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Inactivation of Chromosomal Genes in *Serratia marcescens*

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Abstract

© 2016, Springer Science+Business Media New York. Gram-negative bacterium *Serratia marcescens* is a well-known environmental microorganism and the accepted clinical pathogen causing nosocomial infections. It attracts more attention in recent years due to the emergence of strains with multiple drug resistance. Standard recombinant techniques are difficult to apply to *S. marcescens* due to the presence of numerous hydrolytic enzymes, in particular, extracellular nuclease and restriction endonuclease, which degrade transforming DNAs. We overcame this obstacle by utilizing restrictionless nuclease-deficient mutant strain *S. marcescens* TT392. As a proof of principle, in this genetic background, we generated a knockout strain with deletion of *macAB* locus using lambda red technology. The resulting mutation could be easily moved to a new genetic background by generalized phage transduction. This strategy provides a good tool for evaluation of *S. marcescens* pathogenic potential.

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Keywords

Efflux pump, Lambda red recombinase, MacAB, PCR, *Serratia marcescens*