

Microbiology (Russian Federation) 2013 vol.82 N6, pages 668-679

Efflux systems in *Serratia marcescens*

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Abstract

A widespread bacterium *Serratia marcescens* (family Enterobacteriaceae) is an opportunistic pathogen and exhibits multiple drug resistance. Active removal of antibiotics and other antimicrobials from the cells by efflux systems is one of the mechanisms responsible for microbial resistance to these compounds. Among enterobacteria, efflux systems of *Escherichia coli* and *Salmonella enterica* ser. Typhimurium have been studied most extensively. Few efflux systems that belong to different families have been reported for *S. marcescens*. In this review, we analyzed available literature about *S. marcescens* efflux systems and carried out the comparative analysis of the genes encoding the RND type systems in different *Serratia* species and in other enterobacteria. Bioinformatical analysis of the *S. marcescens* genome allowed us to identify the previously unknown efflux systems based on their homology with the relevant *E. coli* genes. Identification of additional efflux systems in *S. marcescens* genome will promote our understanding of the physiology of these bacteria, will detect new molecular mechanisms of resistance, and will reveal their resistance potential. © 2013 Pleiades Publishing, Ltd.

<http://dx.doi.org/10.1134/S0026261714010093>

Keywords

antibiotic resistance, bioinformatical analysis, efflux pumps, orthologous genes, *Serratia marcescens*