Abstracts book

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bla$_{SHV}$. Carbapenem resistance genes, *bla*$_{KPC-2}$ (15.8 %), *bla*$_{OXA-1}$ (57.9 %), *bla*$_{NDM-1}$ (15.8 %) were also detected. Approximately, 10.5 % - 36.8 % co-occurrence of two or beta-lactamase genes was detected in some isolates. Resistance to cefotaxime and the presence of wide range of beta-lactamase genes showed the potential risks associated with these pathogens occupational exposure

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Lignocellulose digestion by anaerobic rumen microbial consortia from sheep

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Abstract

Rumen microbial community is excessively studied to understand its complex anaerobic microbial interactions. These consortia are not uniform but very diverse. They degrade complex plant biomass into easily metabolizable compounds by cellulolysis. The aim of this study was to enrich anaerobic cellulolytic consortia from sheep rumen fluids and to understand the possible mechanisms of cellulolysis with reference to their lignocellulolytic enzyme production. The rumen fluid samples were enriched in different culture media containing cellulose. The experiment was conducted in an anaerobic glove box with an atmospheric composition of 90% N_2, 5% H_2 and 5% CO_2. After 4 weeks of incubation at 37 ˚C temperature, homogenized cell suspensions were assayed for their total cellulase, xylanase, exoglucanase, endoglucanase and laccase activities. The most efficient cellulolytic enzyme producer-consortium was RF5, producing the highest total cellulase activity of 0.549 FPU/ml, highest xylanase activity of 0.582 U/ml and highest endoglucanases activity of 0.81 U/ml. The exoglucanase activity was 0.0985 U/ml. However, the laccase production of the 28 consortia investigated was negligible and only several consortia were endoglucanase positive. The regression analysis of enzyme activity data revealed that there is a positive correlation between total cellulase, xylanase and exoglucanase activities of consortia investigated. This reveals that the changes in total cellulase activity might affect the expression of xylanase and exoglucanase. These consortia will mainly release xylose, cellobiose and glucose from lignocellulose. Moreover, RF5 being the most efficient mesophilic anaerobic consortium among investigated consortia should have a multicomponent cellulosome with xylanase, endoglucanase and exoglucanase.

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Characterization of the gamma-glutamylpolyamine synthetase GlnA3 in *Mycobacterium tuberculosi*s as a potential drug target

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Abstract

Human intracellular pathogenic actinobacterium *Mycobacterium tuberculosis* has developed strategies to access nutrients from the host and to exploit the host to synthesize more resources for its growth and propagation. *Mycobacterium tuberculosis* can induce the polyamine biosynthesis during the shift in metabolic state of macrophages. The pathogen is able to utilize polyamines as a sole *N*- and *C*-source to support its own intracellular growth in macrophages. In our previous studies in a model actinobacterium *Streptomyces coelicolor* M145, we demonstrated that a protein annotated as glutamine synthetase-like, GlnA3$_{St}$ (SCO6962), is involved in the first step of polyamine utilization pathway[1]. GlnA3$_{St}$ is a gamma-glutamylpolyamine synthetase (GPS) that ensures both nutrients availability (*C*- and *N*-source) and resistance against high polyamine concentrations in *Streptomyces coelicolor*[1]. Since there is a homologue of GlnA3$_{Mt}$ (Rv1878) in *Mycobacterium tuberculosis,* this GPS enzyme is a particularly interesting target for drug development. In our current studies we were able to show that GlnA3$_{Mt}$ can glutamylate polyamines, demonstrating GPS activity. Thus, inhibition of GlnA3$_{Mt}$ may