An improved extraction method reveals varied DNA content in different parts of the shells of Pacific oysters

The DNA in the shell of Crassostrea gigas could have important roles in the shell biomineralization. However, limited by the low efficiency of existing extraction methods, studies investigating the DNA in shells are lacking. In this study, the shell DNA of C. gigas was extracted using the organic solvent extraction (OSE) and guanidine lysis buffer (GLB) methods; the efficiency and quality of these two methods were compared. The sequences of a mitochondrial gene (cytochrome c oxidase subunit I, COI) and a nuclear gene (28S rRNA) of C. gigas were analyzed to verify the origin of the extracted shell DNA. Finally, the DNA contents of the ventral edge, middle part, and dorsal edge of C. gigas shells were compared. The results showed that OSE had a higher DNA extraction efficiency than GLB; the oyster shell DNA was homologous to the oyster genome; the DNA content was higher in the ventral edge than in the middle part or in the dorsal edge of the C. gigas shell. This study not only reports an improved extraction method for the mollusk shell DNA, but also revealed that the DNA in the oyster shell originates from the oyster body and that the DNA content in different parts of the C. gigas shell showed obvious variance. These results provide supporting evidence for the hypothesis that oyster cells participate in shell formation, and also afford a nondestructive method for oyster genetic identification, which can promote the application of molecular biology technology in oyster breeding. In addition, a shell growth pattern of ‘Under Old & Exceeding Old’ was also proposed.

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Obtenir le document : EDP Sciences
Mots clés : Pacific oyster, shell DNA, in vivo sampling, DNA extraction, shell growth
Thème (issu du Text Mining) : POLLUANTS
Date : 2019-02-18
Format : text/xml
Source : https://doi.org/10.1051/alr/2019003
Langue : Anglais
Télécharger les documents : https://www.alr-journal.org/10.1051/alr/2019003/pdf
Permalien : https://www.documentation.eauetbiodiversite.fr/notice/an-improved-extraction-method-reveals-varied-dna-content-in-different-parts-of-the-shells-of-pacific0