

GENETIC CHARACTERIZATION OF TETRACYCLINE RESISTANCE IN SELECTED SOIL ISOLATES OF BACTERIA

Abstract

Antibiotic resistance is becoming increasingly widespread among bacterial organisms. To respond to the situation it is necessary to understand in detail all the mechanisms of resistance as well as expansion possibilities of resistance genes in the environment. In this study we attempted to identify tetracycline resistance determinants in selected soil gram-positive and gram-negative isolates. The isolates originate from unfertilized soil and from soil fertilized with tetracycline-contaminated manure. We tested the soil isolates for the presence of twenty three selected tetracycline resistance determinants and presence of tetracycline resistance determinants in DNA libraries.

We identified one of the tetracycline resistance determinants *tet(K)* in *Staphylococcus* sp. A DNA fragment was amplified with primers for *tet(M)* determinant in *Arthrobacter* sp., but its presence was not confirmed by the sequence analysis. None of the tested tetracycline resistance determinants were present in the genera *Chryseobacterium* and *Stenotrophomonas*. However, we managed to prove the ongoing horizontal gene transfer between the genus *Stenotrophomonas* and the genus *Chryseobacterium*. The transferred sequences encoded hybrid protein and efflux pump SmeW, both of them specific for genus *Stenotrophomonas*. Association of hybrid protein with resistance to tetracycline was not demonstrated in this study. The gene encoded hybrid protein is probably a component of a mobile element, whose transfer was confirmed by conjugation reaction under laboratory conditions.

Keywords:

tetracycline, resistance, MDR pumps, horizontal gene transfer, *Stenotrophomonas maltophilia*, *Staphylococcus* sp., *Chryseobacterium* sp., *Arthrobacter* sp.