

Sequencing of *Idd* regions in the NOD mouse

The National Institute of Allergy and Infectious Diseases (NIAID), the National Institute of Diabetes, Digestive and Kidney Diseases (NIDDK), and the Juvenile Diabetes Research Foundation (JDRF) are pleased to announce the availability of resources for sequencing *Idd* regions in the NOD mouse:

- The Wellcome Trust Sanger Institute, Cambridge, UK, has completed full BAC end-sequencing of the NOD BAC library from the Diabetes and Inflammation Laboratory at the University of Cambridge, which was developed from the NOD/MrkTac mouse strain.

Sequences have been deposited in the Ensembl trace archive and are mirrored in the NCBI trace archive. The BAC end sequences have been mapped to Build 32 of the mouse genome sequence, and will be mapped to Build 33 of the mouse genome as soon as it is available. Their alignment can be viewed as tracks in the Contigview or Cytoview windows of the Ensembl mouse genome browser, accessed through the DAS sources menu. The data can be accessed from the entry point: (http://www.ensembl.org/Mus_musculus/).

- The Sanger Institute is end-sequencing and fingerprinting a second NOD BAC library (CHORI-29; Peter de Jong, Research Genetics), which was developed from the NOD/LtJ mouse strain.

To date, 50,000 clones from CHORI-29 have been end sequenced, with a potential average genome coverage of 1.5X. An additional set of 50,000 clones will be sequenced, and data will be deposited and available in Ensembl. This data is expected to be available in September 2004.

There is now an opportunity for all interested investigators to propose *Idd* intervals for full, finished sequencing.

Investigators proposing intervals must provide the following information, defining the proposed interval using congenic strains of NOD mice, on no more than one page:

1. Statistical evidence showing that the interval alters the frequency of diabetes
2. Boundary markers under consideration – intervals may not exceed 3 Mbp, and should include as much marker information as possible
3. Information on independent congenics that support the definition of the *Idd* interval.

Proposals may be submitted at any time, via email to: John Ridge (jridge@niaid.nih.gov) or to Beena Akolkar (akolkarb@extra.niddk.nih.gov).

Proposals will be considered by the External Advisory Committee for this project. Investigators will be notified by email, and will receive instructions on how to proceed. A list of intervals in the sequencing queue, with a time estimate for completion, will be posted on this site. **All sequence data will be released according to Bermuda rules: there will be no provision for any exclusive access to the sequence data.**

For more information, or in case of questions, please contact John Ridge (jridge@niaid.nih.gov), Beena Akolkar (akolkarb@extra.niddk.nih.gov), or Marie Nierras (cnierras@jdrf.org).