Abstract

The genus *Streptomyces* produces more than a half of the known bioactive substances, ranking it among the most important bacterial taxons. *Streptomyces lincolnensis* ATCC 25466 encodes a biosynthetic gene cluster for lincomycin biosynthesis in its genome. Apart from the biosynthetic and regulatory genes, the cluster also contains three resistance genes, *lmr(A)*, *lmr(B)* a *lmr(C)*, which could protect of the host from the toxicity of a synthesized antibiotic. The Lmr(C) protein belongs to ARE proteins which generaly confer resistance to clinically important classes of antibiotics: macrolides, streptogramins, lincosamides and pleuromutilins. In addition to antibiotic producers, ARE proteins are also present in pathogenic microorganisms. However, the resistance mechanism conferred by these protins which belong to ABC transporters, even though they lack the transmembrane domain, have not been characterized yet. This makes the ARE proteins an interesting subject of the research.

Using deletion mutants in resistance genes *lmr(A)*, *lmr(B)* a *lmr(C)* we studied their effect on the lincomycin production and resistance to lincosamides, lincomycin and clindamycin with special focus on the function of the *lmr(C)*. We have found that deletion of *lmr(C)* does not significantly influence lincomycin production and resistance, however it has a significant impact on the resistance to clindamycin. Using a two-step immunodetection of fusion protein Lmr(C) - 6His we have found that the Lmr(C) is located mainly in cytoplasm.

Keywords: ABC proteins, ARE proteins, *lmr(C)*, antibiotic resistance, *Streptomyces lincolnensis*.