Z 120 중금속 오염에 의한 총알고둥 (Littorina brevicula)의 mtDNA cyt b gene의 유전적 다양성

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한국산 총알고둥 (Littorina brevicula)의 유전적 다양성을 조사하기 위하여 동해안 4개 지역, 남해안 4개 지역, 서해안 2개 지역 등 총 10개 지역을 선정하여 mitochondrial DNA cytochrome b gene의 염기서열 분석을 실시하였다. 또한 중금속 (Cd, Zn, Cu, Pb)의 유입량이 많은 마산만과 온산만의 오염지역과 비오염지역에서 총알고둥의 mtDNA cyt b gene의 haplotype과 각고 및 습중량을 비교하였다. 한국연안 동해, 남해, 서해의 10개 지역에서 조사된 총알고둥의 염기서열은 9개의 haplotype으로 구분되었으며 지역 집단간 유전적 변이는 유의적 차이를 보이지 않았다. 중금속에 의한 오염지역과 비오염지역의 총알고둥은 5개의 haplotype (A, B, C, D, E)으로 구분되었으며 A type의 빈도는 0.80 이었고 B, C, D, E type의 빈도는 각각 0.05 이었다. 오염지역에서는 A type이 0.90의 빈도를 보였고 비오염지역에서는 A type이 0.70의 빈도를 보였다. 그리고 오염지역과 비오염지역의 각고에 대한 습중량의 비를 조사하였을 때 오염지역 개체의 각고에 대한 습중량의 비는 비오염지역 개체의 것에 비해 습중량이 낮게 나타났다.

Z 121 Phylogenetic Analysis of Perkinsus Found in the Manila clam, Ruditapes philippinarum in Korean Waters

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The protozoan parasites belonging to genus Perkinsus have been associated with mass mortalities of marine bivalves throughout the world. Four species of Perkinsus including P. marinus, P. atlanticus, P. olseni and P. qugwadi are reported to date. Recently Perkinsus has been reported in Korean waters and its taxonomic position is not known yet. Polymerase chain reaction (PCR) and zoosporulation of Perkinsus sp. found in the Manila clam Ruditapes philippinarum, were conducted to establish the phylogenetic position of the species. The region of rRNA of Perkinsus sp. from the hemolymph of the R. philippinarum collected from Wan-Do was cloned and sequenced. Sequences of the non-transcribed spacer (NTS), and the internal transcribed spacer (ITS) 1, ITS 2 from the rRNA were compared to sequences reported for P. atlanticus and P. marinus. Zoospores were derived from hypnospores harvested from fluid thioclycollate medium and incubated in filtered seawater. The NTS sequence was 100% identical to that of P. atlanticus, and has 71.29% similarity to that of P. marinus. The ITS 1 sequence is identical to P. atlanticus ITS 1 (100% similarity), and has 76.1% similarity to P. marinus ITS 1. The ITS 2 sequence was also identical to that of P. atlanticus (100% similarity) and showed 91.7% similarity to that of P. marinus. Morphological features and nucleotide sequences analyzed in this study suggested that Perkinsus sp. found in Korea waters was P. atlanticus found in Portugal, Spain and France. It was also believed that NTS-based PCR assay developed in this study is a useful tool for detection of Perkinsus.