Gene expression of porin and beta-lactamases genes during the beta-lactam antibiotic treatment and effect of inoculum size on *Klebsiella pneumoniae* clinical isolates

ABSTRACT

In recent years, *Klebsiella pneumoniae* has been increasingly reported to be one of the most important nosocomial pathogens, and it is usually resistant to many antibiotics. In this work, we focused on the expression of the *AmpC* group β-lactamase DHA-1 and its negative regulator *AmpR*, as well as the porins OmpK35 and OmpK36 and on effect of inoculum. We used well-characterized *Klebsiella pneumoniae* strains in this study. Plasmids obtained from these strains were also transformed into different wild-type *Klebsiella pneumoniae* strains, which were typed by pulsed-field gel electrophoresis (PFGE) and multi-locus sequence typing (MLST). Gene expression analysis was performed by RT-PCR using specific primers and TaqMan probes. In most strains, expression was dependent on the presence of an inducer. The highly resistant strain showed a different expression pattern, but the expression of bla_{DHA-1} remained inducible by cefoxitin. Different regulation was also observed in the transformants. Based on our data, we suggest that the previously described regulatory pathway for *AmpC* is not generally suitable, and we propose that there are more regulatory factors in the pathway. The fact that AmpC behaves differently in different clones also complicates the establishment of general interpretation criteria as well as the statistical analysis of clinical outcomes.

Keywords

AmpC, *β*-lactamase, ST11, OmpK35, OmpK36, inoculum efect