

Home  
About IR

Journals ▶

- MEPS
- AB
- AEI
- ▶ AME
  - AME Home
  - Most Recent Issue
  - About the Journal
  - Editors
  - AME Forthcoming
  - AME Specials
- CR
- DAO
- ESEP
- ESR
- SEDAO
- Guidelines For Authors
- Editorials
- Subscription Information 2017
- Subscription Information 2018
- Terms of Use
- Open Access
- Contents Mailing Lists
- Rights & Permissions
- Promotional Posters

- Book Series
- Ecology Institute
- Otto Kinne Foundation
- Job Openings
- For librarians

Search:



You are at: [Inter-Research](#) > [AME](#) > [v79](#) > [n3](#) > [p177-195](#)

**AME 79:177-195 (2017)** - DOI: <https://doi.org/10.3354/ame01826>

*AME Special 6: 'SAME 14: progress and perspectives in aquatic microbial ecology'*

**REVIEW**

**Microbial community assembly in marine sediments**

**Caitlin Petro\*\***, **Piotr Starnawski\*\***, **Andreas Schramm\***, **Kasper U. Kjeldsen**

Section for Microbiology and Center for Geomicrobiology, Department of Bioscience, Aarhus University, 8000 Aarhus C, Denmark

\*Corresponding author: [andreas.schramm@bios.au.dk](mailto:andreas.schramm@bios.au.dk)\*\*These authors contributed equally to this work

**ABSTRACT:** Marine sediments are densely populated by diverse communities of archaea and bacteria, with intact cells detected kilometers below the seafloor. Analyses of microbial diversity in these unique environments have identified several dominant taxa that comprise a significant portion of the community in geographically and environmentally disparate locations. While the distributions of these populations are well documented, there is significantly less information describing the means by which such specialized communities assemble within the sediment column. Here, we review known patterns of subsurface microbial community composition and perform a meta-analysis of publicly available 16S rRNA gene datasets collected from 9 locations at depths from 1 cm to >2 km below the surface. All data are discussed in relation to the 4 major processes of microbial community assembly: diversification, dispersal, selection, and drift. Microbial diversity in the subsurface decreases with depth on a global scale. The transition from the seafloor to the deep subsurface biosphere is marked by a filtering of populations from the surface that leaves only a subset of taxa to populate the deeper sediment zones, indicating that selection is a main mechanism of community assembly. The physiological underpinnings for the success of these persisting taxa are largely unknown, as the majority of them lack cultured representatives. Ecological explanations for the observed trends are presented, including the possible influence of energy depletion and the physiological basis of major taxonomic shifts.

**KEYWORDS:** Marine sediment · *Bacteria* · *Archaea* · Microbial diversity · 16S rRNA

 [Full text in pdf format](#)     
 [Supplementary material](#)

**Cite this article as:** Petro C, Starnawski P, Schramm A, Kjeldsen KU (2017) Microbial community assembly in marine sediments. *Aquat Microb Ecol* 79:177-195. <https://doi.org/10.3354/ame01826>

[Next ▶](#)

**Export citation**  
 [Mail this link - Contents Mailing Lists - RSS](#)  
 - Tweet -  [Share](#)

[Cited by](#)

Published in *AME* Vol. 79, No. 3. Online publication date: June 12, 2017  
 Print ISSN: 0948-3055; Online ISSN: 1616-1564  
 Copyright © 2017 Inter-Research.