




DATA NOTE

# First *de novo* draft genome sequence of *Oryza coarctata*, the only halophytic species in the genus *Oryza* [version 1; referees: 2 approved, 1 approved with reservations]

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**Abstract**



*Oryza coarctata* plants, collected from Sundarban delta of West Bengal, India, have been used in the present study to generate draft genome sequences, employing the hybrid genome assembly with Illumina reads and third generation Oxford Nanopore sequencing technology. We report for the first time that more than 85.71 % of the genome coverage and the data have been deposited in NCBI SRA, with BioProject ID [PRJNA396417](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA396417).





This article is included in the [Global Open Data for Agriculture and Nutrition gateway](#).

**Open Peer Review**

Referee Status:   

	Invited Referees		
	1	2	3
<b>version 1</b>			
published 25 Sep 2017	report	report	report

- 1 **Sandip Das** , University of Delhi, India
- 2 **Stephen P. Moose** , University of Illinois at Urbana-Champaign, USA
- 3 **Kashmir Singh**, Panjab University, India

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Comments (0)

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**Author roles:** **Mondal TK:** Conceptualization, Data Curation, Investigation, Methodology, Resources, Writing – Review & Editing; **Rawal HC:** Data Curation, Formal Analysis; **Gaikwad K:** Data Curation, Formal Analysis, Supervision, Validation; **Sharma TR:** Conceptualization; **Singh NK:** Conceptualization, Data Curation, Formal Analysis, Project Administration

**Competing interests:** No competing interests were disclosed.

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## Introduction

Soil salinity is a major abiotic stress of rice cultivation globally (Molla *et al.*, 2015), and rice cultivation areas under soil salinity stress are increasing gradually. Genetic potential for salt tolerance of rice that exists among the natural population has been largely exploited, and alternative useful alleles may further enhance salinity tolerance. Wild species are a potential source of many useful genes and QTLs that may not be present in the gene pool of the domesticated species.

*Oryza coarctata*, known as Asian wild rice, grows naturally in the coastal region of South-East Asian countries. It flowers and set seeds under as high as 40 E.Ce dS m<sup>-1</sup> saline soil (Bal & Dutt, 1986). It is the only species in the genus *Oryza* that is halophyte in nature. However, with the exception of one transcriptomic (Garg *et al.*, 2014) and one miRNA (Mondal *et al.*, 2014) experiment, no large scale generation of any other genomic resource is available for this important species, although several pinitol biosynthesis pathway genes have been cloned to study the functional genomics (Sengupta & Majumder, 2009).

## Methods

The plants were collected from its native place, Sundarban delta of West Bengal, India (21°36'N and 88°15' E) and established to our institute NET house. To determine the genome size, 20 mg of young leaf tissue from Net house grown plants was chopped into small pieces and stained with RNase containing propidium iodide (50 µg/ml) (BD Science, India) as per the protocol of Dolezel *et al.* (2007). The samples were filtered through a 40-µm mesh sieve (Corning, USA), before analysis in (CFM) BD FACS Calibur (BD Biosciences, San Jose, CA, USA). *Pisium sativum* leaf was used as standard for calculating the genome size. Further, high-quality genomic DNA from 100 mg young leaf was extracted using CTAB method (Ganie *et al.*, 2016) for the preparation of various genomic DNA libraries. We used Illumina 4000 GA Ix sequencer (San Diego, CA, USA), with 150-bp paired-end libraries, four mate-pair library (with 150-bp paired-end libraries) of four different sizes (average of 2, 4, 6 and 10 kb size). In addition, we also used third generation sequencing (Oxford Nanopore) technology for better assembly. Sequencing was performed on MinION Mk1b (Oxford Nanopore Technologies, Oxford, UK) using SpotON flow cell (R9.4) in a 48h sequencing protocol on MinKNOW 1.4.32. Base calling was performed using Albacore. Base called reads were processed using poRe version 0.24 (Watson *et al.*, 2015) and poretools version 0.6.0 (Loman & Quinlan, 2014). The simple sequence repeats (SSRs) of each scaffold were identified by MISA perl script (Thiel *et al.*,

2003). Gene model prediction was done by AUGUSTUS 3.1 (Stanke & Waak, 2003) and genes were functionally analysed using InterProScan version 5.16.55 (Jones *et al.*, 2014). The InterProScan results were further parsed for additional functional evidence (GO terms and KEGG pathway) using interproscan-Parser script available at iPlant (Brozynska *et al.*, 2017). Noncoding RNAs, such as miRNA, tRNA, rRNA, snoRNA, snRNA, were identified by adopting Infernal v1.1.2 (Nawrocki & Eddy, 2013) using Rfam (Nawrocki *et al.*, 2015). Transfer RNA was predicted using tRNAscan-SE v 1.23 (Schattner *et al.*, 2005)

## Discussion

The genome (KKLL) of *O. coarctata* is tetraploid (2n=4X=48) with a genome size estimated by flow cytometer is found to be approximately 665Mb. The Illumina 4000 GA Ix sequencer pair-end generated 137 Gb data. Further four mate-pair libraries together generated 104.35 Gb and Nanopore generated 6.35 Gb sequence data. Hence, we achieved 372.48 X depth of the genome of *O. coarctata*. The final assembly generated 58362 number of contigs with a minimum length of 200 bp to maximum length of 7,855,609 bp and 1,858,627 bp N50 value, making a total contig length of 569994164 (around 570 Mb) assembled genome, resulting 85.71 % genome coverage. It has been calculated that data contain very small amount of non-ATGC character. Further, we also found that the repeat contain 19.89% of the genome. We also identified approximately 1605 different non-coding RNAs and around 105673 SSRs. Gene ontology analysis identified several salt responsive genes.

## Data availability

Raw sequence data are available at NCBI SRA under the BioProject ID: PRJNA396417.

## Competing interests

No competing interests were disclosed.

## Grant information

The author(s) declared that no grants were involved in supporting this work.

## Acknowledgements

TKM is also grateful to Mr Sukdev Nath, who provided the planting material. TRS is thankful to the DST, Govt. of India for JC Bose National Fellowship. The authors are thankful to M/S Genotypic Technology Private Limited, Bengaluru, India for sequencing work and M/S BD Biosciences, India for Flow Cytometer work.

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# Open Peer Review

Current Referee Status:



Version 1

Referee Report 20 October 2017

doi:10.5256/f1000research.13443.r26359



**Kashmir Singh**

Department of Biotechnology, Panjab University, Chandigarh, India

The work describe the whole genome sequence of wild species of *Oryza coarctata* species that exclusively grow under saline water and thus will be an important source of salinity tolerance genes. These genes can later be used to introduce salinity tolerance in commercial cultivars of rice. The authors used Illumina and Oxford nanopore sequencing platforms to generate 372.48X data.

The genome sequencing methods seems good enough but authors have discussed very little about the annotation of the genome data. I can understand that there is word limit under Data Note in F1000Research, but still by looking at the discussion, I think analysis portion is weak point in this paper. Authors should provide a comparative note on the genome of *Oryza sativa* and *Oryza coarctata*. How this species is tolerating such a high saline conditions, which kind of genes/osmoregulators are involved in this adaptation should be discussed along with comparison to *O. sativa*. How many different genes were predicted should be mentioned. Authors found approximately 1605 non-coding RNAs? I am not sure, what are trying to tell here, this number should be high as per my opinion.

There are some minor mistakes like; in the affiliation the word "Delhi" is not required. The word, "Primary" should be inserted in the first paragraph last line of Introduction. So the correct sentence will be "...in the primary gene pool...".

**Is the rationale for creating the dataset(s) clearly described?**

Yes

**Are the protocols appropriate and is the work technically sound?**

Yes

**Are sufficient details of methods and materials provided to allow replication by others?**

Yes

**Are the datasets clearly presented in a useable and accessible format?**

Yes

**Competing Interests:** No competing interests were disclosed.

**I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.**

Referee Report 13 October 2017

doi:10.5256/f1000research.13443.r26486



**Stephen P. Moose** 

Department of Crop Sciences, University of Illinois at Urbana-Champaign, Champaign, IL, USA

The authors report a whole genome sequence dataset for a halophytic wild rice species. These data will be useful for discovery of novel alleles for rice improvement, and for comparative/evolutionary genomics within the *Oryza* genus.

1. The report would benefit from more details on the plant accession used as source of DNA for sequencing. It is stated *O. coarctata* is tetraploid. Was that determined by the authors, or is there a citation to include? Is it known whether *O. coarctata* is typically self or cross-pollinated, or other information about expected degree of heterozygosity? When grown in greenhouse to generate the plant tissue used for DNA extraction, were the plant(s) established from seeds, or via clonal propagation? Was the genomic DNA used to prepare sequencing libraries from a single plant, or a pool from multiple plants? This information is important to assess expected frequencies of variant types such as alleles or homeologs due to tetraploidy, which are likely collapsed to varying degrees in the subsequent assembly.
2. There is mention of an assembly and its quality, but not about the method(s) used to produce it or key parameters that guided the assembly. Can the authors provide that information, so that others have a benchmark upon which to compare future assemblies using the datasets?
3. The sentence "Further, we also found that the repeat contain 19.89% of the genome." Is not completely clear. I believe what the authors intend to say is that approximately 20% of the genome assembly is comprised of repeats. How was this sequence fraction defined as repeats, via tool for matching to known repeat sequences, or a de novo approach? By inference, it is also likely that the approximately 100-kb of the estimated genome size not covered by the assembly is comprised of high-copy repeats, leading to an estimate of about 30% total repeat content.

**Is the rationale for creating the dataset(s) clearly described?**

Yes

**Are the protocols appropriate and is the work technically sound?**

Yes

**Are sufficient details of methods and materials provided to allow replication by others?**

Partly

**Are the datasets clearly presented in a useable and accessible format?**

Yes

**Competing Interests:** No competing interests were disclosed.

**I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.**

Referee Report 11 October 2017

doi:10.5256/f1000research.13443.r26360



**Sandip Das** 

Department of Botany, University of Delhi, Delhi, India

The authors report a draft genome sequence of a halophyte *Oryza* species collected from Sunderbans, and provides a glimpse into the adaptive strategies employed by *Oryza* against salinity stress. Undoubtedly, it will be an useful resource for future functional characterization, comparative genomic studies, and developing salinity tolerance in rice. I understand that the present format is only for reporting, and look forward to reading the full manuscript with all the analysis. There are small language edits that that authors need to incorporate.

Comments:

Please add a reference or sufficient information for general readers as to how genome types of rice (for instance, KKLL in case of *O. coarctata*) was assigned.

Language corrections:

1. Change “have been used” to “has been used”
2. Change “We report for the first time that more than 85.71 % of the genome coverage and the data have been deposited in NCBI SRA, with BioProject ID PRJNA396417” to “deposited in NCBI SRA, with BioProject ID PRJNA396417”
3. Change “and established to our institute NET” to “and established at our institute NET”
4. Change “resulting 85.71 % genome coverage” to “resulting in 85.71 % genome coverage”
5. Change “we also found that the repeat contain 19.89% of the genome.” to “we also found that the 19.89% of the genome is repetitive in nature”.

**Is the rationale for creating the dataset(s) clearly described?**

Yes

**Are the protocols appropriate and is the work technically sound?**

Yes

**Are sufficient details of methods and materials provided to allow replication by others?**

Yes

**Are the datasets clearly presented in a useable and accessible format?**

Yes

**Competing Interests:** No competing interests were disclosed.

**Referee Expertise:** Comparative genomics, brassica, polyploidy, regulatory evolution

**I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.**

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