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Research paper

Dynamics of bacterial community structure on intertidal sandflat inhabited by the ghost shrimp *Nihonotrypaea harmandi* (Decapoda: Axiidea: Callianassidae) in Tomioka Bay, Amakusa, Japan

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ABSTRACT

Callianassid (ghost) shrimp has been claimed as an ecosystem engineer, as it is one of the most powerful bioturbating macrobenthos in intertidal sandflats. However, our knowledge about the relationship between areal distribution of bottom-dwelling ghost shrimps and dynamics of sediment microbial community structure remains obscured. We used automated ribosomal intergenic spacer analysis (ARISA) to reveal the bacterial community dynamics in the sediment of intertidal sandflat of Tomioka Bay, Kyushu, Japan, which is predominantly inhabited by a burrow-dwelling callianassid shrimp *Nihonotrypaea harmandi*. We found that the bacterial community structures of high and middle shrimp population areas were significantly differentiated from those of low population area (ANOSIM, $R = 0.10–0.18$, $p < 0.01$), while the former two areas were statistically indistinguishable (ANOSIM, $R = -0.015$, $p > 0.1$). These results illustrated the potential importance of shrimp population density as a key factor in shaping the bacterial community structure and interpreting their dynamics in the sandflat. Furthermore, greater similarity between burrow and non-burrow communities was found in samples taken in autumn through winter than in those in summer (one-way ANOVA, $p < 0.05$), whereas the phylotype richness was not simply differentiated by seasons. These results suggest not only that environmental variables including water temperature and salinity of the water column overlying the sandflat could exert notable impacts on the sediment bacterial community dynamics, but that the bio-irrigation and mixing by the ghost shrimp in permeable sandflat would strongly homogenize sediment particles, enhance solute transport surrounding the burrow and ambient subsurface substrate, and therefore reduce spatial differentiation of the bacterial community structure between the two sites. A comparison between present and previous studies of axiidean (former taxonomic group name, thalassinidean) ghost shrimps provides us with a comprehensive understanding of the shrimps' impacts on bacterial community dynamics, highlighting the importance of sediment permeability, a characteristic determined by the type of sediment, as a key controlling factor to shape spatial heterogeneity of bacterial community structure around burrow.

1. Introduction

Callianassid (ghost) shrimp has been claimed as an ecosystem engineer, as it is one of the most powerful bioturbating macrobenthos in intertidal sandflats (Pillay and Branch, 2011). The population of *Nihonotrypaea harmandi* inhabiting an intertidal sandflat in western Kyushu, Japan is among such bioturbating shrimp (Flach and Tamaki, 2001). This species creates a Y-shaped burrow with two surface openings, reaching down to 60-cm depth (Tamaki and Ueno, 1998). The shrimp burrowing activity is so strong that amounts of sand ejected from its burrow can bury juveniles of the trochid gastropod, *Umbonium moniliferum*, leading to its local population extinction (Flach and Tamaki, 2001; Tamaki, 1994). Not only can ghost shrimp bioturbation influence the population dynamics of other benthos, but also it can have strong impacts on sediment biogeochemical processes. Particulate organic matter derived from the overlying water column or the sediment surface could be accumulated in the burrow lining of the shrimp as illustrated in previous works (de Vaugelas and Buscail, 1990; Kinoshita et al., 2003; Papaspyrou et al., 2005), which would lead to greater activities and abundance of microbes in the burrow compared with those in non-burrow sediment. In fact, increase in bacterial abundance on ghost shrimp burrow has been reported (Branch and Pringle, 1987; Laverock et al., 2010; Papaspyrou et al., 2005). Furthermore, metabolic activity of the microbial community has recently been shown to correlate positively with burrow opening density and hence the

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Abbreviations: rITS, ribosomal intergenic transcribed spacer; ARISA, automated ribosomal intergenic spacer analysis; rRNA, ribosomal RNA; OTU, operational taxonomic units; nMDS, non-metric multi-dimensional scaling; ANOSIM, analysis of similarity; TOC, Total organic carbon.

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population density of the mud shrimp, *Upogebia pugettensis* (see D'Andrea and DeWitt, 2009). These authors reported that the shrimp population density correlated pretty well with net organic carbon remineralization rates and dissolved inorganic nitrogen fluxes from the sediment. However, to our knowledge, there have been no systematic reports on the relationship between areal distribution of bottom-dwelling ghost shrimps and dynamics of sediment microbial community structure.

Furthermore, active movement of the shrimps for burrow construction and maintenance are believed to enhance solute transport through permeable sediment, playing a central role in the formation of micro-niches where distinct microbial community would develop on the burrow lining and nearby sediments (Kristensen and Kostka, 2005; Volkenborn et al., 2012). However, as previous studies report seemingly contrasted results (Bertics and Ziebis, 2009; Laverock et al., 2010; Papaspyrou et al., 2005), a more comprehensive understanding of ghost shrimp impacts on microbial community is clearly needed.

The site for the present study is located within a shallow embayment (Tomioka Bay: water depths ≤20–25 m; 8.5 km alongshore × 2 km cross-shore) at the northwestern corner of Amakusa-Shimoshima

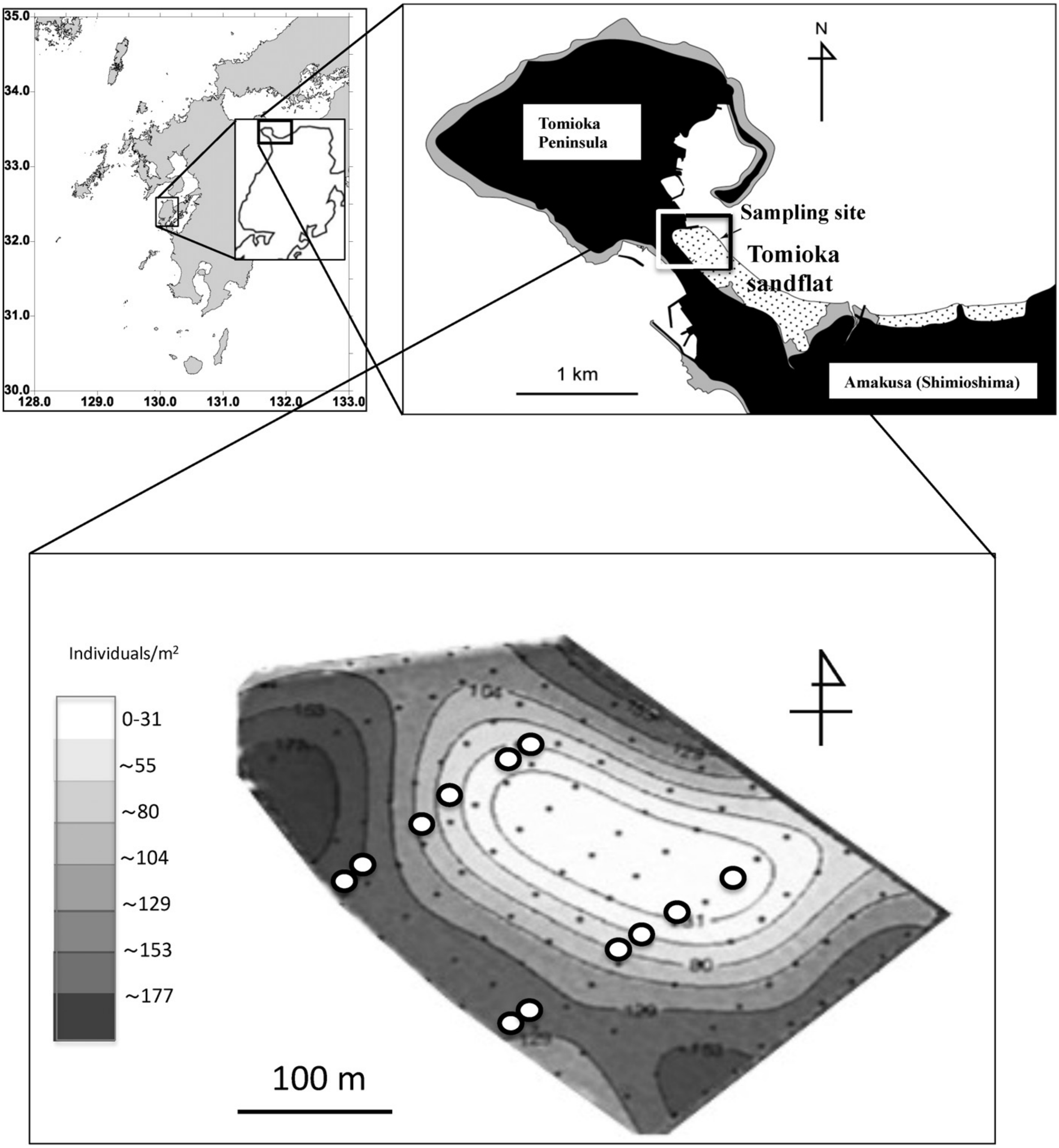

Fig. 1. Map of Tomioka Bay and spatial distribution of *N. harmandi* population density (individuals/m2) on Tomioka sandflat with locations of the sampling points.