



Global genetic homogeneity in the deep-sea foraminiferan *Epistominella exigua* (Rotaliida: Pseudoparrellidae)*

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Abstract

Epistominella exigua is one of the most common deep-sea foraminiferal morphospecies and has a world-wide distribution. A recent molecular study revealed high genetic similarity between Arctic, Atlantic and Antarctic populations of this species. Here, we show that the small-subunit (SSU) and internal transcribed spacer (ITS) rDNA sequences of an *E. exigua* population from Pacific are almost identical to those reported previously from the other three oceans. This result confirms the genetic homogeneity of *E. exigua*, which contrasts with the prevalence of highly differentiated populations in planktonic and shallow-water benthic foraminiferans. We discuss special features of diversification mechanisms in the deep sea that may be responsible for the lack of genetic differentiation and global distribution of some meiofauna species.

Keywords: deep-sea diversity, meiofauna, Foraminifera, SSU rDNA, ITS rDNA, geographic distribution

Introduction

At a local scale, deep-ocean sediments contain some of the most species rich communities on Earth (Grassle & Maciolek 1992). Recently, there has been an increasing emphasis on the relationship between local diversity and diversity at larger (regional to global) scales (Levin *et al.* 2001). However, there is still little information available about how widely species are distributed or about biodiversity at the genetic level (Etter *et al.* 1999, 2005). There is a particular need to increase the genetic database on small size deep-sea benthic organisms in order to learn whether the biodiversification mechanisms operating there are different from those in shallow-water.

Deep-sea benthic foraminiferans provide particularly good models to tackle these questions. They occur in all marine environments and their rich fossil record reveals their morphological evolution over geological time. Molecular studies, focused mainly on planktonic and shallow-water foraminiferal species, have demonstrated considerable cryptic diversity (reviewed in Pawlowski and Holzmann 2008, Darling *et al.* 2008). In striking contrast, three deep-sea species showed very low levels of genetic differentiation between populations in the Arctic and Antarctic sectors of the Atlantic, separated by a distance of up to 17,000 km (Pawlowski *et al.* 2007).

To explore whether this surprising degree of genetic homogeneity along a north-south axis was indicative of a global distribution for some deep-sea benthic meiofauna, we examined molecular diversity in *Epistominella exigua* from the Pacific Ocean and compared it to the earlier data on Arctic, Atlantic and