Population Structure of *Scylla serrata* from Microsatellite and mtDNA Markers

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Abstract

Determination of the population structure and connectivity of natural populations of *Scylla serrata* are useful tools for decision making related to conservation and management efforts of this species. They provide important considerations as recovery and sustainability of the industry relies on the availability of hardy recruits that can replenish harvested resources from the system. In the case of marine domesticated species, admixture is expected due to commodity trade and exchanges.

Current population structure of five wild populations of S. serrata from Pangasinan, Bataan, Cagayan, Quezon, and Panay was determined using five microsatellite markers, cross-amplified from Scylla paramamosain in a total of 259 samples. Mitochondrial 16S rDNA sequences of 25 representative individuals from the same locations were used to provide a comparison with original evolutionary patterns. Quality check of microsatellite data revealed no null alleles in the data set, with all loci and populations exhibiting Hardy-Weinberg Equilibrium. Pairwise FST analysis reveals FST values between 0.001-0.08432 with 9 out of the 16 possible comparisons considered significant. Phylogenetic analysis was performed on the 16S rDNA sequences, supported by bootstrap values. Both sets of data suggest 2 distinct groupings: the east coast populations of Cagayan and Quezon, the west coast populations of Pangasinan and Bataan, with admixture observed in the group from Panay. Additional data from 5 microsatellite markers specifically developed for S. serrata and the D-loop region will be added to the analysis.

The results from both mitochondrial and microsatellite markers, revealing an East-West separation of *S. serrata* populations, suggest that current and evolutionary population patterns are matching. Aquaculture practices appear to have not yet significantly affected the population structure of this domesticated species, as initially speculated.