



Construction and preliminary characterization of a river buffalo bacterial artificial chromosome library

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ABSTRACT. River buffalo genome analyses have advanced significantly in the last decade, and the genome sequence of *Bubalus bubalis* will be available shortly. Nonetheless, large-insert DNA library resources such as bacterial artificial chromosomes (BAC) are still required for validation and accurate assembly of the genome sequence. We constructed a river buffalo BAC library containing 52,224 clones with an average insert size of 97 kb, representing $1.7 \times$ coverage of the genome. This genomic resource for river buffalo will facilitate further studies in this economically important species allowing for instance, whole genome physical mapping and isolation of genes and gene clusters, contributing to the elucidation of gene organization and identification of regulatory elements.

Key words: BAC library; *Bubalus bubalis*; Cloning; Pulse-field gel electrophoresis