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Cluster Analysis and Correlation Study for Yield Attributing Traits in Aromatic Rice Landraces (*Oryza sativa* L.)

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A B S T R A C T

Quantum of genetic variability and the extent to which heritable and non-heritable variations are related to the characters, determines the extent of genetic amelioration. The present investigation was carried out in *kharif,* 2019 to understand the clustering pattern and correlation for yield attributing traits in aromatic landraces of rice. Here 90 aromatic rice landraces along with six check varieties were evaluated for 10 quantitative characters. Cluster analysis divided these 96 rice genotypes into 4 clusters. Highest inter cluster distance was observed between Cluster II and III suggesting maximum variability between them. Maximum heterotic crosses can be obtained by crossing between genotypes of Cluster II and Cluster III which can be used for rice improvement programme. Correlation analysis revealed that grain yield plant^{-1} was having positive and significant correlation with panicle weight, thousand grain weight and grain length indicating the importance of these traits for yield improvement. Selection on any of these characters will have a direct response on grain yield of aromatic rice.

Keywords

Aromatic rice, cluster analysis, correlation analysis, rice, landraces

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Introduction

India has a rich and diverse genetic wealth of aromatic rice. Every state in India has its own set of aromatic rice which is used for special dish preparation. Aromatic rice landraces are the basic indispensable ingredient in their breeding programmes. Exploring diversity in landrace collection of aromatic rice is very important for identifying new genes for its further improvement. To recognize the useable variability, grouping or classification of genetic stocks based on minimum divergence or resemblance between them is quite essential (Chakraborty and Chaturvedi, 2014). Majority of Indian aromatic rice genotypes are having small to medium grains. These indigenous aromatic rice genotypes are endowed with tremendous genetic variability and are vital genetic resources for biotic and abiotic stress tolerance and improved nutritional characteristics. The improvement of these indigenous aromatic rice which possess outstanding quality like aroma, kernel elongation after cooking, fluffiness and taste were somewhat neglected because of their low yield. Aroma and taste of Badshahbhog and Dubraj short grained aromatic rice is known to be superior to Basmati types (Hossain *et al.*, 2009). Genetic diversity of morphological traits can directly provide information on germplasm richness. According to Wattoo *et al.*, (2010), grain yield is a complex trait that depends upon different yield attributing traits. Correlation of different characters with yield enables the breeder to understand the mutual component characters on which selection can be based for genetic improvement. The present study was therefore undertaken to study the clustering pattern and correlation in aromatic rice landraces for yield attributing traits.

Materials and Methods

This experiment was carried out at Research cum Instructional Farm of Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh), India during *kharif* 2019. Geographically, Chhattisgarh state lies between 17°14' to 24°06' North Latitudes and 80°14' to 84°24' East Longitude. Raipur, the capital of Chhattisgarh, is situated in East Central part of state at latitude of 21°16' N, longitude 81°36' E and at an altitude of 289.6 meters above mean sea level. The climate of the region is sub-humid with mean annual rainfall of about 1489 mm. The experimental material consists of 96 rice genotypes. Here, a core set of 90 aromatic landraces was prepared from 571 aromatic germplasm lines of I.G.K.V., Raipur, Chhattisgarh based on the aroma content of their leaves by KOH Sensory test method (Sood and Siddique, 1978). These 90 aromatic rice landraces along with six check varieties namely, Mahamaya, Tarun Bhog Selection1, C.G. Devbhog Selection1, Badshah Bhog Selection1, Vishnu Bhog Selection1 and Dubraj Selection1 were taken in the present study.

Nursery sowing was done in well prepared raised seed bed in first week of July 2019. Twenty eight days old seedlings were transplanted in well puddle field in Augmented Block Design as suggested by Federer, 1956. Each rice genotype was transplanted in two rows of 2m row length. The distance between each block was maintained at 50cm. The randomization of check varieties was done within each block. Each genotype was transplanted without replication. All the recommended package of practices were followed to raise a healthy crop with proper expression. Five random plants were tagged from each plot for data collection. Observations were recorded for ten quantitative traits *viz*., days to 50% flowering, plant height (cm), effective tillers plant^{-1}, panicle weight, grain yield plant^{-1}(g), thousand grain weight (g), grain length (mm), grain breadth (mm), grain length breadth ratio and filled grain% were measured at the particular stages of their expression. Recorded observations were statistically analyzed using OP STAT software.

Results and Discussion

Cluster analysis divided these 96 rice genotypes into 4 clusters. Among all the four clusters, Cluster IV is the largest one comprising of 87 genotypes and Cluster I is the smallest cluster consisting of a single genotype. Cluster II and Cluster III are having 4 genotypes each. Highest inter cluster distance was observed between Cluster II and III suggesting maximum variability between them, followed by Cluster I and II. Genotypes belonging to Cluster II are Aatma Shital, Bag Muchh, Wasmati and Banspatri. Genotypes belonging to Cluster III are Aama gohi, Atma Shital, Barang and Badshah bhog (B: 484). Maximum heterotic crosses can be obtained by crossing between genotypes of Cluster II and Cluster III. Cluster I includes the cultivars which were superior for filled grain% followed by length by breadth ratio and days to 50% flowering. Cluster II includes genotypes having highest grain length, more thousand grain weight and early flowering. Cluster III is having genotypes with decreased plant height, high tillering and late flowering genotypes. Genotypes belonging to Cluster II and Cluster III can be used in hybridization programme for increasing yield in aromatic rice.

Larger distance among the clusters indicates wider genetic diversity among the genotypes. Therefore, hybridization programme should always be formulated in such a way that parents belonging to different clusters with maximum divergence could be utilized to get desirable transgrassive segregants. Cluster analysis provided with a complete view of the variation present among the aromatic rice genotypes and it might be use for the plant breeders for their genetic improvement.

Correlation between grain yield per plant and its components

Grain yield plant^{-1} was found to be positively and significantly associated with panicle weight, thousand grain weight, grain length and plant height indicating the importance of these traits as selection criterion in yield enhancement program. Selection on any of these characters will have a direct response on grain yield of scented rice breeding where multiple selection criteria are essential. Lakshmi *et al.*, (2014) also reported significant positive correlation of grain yield with plant height and grain length. Days to 50% flowering and grain length/breadth ratio showed significant and negative association with grain yield plant^{-1}. Nayak *et al.,* (2001) also found significant negative association of grain yield with grain length/ breadth ratio. Number of effective tillers plant^{-1} was positively and non-significantly correlated with grain yield plant^{-1}. Similar result was found by Borbora *et al.,* (2005) and Madhavilatha *et al.,* (2005).

Inter correlation among yield complements

Days to 50% flowering exhibited positive and significant association with number of effective tillers plant^{-1} (Sawant *et al.*, 1995) grain breadth, grain length/breadth ratio and filled grain%. It had negative and significant association with plant height, thousand grain weight and grain length.

Plant height recorded positive and significant association with grain yield plant^{-1}. Similar results were found by Yadav *et al.*, (2010); Akhtar *et al.*, (2011); Yadav *et al.*, (2011); Seyoum *et al.*, (2012) and Lakshmi *et al.*, (2014). It has also positive and significantly association with thousand grain weight and grain length. It had negative and significant association with days to 50% flowering, tiller number, grain breadth, grain length/breadth ratio and filled grain%. It was positively and non-significantly associated with panicle weight. Number of effective tiller plant^{-1} was positively and significantly associated with days to 50% flowering, panicle weight, grain breadth, grain length/breadth ratio and filled grain%. It had negative and significant association with plant height, thousand grain weight and grain length. Panicle weight was positively and significantly associated with number of effective tillers plant^{-1}. It had positive and non-significant association with plant height, thousand grain weight and grain length. It had negative and non-significant association with days to 50% flowering, grain breadth, grain length/breadth ratio and filled grain%.

Table.1 List of 96 Rice Genotypes used in this study

S.N.	NAME	S.N.	NAME
1	AAMA GOHI	49	KALI MUCHH
2	AATMA SHITAL	50	KALI MUCHHA
3	ATMA SHITAL	51	LOKTI MACHHI
4	AKBAR BADSHAH	52	SUKRA PHOOL
5	BAG MUCHH	53	TENDU PHOOL
6	WASMATI	54	BASMATI
7	BANSPATRI	55	CHHATRI (C: 194)
8	BARANG	56	CHHATRI (C: 808)
9	BADSHAH BHOG (B: 484)	57	BHATTA PHOOL
10	BADSHAH BHOG (B: 497)	58	TIL KASTURI
11	BADSHAH BHOG (B: 2355)	59	KUBRI MOHAR
12	BASHA BHOG	60	LALLOO
13	BASSA BHOG	61	ANGAR MOTI
14	BISNU BHOG (B:1094)	62	KADAM PHOOL
15	MUNI BHOG	63	LAICHI PHOOL
16	CHINI KAPOOR (C:30)	64	LALLU
17	CHINI KAPOOR	65	CHINI K APOOR (C: 459)
18	CHINNUR	66	BAG MUCHH
19	CHINNOUR	67	TULSI MANJARI II
20	CHIRAI NAKHI	68	SUKLA PHOOL
21	DUBRAJ (D: 268)	69	GANGA BARU
22	DUBRAJ (D: 421)	70	JAI GUNDI
23	DUBRAJ (D: 433)	71	BAYASA BHOG
24	DUBRAJ (D: 874)	72	BISNU BHOG
25	DUBRAJ (D: 1420)	73	RAJA BHOG
26	DUBRAJ DHAN DESHI	74	VISHNOO BHOG
27	MAJHALI DUBRAJ	75	VISHNU BHOG
28	GANGA BALU	76	BIKONI
29	BAM BAIJIRA	77	URAI BUTA
30	BHANTA PHOOL (B: 1087)	78	CHENDARA CHHAL
31	JUI PHOOL	79	CHINNOUR
32	RAMKALI	80	DUBAN MUA
33	DUBRAJ (D: 925)	81	BADSHAH BHOG (B: 562)
34	SAMUND CHINI	82	BASA BHOG
35	SAMUNDAR FEN	83	DUBRAJ (D: 33)
36	SANSARI	84	DUBRAJ (D:80)
37	SARSARIYA	85	DUBRAJ (D: 90)
38	JIRA SHANKAR	86	DUBRAJ (D: 272)
39	TIL KASTURI	87	DUBRAJ (D: 934)
40	TULSI AMRIT	88	DUBRAJ (DESHI)

41	TULSI BAS	89	DUDH NAG
42	TULSI MALA	90	BHANTA PHOOL
43	TULSI MANJARI	91	MAHAMAYA (C)
44	BADSHAH BHOG (B:1294)	92	TARUN BHOG SELECTION 1 (C)
45	BADSHAH BHOG (B: 1510)	93	C.G. DEV BHOG SELECTION 1 (C)
46	CHHATRI BHOG	94	BADSHAH BHOG SELECTION 1 (C)
47	GOBIND BHOG	95	VISHNU BHOG SELECTION 1 (C)
48	RAJA BHOG (R: 399)	96	DUBRAJ SELECTION 1 (C)

Table.2 Cluster Composition of 96 Rice Genotypes

CLUSTER	NUMBER OF GENOTYPES	NAME OF GENOTYPES
I	1	BADSHAH BHOG (B: 497)
II	4	AATMA SHITAL, BAG MUCHH, WASMATI, BANSPATRI
III	4	AAMA GOHI, ATMA SHITAL, BARANG, BADSHAH BHOG (B: 484)
IV	87	AKBAR BADSHAH, BARANG, BADSHAH BHOG (B: 2355), BASHA BHOG, BASSA BHOG, BISNU BHOG (B:1094), MUNI BHOG, CHINI KAPOOR (C:30), CHINI KAPOOR, CHINNUR, CHINNOUR, CHIRAI NAKHI, DUBRAJ (D: 268), DUBRAJ (D: 421), DUBRAJ (D: 433) DUBRAJ (D: 874), DUBRAJ (D: 1420), DUBRAJ DHAN DESHI, MAJHALI DUBRAJ, GANGA BALU, BAM BAIJIRA, BHANTA PHOOL (B: 1087), JUI PHOOL, RAMKALI, DUBRAJ (D: 925), SAMUND CHINI, SAMUNDAR FEN, SANSARI, SARSARIYA, JIRA SHANKAR, TIL KASTURI, TULSI AMRIT, TULSI BAS, TULSI MALA, TULSI MANJARI, BADSHAH BHOG (B:1294), BADSHAH BHOG (B: 1510), CHHATRI BHOG, GOBIND BHOG, RAJA BHOG (R: 399), KALI MUCHH, KALI MUCHHA, LOKTI MACHHI, SUKRA PHOOL, TENDU PHOOL, BASMATI, CHHATRI (C: 194), CHHATRI (C: 808), BHATTA PHOOL, TIL KASTURI, KUBRI MOHAR, LALLOO, ANGAR MOTI, KADAM PHOOL, LAICHI PHOOL, LALLU, CHINI KAPOOR (C: 459), BAG MUCHH, TULSI MANJARI II, SUKLA PHOOL, GANGA BARU, JAI GUNDI, BAYASA BHOG, BISNU BHOG, RAJA BHOG, VISHNOO BHOG, VISHNU BHOG, BIKONI, URAI BUTA, CHENDARA CHHAL, CHINNOUR, DUBAN MUA, BADSHAH BHOG (B: 562), BASA BHOG, DUBRAJ (D: 33), DUBRAJ (D: 80), DUBRAJ (D: 90), DUBRAJ (D: 272), DUBRAJ (D: 934), DUBRAJ (DESHI), DUDH NAG, BHANTA PHOOL, MAHAMAYA (C), TARUN BHOG SELECTION 1 (C), C.G. DEV BHOG SELECTION 1 (C), BADSHAH BHOG SELECTION 1 (C), VISHNU BHOG SELECTION 1 (C), DUBRAJ SELECTION 1 (C)

Table.3 Inter Cluster Distances

Cluster No	1	2	3	4
1	0.000	3.345	1.147	1.541
2		0.000	3.967	1.926
3			0.000	2.076
4				0.000

Table.4 Final Cluster Centers

Cluster No	Centres									
	Days to 50% flowering	Plant Height (cm)	Effective tiller plant^{-1}	Panicle Weight (g)	Grain Yield plant^{-1}(g)	Thousand Grain Weight (g)	Grain Length (mm)	Grain breadth (mm)	Grain L/B Ratio	Filled grains%
1	0.423	-0.486	0.213	-0.199	-0.161	-0.392	-0.531	0.312	0.475	1.000
2	-0.693	0.724	-0.535	0.298	0.524	0.739	0.777	-0.509	-0.721	-0.393
3	0.761	-0.833	0.750	0.005	-0.226	-0.612	-0.787	0.738	0.853	0.381
4	-0.002	0.002	0.004	0.011	0.008	0.002	0.002	-0.001	-0.001	-0.002

Table.5 Pearsons correlation coefficient among the ten yield attributing traits

Characters	Days to 50% flowering	Plant Height (cm)	Effective tiller plant^{-1}	Panicle Weight (g)	Grain Yield plant^{-1}(g)	Thousand Grain Weight (g)	Grain Length (mm)	Grain breadth (mm)	Grain L/B Ratio	Filled grains%
Days to 50% flowering	1.000									
Plant Height (cm)	-0.848**	1.000								
Effective tiller plant^{-1}	0.621**	-0.753**	1.000							
Panicle Weight (g)	-0.169NS	0.154NS	0.305**	1.000						
Grain Yield plant^{-1}(g)	-0.353**	0.348**	-0.147NS	0.723**	1.000					
Thousand Grain Weight (g)	-0.748**	0.677**	-0.546**	0.169NS	0.394**	1.000				
Grain Length (mm)	-0.823**	0.871**	-0.695**	0.145NS	0.352**	0.885**	1.000			
Grain breadth (mm)	0.584**	-0.781**	0.588**	-0.050NS	-0.101NS	-0.428**	-0.725**	1.000		
Grain L/B Ratio	0.840**	-0.951**	0.789**	-0.066NS	-0.303**	-0.724**	-0.906**	0.781**	1.000	
Filled grains%	0.423**	-0.486**	0.213*	-0.199NS	-0.161NS	-0.392**	-0.531**	0.412**	0.475**	1.000

*Note: *Significant at 5%, ** Significant at 1%*

Thousand grains weight was positively and significantly associated with plant height and grain length. Nayak *et al.*, (2001) also found significant positive association of thousand grain weight with grain length. It had positive and non-significant association with panicle weight. Grain length was positively and significantly associated with plant height and thousand grain weight. It had positive and non-significant association with panicle weight. Lakshmi *et al.*, (2014) also reported negative significant association of grain breadth with grain length.

Grain breadth was having positive and significant association with days to 50% flowering, number of effective tillers plant^{-1}, grain length/breadth ratio and filled grain%. Grain length/breadth ratio was positively and significantly associated with days to 50% flowering, number of effective tillers plant^{-1}, grain breadth and filled grain%. It had negative and significant association with plant height, thousand grain weight and grain length. It had negative and non-significant association with panicle weight. Filled grain% was having positive and significant association with days to 50% flowering, tiller number plant^{-1}, grain breadth and grain length/breadth ratio.

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