Sugarcane CBMs from Expansins and Xyloglucan endotransglycosylase

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The sugarcane is the most important species for the generation of sustainable bioethanol in Brazil, the second largest producer in the world. One of the biggest promises for an increase in ethanol production is the second-generation ethanol produced with lignocellulosic biomass. For such, it is necessary to degrade the biomass using glycoside hydrolases to generate C5 and C6 carbohydrates, aiming at fermentation by microorganisms. Carbohydrates are biomolecules involved in many life processes. Because of this multiplicity of functions, several proteins involved in processes that include carbohydrates have acquired non-catalytic modules, such as carbohydrate binding modules (CBMs) that interact specifically with mono-, oligo- and polysaccharides. In some cases, CBMs can also be found isolated as single proteins. In carbohydrate-active enzymes, like glycoside hydrolases, CBMs can be found as a single unit arranged in tandem at different positions. CBMs recognize and bind specifically to carbohydrates, which lead to biological consequences: enhanced hydrolysis of insoluble substrates, increased accessibility of the catalytic domain to the substrate, disruption of polysaccharide structure and cell surface protein anchoring. The study of CBMs found in sugarcane proteins can help produce better material for second-generation ethanol from sugarcane lignocellulosic waste. Xyloglucan endotransglycosylases (XET) and Expansins are plant enzymes involved in cell wall processes. Some of these enzymes have a CBM. The aim of this project is to characterize some CBMs found in XET and Expansins of sugarcane. The prospection of these enzymes was done *in silico* with the Gene Index data base. A total of 181 XET and 167 expansin sequences were analyzed by the Motif Scan software. As a result, 11 CBMs in 8 XET sequences and 4 CBMs in 3 Expansin sequences were found. Primers were designed to amplify these CBMs. They will be cloned in a plasmid in order to be completely sequenced. In addition, these CBMs will be produced in heterologous expression systems so they can be characterized.