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Assembling the largest diploid rice genome for discovery of novel genes

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The Australian wild relatives of rice represent largely untapped genetic reservoirs that can be harnessed for cultivated rice improvement. *Oryza australiensis* is an endemic Australian wild rice relative that possesses a number of agronomically attractive traits, including resistances to blast disease (*Pyricularia oryzae*) and brown plant hopper (*Nilaparvata lugens*), as well as heat, salinity, and drought tolerances. Consequently, *O. australiensis* is a promising genetic resource for cultivated rice. The development of a high-quality genome assembly is foundational for exploring the gene content of this species. Here, we present a chromosome-level de novo genome assembly of *O. australiensis*. PacBio HiFi long read data from *O. australiensis* was assembled using the Hifiasm Denovo assembler. The final length of the *O. australiensis* genome was 909 Mb. Genome assembly completeness, assessed using Benchmarking Universal Single-Copy Orthologues (BUSCO) from the viridiplantae lineage, was 99.3%. Eleven out of the 12 assembled pseudochromosomes had telomeres on both the forward and reverse strands, representing full chromosomes. The finalised assembly provides a high-quality, near-complete representation of the *O. australiensis* genome, that can be used to identify novel genetic material. Ongoing functional annotation of the *O. australiensis* genome will further elucidate the genes that control beneficial traits in this species.

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