



Polymorphic microsatellite loci developed from the Hong Kong oyster (*Crassostrea hongkongensis*)

H.T. Ma^{1,2}, S. Xiao^{1,2}, Y. Zhang^{1,2}, X.M. Li³, J. Li^{1,2} and Z.N. Yu^{1,2}

¹Key Laboratory of Tropical Marine Bio-resources and Ecology, Guangdong Provincial Key Laboratory of Applied Marine Biology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China

²South China Sea Bio-Resource Exploitation and Utilization Collaborative Innovation Center, Guangzhou, China

³College of Tropical Biology and Agronomy, Hainan Tropical Ocean University, Sanya Hainan, China

Corresponding author: Z.N. Yu

E-mail: carlzyu@scsio.ac.cn

Genet. Mol. Res. 15 (4): gmr.15048676

Received March 30, 2016

Accepted May 6, 2016

Published October 5, 2016

DOI <http://dx.doi.org/10.4238/gmr.15048676>

Copyright © 2016 The Authors. This is an open-access article distributed under the terms of the Creative Commons Attribution ShareAlike (CC BY-SA) 4.0 License.

ABSTRACT. Forty polymorphic microsatellite loci were developed from *Crassostrea hongkongensis* using an enriched partial genomic library with magnetic beads. The polymorphism of these loci was assessed in 30 individuals from a wild population. The allele number of the polymorphic markers ranged from 2 to 13, with an average of 5.8 per locus. The polymorphism information content ranged from 0.032 to 0.891 and 37 loci presented a medium or high level of polymorphism. The observed and expected heterozygosity values

ranged from 0.033 to 1.000 and 0.033 to 0.931, respectively. Of the 40 loci, 28 were found to conform to Hardy-Weinberg equilibrium (HWE), whereas the remaining 12 showed a significant departure from HWE. The availability of these markers will aid future genetic studies in *C. hongkongensis*.

Key words: *Crassostrea hongkongensis*; Microsatellite loci; Polymorphism