

Abstract

Acinetobacter baumannii is an important nosocomial pathogen characterized by the ability to acquire and develop complex resistance to antimicrobial agents. This capability is caused by efflux systems removing molecules of antibiotics from bacterial intracellular space. AdeABC is an RND-type chromosomal efflux system specific for *A. baumannii* which has a broad substrate spectrum. In this work, we focused on functional analysis of AdeABC to define its role in the resistance development to aminoglycosides in genetically different strains. We studied a set of 15 epidemiologically and genotypically well characterized strains of *A. baumannii* which were fully susceptible to aminoglycosides and other antibiotics primarily effective against this species. We determined genotyp of AdeABC for these strains and performed a selection for resistant variants in the presence of netilmicin. Using real-time qRT-PCR we compared the expression of the transporter gene *adeB* in originally sensitive strains and selected variants. The obtained results confirmed that the increased expression of AdeABC significantly reduces susceptibility to aminoglycosides and other antibiotics. The results also suggest that the efflux system provides a significant selective advantage for nosocomial strains of *A. baumannii*.