Poster J-49

Analysis of Adaptation Behaviour of Fungi Under Biotic Stress Caused by Biofilm Formation

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Short Abstract: Biofilms have been found to be cause of many human infections. The composition of biofilm is not known entirely, but supposed to be mixture of various polysaccharides. Fungi are capable of degrading complex polysaccharides. Aim of this study is to explore adaptation of Aspergillus to Salmonella biofilms via microarray analysis.

Long Abstract:
A biofilm can be described as the population of one or more organisms attached to each other and a surface by means of a bacterium-initiated matrix. Biofilms have recently been implicated as the cause of many chronic infections in humans. Biofilms form in many extreme environments. The matrix provides a very stable environment and results in high levels of resistance to antimicrobial agents. Often, it is difficult to clear the infection unless the substrate to which the bacteria are attached is removed. This biofilm composition is not known exactly, but what is known is that it is a mixture of various polysaccharides. Filamentous fungi are capable of degrading complex polysaccharides very efficiently. They are also resistant to harsh environmental conditions, both abiotic stresses and biotic stresses to a great extend. The aim of this study is to explore the adaptation period of Aspergillus species towards the biofilm formed by pathogenic Salmonella via the tools microarray and gene-specific analysis. Pathogenicity of Salmonella and other pathogenic bacteria is related to the biofilm formed by these microorganisms. There are certain fungi which can produce a variety of enzymes capable to degrade the biofilm formed by pathogenic bacteria. To explore which specific enzymes are particularly activated, Salmonella species and Aspergillus species are going to be co-cultivated. A number of pathogenic Salmonella and Aspergillus will be screened to determine the suitable couple. The adaptation period of Aspergillus to Salmonella and the biofilm produced; will be under control and in specified time intervals samples are going to be taken from Aspergillus species to be analyzed with microarray. The data obtained from Aspergillus microarray is going to be further mined to find which specific genes are responsible for resisting the biofilm formed by Salmonella. Those overexpressed genes will be studied detailly to find out a target enzyme which is capable of degrading biofilms. This may lead to development of compounds, enzyme mixtures to destroy Salmonella in contaminated food, patients carrying Salmonella.