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Improvement of stillage-based forage by lignocellulolytic bacteria

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As a byproduct of corn-based ethanol production, stillage can be an excellent feed material in view of the ingredients. The main limitations of its use are the accumulation of mycotoxins as well as high hemicellulose (especially xylan) and fiber contents. Reduction of hemicellulose and fiber content of stillage can be achieved by cellulolytic-hemicellulolytic bacteria. Additionally, with cleavage of highly viscous xylan, prebiotic xylo-oligomers are produced, which may also increase the efficiency of feeding. Two members of our strain collection (K07 and *Xylanibacillus composti* K13) are particularly promising as they form a strong hydrolysis zone on polysaccharide-containing agar plates and according to de novo genome projects they encode many glycoside hydrolases (GHs) in their genomes. Strain K07 is a new species and new genus candidate bacterium in the Pseudomonadaceae family. Based on the 16S rDNA sequence, the closest relatives of the strain are members of the *Cellvibrio* and *Saccharophagus* genera, which are well known for their great cellulolytic-hemicellulolytic activities. Strain K07 was isolated from mesophilic region of compost and its genome consists of 4.243 Mbp. Based on the complete genome sequence, 62 glycoside hydrolase genes are found, which belong to 28 different GH families. In the genome of K07, there is a noticeably high number of annotated genes in the GH 43 family, which contains enzymes mainly involved in xylan degradation. *Xylanibacillus composti* K13 belongs to the Paenibacillaceae family. Its genome size is 4.28 Mbp and contains 40 GH genes belonging to a total of 24 families. Seventeen of its hypothetical GH genes are endoxylanases. Based on this preliminary investigation of their metabolic potential, the two strains are a promising component of a biotechnology process for reduction of hemicellulose (mainly xylan) and fiber content of stillage-based forages.

Biography

Akos Toth is a Research Fellow of the Department of Environmental and Applied Microbiology of the Agro-environmental Research Institute, NARIC. He has received his PhD degree in Environmental Science in 2016. His current research fields include microbial lignocellulose degradation, microbiology of composts and molecular biology of glycoside hydrolases. He is a Member of the Hungarian Society for Microbiology.

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