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Structural, biophysical and biochemical studies of CAZymes with degradation potential of microbial biofilms exopolysaccharids

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Microbial resistance to antibiotics has become one of the major global health threats, considering just antimicrobial resistance alone, it is estimated that up to 700,000 deaths could occur annually. (1) One natural way that certain bacterial species acquire antimicrobial resistance is through the formation of biofilms. Biofilms are complex structures that cluster microbial cells within an extracellular matrix primarily composed of exopolysaccharides (EPS), extracellular DNA, and proteins, with EPS making up about 85% of this matrix. Given the critical role of EPS in the formation and maintenance of biofilms, enzymes active on complex carbohydrates can be used to degrade bacterial biofilms. Consequently, in this study we focus on the usage of glycoside hydrolases (GH) with potential for degrading and preventing bacterial biofilm formation. More specifically, we used a GH from the family GH153, this class of enzymes has been characterized as β -1,6-N-acetylglucosaminidases, however, only 2 enzymes in this family have been structurally and biochemically studied. (2-3) In this study, specifically, we analyzed a GH153 derived from *Serratia marcescens* which presented a high degradation potential of 90% when applied in *Staphylococcus aureus* biofilms that are Poly- β -1,6-N-acetyl-d-glucosamine (PNAG) rich. Moreover, when in synergy with different antibiotics, this enzyme optimizes their action in the biofilm showing a reduction of approximately 50% of viable planktonic cells. Additionally, structural and biochemical experiments were performed in order to characterize this GH153.

Palavras-chave: Biofilm; β -1,6-N-acetylglucosaminidases; PNAG.

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