Nangodar, Barhasal
Cluster-X	6	Dubraj Dubraj (D:26), Dubraj (D:33a), Dubraj (D:35), Dubraj (D:80), Indira Sugandhit Dhan-1
Cluster-XI	2	Thakur Bhog, Tarun Bhog S-1
Cluster-XII	3	Raja Bhog, Bhainsa Punchhi, Kala Jira
Cluster-XIII	6	Bag Muchh, Chhatri-1, Mai Dubraj, Tulsi Manjar, B.Bhog(B:2297), Dubraj (D:33bi)
Cluster-XIV	7	Atma Shital, Nawab Bhog, Dujai, Loung Phool B. Bhog(B:323i), B.Bhog(B:1010), B.Bhog(B:2354)
Cluster-XV	6	Dubraj (D:18ii), Dubraj (D:19i), Dubraj (D:22i), Dubraj (D:76i), Dubraj S-1, C.G. Sugandhit Bhog
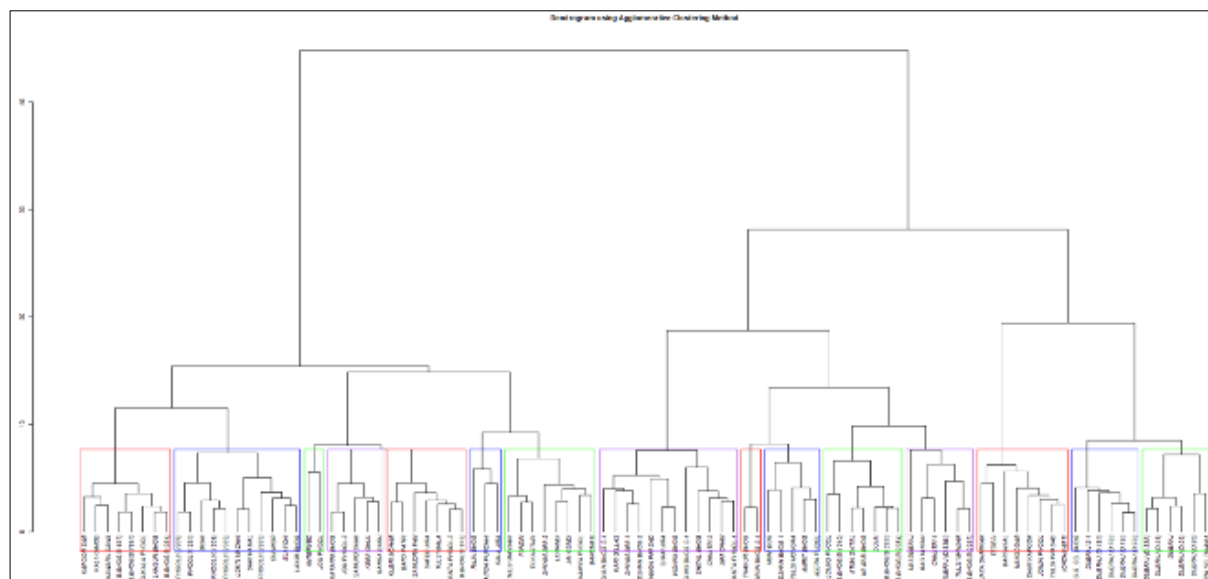
Fig 1: Dendrogram using Agglomerative Clustering Method

Table 3: Cluster Means for 16 yield related characters

Clusters	DTF	PH	ST	NTPP	PT	PL	PNPP	PWPP	NOS	NFS	1000 GW	GL	GW	GYPP	BY	HI
Cluster-I	101.50	127.25	0.55	9.38	8.12	24.50	5.50	4.88	138.88	115.50	7.67	6.65	2.05	1.86	54.25	28.85
Cluster-II	88.36	127.12	0.55	10.11	9.39	24.71	9.43	8.34	148.52	119.80	13.00	6.65	2.34	4.90	25.14	19.49
Cluster-III	94.50	148.81	0.61	8.12	7.88	27.30	7.75	9.72	195.56	166.38	11.50	6.21	2.27	6.47	24.00	26.91
Cluster-IV	105.20	136.22	0.48	9.60	8.95	26.34	9.25	8.20	173.35	137.20	9.01	6.22	2.10	3.68	23.60	16.54
Cluster-V	99.29	138.17	0.54	8.75	8.25	28.29	6.54	7.50	148.68	111.00	11.58	6.79	2.24	4.54	18.29	25.14
Cluster-VI	97.08	148.40	0.58	14.15	12.33	27.78	12.17	15.02	174.10	135.54	10.90	6.66	2.31	9.31	35.04	27.03
Cluster-VII	94.20	142.78	0.55	12.05	11.25	26.79	11.70	16.25	249.85	214.20	8.74	5.94	2.32	12.47	35.35	36.48
Cluster-VIII	97.38	154.99	0.54	11.22	10.56	27.27	10.09	9.97	147.28	116.81	12.86	7.12	2.34	6.14	26.59	23.41
Cluster-IX	93.25	149.10	0.59	9.50	9.12	26.63	8.72	16.34	146.81	125.75	19.01	8.79	2.54	12.84	42.41	30.60
Cluster-X	102.00	119.40	0.56	12.79	11.71	21.02	10.71	14.50	161.21	138.25	16.06	8.30	2.33	10.28	36.21	32.55
Cluster-XI	103.00	133.15	0.56	12.12	11.88	23.19	10.50	23.75	230.12	208.62	11.36	5.70	2.40	17.65	65.75	26.86
Cluster-XII	96.67	147.50	0.56	9.58	8.67	27.43	9.17	10.25	182.58	171.25	12.57	7.47	3.10	7.55	26.00	27.90
Cluster-XIII	99.17	140.71	0.55	11.08	10.58	24.18	10.67	18.92	184.17	146.25	10.76	6.00	2.00	15.36	25.00	40.70
Cluster-XIV	101.14	147.16	0.53	9.57	9.32	26.36	8.89	13.64	197.50	163.00	9.87	5.10	2.10	6.80	24.25	28.05
Cluster-XV	102.00	110.19	0.55	9.25	9.04	20.52	8.46	11.83	155.00	113.75	14.09	6.90	2.00	5.25	20.00	22.07

Note: DTF - Days to 50% Flowering, PH - Plant Height, ST - Stem Thickness, NTPP - Number of Tillers Plant-1, PT - Productive Tillers, PL - Panicle Length of main axis, PNPP - Panicle Number Plant-1, PWPP - Panicle Weight Plant-1, NOS - Number of Spikelets Panicle-1, NFS - Number of Filled Spikelets Panicle-1, 1000 GW- 1000 Grain Weight, GL - Grain Length, GW - Grain width, GYPP - Grain Yield Plant-1, BY- Biological Yield, HI - Harvest Index.

Conclusion
It is clear from the above results that the cluster mean for various quantitative traits related to yield attributes revealed that different cluster respond differentially for various traits. Cluster XI showed highest mean performance for grain yield per plant i.e 17.65 followed by cluster XIII i.e 15.36. Hence, the result recommend genotypes present in these clusters showing high mean performance should be inter-crossed from diverse cluster which will be helpful to produce better recombinants for yield purpose and can be used in our crop improvement programme. Similarly for other traits like earliness, we should select cluster having lowest cluster mean i.e cluster II (88.36), cluster-X (16.06) should be selected for 1000 grain weight whereas if we want to select for dwarf plant height then cluster VIII (154.99) must be selected.

References
1. Ahmed MS, Khaleda Akter, Khalequzzaman M, Rashid ESMH, Bashar MK. Diversity analysis in boro rice (*Oryza sativa* L.) accessions. Bangladesh J Agrl. Res 2010;35(1):29-36.
2. Cuevas-Perez FE, Guimaraes EP, Berrio LE, Gonzalez DI. Genetic base of irrigated rice in Latin America and the Caribbean. Crop. Sci. 1992;32:1054-1059.
3. Dilday RH. Contribution of ancestral lines in the development of new cultivars of rice. Crop. Sci. 1990;30:905-911.
4. Rao CR. Advanced statistical methods in biometrical research. John Wiley and Sons Inc., New York 1952, 236-272.
5. Soni DK, Sarawgi AK, Rastogi NK. Genetic divergence in traditional rice accessions of Madhya Pradesh India. *Oryza* 1999;36(2):118-120.