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Analysis Of BAC End Sequences Of Tilapia (Oreochromis niloticus) Using in silico Approaches.

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Tilapias are the second most important fish group in aquaculture and a primary source of animal protein for millions of people in developing countries. Over the past years a great effort has been done to increase the genomic tools in tilapia by obtaining data on BAC End Sequences (BES), Expressed Sequence tags (EST), restriction fingerprint maps, and radiation hybrid maps. We analyzed BES to develop comparative physical maps, and estimated the number of genome rearrangements, between tilapia and three other model fish species: stickleback, medaka and pufferfish. In order to analyse these BACs, we are using a modeling approach with a standard design notation, namely UML. In this way, both genomic knowledge and in silico analysis results are expressed through sequence diagrams. These diagrams help to define a more precise and valid approach for data confrontation. We used BES from 106,259 tilapia BACs, obtained by the Broad Institute and the Genoscope, to do blast analysis against the genome assemblies of the three fish species. We identified homologies for approximately 25,000 BACs for each species. Rearrangement breakpoints between tilapia and these species occur about every 3Mb across the genome. To visualize the position of BES on the fish genomes, we created a GBrowser available through the database BouillaBase.org. These physical maps are a useful resource for comparative positional cloning of traits in cichlid fishes and comparative genomics between cichlid and other fish family. The paired BES from these clones will be an important resource for assembling the forthcoming tilapia genome.