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SNP markers in growth-related candidate genes of Black tiger shrimp and their significance

K Vinaya Kumar, S Jothivel, J Shanmugakarthik, G Gopikrishna, J Ashok Kumar, and R Pradeep
Central Institute of Brackishwater Aquaculture, India

Penaeus monodon (Black tiger shrimp) is an important cultured shrimp species in India. Although *Litopenaeus vannamei* is dominating shrimp culture and exports in India, the Black tiger shrimp contributed $ 435.79 million through 34,133 MT of exports in 2013-14 (www.mpeda.com). As the domestication and selective breeding of this species is a concern to the hatchery community, Indian shrimp industry continues to depend on wild broodstock for seed production. Till date, Quantitative Trait Loci information does not exist for growth traits of Black tiger shrimp. Hence the objective of this study was to identify Single Nucleotide Polymorphisms (SNPs) in growth-related candidate genes of Black tiger shrimp and to understand their significance for future association studies. A total of 39,397 EST sequences were downloaded from Genbank maintained at NCBI (http://www.ncbi.nlm.gov) and were assembled to 3,773 contigs using CAP3 software (http://seq.cs.iastate.edu/cap3.html).Putative SNPs were identified by manually screening the contigs in Notepad++ version 6.1.1 text editor (http://notepad-plus-plus.org/)with the following criteria;

A. the contig should have at least four accessions at a SNP base
B. both the SNP alleles should be represented by at least 2 accessions
C. no other SNP should be present within 20 bases on either side of the putative SNP.

The identified SNP containing contigs were pulled out from whole assembly using a script written in Python 2.7.2 machine language (http://www.python.org/downloads/script). The gene identities for these 422 SNP-containing contigs were obtained after a similarity search usingblast2go (http://www.blast2go.com/start-blast2go)tool. Based on the gene identities of top blast sequence accessions and their probable functions, various growth-related candidate genes in shrimp were short-listed. A total of 8mis-sense substitution SNPs coding for non-synonymous aminoacids and one non-sense substitutionSNP introducing chain termination codon in 9 genes were documented. The likelihood of these non-synonymous SNPs to cause functional impact on the protein was individually estimated using the PANTHER classification system version 6.1 (www.pantherdb.org) based on substitution position-specific evolutionary conservation score (subPSEC) and Pdeleterious estimates. The non-synonymous SNP in cathepsin B gene might be impairing protein function (subPSEC, -4.77 and Pdeleterious, 0.85). The SNP in beta-tubulin gene that introduces chain termination codon might be producing incomplete protein. The genotype information of these 2 SNP loci is to be considered for future association analyses for growth traits as well as for broodstock selection in commercial seed production.

Biography

K Vinaya Kumar has completed his MVSc and PhD from National Dairy Research Institute, Karnal, India in the subject of Animal Genetics and Breeding. Currently, he is working as scientist at Central Institute of Brackishwater Aquaculture, Chennai, India. He has published 9 papers in reputed journals. His research interests include application of conventional and molecular tools for genetic improvement of candidate aquaculture species.

vinayndri@yahoo.com