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SNP Discovery in the South American Freshwater Fish Tambaqui (*Colossoma macropomum*) by Deep Sequencing of Reduced Representation Libraries

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Tambaqui is the most important native fresh water fish species cultured in Brazil, with current yearly production levels exceeding 200.000mt. Efforts to structure genetic improvement programs for increasing productivity are recent and will greatly benefit from the use of genomic tools for broodstock management and assisted genetic evaluations and breeding. Recent efforts have produced a draft genome sequence for this species. Reduced representation libraries of varying fragment sizes were produced with bulked DNA samples and sequenced with 2x160bp Illumina protocols to produce >720million reads. Generated reads were aligned with the draft reference genome sequence using BWA and SNP discovery was performed using Freebayes. An estimated 12% of the tambaqui genome was sequenced with a depth of >100 reads. A total of 993.935 SNPs were observed with read depths >60 (median: 438) and minor allele frequencies >0.05 (MAF 0.05-0.15: 94.102 SNPs; 0.15-0.25: 326.575; 0.25-0.35: 255.967; 0.35-0.45: 215.054; 0.45-0.50: 102.237). This represents the first report of an extensive effort to identify SNP markers for this species and will be a valuable source of information for designing marker panels with varying applications.

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