

Applying EzRAD Method for SNPs Discovery in Population Genetics of Freshwater and Marine Fish in the South of Vietnam

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Abstract : Enzyme restriction site associated DNA (EzRAD) has recently emerged as a promising genomic approach for exploring fish genetic diversity on a genome-wide scale. This is a simplified method for genomic genotyping in non-model organisms and applied for SNPs discovery in the population genetics of freshwater and marine fish in the South of Vietnam. The observations of regional-scale differentiation of commercial freshwater fish (smallscale croakers *Boesemania microlepis*) and marine fish (emperor *Lethrinus lentjan*) are clarified. Samples were collected along Hau River and coastal area in the south and center Vietnam. 52 DNA samples from Tra Vinh, An Giang Province for *Boesemania microlepis* and 34 DNA samples of *Lethrinus lentjan* from Phu Quoc, Nha Trang, Da Nang Province were used to prepare EzRAD libraries from genomic DNA digested with MboI and Sau3AI. A pooled sample of regional EzRAD libraries was sequenced using the HiSeq 2500 Illumina platform. For *Boesemania microlepis*, the small scale population different from upstream to downstream of Hau river were detected, An Giang population exhibited less genetic diversity (SNPs per individual from 14 to 926), in comparison to Tra Vinh population (from 11 to 2172). For *Lethrinus lentjan*, the result showed the minor difference between populations in the Northern and the Southern Mekong River. The numbers of contigs and SNPs vary from 1315 to 2455 and from 7122 to 8594, respectively ($P \leq 0.01$). The current preliminary study reveals regional scale population disconnection probably reflecting environmental changing. Additional sampling and EzRad libraries need to be implemented for resource management in the Mekong Delta.

Keywords : *Boesemania microlepis*, EzRAD, *Lethrinus lentjan*, SNPs

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