

species within the biogeographically complex Indo-West Pacific and northern Australian regions. We analyzed genetic variation from over 400 individuals from the Solomon Islands, Indonesia, Australia, Vietnam and Papua New Guinea at 6 polymorphic microsatellite loci and one mitochondrial gene region (cytochrome oxidase 1). Analyses based on these genes indicate that significant genetic structure exists within and between Indonesian, Australian and eastern Pacific populations and therefore that *P. maxima* is not genetically homogenous throughout its broader distribution. Knowledge on the population structure of this species will be used to identify genetically differentiated sub-populations that may have desirable traits for aquaculture and future breeding programs.

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Genetic basis of tangerine shell color variation in the Pacific abalone, *Haliotis discus hannai*

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Shell color polymorphisms are known to exist in the Pacific abalone, *Haliotis discus hannai*. The tangerine shell colored individuals, which had occurred rarely in the northern China, were discovered in the early 1990s. After four continuous mass crosses within the variants, the offspring generated the same shell color as the parents. This suggested that the tangerine shell color variation can be inherited reliably. To determine the inheritance nature of the variant, controlled mating experiments were designed to observe the segregation of the F₂ generation between the tangerine-morphs and the greenish-morph. Sixteen F₁ families by four reciprocal crosses between tangerine-morph and greenish-morph were generated. The eight F₁ hybrid families showed greenish shell color, the same with the four F₁ families which parents were both greenish-morphs, whereas four F₁ families generated by both tangerine-morphs showed tangerine shell color. This indicated that the phenotype of the variant is recessive to the greenish individuals. Five crosses between the hybrid F₁ families and three crosses between hybrid F₁ families and F₁ tangerine-morph families were carried out successfully. In the progenies composed of the normal greenish-morph and

the variant tangerine-morph, the expected segregation ratio of 3:1 was consistent with the observation in all the five crosses, and 1:1 consistent with the observation in all the three crosses. This implies that a single gene model controls the inheritance pattern of the tangerine variants. Besides, an interesting phenomenon that some bluish individuals occurred in one 1:1 segregation family was observed. The detailed relationship among the bluish-morph, tangerine-morph and the greenish-morph should be detected by further controlled mating experiments.

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Genomic resources and their informatic analysis for comparative genomics in catfish

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The completion of the Human Genome Project marks the start of the post-genomics era. However, with aquaculture species, genome research is still at the early stages of structural genomics. Recent rapid progress has laid a foundation for exponential growth and development of genome resources and information in aquatic species. Scientists are mandated to make rapid transitions between studies on a single gene to thousands of genes, from development of a few molecular markers to markers with genome coverage, from Northern blot or RT-PCR to high-density microarrays, and from working with clones to entire genome mapping. Such advances have led to the emergence of informatic sciences which in turn will be used to dissect genes and their functions, not only within a species, but also across species. The power of comparative genomics has yet to be realized, which will provide many clues about evolution, and facilitate functional studies. Progress made in the last 5 years in catfish genomics will be reviewed in the areas of molecular marker development, construction of framework linkage maps, development of genomic resources, and analysis of genomic organization and composition. Results of informatic analysis of genomic resources such as expressed sequence tags (ESTs) and BAC end sequences (BES) will be presented in relation to comparative genomics.

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