environments, the aim of this study was to gain insight to the structure and composition of microbial communities and the influence of changing parameters. The first step of this long-term investigation was to reveal the phylogenetic diversity of microbial communities inhabiting the first lake water, sediment and biofilm developed on the reed surface. The spatial and temporal changes were tracked by DGGE, using primers 27fGC and 519r. Exploration of the phylogenetic diversity of bacteria and archaea was carried out by the construction of three clone libraries respectively, and sequencing 16S rRNA coding regions of DNA. Archaeal diversity was examined by the cloning of ribosomal sequences from the community DNA using primers A109f and A958r. Analyses have shown that bacterial communities of the sediment formed separate groups which showed little similarity to the communities of the lake water during the whole year. Both clone library analyses and DGGE patterns have shown that the influent water differed from every other sample. In the case of water samples, representatives of the Phylum Cyanobacteria were present in large proportions. Arthrospira platensis proved to be a constant member of the lake water community. In both biofilm and sediment samples members of the Genus Hydrogenophaga (Proteobacteria), the Ordines Rhodocyclales and Rhodobacterales and purple non-sulfur bacteria were found to be dominant. Archaeal communities were less diverse than bacterial ones based on the processing of three clone libraries and the similarity was more pronounced between the sample types. The archaeal diversity of the sediment was the most diverse among the sample types. The most common archaeal genera were Metanosaeta and Metanocalculus. The majority of bacteria identified from the Reservoir-System was haloalkalophilic, and might be capable of utilizing a wide range of carbon compounds.

## TETRACYCLINE RESISTANCE TET(A) PLASMIDS TRANSFERRING MULTIRESISTANCE IN ENTEROTÖXIGENIC E. COLI STRAINS FROM PIGS

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Enterotoxigenic E. coli (ETEC) bacteria are frequent pathogens causing watery diarrhea in weaned pigs. Plasmids encoding different enterotoxins (estA, estB, elt) and fimbrial adhesins (f4, f18) are of prime importance in the pathogenesis of ETEC strains. Recently, the complete sequence of the ETEC pTC plasmid was described, as a first representative of hybrid ETEC plasmids carrying the tetracycline resistance gene tet(B) in combination with enterotoxin genes estA and estB. Similarly, unrayeling the impact of tet(A)-plasmids in the transfer of resistance and/or virulence would also be important for the efficient therapy of ETEC infections. The main objective of the present study was to provide a comparative description of antimicrobial resistance and virulence profiles of porcine post-weaning ETEC strains representing three middle-European neighboring countries: Hungary, Austria and the Czech Republic. Furthermore, the characterization of genetic vectors for tetracycline resistance was also attempted, with special regard to plasmids responsible for the transfer of tetracycline resistance gene tet(A) and putative co-resistance/virulence genotypes. A total of 87 porcine ETEC strains isolated from post-weaning diarrhea were included in this study. Majority of them were isolated in Europe: Hungary (n=16), Austria (n=34) and the Czech Republic (n=17), and 20 ETEC strains were derived from the USA. Antimicrobial resistance phenotype of the strains was determined for 17 antimicrobial compounds with clinical relevance. Strains resistant to tetracycline were subjected to further studies, including the PCR subtyping of the tet genes, and the detection and characterization of plasmids mediating tetracycline resistance and ETEC-specific virulence in two tet(A)-positive monoplasmidic derivatives of F18+ ETEC strains from Hungary and from the

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Czech Republic (2172/11 and 11732/71 respectively). Regardless of the geographical origin, majority of the ETEC strains shared a common MDR pattern of sulfamethoxazole (91%), tetracycline (84%) and streptomycin (80%) resistance. The tetracyclin resistant phenotype was most frequently covered by the presence of the tet(B) gene (38%), when tet(A) was identified in 26% of the isolates. The virulence gene profile included enterotoxin genes (ett, estA and/or estB), as well as adhesin genes (f4, f18) without geographic differences. Characterization of these tet(A) plasmids revealed, that the IncI1 plasmid of the Hungarian strain mediated the co-transfer of tet(A), aadA1 (streptomycin/spectinomycin) and strA (streptomycin) genes, when the IncF plasmid of the Czech strain carried tet(A) in association with catA1 for chloramphenicol resistance. Furthermore, the tet(A) plasmid of the Hungarian strain carried a class 1 integron with an unusual variable region of estX-aadA1 responsible to streptothricin-spectinomycin/streptomycin resistance phenotype. In conclusion, the presence of IncI1 and IncF type plasmids, responsible for the co-transfer of the tet(A) gene and additional resistance determinants were demonstrated for the first time in F18+ ETEC strains. In addition to the pTC hybrid plasmid of tet(B)-type, the first description of tet(A) plasmids was provided as a vector of multidrug resistance in porcine ETEC strains.

## ENHANCEMENT OF PERFORMANCE OF MICROBIAL FUEL CELLS USING A NEW GEL-TYPE ANODE AND SEMI-CONTINUOUS FERMENTATION

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Microbial fuel cell (MFC) is a device that contains live microorganisms and it is able to convert directly organic chemical bounds to electrical energy. MFC is considered to be a promising sustainable technology, in particular when using wastewaters as substrates, offering the advantage of simultaneously treating wastewater and generating electric power. Unfortunately, so far this technology still face numerous problems such as low converting efficiency comparing with other chemical fuel cells, low electrical potential, capacity of applied bacteria etc. Generally, in MFC bacterial cells attach directly to electrode forming biofilm in anode chamber and transfer extracellular electrons to anode, thus the performance of MFC should be affected by quality of biofilm layer(s). In this study, a new anode-type containing gel-entrapped bacteria was constructed and operated semi-continuously. Shewanella bacteria cells were entrapped in alginate gel with some major modification. Effects of some components such as polyaniline (PANI), titanium-dioxide and ammonium-persulphate as well as graphite powder to increase the conductivity and to enhance the electron transfer were investigated. In case of the conductivity, three levels of PANI (0 g ·ml-1; 0.01 g ml-1; 0.02 g ml-1) and three levels of graphite powder (0 g ml-1; 0.01 g ml-1; 0.05 g ml-1) were applied. The gel electrodes were investigated in three identical size dual-chamber MFCs. The increase in concentration of PANI resulted the rise of the conductivity in the modified gels. Addition of 0.01 g·ml-1 and 0.02 g·ml-1 PANI caused 6-fold (from 10.4 S to 64.5 S) and 10-fold (to 104.4 S) higher conductivity, respectively. Moreover, electrical potentials were 1.5 times in the case of 0.01 g·ml-1 and two times higher in the case of addition of 0.02 g·ml-1 of PANI meaning two and three times increase in power density (from 4.83 W·m-3 to 10.05 and 14.62 W·m-3). Graphite powder had also significant effects on conductivity, voltage and power density performance. Addition of 0.05 g·ml-1 graphite powder caused 10-fold higher conductivity (10 S to 100 S), double higher voltage output (0.17 V to 0.34 V) and 4-fold higher power density (4.83 W·m-3 to 19.24 W·m-3), respectively. It worth to note that combination of PANI and graphite powder resulted 105-fold higher conductivity (10.4 S to 1087 S), 3-fold higher voltage generation (0.17 V to 0.44 V) and 7-