



Hyriopsis cumingii:

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College of Animal Sciences, Zhejiang University, Hangzhou 310058, China
College of Life Science, Shaoxing University, Shaoxing 312000, China

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ABSTRACT

Hyriopsis cumingii (Hc) is a bivalve species widely distributed in the coastal waters of Zhejiang Province, China. This study investigated the genetic diversity and phylogenetic relationships of *H. cumingii* populations from different regions. The results showed that the genetic diversity of *H. cumingii* is high, and the populations are genetically diverse. The phylogenetic analysis revealed that *H. cumingii* is closely related to *Escherichia coli* (fi) and *Pinctada fucata* (CaM, CaLP). The study also found that the genetic diversity of *H. cumingii* is related to its geographical distribution and genetic drift.

1. Introduction

The bivalve *Hyriopsis cumingii* is a species of bivalve in the family Hyriidae. It is widely distributed in the coastal waters of Zhejiang Province, China. The species is characterized by its large size and its ability to form large colonies. The genetic diversity of *H. cumingii* is high, and the populations are genetically diverse. The phylogenetic analysis revealed that *H. cumingii* is closely related to *Escherichia coli* (fi) and *Pinctada fucata* (CaM, CaLP). The study also found that the genetic diversity of *H. cumingii* is related to its geographical distribution and genetic drift.

* Corresponding author. E-mail address: zhangyong@zhu.edu.cn

HcCaM ACATGGGGGACATCGCCTGTACTAAGGTGTTCATCCACAGTAGAAAACAGACGTTTTTCGCCT. 60
HcCaLP -----

HcCaM GATCAAAAGAGTCGTTTACAGCAGAAGCAGCTTTTTAAGGTATTCGTTGTGATTAAGCTAT 12
HcCaLP -----ACATGGGGGATACCTGAACTAGACTTTTTCACTTCCATACACCTGCTCAGCA 5

HcCaM GGGTGACCAACTACACGAAAGAACAGATTGCTGAGTTCBAGGAGGCATTTCAGCCTGTTTTGA 18
HcCaLP GGCAGACCAACTAAGCAGAAGAACAATTTGCTGAGTTCBAGGAGGCATTTCAGCCTGTTTTGA 1

HcCaM CAAGGACGGGGATGGAACCATCCACCAAAAGGAACCTGGGGACAGTGTATGAGCTCTCTGGG 2
HcCaLP CAAGGACGGGGATGGAACCATCCCAACCAAGGAGCTGGGGACGCTGTATGATATTCCTGGG 1

HcCaM ACAGAATCCAACTGAGGGCTGAGCTACAGGACATGATTACAGAACTGGATGCCGATGCTTAA 23
HcCaLP GCAGAACCCACCGGAGGCTGACTTGCATGCGCATGATCAGTGAAGTGCATGCCACATGCCAA 3

360 *HcCaM* TTTAAATATTATTTTCCCAATTCTTAAATATATGCAAAAAATTGAAATATCGG 360
 293 *HcCaLP* TTTCAATAATATTTTCCCAATTCTTAAATATATGCAAAAAATTGAAATATCGG 293

420 *HcCaM* TTTTAAATAATTTTACCCCAATTCCTTAAATTTTAAATAATTTTAAATTTT 420
 353 *HcCaLP* TTTTAAATAATTTTACCCCAATTCCTTAAATTTTAAATAATTTTAAATTTT 353

413 *HcCaLP* AAATTTTGGAAATGAGGAAATTAATTAACAATTTGGAAATTTGGTTA 413

540 *HcCaM* TTTTCAATAATTTTCCGAAATTAATTTTCAATAATTTTCAATAATTTT 540
 473 *HcCaLP* TTTTCAATAATTTTCCGAAATTAATTTTCAATAATTTTCAATAATTTT 473

600 *HcCaM* AATTTTCAATAATTTTCCGAAATTAATTTTCAATAATTTTCAATAATTTT 600
 533 *HcCaLP* AATTTTCAATAATTTTCCGAAATTAATTTTCAATAATTTTCAATAATTTT 533

660 *HcCaM* TAAGTAATGCAAATGTGTGTTTCCAGATATTTTATTTTATACATTTTTATTTTT 660
 593 *HcCaLP* TAAGTAATGCAAATGTGTGTTTCCAGATATTTTATTTTATACATTTTTATTTTT 593

720 *HcCaM* TTTAAACATAAATAAATATACTATCTTAGGGTTCAAAAAATAAATAAATAA 720
 652 *HcCaLP* TTTAAACATAAATAAATATACTATCTTAGGGTTCAAAAAATAAATAAATAA 652

726 *HcCaM* AAAAAA----- 726
 712 *HcCaLP* AGCAATGCAAAATTTCCAAAAGGAAGAATGACTAGGCTGAAAAACCC 712

832 *HcCaM* TTTCTTTCTGGAGCAATGTCAACAACGTCACAGAAATGAAAAGT 832
 765 *HcCaLP* TTTCTTTCTGGAGCAATGTCAACAACGTCACAGAAATGAAAAGT 765

952 *HcCaM* TTTTATTAATAAATAATTTATGCAAGATTTCTTATTTCGGC 952
 885 *HcCaLP* TTTTATTAATAAATAATTTATGCAAGATTTCTTATTTCGGC 885

1132 *HcCaM* CATTAACACTATTTTTTTTTTCCCAAAATAAATTGACAAGAC 1132
 1065 *HcCaLP* CATTAACACTATTTTTTTTTTCCCAAAATAAATTGACAAGAC 1065

1192 *HcCaM* TTGCAGTACGCATTTGTGCAATTAATAATTCCTAGTAT 1192
 1125 *HcCaLP* TTGCAGTACGCATTTGTGCAATTAATAATTCCTAGTAT 1125

1217 *HcCaM* AA 1217
 1150 *HcCaLP* AA 1150

Fig. 1.

HcCaM - *HcCaLP*



