Request to construct a BAC library from the gray squirrel

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This proposal represents an addendum to a previous proposal (Thomas et al., http://www.genome.gov/10001852) requesting prioritization and creation of BAC libraries from representatives of diverse mammalian phylogenetic lineages for which genomic resources are largely unavailable.

Below we propose the gray squirrel (*Sciurus carolinensu*s, (Order Rodentia, Superorder Euarchontoglires) as a candidate for BAC library construction. The squirrel would serve to provide valuable genomic comparisons to species for which BAC libraries or full genomic sequence already exist.

Creation of a BAC library resource for a sciurid rodent would provide the capacity to obtain molecular sequence data for a rodent phylogenetically distant from mouse and rat, which differs from these two murid species by having a conserved genomic organization and lower overall rate of nucleotide evolution. The ability to obtain molecular sequence data from a different, non-accelerated rodent lineage would be extremely useful for molecular evolutionary analyses of the mammalian genome, where the past use of only mouse and rat sequences have resulted in numerous errors concerning general biological phenomena (such as estimation of mutation rates [1]). The ability to obtain non-murid gene

sequence will also be very powerful for annotation of rodent-specific gene regulatory elements.

As requested in our previous proposal, we recommend that the library be constructed at the standard depth of clone coverage equal to at least 10X genome equivalents (the genome size of the gray squirrel is expected to be ~3x10^9 bp), have an average clone insert size of ~150 kb and be made using standard BAC vectors, such as pTARBAC2.1 or pBACe3.6. These specifications are the standard for previous mammalian BAC libraries and therefore should be held to in each of the mammals we are proposing.

References:

1. Kumar S, Subramanian S. 2002. Mutation rates in mammalian genomes. *PNAS* 99:803-808.