

Studies of the cellulolytic system of the gliding bacterium *Cytophaga hutchinsonii*

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ABSTRACT

Cytophaga hutchinsonii is an aerobic gram-negative bacterium originally isolated from sugarcane piles. This microorganism must therefore possess a set of genes allowing it to digest cellulolytic substrates. In this study we examined genes in *C. hutchinsonii* Whole Genome Sequence (WGS) data set encoding cellulases potentially used by this microorganism for degrading high molecular-weight organic biopolymers. Several genes from CAZy (Carbohydrate-Active enZymes) Family Glycoside Hydrolase were BLAST against *C. hutchinsonii* genome sequence and analyzed. The data analysis and homology findings showed some amazing results. We identified several genes believed to encode proteins involved in cellulose degradation. These genes include several endo-beta-1,4-glucanases and several beta-glucosidases, amongst others. However, the most striking feature of *C. hutchinsonii* is the absence of a cellulose-binding domain (CBD) which to date was believed to be imperative in microbial digestion of crystalline cellulose. Our focus on *Cytophaga* was motivated by the desire to understand the role of these bacteria in the utilization of the highly abundant cellulolytic wastes which can be converted into various compounds for use as biofuels and other by-products.