



## Analysis *in silico* of polysaccharides degrading enzymes of *Aspergillus flavipes* FP-500 found in complex carbon sources.

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**Introduction.** *Aspergillus* is capable to produce a lot of carbohydrate degrading enzymes (CDE) which applied in a great variety of industrial processes such as feed and food production. *Aspergillus flavipes* posses interesting capabilities to produce those enzymes. However, its entire genome is not sequenced yet. However, the sequence of *Aspergillus terreus* genome is available: According to the literature the family *flavipes* and *terreus* are so similar that can be joined<sup>1</sup>. Some of (CDE) have been reported to possess carbohydrate binding domains (CBD's); which are sequences for specific union to some polysaccharides<sup>2</sup>.

The aim of this work is the identification to analyze the enzymes secreted by *A. flavipes* growing on complex carbon sources and analyze the probable CBD's in these enzymes by comparison with sequences of *Aspergillus terreus*, polysaccharide degrading enzymes.

**Methods.** Secreted proteins from *Aspergillus flavipes* FP-500 cultures with corn cobs as complex carbon source were analyzed by LC/MS/MS coupled system. Proteins identification and CBD's search were made using Conserved Domain Database tool (CDD) from NCBI or Uniprot databases.

**Results.** Proteins were identified as very similar to *Aspergillus terreus* proteins (table 1). Glucoamylase acts on starch hydrolysis, while  $\alpha$ -galactosidase is involved in degradation of galacto(gluco)mannan<sup>3</sup>. On the other hand, cellobiohydrolase acts on the backbone of cellulose while xylanase and acetylxyylan esterase belong to xylanolytic system. Many references indicate synergistic effect of different enzymatic systems; such as the combined action of Cellobiohydrolases with xylanase and acetylxyylan esterase gives an important

increase of depolymerization of corn stover due to synergistic action of these enzymes<sup>4</sup>. We looked for CBD's and some of them were found using the CDD tool and Blastp protein sequences. Unlike the first three enzymes, xylanase A precursor and Acetylxyylan esterase didn't show CBD's when were analyzed by CDD tool but shows identities near to 57 and 67% respectively to fungal cellulose binding domain (A1CCD3 \_ASPCL Uniprot).The presence of CBD's on these enzymes suggests that may be necessary at least one of each with CBD's as a strategy used by the fungus to improve the polysaccharide hydrolysis.

**Table 1.** Identified enzymes on *Aspergillus flavipes* FP-500 cultures on corn cobs with probable Carbohydrate Binding Domain sequences

Enzyme	NCBI and Uniprot Accession	Score	e-value
Glucoamylase precursor	XP_001213553.1	49.4	4x10 <sup>-6</sup>
	Q0CPK9	109	9x10 <sup>-5</sup>
$\alpha$ -galactosidase	Q0CVX4.2	208	2X10 <sup>-17</sup>
	AAW68437.2	69.8	10 <sup>-2</sup>
Cellobiohydrolase	Q0CMT2	157	6X10 <sup>-11</sup>
	XP_001216082.1	53.7	2X10 <sup>-7</sup>
Endo-1,4-beta-xylanase A precursor	Q0CFS3	119	6X10 <sup>-8</sup>
	Q0CNM5	103	9X10 <sup>-5</sup>
Acetylxyylan esterase			

**Conclusions.** It's possible to identify CDE on proteins secreted by *A. flavipes* on corn cobs. Some of these enzymes likely to own CBM's which were possible to identify by comparison with *A. terreus* proteins.

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### References.

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