**The Oryza BAC library resource: Construction and analysis of 12 deep-coverage large-insert BAC libraries**

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**Abstract**

Rice (Oryza sativa L.) is the most important food crop in the world and a model system for plant biology. With the completion of a finished genome sequence we must now functionally characterize the rice genome by a variety of methods, including comparative genomic analysis between cereal species and within the genus Oryza. Oryza contains two cultivated and 22 wild species that represent 10 distinct genome types. The wild species contain an essentially untapped reservoir of agriculturally important genes that must be harnessed if we are to maintain a safe and secure food supply for the 21st century. As a first step to functionally
characterize the rice genome from a comparative standpoint, we report the construction and analysis of a comprehensive set of 12 BAC libraries that represent the 10 genome types of Oryza. To estimate the number of clones required to generate 10 genome equivalent BAC libraries we determined the genome sizes of nine of the 12 species using flow cytometry. Each library represents a minimum of 10 genome equivalents, has an average insert size range between 123 and 161 kb, an average organellar content of 0.4%–4.1% and nonrecombinant content between 0% and 5%. Genome coverage was estimated mathematically and empirically by hybridization and extensive contig and BAC end sequence analysis. A preliminary analysis of BAC end sequences of clones from these libraries indicated that LTR retrotransposons are the predominant class of repeat elements in Oryza and a roughly linear relationship of these elements with genome size was observed.