



Development of novel polymorphic microsatellite markers for the blood clam *Tegillarca granosa* by pyrosequencing

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ABSTRACT. Large amounts of expressed sequence tags (ESTs) generated using next-generation sequencing technologies provide a cost-effective and valuable genomic resource for the development of microsatellite markers. In this study, we isolated 115 novel polymorphic microsatellite markers for the blood clam *Tegillarca granosa* from ESTs in 454 sequencing data. All the loci were characterized in 30 individual clams from a natural population in Xiangshan (Zhejiang Province, China). The number of alleles per locus varied from 2 to 10, with an average of 3.78. The observed and expected heterozygosities ranged from 0 to 1 and from 0.040 to 0.799, respectively. The polymorphic information content (PIC) ranged from 0.038 to 0.825, and 29 highly polymorphic loci ($PIC \geq 0.5$) and 42 moderately polymorphic loci ($0.25 < PIC < 0.5$) were identified. Thirty-eight of the 115 loci deviated significantly from the Hardy-Weinberg equilibrium ($P < 0.01$) after a Bonferroni correction. A BlastX search revealed that 46 (40%) of the polymorphic loci identified were from transcript regions of known genes. The microsatellite markers developed in the present study

will greatly enrich the microsatellite resources of *T. granosa*, and are available for further population genetic analysis, genetic trait mapping, and molecular-assisted selection.

Key words: *Tegillarca granosa*; Microsatellite; Polymorphic marker; Pyrosequencing