Geophysical Research Abstracts, Vol. 10, EGU2008-A-12370, 2008 SRef-ID: 1607-7962/gra/EGU2008-A-12370 EGU General Assembly 2008 © Author(s) 2008



Phylogeny and diversity of symbionts from the whale falls worm *Osedax mucofloris*

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Long after they die and fall to the ocean floor the skeletal remains of large whales constitute the energy source for a fauna of highly specialized species. Some members of these whale falls ecosystems, discovered twenty years ago, are also found cold seeps and hydrothermal vents in the deep sea. The most spectacular members of whale falls are Osedax, a group of annelids related to the tubeworms at hydrothermal vents. Osedax species lack a gut. Instead their posterior end constitutes a "root" structure filled with symbiotic bacteria and extending into the bone tissue. These bacteria are hypothesized to degrade the lipids in the whale bone to provide their host with nutrition. In this study, we describe the symbiotic community of Osedax mucofloris from North-Atlantic whale falls. Our main objective is to characterize this symbiosis using comparative 16S and ITS rRNA sequence analysis and fluorescence in situ analysis (FISH). We have identified at least three endosymbiotic "phylotypes" that are closely related to the Osedax endosymbionts found in East-Pacific whale falls. This suggests that these symbioses are specific to these whale fall worms and widespread throughout the deep sea. In addition to the endosymbionts in the roots of the worm, we found a highly diverse bacterial community associated with the trunk and mucus tube of O. mucofloris. The high abundance of these ectosymbiotic bacteria on the worm trunk suggests that they may also play a role in providing nutrition to the host.