

Identification of an ABC-type multidrug efflux pump MacAB genes in the genome of *Serratia marcescens* SM6

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Motivation and Aim: Bacterial multidrug resistance is a global problem worldwide. *Serratia marcescens* is an opportunistic pathogen with increasing clinical importance. Infections caused by *S. marcescens* are often difficult to treat due to multiple drug resistance. One of the mechanisms of drug resistance is based on the activation of efflux pumps. A number of efflux pumps that belong to several classes were identified in reference genome *S. marcescens* Db11 [1], including a macrolide-specific ABC-type efflux pump MacAB. The aim of this study was to identify *macAB*-like genes in the genome of laboratory strain *S. marcescens* SM6.

Methods and Algorithms: Analysis of *macAB*-like genes was done in RAST (<http://rast.nmpdr.org/rast.cgi>).

Results: Analysis of *S. marcescens* SM6 genome showed that this strain harbors three independent gene clusters encoding for MacAB-like efflux pumps. Interestingly, *macAB*-like genes in genome locus SM6_1728-1729 share approximately 70 % of homology to similar genes in *E. coli* and *Salmonella enterica* serovar Choleraesuis str. SC-B67 and have a surrounding similar to that in those bacteria. Two additional *macAB*-like loci *S. marcescens* SM6 genome, SM6_875-876 and SM6_1583-1584 are absent from *E. coli* and salmonellae genomes but could be found in other genomes of *Serratia* sp. Function of these additional gene clusters in *S. marcescens* drug resistance is currently unknown.

Conclusion: Therefore, in contrast to a single macrolide-specific MacAB efflux pump present in *E. coli* genome, distantly related bacterium *S. marcescens* possesses three gene clusters encoding for homologues of this efflux pump. Detailed characterization of the impact of these gene clusters on resistance to antimicrobials is needed.

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References

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