195e Functional Genomics Analysis of Glucan Dimer Metabolism in the Hyperthermophlic Bacterium Thermotoga Maritima

Steven R. Gray, Shannon B. Conners, Clemente I. Montero, and Robert M. Kelly

Thermotoga maritima is a hyperthermophlic gram-negative bacterium with an optimal growth temperature of 80oC and the ability to grow on a wide variety of substrates. It is among the most studied of high temperature microbes, with a fully sequenced genome and many characterized metabolic pathways. Here, we present a functional genomics-based study of differential gene expression in T. maritima during growth on cellobiose and maltose, with and without the presence of elemental sulfur. Using cDNA microarrays in batch growth, we found that the substitution of the beta-linked cellobiose compared to the alpha-linked maltose results in dramatic changes in gene expression, with over 14.8% of the genome significantly responding to this change in the presence of sulfur, and 14.4% (mostly a different set of genes) without sulfur. This included many pathways not thought to be involved in the conversion of disaccharides. In addition, in the presence of sulfur only ten genes to respond significantly when grown with maltose, and only nine genes responded in cellobiose-based growth. It is interesting to note a strong agreement between several of the differentially expressed operons, suggesting a generalized sulfur response. Also notable is the small overall sulfur effect, compared to much greater sulfur induced expression changes observed in archeal hyperthermophiles. To examine the effects of carbohydrate linkage and the presence of sulfur in more detail, continuous culture experiments were conducted with T. maritima to examine the utilization of carbon sources in a steady-state environment. In addition, gene expression was examined during the transition between carbon sources was examined to better understand how T. maritima responds to the presence of multiple carbon sources. The goals of this work are to uncover regulatory pathways utilized by hyperthermophiles in responding to changing environmental conditions, and to relate these findings to sugar-responsive genes in distantly related microorganisms such as well-characterized mesophilic pathogens, in order to better understand environmental impact on metabolic pathway evolution.