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ANALYSIS OF *STENOTROPHOMONAS MALTOPHILIA* ANTIPHAGE DEFENSE SYSTEMS*

G. Jdeed¹, V. V. Morozova², N. V. Tikunova²

¹Novosibirsk State University

²Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk

✉ghadeerjdeen@outlook.com

Abstract

Stenotrophomonas maltophilia exhibits intrinsic high-level of resistance to a variety of antibiotics and is an opportunistic pathogen, the World Health Organization lists it as one of the leading drug-resistant pathogens in hospitals worldwide. With the rise of antibiotic resistance, bacteriophages appear to be the promising alternative.

Bacteria have developed a wide array of diverse anti-phage defense mechanism. The goal of the research was to conduct a pangenome analysis of locally and globally sequenced *S. maltophilia* strains in search for anti-phage defense systems, their integration hotspots and their level of conservation.

Pangenome analysis of 72 complete *S. maltophilia* strains genomes revealed a high level of heterogeneity with shared genes present in all strains constituting 4% of all genes.

A total of 71 diverse antiphage defense systems and subsystems were found in *S. maltophilia* complex. The systems varied widely among the strains with the most commons ones being Wadjet type I, which is suggested to be anti-foreign DNA in the form of plasmids or phage ssDNA, followed by restriction modification system type II, then Gabija system and the restriction modification systems (RM type IV, RM type I and RM type IIG), respectively. Interestingly, complete CRISPR/Cas systems were rarely found (8% of studied strains) (Fig. 1), compared with their general percentage of distribution among bacteria (42%). Only Wadjet I and AbiE 4 were found to be highly conserved, while the other systems were very variable among different strains (Fig. 2).

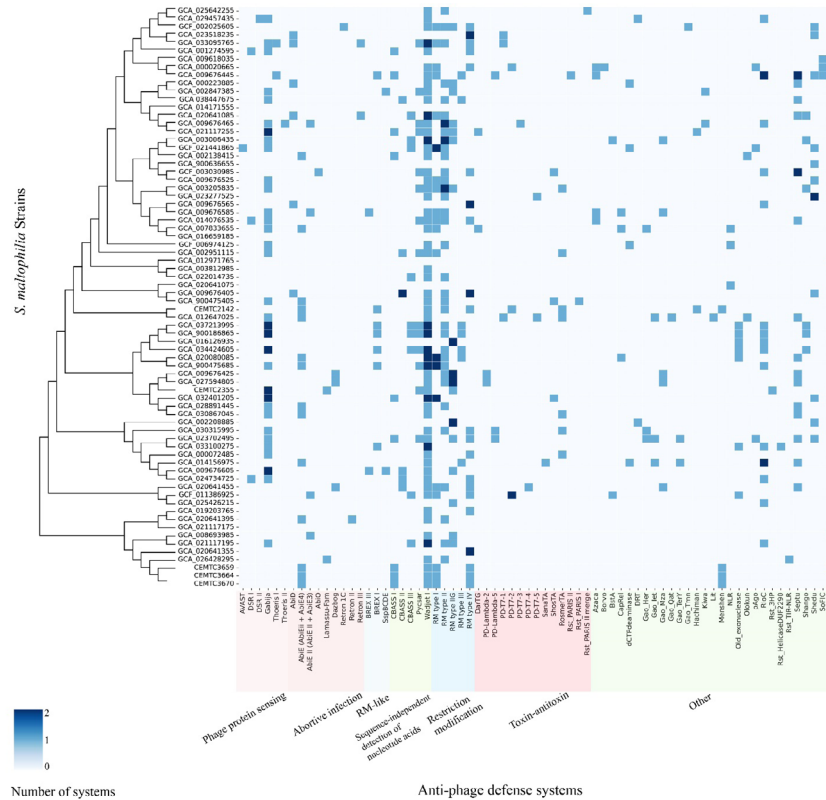


Fig. 1. Distribution of anti-phage defense systems in *S. maltophilia*

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Fig. 2. Conservation of genes constituting anti-phage defense systems in *S. maltophilia*

The anti-phage defense systems were found to be distributed in fixed integration sites across the studied strain, 28 integration sites were found, 4 of them contained more than 50 % of the instances of the anti-phage defense systems (Fig. 3).

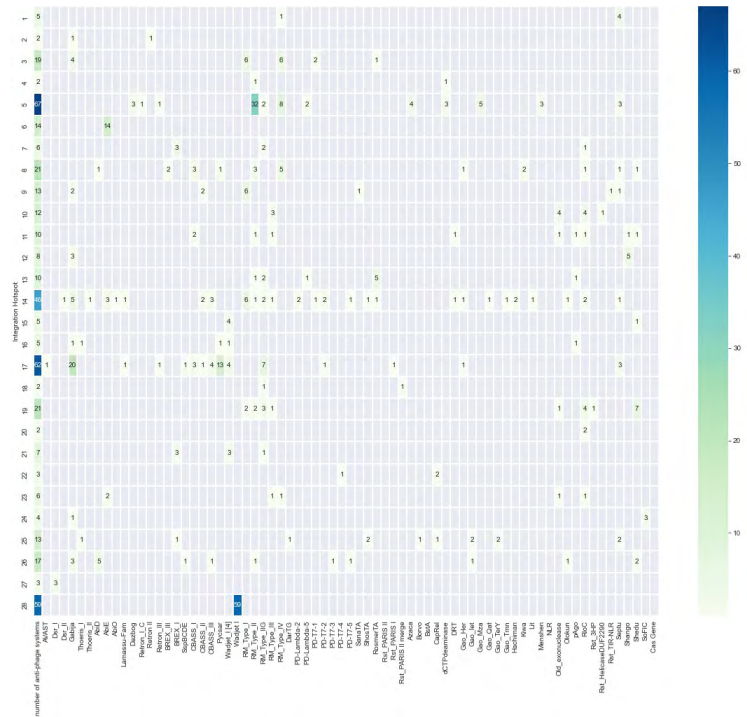


Fig. 3. Integration sites of anti-phage defense systems in *S. maltophilia*