Phenotypic assessment of rice (Oryza sativa L.) genotypes for genetic variability and varietal diversity under direct seeded condition

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Received: January 22, 2016; Revised received: October 24, 2016; Accepted: January 1, 2017

Abstract: The study on variability and diversity of 32 genotypes of rice (Oryza sativa L.) under direct seeded condition revealed significant variability at 5% level among the genotypes for all the characters. High level of broad sense heritability was observed for days to 50% flowering (0.986) followed by filled grains (0.8216) and 1000-grain weight (0.7306). Expected genetic advance was highest for yield per hectare (39.639) and filled grains per panicle (51.39). Genetic divergence analysis using Mahalanobis’s D2 statistic grouped the genotypes into 7 clusters. Cluster II had maximum number (16) of genotypes. Maximum inter cluster distance was found between cluster IV and VII (984.82). However, intra cluster distance was maximum in cluster III (363.58). Genotypes from diverse clusters viz.NR 89, PAU 3284, ARIZE SWIFT, RY 248, Varadhan, RYC489, MTU 1010 and RYC 674 could be recommended for inclusion in hybridization programme for breeding under aerobic rice condition.

Keywords: Aerobic rice, Genetic divergence, Rice, Varietal diversity

INTRODUCTION

Genetic variation is the spice of plant breeding programme as it widens the scope of selection. Therefore, estimation of extent and nature of diversity in the germplasm accessions for yield and other economic traits is critical. The exploitable variability is judged through simple measure of variability through D2 statistics. Estimates of heritability and genetic advance help in understanding the nature of gene action affecting the concerned trait (Srivastava et al., 2012). Genetic diversity and the diverse gene pools is lifeline of any breeding programme that provides opportunity for identification of traits that offer substantial scope for improvement through selection if higher level of productivity is to be achieved and sustained. Genetic divergence is an outcome of several factors such as exchange of breeding material, genetic drift, natural variation and artificial selection other than ecological and geographical diversification (Sirohi and Dar, 2009). The greater the diversity among the parents higher is the chances of achieving heterotic progeny and a broad spectrum variability in segregating generations. Thus, assessment of genetic diversity for different traits in the germplasm is essential for the identification of suitable parents in the hybridization programme (Sharma et al., 2008).

In view of the scarce water situation in most of the rice growing areas in Uttarakhand we have taken up this experiment to judge the inter-trait variability and varietal diversity in rice genotypes under direct seeded condition to screen the genotypes that can be used as cultivar or surrogate parent in hybridization programs for moisture stress regime.

MATERIALS AND METHODS

32 rice genotypes including 1 local check i.e. Pant Dhan 12, were included in present study. The experiment was laid in complete randomized block design (RBD) with three replications. The standard agronomic practices were followed to raise a healthy crop. Observations were recorded on five randomly selected plants for 6 quantitative traits viz. tiller number per plant, days to 50% flowering, panicle length (cm), number of filled grain per panicle, 1000-grain weight (g) and grain yield/hectare (Kg/ha). Statistical tools like analysis of variance (Panse and Sukhmate, 1967), coefficients of variability (Burton, 1952), heritability (Allard, 1960), genetic advance (Allard, 1960) and D2 statistics (Murthy and Arunachalam, 1967) were used for analysis.

RESULTS AND DISCUSSION

Variability: Analysis of variance for 6 yields and its
contributing traits in rice indicated that, mean square
differences among 32 genotypes for all the characters
studied are highly significant at 5% level of probability
(Table 1). Thus, there is sufficient scope for further
improvement in these characters under direct seeded
environment.

Genetic variability: Estimates of variability para-
deters for different quantitative traits among genotypes in
rice are presented in Table 2. Number of tillers per
plant varied from 6 to 11 with coefficient of variation
CV 11.80. Genotypes MTU 1010, NR89 and RYC
248 were superior genotypes with 11, 10 and 10 tillers/
plant respectively. Days to 50% flowering varied from
72 to 93 with CV 2.81. Genotypes Wardhan, PD12, and
NP9161 were superior that flowered in 72, 73 and 74 days
respectively. Panicle length ranged from 24.13 cm (Konark)
to 28.47 cm (RYC248) with CV 5.33. Genotypes RYC248, Tehalka and NP9161 are the best genotypes that have panicle length of
28.47, 28.00 and 27.87 cm respectively. Number of
filled grains per panicle ranged from 108 to 210 with
mean sum of squares

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Degree of freedom</th>
<th>Days to 50% flowering</th>
<th>Panicle length</th>
<th>Tiller no per plant</th>
<th>Filled grain per panicle</th>
<th>1000 grain weight</th>
<th>Yield/ ha (kg/ha)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replication</td>
<td>2.0</td>
<td>0.562</td>
<td>1.15</td>
<td>18.04</td>
<td>61.81</td>
<td>1.771 **</td>
<td>24512.00</td>
</tr>
<tr>
<td>Treatment error</td>
<td>62.0</td>
<td>0.422</td>
<td>2.05</td>
<td>0.987</td>
<td>165.09</td>
<td>5.023</td>
<td>136942.8</td>
</tr>
</tbody>
</table>

*significant @ p=0.05, **significant @ p=0.01

Table 2. Estimates of variability parameters for different quantitative traits among rice genotypes under aerobic condition.

<table>
<thead>
<tr>
<th>Characters</th>
<th>Range</th>
<th>GM</th>
<th>SEM+</th>
<th>PCV</th>
<th>GCV</th>
<th>h²</th>
<th>Gₐ</th>
<th>Gₐ in % of mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>Day To 50% Flowering</td>
<td>72-93</td>
<td>79.86</td>
<td>0.375</td>
<td>6.545</td>
<td>6.499</td>
<td>0.986</td>
<td>10.622</td>
<td>13.30</td>
</tr>
<tr>
<td>Panicle length of main axis</td>
<td>24.13-28.47</td>
<td>26.864</td>
<td>0.826</td>
<td>6.24</td>
<td>1.25</td>
<td>0.404</td>
<td>0.139</td>
<td>0.51</td>
</tr>
<tr>
<td>Tiller / Plant</td>
<td>6-11</td>
<td>8.416</td>
<td>0.573</td>
<td>15.93</td>
<td>7.25</td>
<td>0.207</td>
<td>0.583</td>
<td>6.93</td>
</tr>
<tr>
<td>Filled grain per panicle</td>
<td>108-210</td>
<td>145.95</td>
<td>7.41</td>
<td>20.81</td>
<td>18.86</td>
<td>0.821</td>
<td>51.39</td>
<td>35.21</td>
</tr>
<tr>
<td>1000 grain weight</td>
<td>10.1-28.6</td>
<td>21.583</td>
<td>1.29</td>
<td>20.01</td>
<td>17.11</td>
<td>0.730</td>
<td>6.50</td>
<td>30.12</td>
</tr>
<tr>
<td>Grain yield /ha</td>
<td>3278.46943</td>
<td>3856.083</td>
<td>213.65</td>
<td>12.41</td>
<td>7.86</td>
<td>0.402</td>
<td>39.639</td>
<td>10.27</td>
</tr>
</tbody>
</table>

PCV and GCV: The moderate to high value for PCV
and GCV (Table 2) was recorded for total number of
filled grain per panicle (20.81, 18.86) and test weight
(20.01, 17.11). However, narrow gap between these val-
ues indicate that these traits are least influenced by envi-
ronment. Low value for PCV and GCV were recorded
for days to 50% flowering (6.54, 6.499) and panicle.
Bhadru et al. (2012) reported high PCV and GCV for
number of grains per panicle, and grain yield per plant
in rice. A relatively large gap between PCV and GCV for
these two traits is indicative of environmental influence
on trait expression. The similar results in transplanted
rice were reported by Panwar et al. (2005). Similar
finding of PCV and GCV have also been reported in
rice for days to 50% flowering and Grain yield per
plant by Singh et al. (2006). Similar finding of PCV
and GCV have been reported for total grains per pani-
cle, grain yield per plant and number of effective tillers
per plant, while the lowest in days to maturity and days
to 50 per cent flowering in rice by Khare et al. (2014).

Heritability and genetic advance: Very high level of
broad sense heritability was observed for days to 50 %
flowering (0.9867) followed by filled grain per panicle
(0.821), 1000 grain weight (0.730) and grain yield /ha
(0.402). These results are in accordance with reports
of Nayak et al. (2002) in scented Rice under Rainfed
condition. This serves as an index of transmissibility
of traits from parents to their offspring. But character
exhibiting high heritability may not necessarily give
high genetic advance (Gandhi et al., 1964) because of
involvement of non-additive gene action. Thus, selec-
tion for the characters should be based on high herita-
bility as well as high genetic advance (Johnson et al.,
1955). The genetic advance was highest for grain
yield/ha (39.639) followed by filled grain per panicle
(51.39), while low genetic advance was observed for
panicle length (0.139) (Table 2). Similar results were
also reported by Pratap et al. (2012) and Gangashetty
et al. (2013) in rice. Heritability coupled with expected
genetic advance for a trait will help us in deciding the
scope of improvement of that particular trait through
selection (Johnson et al., 1955).

Diversity: Genetic diversity and the diverse gene pool
are the basis of plant breeding. Genetic diversity is
essential if higher level of productivity is to be
achieved because it providing genetic building blocks
for further improvement. Hence, genetic diversity is
necessary for progress to be made in plant breeding as
well as during selection of parental genotypes for
crossing programme. Based on the D² values, the con-
stellation on genotype into clusters was done as sug-
The results indicated that, suggested by Rao (1952). All the 32 genotype were grouped into seven clusters. (Table 3). Clustering pattern of genotypes showed lack of any relationship between geographic origin and genetic diversity reported by Chandra et al. (2007) and Bhanumathi et al. (2010). Cluster I (Tehlka), VI (SabourSurhit) and VII (RYC674) contained only one genotype each. Cluster II comprises of sixteen genotype (US350, NP9161, NPH24, US375, RXML01, DRH834, SVH027, Lalat, konark, Rajendra kasturi, RYC230, RYC232, RYC238, RYC237, GGV0501, Pant dhan12). The Cluster III having five genotypes (Dhaanya080544, NR89, PAU3284, ARIZE SWIFT, and RYC248). Cluster IV comprises four genotype (PD12, Varadhan, RYC489, MTU1010). Cluster V contains four genotypes (NPH5, PAU3285, RYC667, and Rajendra Suwasini). While cluster VI contains only one genotype (SABOUR SURHIT) and cluster VII contain one genotype (RYC674). The results indicated that, the diversity reported among the genotype is due to both geographical diversification and genotypic differences which played a major role in the clustering along with the similarity and differences in their adaptation, selection criteria, selection pressure and environmental condition (Nayak et al., 2004 and Bose and Pradhana, 2005). 

Intra cluster genetic distance: Intra cluster average D^2 values ranged from 0.0 to 363.59 it was maximum in cluster III with five genotypes (Dhaanya080544, NR89, PAU3284, ARIZE SWIFT, RYC248) followed by cluster IV with four genotypes (PD12, Varadhan, RYC489, MTU1010). According to findings, selection of parents should be done from these two cluster III and cluster IV having wider inter-cluster distance to get more variability and high heterosis effect for yield and its contributing traits. The maximum intra cluster distance was observed in cluster III. Hence under directed seeded condition selection within these cluster may be exercised based on the highest mean for the desirable trait, which could be made use in further improvement through inter varietals hybridization as well as in recombination breeding. Similar findings have been reported by De and Rao (1987), Pradhan and Roy (1990), Mishra et al. (2003) and Chaturvedi and Maurya (2005) in transplanted rice.

The inter cluster genetic distance: The inter cluster average D^2 values was maximum (984.856) between cluster VI with one genotype, (RYC674) and cluster III with five genotype (Dhaanya080544, NR89, PAU3284, ARIZRSWIFT, and RYC248). Therefore choice of divergent parent can be made from these two diversified clusters for hybridization purpose to get high heterotic effects for grain yield and its concerned traits under aerobic environment. The results are close confirmation with the findings of Joshi et al. (2008) clustered eighteen rice varieties on the basis of sixteen quantitative characters using numerical taxonomic approach were grouped into nine different clusters revealing sufficient amount of variability among the varieties.

Conclusion

Ample variability among the genotypes for all the characters studied in Rice under direct seeded condition indicated scope for improvement in seed yield and its related traits. A high level of broad sense heritability for days to 50% flowering filled grains and 1000-grain weight along with high expected genetic advance for yield per hectare and filled grains per panicle can be viewed in the light of scope of genetic progress of these traits under selection cycle. The pattern of clustering proved that geographical diversity

Table 3. Distribution of different rice genotypes into clusters based on D^2 statistics.

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Name of genotypes</th>
<th>Number of genotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>Tehlka</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>US350, NP9161, NPH24, US375, RXML01, DRH834, SVH027, Lalat, konark, Rajendra kasturi, RYC230, RYC232, RYC238, RYC237, GGV0501, Pant dhan12.</td>
<td>16</td>
</tr>
<tr>
<td>III</td>
<td>Dhaanya080544, NR89, PAU3284, ARIZE SWIFT, RYC248</td>
<td>5</td>
</tr>
<tr>
<td>IV</td>
<td>PD12, Varadhan, RYC489, MTU1010</td>
<td>4</td>
</tr>
<tr>
<td>V</td>
<td>NPH5, PAU3285, RYC667, RAJENDRA SUWASINI</td>
<td>4</td>
</tr>
<tr>
<td>VI</td>
<td>SABOUR SURHIT</td>
<td>1</td>
</tr>
<tr>
<td>VII</td>
<td>RYC674</td>
<td>1</td>
</tr>
</tbody>
</table>

Table 4. Average inter cluster (above diagonal) and intra cluster (diagonal) D^2 values in rice.

<table>
<thead>
<tr>
<th>Cluster</th>
<th>I</th>
<th>II</th>
<th>III</th>
<th>IV</th>
<th>V</th>
<th>VI</th>
<th>VII</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>238.359</td>
<td>135.25</td>
<td>258.63</td>
<td>133.14</td>
<td>424.40</td>
<td>760.10</td>
<td></td>
</tr>
<tr>
<td></td>
<td>273.60</td>
<td></td>
<td>257.82</td>
<td>625.10</td>
<td>964.04</td>
<td></td>
<td></td>
</tr>
<tr>
<td>III</td>
<td>363.58</td>
<td>276.42</td>
<td></td>
<td>372.45</td>
<td>709.63</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IV</td>
<td></td>
<td>312.01</td>
<td>280.16</td>
<td>643.63</td>
<td>984.82</td>
<td></td>
<td></td>
</tr>
<tr>
<td>V</td>
<td>164.58</td>
<td></td>
<td>370.87</td>
<td>707.18</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>VI</td>
<td></td>
<td>0</td>
<td></td>
<td>348.45</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>VII</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
need not necessarily be related to genetic diversity and genotypes. Present investigation revealed that, three cluster showed maximum intra and inter cluster D2 values having the diversified genotype including NR 89, PAU 3284, ARIZE SWIFT, RY 248 (in Cluster III), Varadhan, RYC489, MTU 1010 (in cluster IV) and RYC 674 (in cluster VII) should be recommended for inclusion in inter varietal hybridization programme as well as in recombination breeding to improve the yield and its related traits under aerobic rice cultivation.

REFERENCES