



Population structure of the blood clam (*Tegillarca granosa*) in China based on microsatellite markers

Y.J. Wang^{1,2}, Q.G. Zeng¹ and L.N. Xu³

¹Key Laboratory of Applied Marine Biotechnology, Ningbo University, Ministry of Education, Ningbo, China

²Marine Biotechnology Laboratory, Ningbo University, Ningbo, China

³College of Science & Technology, Ningbo University, Ningbo, China

Corresponding author: Y.J. Wang

E-mail: wangyajun@yahoo.cn

Genet. Mol. Res. 12 (2): 892-900 (2013)

Received June 13, 2012

Accepted January 1, 2013

Published April 2, 2013

DOI <http://dx.doi.org/10.4238/2013.April.2.6>

ABSTRACT. The blood clam, *Tegillarca granosa*, is widely cultivated in China. We isolated 6 microsatellite loci from *T. granosa* and used them to investigate genetic diversity and population structure of 5 widely distributed populations of blood clam collected from eastern and southeastern China. The allele number per locus varied from 4 to 9, and the polymorphism information content value was 0.301 to 0.830. The mean observed and expected heterozygosities varied from 0.304 to 0.460 and 0.556 to 0.621, respectively; the population from Yueqing had the smallest observed heterozygosity. In the neighbor-joining tree, Shandong, Fenghua and Yueqing populations clustered together, and there was geographic divergence between Shandong and Guangxi populations. Some microsatellite loci that were isolated from these mainland China samples were not found in blood clams collected from Malaysia.

Key words: *Tegillarca granosa*; Blood clam; Microsatellite; SSR; Population structure