

Whole genome sequencing of wild rice reveals the mechanisms underlying oryza genome evolution

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In a collaborative study published online today in *Nature Communications*, researchers from Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, BGI-Shenzhen, and University of Arizona have completed the genome sequencing of wild rice *Oryza brachyantha*. This work provides new insights for researchers to understand the function and evolution of *Oryza* genomes.

The genus *Oryza* is an idea model system for studying plant comparative genomics, [evolutionary biology](#) and functional biology. There are two [cultivated rice](#) and more than twenty wild rice species. Among them, the wild relatives can provide invaluable genomic resources for rice improvement. As the most diverged wild relative of *O. sativa* (rice), *O. Brachyantha* has resistance against many rice pathogens and various stress environments. It was also proved to have the most compact genome in the genus *Oryza*, suggesting the genome may not experience many changes after the divergence of *Oryza* species.

In this study, researchers generated a high-quality reference [genome sequence](#) of *O. brachyantha* (~261Mb), and 96% genome sequences are anchored on 12 chromosomes based upon BAC-based physical map. After the comprehensive analysis, they found that the compact genome of *O. brachyantha* was caused by the silencing of LTR (Long terminal Repeats) retrotransposons and massive internal deletions of ancient elements.

Compared with the [rice genome](#), the team found that many gene families were expanded in rice, where tandem duplications and gene movements mediated by double-strand break repair are responsible for the amplification of these genes. Researchers also observed that segmental and tandem duplications, further expanded by transposable element insertions, contributed to transition from euchromatin to heterochromatin in the rice genome, reflecting the dynamic nature of the *Oryza* genomes.

Quanfei Huang, Project Manager from BGI, said "This work revealed many important genomic mechanisms underlying *Oryza* genome, such as the genome size variation, gene movement and transition of euchromatin to heterochromatin. In the near future, I believe there will be more genomes of *Oryza* species to be cracked, enabling the genus *Oryza* be an unparalleled system for functional and evolutionary studies in plants."

Provided by BGI Shenzhen

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