Comparative physical mapping between Oryza sativa (AA genome type) and O. punctata (BB genome type)

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Abstract
A comparative physical map of the AA genome (Oryza sativa) and the BB genome (O. punctata) was constructed by aligning a physical map of O. punctata, deduced from 63,942 BAC end sequences (BESs) and 34,224 fingerprints, onto the O. sativa genome sequence. The level of conservation of each chromosome between the two species was determined by calculating a ratio of BES alignments. The alignment result suggests more divergence of intergenic and repeat regions in comparison to gene-rich regions. Further, this characteristic enabled localization of heterochromatic and euchromatic regions for each chromosome of both species.

The alignment identified 16 locations containing expansions, contractions, inversions, and transpositions. By aligning 40% of the punctata BES on the map, 87% of the punctata FPC map covered 98% of the O. sativa genome sequence. The genome size of O. punctata was estimated to be 8% larger than that of O. sativa with individual chromosome differences of 1.5-16.5%. The sum of expansions and contractions observed in regions >500 kb were similar, suggesting that most of the contractions/expansions contributing to the genome size difference between the two species are small, thus preserving the macro-collinearity between these species, which diverged approximately 2 million years ago.