



Category: Animal genomics

Identification of molecular markers in *Labeo rohita* towards better carbohydrate utilization

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Abstract

The contribution of aquaculture products in providing nutritional and food security to human is increasing expeditiously with the increase in animal protein demand. Feed cost contributes more than 60% of the cost of aquaculture production. Henceforth, formulation of cheap fish feed is one of the greatest challenges in aquaculture industry. Carbohydrates are the cheap source of dietary energy. So their level of utilization in fish is an exciting area in research for decreasing the fish feed cost. Molecular markers such as microsatellite and single nucleotide polymorphism (SNP) are used for genetic mapping, quantitative trait loci identification and genome-wide association studies in several aquaculture species. In this experiment, SNPs and microsatellite markers linked to carbohydrate utilization in *Labeo rohita* were identified. Liver tissue samples of *Labeo rohita* and *Labeo bata* were collected from individuals fed with a customized diet with 40% carbohydrate for a period of 21 days. RNA was extracted and cDNA library was prepared and sequenced on Illumina NextSeq 500 platform. 7.5 GB of data was generated from each species. Assembly of rohu data resulted in 70, 225 contigs, out of which 6284 microsatellite markers were identified. Among which, 3838, 1817, 488, 132 and 9 were di-, tri-, tetra-, penta- and hexa-repeats, respectively. Primer modelling was successful for 4190 sequences. Similarly, 2, 14, 071 SNPs were identified using CLC bio v7.0.4 and utilizing Illumina reads obtained from *Labeo bata*. This study can be helpful in efficient use of carbohydrate in *Labeo* species for decreasing feed cost globally.

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