Mechanistic strategies of microbial communities regulating lignocellulose deconstruction

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Abstract

Salt marshes are highly productive intertidal ecosystems. Among the most effective carbon sequestering ecosystems per unit area, they can generate abundant organic carbon, which is produced in the form of lignocellulose, a renewable and sustainable feedstock for fuel production. Once lignocellulose is generated, it is then metabolized by communities of functionally diverse microbes. Unfortunately, the organisms and precise mechanisms regulating this process remain unknown due to the complex and underexplored environment. A new study sought to better understand lignocellulose decomposition. Using proteomics and sequencing, they evaluated the microbes residing in a natural established UK salt marsh. They found that the community was dominated by Gammaproteobacteria, Bacteroidetes, and Deltaproteobacteria. 42 families of lignocellulolytic bacteria were identified, which secrete glycoside hydrolase family enzymes to degrade lignocellulose. And an abundance of putative esterases associated with decoupling lignin from polysaccharides was observed. These results broaden our understanding of the microbial and molecular mechanisms underpinning carbon sequestration in salt marshes.