GENETIC DIVERGENCE FOR YIELD AND RELATED ATTRIBUTES IN AEROBIC RICE UNDER AEROBIC AND NORMAL CONDITION

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INTRODUCTION

Increasing water scarcity has threatened the traditional rice cultivation practices all over the world (Tuong and Bouman, 2003). Decreasing water resources for rice cultivation has prompted research on the development of water efficient aerobic rice varieties by combining the drought-resistant characteristics of upland varieties with the high-yielding traits of lowland varieties (Belder *et al.*, 2005). Aerobic rice is a production system in which specially developed varieties are grown in welldrained,non-puddled and non-saturated soils. Diversity analysis helps in assessing the nature of diversity in order to identify genetically diverse genotypes for their use in breeding programmes. Mahalnobis's D^2 statistic is an unique tool for classifying genetically diverse parents based on quantitative traits which could be appropriately utilized in hybridization programme. The study of diversity of rice genotypes for both aerobic and normal conditions may lead towards enhancing yield and productivity. The estimation of genetic divergence in the available genotypes is important for successful selection of parents for hybridization purpose. The divergent lines belonging to different and distantly located clusters have a higher probability of giving heterotic hybrids or superior progenies than those parental lines belonging to the same cluster or group possessing low genetic distance. Genetic diversity is considered to be important for realizing heterotic response in F_1 and a broad spectrum of variability in segregating generations (Arunachalam, 1981).Several researchers have emphasized the importance of genetic divergence for selection of desirable parents (Ushakumari and Rangaswamy 1997, Vaithiyaligan 2005, Maji *et al.*, 2012,Chandan *et al.*, 2015 and Santosh *et al.*, 2015). Looking into the importance of varietal development in aerobic rice, the present investigation was undertaken to assess the magnitude of genetic divergence among the selected rice genotypes under aerobic and normal conditions.

MATERIALS AND METHODS

The experimental material for the present study comprised of twenty five genotypes of rice based on suitability in aerobic and normal condition laid in randomized block design (RBD) with three replications at the Field Experimentation Centre of Department of Plant Breeding and Genetics, Rajendra Agricultural University, Pusa Samastipur Bihar during *kharif,* 2014. Standard agronomic practices and plant protection measures were taken as per schedule. Each genotype was grown in a plot of 5 x 1 square meters with the spacing 20 x 15 cm row to row and plant to plant respectively.

Observations were recorded for days to 50% flowering, days to physiological maturity, plant height(cm), panicle length(cm), number of spikelets per panicle, number of tillers per plant, 1000-grain weight (g), relative water content (%), maximum root length(cm), Flag leaf area(cm²), Harvest index(%), Chlorophyll content(SPAD), Proline accumulation in leaves μg/g Dry Wt., Peroxidase activity in leaves unit /g Fresh Wt. and grain yield per plot (g) on five randomly selected

ABSTRACT

An investigation were carried out with twenty five rice genotypes to study the nature and magnitude of genetic diversity among them. The genotypes were grouped into six clusters on the basis of D^2 statistics and ward minimum variance under both aerobic and normal conditions. Cluster III and VI (1672.84); Cluster V and VI (550.04) showed maximum inter-cluster distance while cluster II(46.79); Cluster IV (45.55) exhibited maximum intra-cluster distance respectively under both aerobic and normal conditions. Under aerobic condition, the cluster I exhibited higher mean performance for proline accumulation in leaves. Cluster III showed higher mean performance for most of the yield attributing characters. Therefore, selection of parents from this cluster for these traits would be effective under normal condition. Traits like peroxidase activity in leaves (69.67%; 58.00%) followed by relative water content (23.00%;6.70%) and grain yield per plot (0.33%; 25.33%) respectively under aerobic and normal condition were the major contributors to the genetic under aerobic as well as normal condition.

plants from each entry for each replication for above mentioned traits excluding for days to flowering, days to physiological maturity and grain yield (kg/plot) where whole plot data were considered. The data was subjected to Mahalanobis D^2 statistics to measure the genetic divergence as suggested by Rao (1952).

Relative water content in flag leaf (%)

Relative water content (RWC) of the flag leaves was determined using the equation given by Barr and Weatherley (1962).

$$RWC = \frac{F.W - D.W}{T.W - D.W} \times 100$$

Where,

F.W. = Fresh Weight of flag leaf (g)

D.W. = Dry Weight of flag leaf (g)

T.W. = Turgid Weight of flag leaf (g)

Harvest index (%)

The value of harvest index (HI) was calculated from the following formula (Donald 1962).

$$Harvest\ index = \frac{Grain\ yield}{Total\ biological\ yield\ (grain\ yield\ +\ straw)} \times 100$$

Chlorophyll content (SPAD)

Leaf chlorophyll content was recorded by measuring greenness of leaf using a portal chlorophyll meter (Monilta Camera Co. Ltd., Japan). SPAD readings were collected from the middle region of first fully opened leaf and it was averaged across each plot and expressed as SPAD reading per plant.

Proline accumulation in leaves μg/g dry wt.

The method developed by Bates et al. (1973) for three quantification of proline was used.

Peroxidase activity in leaves unit /g fresh wt.

The activity of peroxidase was determined by the method of Palmiano and Juliano (1973).

RESULTS AND DISCUSSION

Twenty five rice genotypes were grouped into six clusters under both aerobic and normal conditions (Table 1) but the clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating that there was no formal relationship between geographical diversity and genetic diversity. The genetic drift and selection in different environment could cause greater diversity than geographical distance (Patel and Patel, 2012). Cluster IV comprises largest number of genotypes (10) followed by Cluster I (7), Cluster VI (3) and Cluster II &III (3), whereas the Cluster V were solitary (monogenotypic), comprising single genotype in under aerobic condition. Similar studied based on D^2 statistic was also performed by Sankar, et al. (2005), Chauhan and Singh (2003), Sood et al. (2005), Raut (2009), Mall et al. (2011), Chandan et al. (2015) and Santosh et al. (2015). However, under normal condition, Cluster VI comprises largest number of genotypes (7) followed by Cluster I (5) and Cluster IV (4). However, the cluster I, III and V contained three genotype. These findings were agreement with Sankar, et al. (2005), Chauhan and Singh (2003) and Kumar and Bala et al. (2005). The genotypes in cluster III and cluster VI, due to maximum inter cluster distance (Table 2) between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. Similar inter varietal crosses may be attempted between genotypes in cluster I and VI, cluster V and VI, cluster III and IV, cluster II and VI and cluster I and IV . The lowest inter cluster distance was observed

Table 1: Clustering pattern of twentyfive genotypes of rice on the basis of D^2 statistic under aerobic and normal condition.
A. Aerobic Condition

Cluster No.	No. of Geno typeswithin cluster	Genotypes in cluster
I	7	RAU1417-2-1-5-7-7, RAU1421-12-1-7-4-3, RAU 1415-35-76-9-5-3-4, RAU 1428-54-35-5-5, RAU1463-16, RAU1471-10, Vandana (Check)
II	2	RAU1451-66-1-1-5-1, RAU1397-18-3-7-9-4-7
III	2	RAU1417-11-1-74-3-2, RAU1415-35-7-6-9-5-1
IV	10	RAU 1401-18-1-4, RAU 1421-15-3-2-5-3-7, RAU1397-25-8-1-2-5-4, RAU 1421-15-3-2-5-7-3, RAU1426-43-2-5-4, RAU1415-8-6-4-3-3, RAU1428-7-3-6, RAU1421-12-1-7-3, RASI, Turanta
V	1	RAU 1415-9
VI	3	RAU 1401-18-1-5, Sahbhagi, Rajendra Bhagwati

B. Normal Condition

Cluster No.	No. of Genotypes within cluster	Genotypes in cluster
I	5	RAU 1401-18-1-4, RAU1451-66-1-1-5-1, RAU1417-11-1-74-3-2, RAU1463-16, RAU1471-10
II	3	RAU 1401-18-1-5, RAU 1428-54-35-5-5, Rajendra Bhagwati
III	3	RAU1415-35-7-6-9-5-1, Sahbhagi, RAU1397-18-3-7-9-4-7
IV	4	RAU1397-25-8-1-2-5-4, RAU 1421-15-3-2-5-7-3, RAU1426-43-2-5-4, RAU1415-8-6-4-3-3
V	3	RAU 1415-9, RAU1421-12-1-7-3, Rasi
VI	7	RAU1417-2-1-5-7-7, RAU1421-12-1-7-4-3, RAU 1415-35-76-9-5-3-4, RAU 1421-15-3-2-5-3-7, Vandana (Check), Turanta

Table 2: Cluster mean values for different quantitative characters in 25 rice genotypes under aerobic and normal condition

A. Aerobic Condition

	DFF	DPM	PH	PL	SPP	TPP	TGW	RWC	MRL	FLA	HI	CC	PRO	PERO	GY/P
Cluster I	81.53	101.40	103.17	22.37	10.07	10.60	24.85	74.25	10.79	21.57	51.17	39.40	10.82	375.91	2.12
Cluster II	80.13	100.63	102.87	22.23	9.87	10.43	23.14	68.40	10.96	19.88	52.42	39.47	11.59	462.71	2.05
Cluster III	76.67	101.33	105.00	22.20	12.00	11.67	27.07	83.70	12.87	23.53	62.07	44.33	10.00	318.37	2.58
Cluster IV	76.00	109.50	113.00	25.68	11.83	13.17	29.53	87.62	18.912	29.15	64.50	44.17	11.62	550.58	2.68
Cluster V	87.00	107.33	105.00	26.47	11.00	10.33	28.43	85.63	13.87	25.70	63.57	45.00	11.13	411.53	2.25
Cluster VI	81.33	105.00	105.67	21.97	10.67	10.00	27.53	83.67	13.53	23.03	63.69	43.00	9.95	660.60	2.58

B. Normal Condition

	DFF	DPM	PH	PL	SPP	TPP	TGW	RWC	MRL	FLA	HI	CC	PRO	PERO	GY/P
Cluster I	79.89	100.26	103.33	22.16	11.85	15.78	27.11	73.79	11.64	32.82	56.18	41.11	10.02	344.62	2.66
Cluster II	84.67	104.58	107.00	24.23	12.83	17.17	29.23	82.97	12.87	40.94	60.67	42.42	10.41	403.43	3.75
Cluster III	83.22	101.89	100.89	21.47	11.33	15.44	25.86	70.39	9.77	23.60	48.99	35.33	10.82	413.26	2.18
Cluster IV	81.76	102.14	106.95	24.11	12.19	16.38	27.08	76.22	12.11	35.26	54.44	41.57	9.75	234.47	3.44
Cluster V	73.67	112.33	117.00	28.23	14.00	20.67	32.57	90.50	16.83	46.65	57.37	47.67	11.48	412.80	5.87
Cluster VI	71.00	101.33	96.67	20.67	10.33	13.33	24.40	64.67	7.83	17.30	56.57	34.67	12.12	215.11	1.70

Table 3: Mean intra and inter cluster distances (D²) among six clusters in rice under aerobic and normal condition

A. Aerobic Condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	45.21	148.82	78.52	627.28	95.22	1302.01
Cluster II		46.79	322.48	313.98	115.28	734.88
Cluster III			0.00	842.61	141.11	1672.84
Cluster IV				31.00	314.09	190.93
Cluster V					0.00	883.79
Cluster VI						0.00

B. Normal Condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	35.09	79.46	95.31	143.63	203.54	142.99
Cluster II		45.55	151.32	208.74	83.97	329.33
Cluster III			30.89	351.39	345.95	193.57
Cluster IV				93.19	262.90	214.46
Cluster V					0.00	550.04
Cluster VI						0.00

between cluster I and III showing this cluster was relatively less divergent and crossing between them cannot produce vigorous offspring (F_1 progenies) under aerobic condition. Under normal condition, the maximum inter cluster distance was observed between cluster V and VI followed by cluster III and IV, cluster III and V and cluster II and VI indicating the chances of getting high yielding recombinants would be better if the crosses are made among the genotypes of these groups. The lowest inter cluster distance was recorded between cluster I and II showing this cluster was relatively less divergent. Similar studied based on D² statistic was also performed by that of Chandra *et al.* (2007). To realize much variability and high heterotic effect, Chaturvedi and Maurya (2005) recommended that parents should be selected from two clusters having wider inter cluster distance.

Under aerobic condition, Cluster III, IV and V showed high cluster mean values (Table 3) for spikelet per panicle, chlorophyll content, days to physiological maturity, plant height, tillers per plant, 1000 grain weight, relative water content, maximum root length, flag leaf area, harvest index, peroxidase activity in leaves, proline accumulation in leaves, grain yield per plot, days to fifty percent flowering and panicle length but Cluster I,II,IV and VI showed low cluster mean for maximum root length, harvest index, peroxidase activity in leaves, days to fifty percent flowering, plant height, spikelet per panicle, 1000 grain weight, relative water content, flag leaf area, chlorophyll content, grain yield/plot, days to physiological maturity, panicle length, tillers per plant and proline accumulation in leaves. Under normal condition, Cluster II,V and VI showed high cluster mean values for days to fifty percent flowering, peroxidase activity in leaves, days to physiological maturity, plant height, spikelet per panicle, 1000 grain weight, relative water content, flag leaf area, chlorophyll content, grain yield/plot, panicle length, tillers per plant and proline accumulation in leaves but Cluster II,V and VI showed low cluster mean values for days to fifty percent flowering, peroxidase activity in leaves, days to physiological maturity, plant height, spikelet per panicle, 1000 grain weight, relative water content, flag leaf area, chlorophyll content, grain yield/plot, panicle length, tillers per plant and proline accumulation in leaves. Selection of genotypes based on cluster mean for the better exploitation of genetic potential also reported by

Table 4: Character contribution (%) towards divergence under aerobic condition and normal condition

S.No.	Source	Times Ranked 1st AEROBIC	Contribution % NORMAL	Times Ranked 1st	Contribution %
1	DFF	0	0.00	0	0.00
2	DPM	0	0.00	0	0.00
3	PH (cm)	0	0.00	0	0.00
4	PL (cm)	1	0.33	3	1.00
5	SPP	1	0.33	0	0.00
6	TPP	0	0.00	0	0.00
7	TGW (g)	3	1.00	0	0.00
8	RWC (%)	69	23.00	20	6.67
9	MRL (cm)	2	0.67	1	0.33
10	FLA (cm²)	6	2.00	14	4.67
11	HI (%)	2	0.67	1	0.33
12	CC (SPAD)	0	0.00	0	0.00
13	PRO (µg/g Dry Wt.)	6	2.00	11	3.67
14	PERO (unit /g Fresh Wt.)	209	69.67	174	58.00
15	GY/P (kg)	1	0.33	76	25.33

Abbreviations

DFF = Days to 50% flowering, DPM = Days to physiological maturity, PH = Plant height, PL = Panicle length, SPP = Spikelet per panicle, TPP = Tillers per plant, TGW = 1000 Grain weight, RWC = Relative water content, MRL = Maximum root length, FLA = Flag leaf area, HI = Harvest index, CC = Chlorophyll content, PRO = Proline accumulation in leaves, PERO = Peroxidase activity in leaves. GY/P = Grain yield per plot.
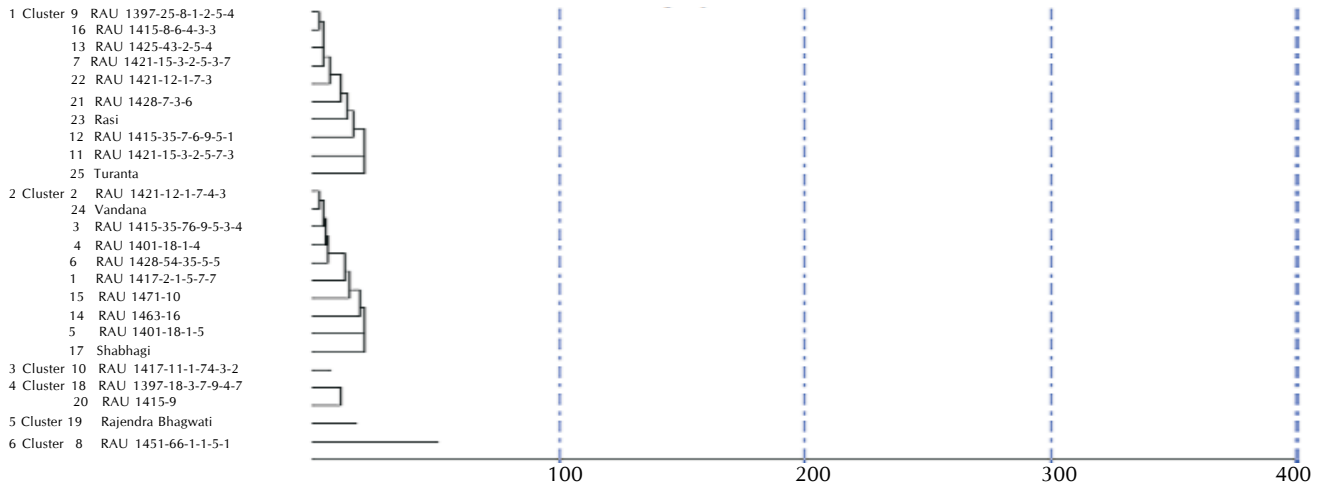

Figure 1: Clustering pattern of 25 aerobic rice genotypes on the basis of D² statistic by Tocher method in aerobic condition
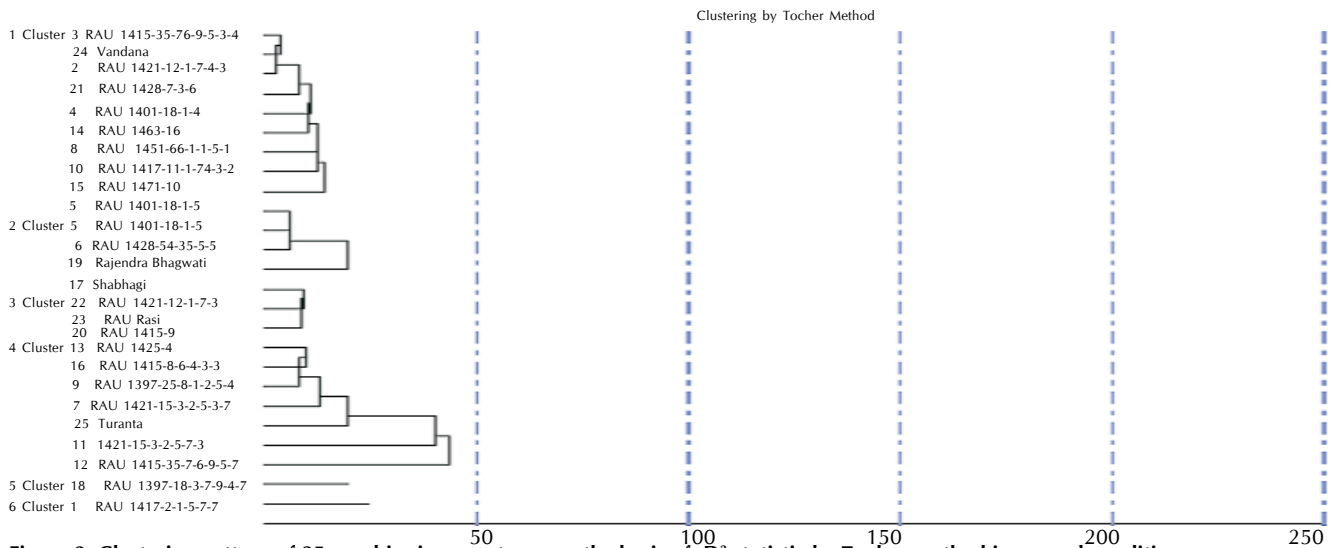

Figure 2: Clustering pattern of 25 aerobic rice genotypes on the basis of D² statistic by Tocher method in normal condition

Abarshahr, *et al.* (2011), Chaturvedi, *et al.* (2011), Raut *et al.* (2009), Ramya and Senthil kumar (2008), Arivoli *et. al.* (2009), Gahalain *et. al.* (2010), Kumar, *et al.* (2009) and Singh *et al.* (2013). Clusters with desired mean value may be used in hybridization programme to achieve desired high yielding segregants (Saraswathi et al. 1996).

The selection and choice of parents mainly depends upon contribution of characters towards divergence (Bose *et al.* 2011). The maximum contribution(Table 4) in the manifestation of genetic divergence was exhibited by peroxidase activity in leaves, followed by relative water content, proline accumulation in leaves, flag leaf area, and 1000 grain weight under aerobic condition suggesting scope for improvement in these characters. Similar result were observed by Chandra *et al.* (2007) for 1000-grain weight. Under normal condition, the maximum contribution in the manifestation of genetic divergence exhibited by peroxidase activity in leaves followed by grain yield per plot, relative water content in flag leaf, flag leaf area, proline accumulation in leaves and panicle length. This indicated that selection of genotypes for these traits may be rewarding for future utilization in breeding programme. Similar observation was recorded by Kumar and Bala (2005), Ramya and Senthil Kumar (2008), Raut *et al.* (2009) and Sankar *et al.* (2005). Such results indicated that these four characters contributed maximum towards diversity. The greater diversity in the present materials is due to these four characters which will offer a good scope for improvement of yield through rational selection of parental genotypes. Waghmare *et al.* (2008) also reflects the high relative genetic contribution of specific traits such as, relative water content and chlorophyll content towards the total divergence under moisture stress in early rice genotypes.

ACKNOLEDGEMENT

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