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# Genomic organization of serratiochelin cluster in the environmental and clinical strains of *Serratia marcescens*

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*Motivation and Aim*: Bacterial siderophores are small secondary metabolites with a strong ferric iron-binding capacity. Availability of iron in the mammal hosts during infection is extremely limited for support of bacterial survival. The non-ribosomal peptide synthetase (NRPS) – mediated combinatorial biosynthesis of siderophores is induced by the iron starvation and functions to replenish iron supply in the bacterial cells [1]. Thus, siderophores play an essential role as a virulence factor of pathogenic bacteria. A goal of this study was to identify the serratiochelin gene cluster in the genomes of the environmental and clinical strains of *S. marcescens,* SM6 and SR 41-8000.
*Methods and Algorithms*: *S. marcescens* genomes were analyzed for the presence of siderophores-encoding gene clusters using AntiSmash software and using RAST platform for gene annotation [2].
*Results*: Genome analysis of *S. marcescens* strains Sm6 and SR41-8000 showed the presence of NRPS modules SM6_200-203 and SR41_3114-3117, respectively. Closely related bacteria *Serratia* sp. V4 was recently showed to synthetize siderophores serratiochelines A, B and C [3]. The BLAST analysis of amino acid sequences of identified NRPS *S. marcescens* SM6 and SR 41-8000 against serratiochelin NRPS *Serratia* sp. V4 demonstrated a high homology. However, a comparison of *Serratia* sp. V4 serratiochelin cluster organization with clusters, identified in *S. marcescens* SM6 and SR 41-8000 strains revealed significant differences.
*Conclusion*: Both strains *S. marcescens* SM6 and SR 41-8000 encode NRPS needed for serratiochelin production. The organization of serratiochelin gene clusters in environmental and clinical strains of *S. marcescens* differs from *Serrati a* sp. V4.
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