The oryza map alignment project: the golden path to unlocking the genetic potential of wild rice species

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Abstract

The wild species of the genus Oryza offer enormous potential to make a significant impact on agricultural productivity of the cultivated rice species Oryza sativa and Oryza glaberrima. To unlock the genetic potential of wild rice we have initiated a project entitled the 'Oryza Map Alignment Project' (OMAP) with the ultimate goal of constructing and aligning BAC/STC based physical maps of 11 wild and one cultivated rice species to the International Rice Genome Sequencing Project's finished reference genome--O. sativa ssp. japonica c. v. Nipponbare. The 11 wild rice species comprise nine different genome types and include six diploid genomes (AA, BB, CC, EE, FF and GG) and four tetraploid genomes (BBCC, CCDD, HHKK and HHJJ) with broad geographical distribution and ecological adaptation. In this paper we describe our strategy to construct robust physical maps of all 12 rice species with an emphasis on the AA diploid O. nivara--thought to be the progenitor of modern cultivated rice.