

**P0231*****de novo* Genome Assembly of the South American Freshwater Fish Tambaqui (*Colossoma macropomum*)**

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Room:

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The Tambaqui (*Colossoma macropomum*) is a freshwater fish species naturally found in the Amazon river basin which has historically been widely exploited by community and commercial fishing. Recent efforts to domesticate, breed and raise the species in aquaculture systems has led to significant increases in production (>10-fold) over the last ten years. Current production is above 120,000 metric tons per year with a strong growth trend, making it the most important native aquaculture species in Brazil. Data for generating the draft assembly were produced from shotgun libraries with two different insert sizes and mate-paired libraries with four different sizes sequenced (2x150bps) with Illumina HiSeq2000 technology. A total of 124.8Gbp quality-filtered nucleotides were sequenced which amount to 85x mean genome coverage, considering previously published information (C-value = 1,5pg = 1.467Gbp). Sequence assembly was performed with SOAPdenovo and generated 8.924 scaffolds spanning 1.54 Gbp (N50: 2,041,733bp (162 scaffolds), N90: 200,945bp (1009 scaffolds), ~500Mbp of unmapped nucleotides). Gene model prediction is underway with MAKER2 using as extrinsic evidence protein and EST data from phylogenetically related taxa. This represents the first report of a draft genome sequence for this species and will be a valuable source of information for marker detection/selection, genetic improvement, conservation and basic biology studies in this species.

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