Phylogenetic Distribution of Potential Cellulases in Bacteria

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Project Goals

The main goal of this project is to connect diverse microbial groups with the extracellular enzyme systems that catalyze the decay of organic material. We will also determine whether different groups of microbes and their enzymes respond to environmental changes, and whether they can recover from such changes. Finally, we will develop mathematical models to predict the responses of microbial communities and their associated functions under new environmental conditions

Abstract:
In most terrestrial ecosystems, the depolymerization of plant cell wall is the rate limiting step in the turnover of organic material. The composition of plant detritus is known to depend mainly on enzymes produced by microorganisms. This raises the question: which phylogenetic lineages of microorganisms can degrade plant cell wall material, including cellulose?
To address this question, we compared the distribution of Glycoside Hydrolases (GH) potentially related to the cellulose degradation among 3744 bacteria.
Some phylogenetic groups are especially rich in GHs whereas some are very poor. For example, in bacteria from the Bacteroidetes phylum ~40 GHs (from the families 1, 3 5, 6, 8, 9, 10, 12, 16, 45, 48) are described (per genome) but in the Chlorobi phylum less than 5 of these protein-encoding genes are observed, per sequenced genome. The others bacteria that lack these GHs belong to the Aquificae, Chlamydiae, Chrysiogenetes, Cyanobacteria, Deferribacter, Elusomicrobia, Fusobacteria, Gemmatimonadetes, Synergistetes, Tenericutes and Nitrospirae phyla.
In addition, when present in genomes, not all the GH families are equally observed. Indeed, enzymes from the family 6, 8, 9, 45, and 48 are 1.5 to 3 times less abundant than enzymes from the family 1, 3 and 5. The over-representation of these enzymes is related to their numerous activities (e.g. GH1: β-glucosidase; β-galactosidase; β-mannosidase; β-glucuronidase; exo-β-1,4-glucanase; etc.) whereas the enzymes with low abundance display only few activities (e.g. GH6: endoglucanase and cellobiohydrolase).
For each phylum, we defined an abundance profile (for GH1, 3, 5, 6, 8, 9, 10, 12, 16, 45 and 48). These profiles were compared and clustered in order to discriminate the potential cellulose degraders from the other organisms. This clustering highlights the adaptation of microorganisms to different “life-styles”. For example, autotrophic bacteria (e.g.

Cyanobacteria) and/or intracellular pathogens (e.g. Tenericutes) generally lack many enzymes involved in polymers degradation, outside the cell (e.g. GH3, 5, 6, 8).
The association of 'Carbohydrate Binding Modules' (CBM) to catalytic domains (GH) is assumed to potentiate the catalytic activity by proximity effects. The association of GHs, from the above mentioned GH families, with CBMs from the family 2, 3 and 4 was thus investigated. Surprisingly, the CBM-GH profiles differ significantly from the profiles of their ‘free enzymes’ relatives. The association of CBM to GHs is a signature for enzymes involved in the catabolism of cellulose whereas the physiological function of ‘free’ enzymes is still pending (anabolism and/or catabolism).