



Bioturbation activity of three macrofaunal species and the presence of meiofauna affect the abundance and composition of benthic bacterial communities

Élise Lacoste^{a,b,*}, Adeline Piot^a, Philippe Archambault^b, Christopher W. McKindsey^{a,c}, Christian Nozais^d

^a Institut des Sciences de la mer, Université du Québec à Rimouski, Rimouski, Canada

^b Québec-Océan, Département de Biologie, Université Laval, Québec, Canada

^c Fisheries and Oceans Canada, Institut Maurice Lamontagne, Mont-Joli, Canada

^d Québec-Océan, Département de Biologie, Université du Québec à Rimouski, Rimouski, Canada

ARTICLE INFO

Keywords:

Biodiversity
Benthic community
Bacteria abundance
High nucleic acid content
Meiofauna
Alitta virens
Mya arenaria
Limicola balthica

ABSTRACT

Given concerns of increasing rates of species extinctions, the relationship between biodiversity and ecosystem functioning has become a major research focus over the past two decades. Many studies have shown that biodiversity *per se* (e.g. species richness) or species-specific traits may be good predictors of changes in ecosystem function. Although numerous studies on this subject have focused on terrestrial systems, few have evaluated benthic marine systems. We used the *Limicola balthica* community as a model to test whether the number or identity of three well-studied macrofaunal species influence the sediment bacterial compartment, which drives important biogeochemical processes and influence ecosystem functioning. We also investigated the poorly known role of meiofauna in the interactions between macrofauna and bacteria. Eight combinations of 0–3 species were maintained in microcosms for 34 days in the presence or absence of meiofauna. The abundance and composition of the bacterial community, defined by the relative percentage of cells with a high (HNA) vs low (LNA) nucleic acid content, were measured. Species identity of macrofauna was a better indicator of changes in the microbial compartment than was species richness *per se*. In particular, the gallery-diffuser behaviour of the polychaete *Alitta virens* likely induced strong changes in sediment physical and geochemical properties with a major impact on the bacterial compartment. Moreover, the presence of meiofauna modulated the influence of macrofauna on bacterial communities. This study provides evidence that species identity provides greater explanatory power than species richness to predict changes in the bacterial compartment. We propose that multi-compartment approaches to describe interactions amongst different size classes of organisms and their ecological roles should be further developed to improve our understanding of benthic ecosystem functioning.

1. Introduction

Given current concerns of high rates of species extinctions, many studies have attempted to understand and predict the effects of biodiversity on ecosystem functions and services (see reviews by Cardinale et al., 2011; Loreau et al., 2001; Naeem et al., 2009). Most such studies have evaluated how changes in species richness *per se* modify ecosystem properties (i.e., the size of compartments and rates of processes, as defined by Hooper et al., 2005). More recently, there has been a growing interest about the effects of species-specific traits on these properties (Cernansky, 2017). Numerous studies suggest that the properties used to measure ecosystem functioning (e.g., decomposition

rate, nutrient uptake rate) are more dependent on species-specific traits than on species richness *per se* (Gagic et al., 2015; Mouillot et al., 2011; Strong et al., 2015). Much research in this field of study has focused on terrestrial systems (Gamfeldt et al., 2014), although the number of manipulative experiments to assess links between biodiversity and ecosystem functioning in marine systems has also rapidly increased (Cardinale et al., 2011; O'Connor and Byrnes, 2013; Solan et al., 2012). Karlson et al. (2010) and Norling et al. (2007) manipulated marine invertebrate species richness and composition and concluded that differences between measured functions were only a function of species-specific traits. O'Connor and Crowe (2013) studied tidepools and concluded that species identity in a gastropod assemblage (grazers), but not

* Corresponding author. Institut des Sciences de la mer, Université du Québec à Rimouski, Rimouski, Canada.
E-mail address: eliz.lacoste@gmail.com (É. Lacoste).

<https://doi.org/10.1016/j.marenvres.2018.02.024>

Received 14 September 2017; Received in revised form 21 February 2018; Accepted 21 February 2018
0141-1136/ © 2018 Elsevier Ltd. All rights reserved.

the diversity, affected algal cover and biomass, which were used as indicators of ecosystem functioning. According to Ieno et al. (2006) and Solan et al. (2008), increased benthic species richness enhances nutrient regeneration, but such effect is, at least partly, a function of the intensity of bioturbation, which itself reflects species-specific activity. Mermillod-Blondin et al. (2005) and Piot et al. (2014) thus suggested that functional traits of benthic species – defined with respect to bioturbation mode, depth of burrowing, and feeding behaviour – may be more important than species richness *per se* in predicting the impact of biodiversity change on ecosystem functioning, as defined by nutrient flux intensity. Finally, Wrede et al. (2017) highlighted the ability of species to rework sediment and influences biogeochemical cycling.

Since bacteria drive globally important biogeochemical processes, some studies also used characteristics of the microbial compartment to describe the link between macrofaunal diversity and ecosystem functioning. Mermillod-Blondin et al. (2004) demonstrated that, due to its strong bioturbation activity, the occurrence of *Alitta* (formerly *Nereis*) *diversicolor* increased total active bacterial abundance but reduced the activity of sulphate-reducing bacteria in benthic sediments. Subsequently, Michaud et al. (2009) and Chen et al. (2017) showed that the presence of macrofauna, which indirectly oxygenated the sediment through bioturbation, affected bacterial activity and composition. Although microbial communities inhabiting sediment mediate key processes that control ecosystem carbon and nitrogen cycling and play thus a key role in the functioning of aquatic ecosystems, the factors controlling the abundance and composition of benthic bacterial communities are still poorly understood.

In this study, we tested the influence of species richness and identity of three functionally different macrofaunal species (different bioturbation and feeding modes) on the microbial compartment, described using bacterial abundance and proportion of high nucleic acid content bacteria. High nucleic acid (HNA) content bacteria can be distinguished from low nucleic acid (LNA) bacteria by cytometry, due to higher fluorescence intensity (NA content) and cell size (SSC = sizeward scatter) (Gasol et al., 1999; Lebaron et al., 2001). Until recently, HNA bacteria were considered as the active components of the flow cytometrically sorted subpopulations (i.e. HNA and LNA bacteria) (Lebaron et al., 2001, 2002, Servais et al., 2003). However, there are contrasting reports showing that the LNA bacterial group was at least as active as HNA (Longnecker et al., 2005; Wang et al., 2009; Zubkov et al., 2001) and may be phylogenetically distinct groups, regulated by different factors and playing different ecological roles (Liu et al., 2016; Mary et al., 2006; Schattenhofer et al., 2011). In this regard, we used the proportion of HNA bacteria (%HNA) as a proxy of bacterial assemblage composition. We also evaluated the influence of meiofauna on the interactions between macrofaunal species and bacteria. Meiofauna constitute a link between smaller (e.g. bacteria) and larger (e.g. macrofauna) organisms in benthic sediments. While they may play a significant role in benthic ecosystem processes and services (Schratzberger and Ingels, 2017), they are less-well studied relative to other taxa (Giere, 2009, but see Piot et al., 2014).

We hypothesized that macrofaunal species identity (i.e. particular species defined by different functional traits), is a better predictor of changes in the microbial compartment compared with species richness, and that each macrofaunal species plays idiosyncratic roles through different bioturbation and feeding modes. Moreover, we predicted that the effect of macrofauna on the microbial compartment is influenced by the presence of meiofauna.

2. Material and methods

2.1. Field sampling

Sediments and organisms were haphazardly collected along the Pointe-au-Père intertidal area (48°31'N, 68°28'W), located on the south shore of the St. Lawrence maritime estuary, eastern Canada. About

1.2 dm³ of sediments was sampled with a grab (from the top 10 cm surface layer) and sieved on a 1 mm mesh to exclude the largest particles and macrofauna, and frozen for 1 month (–20 °C) to remove most viable meiofauna, i.e. by significantly decreasing the abundance of nematodes (Quaresma et al., 2004). Macrofauna and a mixture of meiofauna (size < 500 µm) living in the upper 2.5 cm sediment layer were subsequently collected using a grab and sieves of various mesh sizes. All organisms were acclimated for 15 days under controlled conditions (temperature: 12 ± 1 °C, salinity: 27, photoperiod: 12 h light/12 h dark).

Macrofaunal communities in the intertidal zone of the St. Lawrence estuary are characterized by low species richness and are dominated by the polychaete *Alitta virens* and the bivalves *Limecola balthica* and *Mya arenaria*, which served as model organisms in this study. The main characteristics and roles played by these three species on multiple ecosystem properties are well-described (Mermillod-Blondin et al., 2003, Michaud et al., 2005, 2006, 2009). Briefly, the omnivorous polychaete *A. virens* is a gallery-diffuser that modifies sediment geochemical conditions (Michaud et al., 2005, 2006, 2009, Nilsen et al., 1995). The bivalve *L. balthica*, a biodiffuser, is mainly a deposit-feeder under laboratory conditions which strongly interacts with surface sediments (Hummel, 1985; Olafsson, 1986), and may also cause non-local transport of particles (Morys et al., 2017). Finally, the bivalve *M. arenaria* strongly affects the overlying water due to its suspension feeding mode (Forster and Zettler, 2004), but this biodiffuser can also modify sediment characteristics (Hansen et al., 1996; Michaud et al., 2006).

2.2. Microcosms and experimental setup

2.2.1. Experimental design

The experimental design (Table 1) consisted of three mono-specific treatments (*M. arenaria* (A), *L. balthica* (B), *A. virens* (V)), three treatments with combinations of two species (AB, AV, BV), one combination of the three macrofaunal species (ABV) and one control treatment without macrofauna (X). These 8 treatments were crossed with two levels of meiofauna (with (+) or without (–)). Each treatment and level was triplicated giving a total of 48 microcosms.

2.2.2. Day 1: microcosm set-up

Each of the 48 microcosms was made of an opaque PVC tube (diameter: 10 cm, length: 21 cm) that was hermetically sealed at the bottom. Each was initially filled with homogenised and thawed

Table 1
Biovolume, abundance, species richness and biomass for each treatment (X = control, A = *Mya arenaria*, B = *Limecola balthica*, V = *Alitta virens*).

Treatment	Biovolume (mL ± SD)	Abundance			Total	Species		Biomass (g ± SD)
		A	B	V		Richness		
Without meiofauna								
X								
A	11.9 ± 0.7	6	0	0	6	1		16.1 ± 1.5
B	9.2 ± 0.7	0	24	0	24	1		12.2 ± 0.9
V	8.6 ± 0.8	0	0	12	12	1		5.2 ± 0.9
AB	10.9 ± 0.5	3	12	0	15	2		15.3 ± 1.9
AV	10.9 ± 0.5	3	0	6	9	2		11.9 ± 1.6
BV	9.2 ± 0.5	0	12	6	18	2		10.2 ± 0.3
ABV	10.4 ± 0.7	2	8	4	14	3		13.5 ± 1.6
With meiofauna								
X								
A	11.0 ± 0.9	6	0	0	6	1		15 ± 1.0
B	8.8 ± 1.2	0	24	0	24	1		12.3 ± 1.2
V	9.5 ± 1.1	0	0	12	12	1		6.9 ± 0.8
AB	10.7 ± 0.6	3	12	0	15	2		15.2 ± 0.5
AV	9.7 ± 1.0	3	0	6	9	2		10.4 ± 0.8
BV	9.0 ± 0.6	0	12	6	18	2		10.1 ± 1.3
ABV	10.3 ± 0.4	2	8	4	14	3		12.5 ± 0.1

Download English Version:

<https://daneshyari.com/en/article/8886331>

Download Persian Version:

<https://daneshyari.com/article/8886331>

[Daneshyari.com](https://daneshyari.com)