

1 ***Oryza* genome evolution through a tetraploid lens**

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Abstract

Oryza is remarkable genus - with two domesticated (i.e. Asian and African rice) and 25 diploid and tetraploid wild species, 11 extant genome types, and a ~3.4-fold genome size variation - that possesses a virtually untapped reservoir of genes that can be used for crop improvement. Here we unveil and interrogate 11 new chromosome-level assemblies of nine tetraploid and two diploid wild *Oryza* species in the context of ~15 million years of evolution of the genus. We show that the core *Oryza* (sub)genome across all genome types is only ~200 Mb and largely syntenic, while the remaining nuclear fractions, spanning ~80-600 Mb, are intermingled, extremely plastic and rapidly evolving. For the halophyte *O. coarctata*, we show that - despite the detection of gene fractionation in the subgenomes - homoeologous genes are expressed at higher levels in one subgenome over the other in a mosaic form, thereby showing subgenome equivalence. The integration of these 11 new ultra-high quality reference genomes with our previously published genome data sets provide a nearly complete picture of the consequences of natural and artificial selection across the evolutionary history of *Oryza*. This in turn opens the door to unlock their genetic potential for future crop improvement and neodomestication.