TITLE: IDENTIFICATION OF GENES ENCODING FOR ENZYMES INVOLVED IN GELLAN GUM DEGRADATION IN *MUCILAGINIBACTER*

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ABSTRACT:
Gellan gum is a polysaccharide produced by soil bacteria used to solidify culture medium. It is widely used in food industry as a gelation agent; however, its applications are restricted due to its high viscosity. A strain of *Mucilaginibacter* was isolated from Amazonian soil and exhibited the phenotype of gellan gum degradation. There are four known enzymes involved in gellan degradation: a gellan lyase, which releases the tetramer that constitutes gellan; and three enzymes involved in the release of each monomer that compose the tetramer: an unsaturated glucuronyl hydrolase (UGH), an α-L-rhamnosidase, and a β-D-glucosidase. The objective of this study was to identify putative enzymes responsible for gellan degradation in the genome of a *Mucilaginibacter* PPCGB 2223, a strain isolated from Amazonian soils. The genome of strain PPCGB 2223 was sequenced and annotated. Genes coding for the enzymes involved in gellan degradation were identified and analyzed. *Mucilaginibacter* sp. PPCGB 2223 presented 13 copies of genes encoding for α-L-rhamnosidase and 9 gene copies for β-D-glucosidase. These enzymes are widespread among bacteria, since they are involved in degradation of plant material. Two sequences with similarity to UGH were identified, but one of them was annotated as “unsaturated chondroitin disaccharide hydrolase”. Chondroitin is a disaccharide of N-acetylgalactosamine and glucuronic acid and, it has been shown that UGH can also degrade chondroitin. The final enzyme involved in gellan degradation is gellan lyase, but no ORF was found with high similarity to the only sequence of gellan lyase published. This enzyme was previously described in a *Bacillus* strain, and contains 2475 amino acids. However, it was identified one gene for polysaccharide deacetylase in the genome of PPCGB 2223 presenting a similarity with gellan lyase from *Bacillus* but, the sequence is only 264 aa long. Therefore, we cannot infer its functional role, since this enzyme is yet poorly described. *Mucilaginibacter* sp. PPCGB 2223 strain presents genes encoding for three of the four enzymes responsible for gellan depolymerization and one candidate for the final enzyme. Nevertheless, we have yet to evaluate if these genes are active and if the enzymes are functional aiming further biotechnological applications.

Keywords: EPS, genomics, *Mucilaginibacter*, Amazonian soil.

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