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Impact of feeding by *Arenicola marina* (L.) and ageing of faecal material on fatty acid distribution and bacterial community structure in marine sediments: An experimental approach

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Abstract

The fate of ingested eukaryotic photoautotrophic fatty acids during gut transit in the lugworm Arenicola marina (L.) and the influence of A. marina's faces on the evolution of fatty acid distribution and bacterial community structure in superficial sediments were studied under laboratory conditions. Dead phytoplanktonic cells (food portions) were fed to individual A. marina and subsequently incubated, or allowed to directly incubate in the presence of fresh egesta or non-ingested sediment. Changes in fatty acid composition and genetic structure of bacterial communities during gut transit and/or incubation were monitored using gas-chromatography/mass-spectrometry and a DNA fingerprint approach (RISA), respectively. Results, supported by principal component analyses, suggest that A. marina's feeding activity can directly and indirectly affect the lipid biomarker composition and the bacterial community structure of inhabited sediments. Faecal casts produced from food portions appeared qualitatively enriched in saturated fatty acids relative to (poly)unsaturated ones due, partly, to an increase of some bacterial fatty acids and to the preferential removal of some polyunsaturated fatty acids (PUFAs). The incubation of food portions in the presence of fresh A. marina's egesta (designed to study the indirect impact of feeding by A. *marina*) induced a significant increase in the concentrations of C_{20} and C_{22} polyunsaturated fatty acids (PUFAs), whereas these compounds almost disappeared following direct feeding and subsequent incubation, indicating that some dietary fatty acids may be more accessible to biodegradation following passage through the gut of A. marina. The aforementioned increase in PUFAs was attributed to a bacterial production during incubation, suggesting the presence of PUFA-producing bacteria in the fresh egesta of A. marina. Those bacteria were either enteric bacteria that were released with the egesta or ingested bacteria that have survived gut passage, as suggested by the variations of the bacterial community structure (i.e. RISA profiles) during incubation. The results suggest that aged faeces from A. marina might be, in some circumstances, of relatively high nutritional value to trophic levels which are unable to synthesize essential PUFAs de novo. The presence of PUFA-producing bacteria in guts of marine lugworms deserves further attention. © 2006 Elsevier B.V. All rights reserved.

Keywords: Arenicola marina; Feeding activity; Fatty acids; PUFA-producing bacteria; Bacterial community structure; RISA; Superficial sediments

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1. Introduction

Benthic macrofauna have a significant impact on the biogeochemical processes in marine sediments, through activities such as particle reworking, irrigation, feeding and bacterial gardening/stimulation (Banta et al., 1999; Aller et al., 2001). To meet their nutritional needs, deposit feeders ingest massive volumes of sediment by bulk feeding, and extract organic matter (OM) from different food sources such as digestible detritus (e.g. phytoplanktonic remains), microbes and benthic microbiota (Lopez and Levinton, 1987; Andresen and Kristensen, 2002). As a result of the ingestion process, marine worms produce faeces which can represent a potential food source for other consumers and be the site of intense geochemical transformation of OM (Wilde and Plante, 2002; Plante and Wilde, 2004).

Feeding by deposit-feeders can significantly affect the qualitative and quantitative distribution of specific components of OM (Bradshaw and Eglinton, 1993 and references therein). Among those compounds, lipids (such as fatty acids) appear particularly important due to their key role in the transfer of carbon and energy through aquatic food webs (Müller-Navarra et al., 2000). Moreover, the specific structure of some lipids allow them to be widely used as biomarkers in geochemical studies for determining the source, the transformation and the fate of OM (Grossi et al., 2003 and references therein).

The differential digestion of bacteria and the release of enteric bacteria by marine deposit-feeders have been demonstrated. This can lead to structural shifts of the bacterial assemblages in faeces compared to the ingested sediment, and affect bacterial population dynamics by cellular destruction (bacteriolytic activity) and/or by stimulating growth during passage through the digestive tract (Dobbs and Guckert, 1988; Wilde and Plante, 2002; Lucas et al., 2003).

It is thus evident that the overall feeding activity of worms (ingestion of sediment/egestion of faecal material) influences the quality and the quantity of the OM, but also its subsequent evolution. However, to the best of our knowledge, there have been few studies at the molecular level on both the direct (i.e. gut transit) and the indirect (i.e. bacterial inoculation and ageing) impact

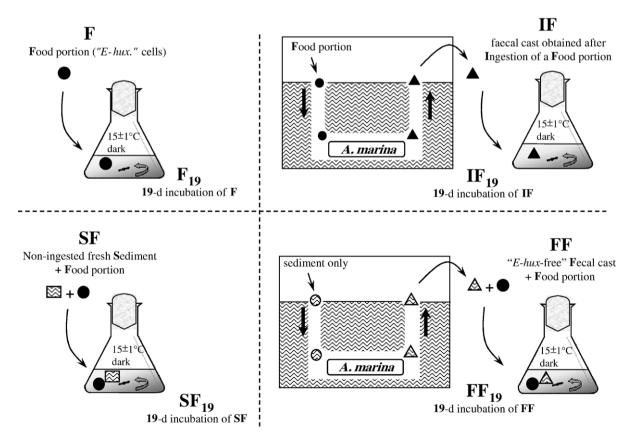


Fig. 1. Outline of the experimental design.

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