Data Article

Data on genetic potentiality of folk rice (Oryza sativa L.) genotypes from Koraput, India in reference to drought tolerance traits

Debabrata Pandaa,*, Swati S. Mishraa, Sangram K. Mohantyb, Prafulla K. Beheraa, Sangram K. Lenkac

a Department of Biodiversity and Conservation of Natural Resources, Central University of Orissa, Koraput, 764 021, Odisha, India
b National Rice Research Institute (ICAR), Cuttack, 753 006, Odisha, India
c TERI-Deakin NanoBiotechnology Centre, The Energy and Resources Institute, Gurugram, Haryana, 122 001, India

ARTICLE INFO

Article history:
Received 6 May 2019
Received in revised form 27 July 2019
Accepted 29 July 2019
Available online 12 August 2019

Keywords:
Drought tolerance
Indigenous rice
Simple sequence repeat
Microsatellite panel

ABSTRACT

Precise physiological and molecular marker-based assessment provides information about the extent of genetic diversity, which helps for effective breeding programmes. We have conducted detailed physiological and molecular marker-based assessment of selected eight indigenous rice landraces from Koraput, India along with tolerant (N22) and susceptible (IR64) check varieties under control and simulated drought stress using polyethylene glycol (PEG) 6000. After exposure to different levels of drought stress, relative germination performance (RGP), seedling vigour index (SVI) and relative growth index (RGI) were significantly declined in all the rice landraces compared to the control plants and significant varietal differences were observed. Genetic relationship among the studied rice landraces was assessed with 24 previously reported drought tolerance linked Simple Sequence Repeat (SSR) markers. A total of 53 alleles were detected at the loci of the 24 markers across the 10 rice accessions. The Nei’s gene diversity (He) and the polymorphism information content (PIC) ranged from 0 to 0.665 and 0 to 0.687, respectively. Six SSR loci, RM276, RM411, RM3, RM263, RM216 and RM28199, provided the highest PIC values and are potential for exploring the genetic diversity of studied rice lines for drought tolerance. Four rice genotypes

* Corresponding author.
E-mail address: dpanda80@gmail.com (D. Panda).

https://doi.org/10.1016/j.dib.2019.104363
2352-3409/© 2019 The Author(s). Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).
Butkichudi, Haldichudi, Machakanta and Kalajeera) showed the highest genetic distance with tolerant check variety (N22) and can be considered as valuable genetic resources for drought breeding program.

© 2019 The Author(s). Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

1. Data

The dataset contains tables, graphs and images derived from the analysis of the raw data obtained from the various growth and genetic diversity parameters of the folk rice varieties from Koraput, India under control and drought condition. Details of genotypes with their origin, ecotype and special characters were presented in Table 1. Variations of relative germination performance (RGP), relative growth index (RGI) and seedling vigour index (SVI) of studied rice genotypes in different concentration of PEG induced drought stress was shown in Fig. 1. Analysis of variance (ANOVA) of studied parameters in rice seedlings grown under different levels drought stress was presented in Table 2. Genotyping of the studied genotypes was carried out by taking 24 reported simple sequence repeat (SSR) markers.
Different alleles, in form of variation in molecular weight of each amplified products for each SSR marker against studied ten genotypes are given in a Microsatellite Panel (Fig. 2). The markers amplified a total of 53 alleles with an average of 2.2 per locus. Genetic diversity parameters such as number of alleles, number of effective alleles, expected homozygosity, expected heterozygosity, Nei’s genetic diversity, Shannon’s information index and polymorphism information content was presented in Table 4. The pair-wise genetic similarity calculated for all the studied genotypes with 24 SSR markers ranged from 0.431 to 0.813 (Table 5). Cluster analysis based on the Bray-Curtis paired linkage revealed the percent of similarity in SSR marker data among studied rice genotypes were presented in Fig. 3.

2. Experimental design, materials, and methods

2.1. Plant materials and growth conditions

The experiment was conducted by taking eight folk rice genotypes from Koraput, India along with N22 (drought-tolerant improved rice variety) and IR64 (drought-susceptible irrigated variety) as check varieties. The details of the rice landraces used in this study are presented in Table 1. Uniform sized seeds of each variety were selected, surface sterilized and kept for germination. The seeds were

| Variety No | Variety          | Origin            | Ecotype | Characters                                                                 |
|------------|------------------|-------------------|---------|---------------------------------------------------------------------------|
| 1          | Dangarabayagundar| Landraces of Koraput | Up land | Short Duration of maturity (103 days), medium and bold grain, white grain, coarse white rice, drought escaping. |
| 2          | Machhakanta      | Landraces of Koraput | Low land | Long duration of maturity (135–145 days), slender grain, popular variety, drought tolerant. |
| 3          | Kalajeera        | Landraces of Koraput | Low land | Long duration of maturity (140–150 days), aromatic, small oval grain with black husk color |
| 4          | Butukichudi      | Landraces of Koraput | Low land | Long duration of maturity (135–140 days), brown grain, white coarse rice, strong straw and drought tolerant. |
| 5          | Bhatachudi       | Landraces of Koraput | Medium land | Medium duration of maturity (130 days), yellow grain, white coarse rice, non-lodging, white seed coat color, drought tolerant. |
| 6          | Haladichudi      | Landraces of Koraput | Medium land | Medium duration of maturity (125–135 days), medium slender grain, deep yellow husk color, popular variety, drought tolerant. |
| 7          | Pandakagura      | Landraces of Koraput | Up land | Long duration of maturity (145–150 days), drought tolerant, white grain, coarse white rice. |
| 8          | Mugudi           | Landraces of Koraput | Low land | Medium duration of maturity (130–135 days), drought tolerant, strong straw, bold kernel. |
| 9          | N 22             | Eastern India     | Up land | Short duration of maturity (80–95 days), deep-rooted, drought and heat tolerant aus rice variety. |
| 10         | IR 64            | IRRI, Philippines | Low land | Short duration of maturity (115 days), high yielding hybrid variety, long slender grain, rainfed lowland area, susceptible to drought stress. |
Fig. 1. Variations of relative germination performance (RGP), relative growth index (RGI) and seedling vigour index (SVI) of studied rice genotypes in different concentration of PEG induced drought stress. Data are the mean of three replications (n = 3) with vertical bar represents standard deviation. The treatment C: control and –0.5 MPa, –1.0 MPa and –1.5 MPa are different levels of drought. LSD: least significance difference. Genotypes 1: Dangarabayagundar; 2: Machhakanta; 3: Kalajeera; 4: Butukichud; 5: Bhatachudi; 6: Haladichudi; 7: Pandakagura; 8: Mugudi; 9: N 22; 10: IR 64.
placed in sterilized petriplates over saturated tissue paper and transferred to an incubator with a 12-h light/12-h dark photoperiod with daily maximum photosynthetic photon flux density (PPFD) about 380 ± 40 mol m⁻² s⁻¹ at 25 °C in the laboratory. After sowing seeds immediately the drought stress was simulated with variations in osmotic potential by application of different concentrations (19.6%, 29.6% and 36.0%) of polyethylene glycol (PEG) that produced -0.5, -1.0 and -1.5 MPa water potential, respectively for 15 days. A control set was also run along with the treatment without application of PEG.

2.2. Determination of early growth performances

The seed germination rate was recorded 9 days after sowing. The seedling vigour characteristics of 15-days-old seedlings were measured by taking root and shoot length, fresh and dry weight of five

Table 2
Sum square is the absolute value and percentage of total (in bracket) of main effect resulting from analysis of variance (ANOVA) of studied parameters in rice seedlings grown under different levels drought stress. df, Degrees of freedom; Total df = 49; The P of overall ANOVA for variety, treatment and variety x treatment interaction for each parameters *P < 0.05,**P < 0.01.

| Parameters | Source of Variation | Variety (df = 9) | Treatment (df = 3) | Variety x Treatment (df = 37) |
|------------|---------------------|------------------|-------------------|-----------------------------|
| RGP        |                     | 19571** (62)     | 4760** (15)       | 6843** (21)                 |
| RGI        |                     | 2993** (18)      | 11611** (70)      | 1834** (11)                 |
| SVI        |                     | 1046610** (64)   | 384915** (23)     | 174011** (10)               |

RGP: relative germination performance; RGI: relative growth Index; SVI: seedling vigour index.

Table 3
Details of SSR markers used in this study.

| Sl. No. | Primer Repeat motive | Forward primer | Reverse primer | Chromosome No. |
|---------|----------------------|----------------|----------------|----------------|
| 1       | RM339 (CTT)8CTT (CTT)5 | GTAATGATGCTTGTTGGAAG | GAGTCATGTAGCGCATGACATG | 8 |
| 2       | RM411 (GTT)7         | ACAAACACTTCGCTTGATAC | TGAACGAAACAACACTGACGTA | 3 |
| 3       | RM517 (CT)15         | GGCTTACTGGCTTCGATTTG | CGTCTCCTTTGGTATGC | 3 |
| 4       | RM3 (GA)2GG (GA)25   | ACAGTGGAGCCGACCTG | CTTCCACTTGCCACATCTT | 6 |
| 5       | RM52 (TC)14          | AGGCGGTCGTGATACGAGG | GACATTTGGGATGTCGTT | 2 |
| 6       | RM231 (CT)16         | CCAGATTTATTTCGGAGTGC | CACCTGAGATATCTGTT | 3 |
| 7       | RM215 (CT)16         | CAAAAGGAGGACCAAGACG | TGAACGACCTTCTTTGCTAG | 9 |
| 8       | RM263 (CT)34         | CCCAGGCTTGATGCAAGGAC | GCTCTTTGGTGACTACAG | 2 |
| 9       | RM463 (TTAT)5        | TTTCCCTCACATGACGTCG | TTTCTTCTCAGCTACTGG | 12 |
| 10      | RM136 (AGG)7         | GAGACGCTACGTCGCTTCTACG | GAGGAGGCGCGACCCACGTACCG | 6 |
| 11      | RM28048 (CCG)8       | TTCAAGCCGCATCTCATTCC | GCTTATTTGAAAAATGTTTAC | 12 |
| 12      | RM28052 (TA)26       | ACTAAAGATCTTCGAGCTGC | GCTGACATGAGTTCTGTTTC | 12 |
| 13      | RM276 (AG)8A3 (GA)33 | CTGACCTTAGGACACCTCTGT | TCTCCTCATGACAGATATCA | 6 |
| 14      | RM22 (GA)22          | GGTTCGGGGACCCATATCC | CTGCCCCTCTCCTCCTACTG | 3 |
| 15      | RM337 (CTT)4-19-(CTT)8 | GTAGGGAAAGGAGGGCGACAG | CGATAGATAGTGATGTGCTG | 8 |
| 16      | RM28076 (CT)13       | GGGACTTGGGACCCAGATTATG | TCATCGCTGCTGCTGCTATG | 12 |
| 17      | RM7332 (ACAT)11      | ACACGCTGACCACTGACAGC | CAGGGAATGACACGTGTC | 3 |
| 18      | RM60 (AATT)5AATCT (AATT) | AGTCTCATTGGCGCTTCC | AGTCTCATTGGCGCTTCC | 3 |
| 19      | RM216 (CT)18         | GCAATGCGGCAAGTGTTTAA | TGATATAACCAACACGCGAG | 10 |
| 20      | RM518 (CT)15         | CTCTCATTGACACCTACCATG | ATTCAGTGGGACCAACCAA | 4 |
| 21      | RM28199 (ATAG)5      | CGGTCGCTGAGGCCTGTCG | GCTGACATGAGTTCTGTTTC | 12 |
| 22      | RM345 (CTT)9         | ATGGGAACTTCAACGAGAAC | GTGCAACAACCCACATG | 6 |
| 23      | RM1261 (AG)16        | GTCATGCGCAGAGCACAAC | GTGCAACAACCCACATG | 12 |
Fig. 2. Microsatellite panel of studied SSR primers in different genotypes. Genotypes 1: Dangarabayagundar; 2: Machhakanta; 3: Kalajeera; 4: Butukichudi; 5: Bhatachudi; 6: Haladichudi; 7: Pandakagura; 8: Mugudi; 9: N 22; 10: IR 64.

Table 4
Genetic diversity parameters calculated on SSR data. Na: number of alleles; Ne: number of effective alleles; Ho: expected homozygosity; He: expected heterozygosity/Nei’s genetic diversity; I: Shannon’s information index; PIC: polymorphism information content.

| Locus | Na | Ne  | Ho  | He  | I   | PIC |
|-------|----|-----|-----|-----|-----|-----|
| RM339 | 1  | 1.000 | 1.000 | 0.000 | 0.000 | 0   |
| RM411 | 3  | 2.415 | 0.375 | 0.586 | 0.984 | 0.603 |
| RM517 | 3  | 1.852 | 0.516 | 0.460 | 0.802 | 0.460 |
| RM3  | 3  | 2.740 | 0.332 | 0.635 | 1.049 | 0.639 |
| RM452 | 2  | 2.000 | 0.474 | 0.500 | 0.693 | 0.460 |
| RM523 | 2  | 1.724 | 0.558 | 0.420 | 0.611 | 0.420 |
| RM231 | 2  | 1.342 | 0.732 | 0.255 | 0.423 | 0.355 |
| RM215 | 2  | 1.923 | 0.495 | 0.480 | 0.673 | 0.486 |
| RM263 | 3  | 2.817 | 0.321 | 0.645 | 1.067 | 0.661 |
| RM463 | 1  | 1.000 | 1.000 | 0.000 | 0.000 | 0   |
| RM136 | 2  | 1.724 | 0.558 | 0.420 | 0.611 | 0.420 |
| RM28048 | 2  | 1.923 | 0.495 | 0.480 | 0.673 | 0.480 |
| RM28052 | 2  | 1.976 | 0.477 | 0.494 | 0.687 | 0.493 |
| RM276 | 4  | 2.985 | 0.300 | 0.665 | 1.192 | 0.687 |
| RM22 | 1  | 1.000 | 1.000 | 0.000 | 0.000 | 0   |
| RM337 | 2  | 1.835 | 0.521 | 0.455 | 0.647 | 0.462 |
| RM28076 | 2  | 1.724 | 0.558 | 0.420 | 0.611 | 0.420 |
| RM7332 | 2  | 1.849 | 0.506 | 0.459 | 0.652 | 0.468 |
| RM60 | 2  | 1.960 | 0.473 | 0.490 | 0.683 | 0.489 |
| RM216 | 3  | 2.946 | 0.301 | 0.661 | 1.089 | 0.648 |
| RM518 | 2  | 1.960 | 0.473 | 0.490 | 0.683 | 0.489 |
| RM28199 | 3  | 2.151 | 0.437 | 0.535 | 0.845 | 0.549 |
| RM345 | 2  | 1.220 | 0.811 | 0.180 | 0.325 | 0.277 |
| RM1261 | 2  | 1.976 | 0.477 | 0.494 | 0.687 | 0.493 |
| **Mean** | **2.208** | **1.918** | **0.549** | **0.426** | **0.654** | **0.437** |
| **St. Dev** | **0.721** | **0.570** | **0.210** | **0.199** | **0.325** | **0.194** |
different plants in each replication under drought as well as at control conditions. For analysing early growth performances, relative germination performance (RGP), relative growth index (RGI), and seedling vigour index (SVI) were calculated according to Rubio-Casal et al. [3] and Bhattacharjee [4] as follows.

\[
\text{RGI} = \frac{\text{average dry mass of five treated seedling}}{\text{average dry mass of five control seedlings}} \times 100.
\]

\[
\text{RGP} = \frac{\text{percentage of germination under treatment}}{\text{percentage of germination under control}} \times 100.
\]

\[
\text{SVI} = \frac{\text{mean shoot length} + \text{mean root length}}{\text{percentage of final germination}}.
\]

2.3. Genotyping with drought tolerance linked rice microsatellite loci

Genotyping with drought tolerance linked rice microsatellite loci was done by taking 24 reported simple sequence repeat (SSR) markers linked to different drought tolerance QTL. Total genomic DNA was extracted and purified from the young leaves by a modified CTAB (cetyl-trimethylammonium bromide) method described by Murray and Thompson [5]. The PCR amplification was performed in thermal cycler (BioRad, USA) by taking 20 µl volumes mixed with 2 µl of genomic DNA (25 ng ml\(^{-1}\)), 1.5 µl of MgCl\(_2\) (25 mM L\(^{-1}\)), 0.3 µl of dNTP mixtures (10 mM L\(^{-1}\)), 2 µl of 10 PCR buffer, 2 µl of SSR primer (2 µM L\(^{-1}\)), 0.2 µl of Taq polymerase (10 U ml\(^{-1}\)) and 12 µl of ddH\(_2\)O, following the method of Panaud et al. [6]. The PCR amplification was an initial denaturation at 94 °C for 5 min followed by 35 cycles of denaturation at 94 °C for 30 sec, annealing (depending on TM value of primer) at 50–60 °C for 45 sec, extension at 72 °C for 1 min and a final extension of 7 min at 72 °C. The amplified products were resolved through 2.5% ethidium bromide stained (1 µg ml\(^{-1}\)) agarose gel and documented using a gel documentation system (BioRad, USA). The different allelic forms (variation in molecular weight of the amplicons) of individual SSR loci were scored as 1 or 0 based on their presence or absence, respectively across the studied rice genotypes. A proximity matrix was constructed from the 1/0 matrix using PAST-3 (Palaeontological Statistics) software to construct a dendrogram using average linkage among the studied genotypes. Marker based population genetics study was performed with calculation of polymorphic information content (PIC), effective number of alleles (Ne), Shannon’s Information index (I), and Nei’s heterozygosity (He) was performed using genetic diversity analysis software POPGENE 1.31 [7].

2.4. Statistical analysis

Growth parameters were analyzed by two-way analysis of variance (ANOVA) with the variety and different treatment levels by using CROPSTAT (International Rice Research Institute, Philippines) software.
Acknowledgments

The study was supported by Science and Technology Department, Government of Odisha, India [Ref. No. 3340 (Sanc.)/ST/22.06.17]. The authors are grateful to Head, Department of Biodiversity and

Fig. 3. Dendrogram showing the percentage of similarity between the rice genotypes based on SSR amplified products.

Acknowledgments

The study was supported by Science and Technology Department, Government of Odisha, India [Ref. No. 3340 (Sanc.)/ST/22.06.17]. The authors are grateful to Head, Department of Biodiversity and
Conservation of Natural Resources for providing necessary facilities for the work. The Regional Director, MS Swaminathan Research Foundation (MSSRF), Jeypore, Odisha and the Director, National Rice Research Institute, Cuttack, Odisha are highly acknowledged for providing the rice seeds for the experiment.

Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.dib.2019.104363.

References

[1] S.S. Mishra, D. Panda, Leaf traits and antioxidant defense for drought tolerance during early growth stage in some popular traditional rice landraces from Koraput, India, Rice Sci. 24 (2017) 207–217.
[2] P. Vikram, S. Kadam, B.P. Singh, J.K. Pal, S. Singh, O.N. Singh, B.M. Swamy, K. Thiyagarajan, S. Singh, N.K. Singh, Genetic diversity analysis reveals importance of green revolution gene (Sd1 Locus) for drought tolerance in rice, Agric. Res. 5 (2016) 1–12.
[3] A.E. Rubio-Casal, J.M. Castillo, C. Lucue, M.E. Fig Ureo, Influence of salinity on germination and seed viability of two primary colonizers of Mediterranean salt plants, J. Arid Environ. 53 (2003) 145–152.
[4] S. Bhattacharjee, Calcium-dependent signaling pathway in heat induced oxidative injury in Amaranthus lividus, Biol. Plant. 52 (2008) 1137–1140.
[5] M.G. Murray, W.F. Thompson, Rapid isolation of high molecular weight plant DNA, Nucleic Acids Res. 8 (1980) 4321–4326.
[6] O. Panaud, X. Chen, S.R. McCouch, Development of microsatellite markers and characterization of simple sequence length polymorphism (SSLP) in rice (Oryza sativa L.), Mol. Gen. Genet. 252 (1996) 597–607.
[7] F.C. Yeh, Population genetic analysis of co-dominant and dominant markers and quantitative traits, Belg. J. Bot. 129 (1997) 157.