

Genetic diversity of wild and domesticated stocks of Thai abalone, *Haliotis asinina* (Haliotidae), analyzed by single-strand conformational polymorphism of AFLP-derived markers

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Genet. Mol. Res. 9 (2): 1136-1152 (2010)

Received February 24, 2010

Accepted March 22, 2010

Published June 15, 2010

DOI 10.4238/vol9-2gmr808

ABSTRACT. Amplified fragment length polymorphism (AFLP) analysis was carried out on representative individuals of wild *Haliotis asinina* using 64 primer combinations. Nine polymorphic AFLPs were cloned and sequenced. Sequence-specific primers were designed from six AFLP-derived fragments. Three sequence-characterized amplified region (SCAR) markers (HaSCAR₃₂₀, HaSCAR₂₉₅, HaSCAR₃₂₇) were selected for genotyping of 8-month-old domesticated stocks of *H. asinina* cultured separately at Sichang Marine Science Research and

Training Station (N = 95) and at a hatchery in Trang province (N = 40) using single-strand conformational polymorphism analysis. Genotypes of wild abalone originating from Talibong Island (N = 25), Cambodia (N = 22), and the P₀ progeny established from Samet Island founders (N = 20) were also investigated. Significant genetic differentiation (P < 0.0001 for the exact test and $F_{ST} = 0.8759-0.8919$, P < 0.001) between abalone from the Gulf of Thailand (Cambodia and Samet Island - east) and the Andaman Sea (Talibong Island - west) were observed. This demonstrated the strong biogeographic structure of *H. asinina* in Thai waters. Non-overlapping composite genotypes for wild abalone from different coastal regions allow us to determine founder contributions in domesticated abalone stocks. Almost all Sichang Marine Science Research and Training Station and the Trang province hatchery stocks exhibited the east coast genotypes (97% of the 135 samples). We suggest that abalone from the east coast population have better survival rates under cultivated conditions than those from the west coast population.

Key words: AFLP; SSCP; Abalone; Genetic diversity; Domestication; Stock identification