Differences in Gut Microbial Communities Between Mussels and Oysters Reflect Differences in Food Resource Utilization

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Abstract

The ribbed mussel Geukensia demissa and the Eastern oyster Crassostrea virginica are commonly found in salt marshes along the east coast of the United States and the Gulf of Mexico. Although both bivalves are estuarine, G. demissa is intertidal whereas C. virginica is intertidal but accounts for less than 3% of the oyster’s carbon requirement. To determine whether this difference in food resource utilization may be reflected in a difference in their gut microbial community, we: 1) characterized the gut microflora of the two bivalves; 2) determined whether the gut microbial communities vary across season; and 3) determined whether cellulytic microbes are present in the gut of the bivalves. Gut microbial communities were analyzed quarterly using universal bacterial primers to PCR amplify the 16S rRNA gene. Clone libraries were then analyzed using RFLP and the dominant members sequenced. Sequence results indicate significant differences in gut bacterial community between the two bivalve species that vary seasonally. Carnobacteria are the only shared dominant community members in the bivalves during March and June, but are absent from both in September. Mycoplasma spp. are dominant community members in the gut of G. demissa during all seasons but not in that of C. virginica. Other gut bacteria in G. demissa included Spiroplasma spp., Entoplasma somnilux, and Pseudomonas sp. In contrast, dominant bacteria in oysters are Wolbachia sp., Raetonia sp., Haemophilus sp., and Escherichia coli. A total of 172 cellulytic CFUs were isolated from the bivalves and 96% were isolated from Geukensia. Our results show a substantial difference in the gut bacterial community between two bivalve species that often live only centimeters apart. Cellulolytic bacteria were present in bivalve guts but they were found almost exclusively in G. demissa.

Objectives

Ribbed mussels and Eastern oysters are both estuarine bivalves but ribbed mussels ingest cellulose-rich detritus whereas Eastern oysters do not. We hypothesize that their gut microbial communities differ. The objectives of the study were to:

- Identify major members of their gut bacterial community
- Isolate cellulytic bacteria from the intestine of the two bivalves

Methods

Extract genomic DNA from gut content
PCR amplify 16S rDNA using universal bacterial primers 63F and 1388R
Construct 16S rDNA libraries
Fingerprint 96 isolates and sequence those that are unique
Assign identity using BLAST

Summary

- Gut microbial communities differed significantly between mussels and oysters reflecting likely differences in food resource utilization.
- Seasonal differences in bivalve gut bacteria indicate transient food resources.
- Most (96%) of the cellulytic bacteria isolated originated from mussels suggesting that detritus is much more important in the diet of mussels than in that of oysters.

References