

Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice**2017**

Posted by : webmaster

Posted on : 2017/11/28 15:50:00

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Volume 15, Issue 6

June 2017

Pages 765–774

Keywords

assembly; molecular clock; sequencing; Oryza ; phylogeny; wild rice

Publication History

Issue online:

10 May 2017

Version of record online:

23 January 2017

Accepted manuscript online:

27 November 2016

Manuscript Accepted:

23 November 2016

Manuscript Revised:

10 October 2016

Manuscript Received:

14 July 2016

Summary

The related A genome species of the Oryza genus are the effective gene pool for rice. Here, we report draft genomes for two Australian wild A genome taxa: *O. rufipogon*-like population, referred to as Taxon A, and *O. meridionalis*-like population, referred to as Taxon B. These two taxa were sequenced and assembled by integration of short- and long-read next-generation sequencing (NGS) data to create a genomic platform for a wider rice gene pool. Here, we report

that, despite the distinct chloroplast genome, the nuclear genome of the Australian Taxon A has a sequence that is much closer to that of domesticated rice (*O. sativa*) than to the other Australian wild populations. Analysis of 4643 genes in the A genome clade showed that the Australian annual, *O. meridionalis*, and related perennial taxa have the most divergent (around 3 million years) genome sequences relative to domesticated rice. A test for admixture showed possible introgression into the Australian Taxon A (diverged around 1.6 million years ago) especially from the wild indica/*O. nivara* clade in Asia. These results demonstrate that northern Australia may be the centre of diversity of the A genome *Oryza* and suggest the possibility that this might also be the centre of origin of this group and represent an important resource for rice improvement.

<http://onlinelibrary.wiley.com/doi/10.1111/pbi.12674/abstract>