**The Whole Genome Sequence of *Faxonius wrighti***

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*Faxonius wrighti* (Hardin crayfish) is a stream-dwelling crayfish found in the Tennessee River at Beason, Snake, Chambers, and Robinson creek basins near Hardin and McNairy counties in Tennessee. Conservation concerns for the Hardin crayfish have led to potential Federal Endangerment listing, such as reduced habitat and excess sedimentation. This study focuses on sequencing the whole genome of a Hardin crayfish for use as a reference genome to assist population genetics analysis and evidence of adaptation. **To obtain genomic data, a form-one male was collected from the type locality, Robinson Creek, State Highway 57, Hardin County, Tennessee. Abdominal tissue DNA was extracted from this individual and the whole genome was sequenced with high coverage using a combination of short reads (Illumina) and long reads (Pacific Biosciences). The short reads were first constructed into *contigs,* then long reads were overlapped and filled in gaps between the *contigs* to make longer *scaffolds.* The individual sequences were assembled through this process, *de novo* assembly, and the genome was annotated**. **The whole genome is 3.5 billion base pairs in length and now acts as the high-quality reference genome for studies to follow1.** This work is applicable to genome resequencing, using low coverage sequences of additional Hardin crayfish individuals and aligning those to the reference. Genome resequencing makes it much easier to identify genome-wide single nucleotide polymorphisms (SNPs), which are used to measure genetic variability and structure, within and between populations. Another important function of the whole genome is studying loci under selection. This includes searching the genome for loci that seem to have undergone positive selection and connecting that to potential adaptation and phenotypic variation. Whole genome sequencing of non-model organisms, like Hardin crayfish, has become invaluable, giving us access to more information about a species than we have ever had.

Word count = 296

**1All sentences in bold have been fabricated for the purposes of this class assignment.**

Check corrections that Dr.Mattingly Made