

Extensive sequence divergence between the reference genomes of two elite indica rice varieties Zhenshan 97 and Minghui 63

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Abstract

Asian cultivated rice consists of two subspecies: *Oryza sativa* subsp. *indica* and *O. sativa* subsp. *japonica*. Despite the fact that *indica* rice accounts for over 70% of total rice production worldwide and is genetically much more diverse, a high-quality reference genome for *indica* rice has yet to be published. We conducted map-based sequencing of two *indica* rice lines, Zhenshan 97 (ZS97) and Minghui 63 (MH63), which represent the two major varietal groups of the *indica* subspecies and are the parents of an elite Chinese hybrid. The genome sequences were assembled into 237 (ZS97) and 181 (MH63) contigs, with an accuracy >99.99%, and covered 90.6% and 93.2% of their estimated genome sizes. Comparative analyses of these two *indica* genomes uncovered surprising structural differences, especially with respect to inversions, translocations, presence/absence variations, and segmental duplications. Approximately 42% of nontransposable element related genes were identical between the two genomes. Transcriptome analysis of three tissues showed that 1,059–2,217 more genes were expressed in the hybrid than in the parents and that the expressed genes in the hybrid were much more diverse due to their divergence between the parental genomes. The public availability of two high-quality reference genomes for the *indica* subspecies of rice will have large-ranging implications for plant biology and crop genetic improvement.

Oryza sativa | reference genomes | BAC-by-BAC | strategy transcriptome

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