



## PO0249: Genome Sequencing and *de novo* Assembly of the South American Tiger Catfish (*Pseudoplatystoma Punctifer*) Using 10X Sequencing Data

The South American Tiger Catfish (*Pseudoplatystoma punctifer*) is a freshwater fish species naturally found in the Amazon river basin with an important role in local community and commercial fishing. Recent efforts to domesticate and raise the species in aquaculture systems has led to >10-fold production increases in the last decade. Current production levels are >15,000mt/year. Recently established initiatives to structure genetic improvement programs for increasing productivity-associated traits could greatly benefit from using genomic tools for broodstock management and assisted genetic evaluations and breeding. Multiple shotgun libraries with two different insert sizes and multiple Nextera mate pair libraries with three different sizes were sequenced (2x160bps) with Illumina HiSeq2000 technology. A total of 252.8Gbp quality-filtered nucleotides were sequenced which amount to 230x mean genome coverage, considering previously published information (C-value = 1.12pg = 1.095Gbp). Initial sequence assembly was performed with SOAPdenovo and generated 25,778 scaffolds spanning 1.12 Gbp (N50 scaffold length: 3.02Mb, L50 scaffold count: 101). An additional long-read library was sequenced with 10x genomics technology and the initial assembly using the software Supernova generated 106,397 scaffolds with average length of 7.5 Kb (longest: 1.8 Mb). The hybrid data assembly is underway, in which different software and protocols are being evaluated in order to obtain the best genome assembly. This represents the first report of a draft genome sequence for this species, which will be a valuable resource for basic biology studies, and marker detection/selection for use in genetic improvement and resource conservation activities.

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