

Occurrence and Community Structure of Bacteria Resistance to High Concentration of Sulfamethoxazole in MBR

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ABSTRACT

Membrane Bioreactor (MBR) technology is becoming an increasingly popular choice for the treatment of wastewaters. MBR microbial community structure of resistance to antibiotic sulfamethoxazole (SMX) was investigated based on 16S rDNA analysis. Sulfamethoxazole is an anti-bacterial sulfonamide. It prevents the formation of dihydrofolic acid, a compound that bacteria must be able to make in order to survive. Twenty different colonies grown on nutrient agar including 1mM SMX were randomly isolated. Through partial sequence analysis of PCR-amplified 16S rDNA, SMX resistance bacteria were divided into seven groups, which were 98% similarities to *Aeromonas caviae*, *A. hydrophila*, *Acinetobacter johnsonii*, *A. haemolyticus*, *Pseudomonas rhodesiae*, *P. graminis*, and *P. stutzeri* respectively. These isolated bacteria also were tested resistant to three other sulfa drugs, sulfanilamide, sulfaguanidine, and sulfadiazine. Antibiotic resistance is a public health concern of great urgency due to a growing inefficacy of antimicrobial agents to treat infectious diseases. Therefore, antibiotic resistance could be considered as an environmental pollution problem.

Key words : Membrane Bioreactor, Sulfamethoxazole, Resistance