Prevalence and Diversity of a Ring-Cleaving Dioxygenase Gene, pcaH, in a Salt Marsh Community
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Abstract
The degradation of lignin-related aromatic compounds is an important ecological process in the highly productive salt marshes of the southeastern U.S. Despite the known role of the endocytical pathway in lignin degradation, there are limited data on the diversity and metabolism of these systems.

Materials and Methods
We report the diversity of genes encoding halo-tolerant ring-cleaving dioxygenases of the [4Fe-4S] halo-tolerant enzyme from bacterial communities associated with decaying Spartina alterniflora, the salt marsh grass dominating these coastal systems, as well as from enrichment cultures with aromatic substrates (p-hydroxybenzoate, vanillate, syringate, or chlorocate). Sequences of halo-tolerant ring-cleaving enzymes from these enrichment cultures and from natural communities were amplified using primers designed to target the pcaH gene from Roseobacter class isolates. The prevalence of pcaH in natural communities were analyzed by T-RFLP fingerprinting of 16S rDNA amplicon pools.

Results
Fifty-two percent of the clones could be classified as marine isolates. The salt marsh community associated with decaying Spartina alterniflora harbored ca. 40 unique members of the Roseobacter class. Enriched communities with those from isolates shows a predominance of Roseobacter class isolates; a predominance of Roseobacter-like proteobacteria suggests enrichment of this lineage may be pivotal in the degradation of aromatic compounds in salt marsh environments.

Conclusions
The abundance and diversity of pcaH genes suggests the [4Fe-4S] halo-tolerant pathway is a major catabolic route for the degradation of aromatic compounds in salt marsh ecosystems.

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Dedicated to Dr. L. Nicholas Bresnick
In gratitude for his outstanding scientific leadership and dedication to our institute's success.
Professor Emeritus, Penn State University