



SNP Discovery in Three South American Freshwater Characiformes Species by Deep Sequencing of Reduced Representation Libraries (RRL)

Saturday, January 12, 2019

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Tambaqui (*Colossoma macropomum*) is the most important native aquaculture freshwater fish species raised in Brazil. A total of 180,000mt are produced annually, accounting to 43% of all finfish cultured domestically. Cross-species hybridization with two other Characiformes species, Pacu (*Piaractus mesopotamicus*) and Pirapitinga (*Piaractus brachypomus*), has been systematically used in the last two decades in terminal crosses to obtain individuals resistant to lower temperatures, diseases and faster growing destined to grow-out. Resulting hybrids are often phenotypically indistinguishable and fully fertile. Recent studies revealed hybrids in specimens sampled in farms as pure Tambaqui. To prospect SNP markers with species-specific alleles, reduced representation libraries (RRL) with fragments between 400–500bp, 500–650 bp, and 650–850bp for each of the three species were produced using bulked DNA samples. Around 12% of the Tambaqui, 11 % of Pacu and 9,5% of Pirapitinga genomes were sequenced using 2x160bp Illumina protocols with an average depth of >100x. Generated reads were aligned with the Tambaqui draft reference genome sequence using BWA and SNP discovery was performed using Freebayes. About 2.4 million SNPs were observed with read depths (RD) >50 and minor allele frequencies >0.05 in Tambaqui, 2.5 million in Pacu and 2 million in Pirapitinga. A total of 16,336 SNPs with species-specific alleles (Tambaqui≠Pacu≠Pirapitinga) helpful for development of tools for hybrid detection were observed (RD>50). This represents the first report of a large-scale effort to identify SNP markers for Pacu and Pirapitinga species, useful for prospecting species-specific SNPs for species-purity certification of commercial Tambaqui broodstocks.

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