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time and cause epidemic outbreaks in hospitals. We compared the virulence factors and resistance patterns of \textit{A. baumannii} strains isolated from samples of patients and staff in intensive care units between 2008-2011. Biofilm formation, serum resistance, siderophore production were investigated and resistance patterns were compared. PCR method was used to detect integrase genes. Most of the strains produced biofilm and siderophore. Only few strains were sensitive to serum. The multidrug resistant (MDR) \textit{A. baumannii} strains belonged to three different resistance patterns and each strain carried the integrase gene. Multidrug resistant \textit{A. baumannii} strains originated from ICU may occur due to the selection effect of broad-spectrum antibiotic therapy. MDR \textit{A. baumannii} strains with three different types of resistance patterns have circulated for years. Biofilm formation may play role in surviving and in the virulence process. The serum resistance helps the bacteria to cause bloodstream infection. These MDR \textit{A. baumannii} strains have adapted to hospital environment and became more virulent.

**GENETIC VARIABILITY OF BLACK ASPERGILLUS ISOLATES ORIGINATED FROM CEREALS IN HUNGARY**

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Black Aspergilli (\textit{Aspergillus} section Nigri) are commonly found as soil organisms decomposing dead plant residues and they are pathogenic on several crops. The plant pathogens are of concern not only for their ability to destroy several agronomically important food crops, but also due to their ability to produce several mycotoxins including ochratoxins and fumonisins. Black Aspergilli associated with any plant pathological problem are usually mentioned as \textit{A. niger} in early publications. However, \textit{Aspergillus} section Nigri is one of the more difficult groups concerning classification and identification and closely related species belonging to this taxa are difficult to assign based solely on their phenotypic characters, but all species can be distinguished from each other using calmodulin or \textit{\beta-}tubulin sequence data. In this study 57 isolates originated from cereals (corn, wheat, barley) and soil were identified at the species level based on partial calmodulin sequence data. 47 isolates were found to belong to the \textit{A. niger}, while 10 isolates to the \textit{A. tubingensis} species. The genetic variability of the isolates was analysed using the UP-PCR method using eight primers. All of the isolates were found to belong to unique haplotypes. Distribution of the mating type genes was examined using a diagnostic PCR approach and 74.4% of the \textit{A. niger} isolates were found to belong to the MAT1-2, while 99% of the \textit{A. tubingensis} isolates belonged to the MAT1-1 mating type. It indicates a clonal population structure, what was also supported by the population genetic analysis of UP-PCR data (index of association and parsimony tree-length permutation tests). Further studies are in progress to examine the mycotoxin producing abilities of the isolates.

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**FILOGENETIC DIVERSITY OF BACTERIAL COMMUNITIES INHABITING A COOLING RESERVOIR USED FOR STORAGE OF THERMAL WATERS**

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Lake Therm-Organ located near Szarvas is a cooling reservoir used for the temporary storage of thermal waters before being redirected into the river Hármas-Körös. Water of this lake is anaerobic, alkaline, rich in phenol and is of high salinity. The aim of this research was the examination of the chemical composition as well as the phylogenetic diversity of bacterial communities inhabiting the lake water and sediment, the thermal water of the well and the utilized thermal water. The bacterial phylogenetic diversity was examined by cultivation based and molecular biological denaturing gradient gel electrophoresis (DGGE) and clone library methods. Depending on the time of residence and season, the chemical composition and biological quality of the thermal inflow transformed in the reservoir. Significant reduction of the concentration of some chemical parameters was observed. Compared to the thermal inflow, the concentration of COD, BOD5 and total phenol decreased significantly in the reservoir in summer. Regardless of the date of sampling, bacterial communities of water samples showed the highest similarity to each other on the basis of the results of 16S rDNA DGGE analysis which indicates a uniform distribution of planktonic bacteria in the water body. Sediment samples formed distinct similarity groups from the water samples. In the structure of water and sediment bacterial communities, temporal changes were more pronounced than spatial differences among the sampling sites. Bacterial communities of the thermal inflow each time had a unique band pattern which differed from the water and sediment samples, as well. Members of a total of 13 phylogenetic phyla, such as: Proteobacteria, Deinococcus-Thermus, Aquificae, Nitrospirae, Firmicutes, Caldariaceae, Chloroflexi, Cyanobacteria, Tenericutes, Bacteroidetes, Actinobacteria, Spirochaetes, Deferrribacteres were detected by the applied cultivation-based and cultivation-independent methods. The greatest diversity was revealed using the clone library method. Altogether 82 ARDRA representatives of molecular clones from the influent water, 54 from the lake water, and 60 from the sediment samples were sequenced. By cultivation, the presence of strains belonging to Alpha- and Beta-Proteobacteria was detected. Members of the following genera were the most abundant: \textit{Spirochaeta}, \textit{Thauera}, \textit{Rhodobacter}, \textit{Alkalifexas}, \textit{Dehalogenimonas}, \textit{Desulfbacterium}, \textit{Achromobacter}. Based on literature data, the majority of microorganisms

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