Construction of the BAC library for ***Biomphalaria glabrata***

New copies of the BAC libray are no longer available since the supporting NHGRI program ended in 2018.

The BAC library was acquired and may still be available, however, by some research groups

Background

On behalf of the ***Biomphalaria glabrata*** genome initiative, a white paper requesting the construction of a bacterial artificial chromosome (BAC) library for the snail ***Biomphalaria glabrata***, was submitted to the National Human Genome Research Institute (NHGRI). In July 2002, review by the Genome Resources and Sequencing Priorities Panel (GRASPP) of the NHGRI BAC Resource Steering Panel resulted in a "high priority" recommendation, concluding that the proposal was "worth accepting based on the medical importance alone". This project was assigned to the laboratory of Rod Wing, Arizona Genomics Institute, University of Arizona, Tucson AZ, which belongs to the National Institutes of Health (NIH) BAC Resource Network. The library was produced to meet a predetermined set of BAC Library Quality Assessment Standards. Details regarding this ***Biomphalaria glabrata*** project are publicly posted on the BAC Library Proposals and Information web page of NHGRI. Since the positive recommendation from the Prioritization Panel, NHGRI and the ***Biomphalaria glabrata*** Genome Initiative have interactively agreed to employ a ***Biomphalaria glabrata*** strain (field isolate) that is **susceptible** to *Schistosma mansoni* to generate the BAC library. Thus, molecular data collected from the ***Biomphalaria glabrata*** BAC library will provide a relevant context for study of the intramolluscan biology of schistosomes.

Working with the Arizona Genomics Institute in Tucson AZ, methods were adapted for isolation of high molecular weight genomic DNA from ***B. glabrata***. Exploratory efforts using M-line snails identified the ovotestis of adult snails (shell diameter at least 10mm) as preferred tissue for the required DNA.

For production of the BAC library, template DNA was isolated from multiple BB02 snails (F2) bred from a single parent snail by selfing. HindIII restriction fragments were cloned into pAGIBAC. In total 61,824 clones were picked and the average insert size is estimated at ~136kb, this yields about 9.05x genome coverage.

For quality assesment both ends of 96 BAC clones were sequenced (GenBank DX360154-360158, DX360097-360114), and ptobing of high density filters of the BAC library with (single- and) low copy genes indicated adequate coverage of the genome by the library.

The quality control phase was completed satisfactorily and the production of the BAC library was reported in Memórias do Instituto Oswaldo Cruz.

Adema CM, Luo MZ, Hanelt B, Hertel LA, Marshall JJ, Zhang SM, DeJong RJ, Kim HR, Kudrna D, Wing RA, Soderlund C, Knight M, Lewis FA, Caldeira RL,
Jannotti-Passos LK, Carvalho Odos S, Loker ES. A bacterial artificial chromosome library for ***Biomphalaria glabrata***, intermediate snail host of ***Schistosoma mansoni***. Mem Inst Oswaldo Cruz. 2006 Sep;101 Suppl 1:167-77. PubMed PMID: 17308766 doi 10.1590/s0074-02762006000900027