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Research Note

Genetic divergence in Indigenous aromatic rice (*Oryza sativa* L.)

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Abstract
India is home to a large number of indigenous rice varieties. Sixty indigenous aromatic rice genotypes from different geographical regions of India were raised at Agriculture Research Farm, BHU, Varanasi during Kharif 2014 to identify variability among them. They were evaluated for seventeen yield and quality characters using D^2 analysis, to study the diversity pattern among the genotypes. Based on the analysis, the genotypes were grouped into 8 clusters. Thirteen genotypes each were grouped under cluster V and VIII, while minimum number of genotype (1) was grouped under cluster II. Maximum inter cluster D^2 value was observed between cluster I and VIII (85.56) followed by cluster II and VIII (80.90). The greater the distance between the two clusters indicates wider the genetic diversity between genotypes. The intra cluster distance was maximum in cluster VII (28.10) followed by cluster V (24.12) indicates hybridization involving genotypes within the same clusters may result in good cross combinations. Among the seventeen traits studied, maximum contribution was made by Days to 50% flowering (32.65), Kernel length after cooking (20.07) and amylose content (20.11). Hence, days to 50 percent flowering, Kernel length after cooking and amylose content together contribute 72.83 % towards total divergence. Therefore, these characters may be given importance during selection of parents in hybridization programmes.

Keywords
Aromatic, cluster, genetic divergence, indigenous, rice.

Rice is an important cereal crop, grown under diverse agro-ecological conditions. It is one of the very few crop species endowed with rich genetic diversity which account over one lakh landraces and improved cultivars (Samal, 2014). The success of any breeding programmes depends upon the genetic variability present among populations. Genetic uniformity is an alarming situation among new rice varities (Morishima and Oka 1995) as it increases the chance of disease epidemics and insect infestation. Genetic divergence among the genotypes plays an important role in the selection of parents having wider variability for different yield and quality characters (Sarawgi and Binse, 2007) which may be useful for breeding programmes. The genetic divergence among the aromatic rice genotypes is also a vital tool to the plant breeders for an efficient choice of parents for plant improvement as genetically diverse parents are likely to contribute desirable segregants and to produce high heterotic crosses (Samal, 2014). In the present study, an attempt has been made to understand the nature and magnitude of genetic diversity by classifying the sixty rice varieties using different clustering procedures.

Sixty indigenous rice genotypes were raised at Agriculture Research Farm, Department of Genetics and Plant Breeding, BHU,Varanasi during *Kharif*, 2014 to identify diverse genotypes. The experiment was laid out in randomized block design with three replications. The genotypes were raised in plot of 5 rows with each row of 5 meter length. Row to row and plant to plant spacing was maintained at 20 x 15 cm. The recommended agronomic practices were followed to raise a good crop. They were evaluated for seventeen yield and quality traits viz., Days to 50% flowering, Days to maturity, Plant height (cm), Effective tillers/plant (no.), Panicle length (cm), Seeds/Panicle (no.), 100 Seed Weight (gm), Yield/plant (gm), Brown Rice Length (mm), Brown Rice Breadth (mm), Kernel Length (mm), Kernel Breadth (mm), Kernel Length After Cooking (mm), Kernel Breadth After Cooking (mm), Elongation Ratio, Alkali Spread Value and Amylose Content (Juliano,1971).Ten random plants per replication per genotype were tagged for recording observations. The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of genotypes into clusters was done following the Tocher's method given by Rao, 1952. For statistical analysis, Windostat Version 9.1 software was used. The genotypes used in study are listed in Table-1.

Analysis of variance showed significant differences for all the seventeen characters studied among the genotypes. Based on D^2 values, 60 genotypes were grouped into 8 clusters (Table 2). Among the different clusters cluster V and VIII consisted maximum number of genotypes (13 genotypes) followed by cluster VI (12 genotypes), cluster IV (8 genotypes), cluster III (6 genotypes), cluster I (5

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genotypes), cluster VII (2 genotypes) and cluster II (1 genotype).

The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were present in same clusters as they showed similarity. Similar finding has been reported by Singh *et al*., 2008. Allam *et al.,* 2014. Some of the genotypes of same geographic origin were distributed in different clusters. Similar results has been reported by Sharma *et al*,. 2011, Allam *et al.,* 2014).The Accessions of genotype Basmati LC, Juhi Bengal, Kanak Jeera, Badshahbhog and Adamchini were clustered in individual groups. Kala namak has been kept in both cluster IV and cluster I. Kala Namak is an ancient cultivar and farmers have been using their own seed for cultivation since hundreds of years. There is lack of seed purification, production, and distribution system for this cultivar. So, variability exists in the accessions of this cultivar. This variability has resulted in decline in productivity and quality but at the same time it has probably helped in survival of the cultivar in its native area of cultivation. A mixed seed lot behaves as a multiline under natural condition. Probably because of this variability Kalanamak suffers less from different diseases and pests in its native area of cultivation as compared to evolved varieties in the same area (Singh *et al*., 2003).

The intra and intercluster distance are presented in (Table 3). Inter cluster distance was higher than intra cluster distance which indicates that there is wider genetic diversity among the genotypes (Subudhi, *et al.,* 2009, Mohanty, *et al.,* 2010).The maximum inter cluster distance was observed between cluster I and VIII (85.56) followed by between cluster II and cluster VIII (80.90) and between cluster III and VIII (76.13) indicating wider genetic diversity among the genotypes between the groups. This can be useful in selection of parents to help recombination process in hybridization programmes. The minimum inter cluster distance was found between cluster I and cluster III (23.64) followed by between cluster II and cluster III (27.7). This shows that the genotypes in these clusters are genetically similar and use of these genotypes in hybridization programme may not give desired results. The average intracluster values ranged from cluster VIII (11.04) to cluster VII (28.10). The maximum intra cluster distance was observed in cluster VII (28.10) followed by cluster V (24.12) and cluster II (22.81). Cluster VII includes two genotypes i.e. Lalmati-40 and Krishna Hamsa. Hence, selection of genotypes based on desirable traits can be practiced within these clusters.

The results of cluster means (Table 4) revealed that cluster I showed highest value for Alkali spread value and lowest value for panicle length,100 seed weight, brown rice length, Kernel length and kernel length after cooking. Cluster II showed highest value for days to 50% flowering, days to maturity, effective tillers/plant, yield/plant and lowest value for Alkali spread value. Cluster III recorded highest value for panicle length, seeds per panicle and amylose content. Cluster IV showed highest mean value for the character plant height in cm and lowest value for amylose content. Cluster V showed highest value for brown rice breadth, kernel breadth and kernel breadth after cooking. Cluster VI recorded highest value for kernel length after cooking and elongation ratio. Cluster VII recorded lowest value for brown rice breadth. Cluster VIII recorded highest value for 100 seed weight, brown rice length and kernel length. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters.

The contribution of each trait to total divergence is presented in (Table 5). Among the traits studied, days to 50% flowering contributed maximum divergence (32.65%) followed by amylose content (20.11%) and kernel length after cooking (20.07%). Similar results are reported by Mohanty, *et al.,* 2010 and Yadav, *et al.,* 2011. The minimum percentage of contribution was observed in panicle length and effective tillers per plant (0.06) followed by kernel breadth (0.23), seeds per panicle (0.68), plant height (0.73), Alkali spread value (0.85), days to maturity (0.90) and kernel length (1.36). The traits days to 50 percent flowering, Kernel length after cooking and amylose content together contribute 72.83 % towards total divergence, Hence these characters should be given importance during choice of parents for hybridization and selection in the segregating populations.

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Table 1. List of genotypes used in this study

Genotypes	No. of Accessions	Origin
Adamchini	7	Uttar Pradesh
Jeera Battis	1	Uttar Pradesh
Thurun bhog	1	Orissa
Dhanaprasad	1	Orissa
Chinoor	1	Madhya Pradesh
Jaiphula	1	Orissa
Dubraj	1	Chhattisgarh
Chini Shakkar	1	Uttar Pradesh
Ketki Joha	1	Assam
Lal Chandan	1	Madhya Pradesh
Jeeriga Sambha	1	Tamil Nadu
Jawa Phool	1	Madhya Pradesh
Indra Bhog	1	Uttar Pradesh
Lanjhi	1	Madhya Pradesh
Tulsi manjari	1	Bihar
Lalmati	1	Uttar Pradesh
Basmati Local	6	Uttar Pradesh
Kala Namak	11	Uttar Pradesh
Juhi Bengal	3	West Bengal
Kanak Jeera	7	Uttar Pradesh
Ram Bhog	1	Uttar Pradesh
Dhania	1	Uttar Pradesh
Hariram	1	Uttar Pradesh
Shyam Jeera	1	Uttar Pradesh
Govind Bhog	1	Orissa
Krishna Hamsa	1	Andhra Pradesh
Badshahbhog	5	Assam

Table 2. Distribution of 36 rice genotypes into different clusters

Cluster No.	Genotypes	No. of genotypes
I	Chinni Shakkar, Ketki Joha, Kala Namak-2, Kala Namak-5, Ram Bhog-52	5
II	Lanjhi	1
III	Basmati LC-1, Basmati LC-2, Basmati LC-3, Basmati LC-4, Basmati LC-5, Basmati LC-6	6
IV	Jawa Phool, Kala Namak 3119, Kala Namak-3, Kala Namak-6, Kala Namak-7, Kala Namak-8, Kala Namak-9, Kala Namak-10	8
V	Dhanaprasad, Jaipula, Dubraj, Tulsi Manjari, Juhi Bengal-23, Juhi Bengal-24, Juhi Bengal-25, Juhi Bengal-26, Kanak Jeera-30-1, Kanak Jeera-30-2, Hariram-48, Shyam Jeera, Govind Bhog	13
VI	Adamchini, Chinoor, Lal Chandan, Jeeriga Sambha, Indra Bhog, Kala Namak-11, Kala Namak-12, Kanak Jeera-27, Kanak Jeera-28, Kanak Jeera-29, Kanak Jeera-31, Dhaniya-78	12
VII	Lalmati-40, Krishna Hamsa	2
VIII	Jeera Battis, Thurun Bhog, Badshahbhog-1, Badshahbhog-2, Badshahbhog-3, Badshahbhog-4, Badshahbhog-5, Adamchini-1, Adamchini-2, Adamchini-3, Adamchini-4, Adamchini-5, Adamchini-6	13

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Table 3. Intra (diagonal) and inter-cluster average distances (D^2) in rice genotypes

	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster	VII Cluster	VIII Cluster
I Cluster	193.90 (13.92)	893.47 (29.89)	558.92 (23.64)	1048.98 (32.38)	920.38 (30.33)	1982.62 (44.53)	3464.14 (58.85)	7321.35 (85.56)
II Cluster		520.33 (22.81)	772.62 (27.7)	923.74 (30.39)	1477.16 (38.43)	1253.68 (35.40)	3424.00 (58.5)	6544.67 (80.90)
III Cluster			298.33 (17.27)	792.18 (28.14)	915.68 (30.26)	1110.60 (33.32)	2538.67 (50.38)	5795.37 (76.13)
IV Cluster				443.72 (21.06)	978.43 (31.27)	906.15 (30.10)	2354.30 (48.52)	5194.74 (72.07)
V Cluster					581.80 (24.12)	1768.20 (42.04)	2422.88 (49.22)	5742.68 (75.78)
VI Cluster						488.095 (22.09)	1776.22 (42.14)	3724.11 (61.0)
VII Cluster							790.15 (28.10)	1314.08 (36.25)
VIII Cluster								122.08 (11.04)

Table 4. Cluster mean of different yield characters in 36 rice genotypes

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1 Cluster	133.17	157.50	150.03	9.58	23.77	218.33	1.14	20.77	4.15	1.88	4.08	1.82	6.74	2.44	1.65	4.77	23.99
2 Cluster	140.75	171.33	161.33	11.67	23.87	248.42	1.65	26.79	5.46	1.86	5.76	1.86	8.99	2.82	1.56	4.08	23.66
3 Cluster	127.52	157.90	159.90	8.00	30.12	274.81	1.37	19.19	4.55	2.04	4.5	1.97	8.61	2.57	1.91	4.69	24.86
4 Cluster	128.15	158.44	173.49	8.26	28.36	231.41	1.65	20.41	5.27	2.04	5.12	1.97	9.19	2.87	1.8	4.54	20.89
5 Cluster	120.50	150.33	145.50	10.33	27.38	223.67	1.67	25.31	4.48	2.31	4.35	2.17	7.20	3.46	1.66	4.25	22.72
6 Cluster	123.47	153.81	164.83	8.67	27.46	193.14	2.00	21.74	5.96	2.05	5.85	1.96	11.56	2.83	1.99	4.56	22.86
7 Cluster	91.17	121.00	112.00	8.33	25.87	124.33	1.74	19.00	6.22	1.64	6.18	1.63	9.86	3.07	1.60	4.33	23.38
8 Cluster	78.39	108.72	90.22	7.33	24.68	107.39	2.53	12.03	8.33	1.64	8.19	1.45	10.93	1.94	1.33	4.34	23.46

1.Days to 50% flowering, 2. Days to maturity, 3.Plant height (cm), 4. Effective tillers/plant 5. Panicle length (cm), 6. Seeds/panicle 7. 100 seed weight, 8. Yield/plant 9. Brown rice length (mm) 10.Brown rice breadth (mm), 11. Kernel length (mm), 12. Kernel breadth (mm), 13.Kernel length after cooking, 14. Kernel breadth after cooking, 15. Elongation Ratio, 16. Alkali Spread Value, 17. Amylose content

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Table 5. Percentage of contribution of each character towards total divergence

Source	Times Ranked 1st	Contribution %
1. Days to 50% Flowering	578	32.65
2. Days to Maturity	16	0.90
3. Plant Height (cm)	13	0.73
4. Effective Tillers/ Plant	1	0.06
5. Panicle Length (cm)	1	0.06
6. Seeds/ Panicle	12	0.68
7. 100 Seed Weight	57	3.22
8. Yield/ Plant	135	7.61
9. Brown Rice Length	103	5.82
10. Brown Rice Breadth	62	3.50
11. Kernel Length	24	1.36
12. Kernel Breadth	4	0.23
13. Kernel Length After Cooking	490	20.07
14. Kernel Breadth After Cooking	38	2.15
15. Elongation Ratio	0	0.00
16. Alkali Spread Value	15	0.85
17. Amylose Content	356	20.11

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