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Pangenome analysis of *Stenotrophomonas maltophilia* antiphage defence systems

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Motivation and Aim: *S. maltophilia* is a highly heterogeneous species known for its ability to adapt to various environments [1, 2]. The study aimed to investigate the distribution and conservation of antiphage defense systems in five newly isolated *S. maltophilia* strains from different ecosystems in Novosibirsk, Russia, and compare them with other available *S. maltophilia* strains in the NCBI GenBank.

Methods and Algorithms: The genomes of the isolated strains were assembled and processed using SPAdes [3] and Ragtag [4] among other tools, searching for antiphage defense systems was done using defense-finder [5], determining conservation was done using MUSCLE alignment [6] with additional calculations, searching for prophages and CRISPR/Cas systems was done using Phigaro [7] and CRISPR/Cas Finder [8], respectively, pangenome analysis was done mainly using Roary [9].

Results: The results showed that the five locally sequenced *S. maltophilia* strains shared 65 % of their genes, compared to 4 % shared among most strains in the pangenome matrix. Only 8 % of the studied strains had complete CRISPR/Cas systems, which is lower than the general distribution in bacteria (42 %) [10]. A total of 72 different antiphage systems and subsystems were identified, with the anti ssDNA phages Wadjet I system, restriction modification systems, Gabija system with endonuclease activity, and the abortive infection system AbiE 4 being the most common (Fig. 1). The distribution of these systems did not follow a trend related to the site of isolation of the strains or their evolutionary history, suggesting that the acquisition of these systems is linked to the presence of phages and other bacterial strains in the microecosystems. Most of the widely distributed systems were highly variable, except for Wadjet I and AbiE, which were conserved, the essential *JetD* gene of the topoisomerase IV activity was absent from half Wadjet I systems, suggesting that those systems are inactive [17] (Fig. 2).

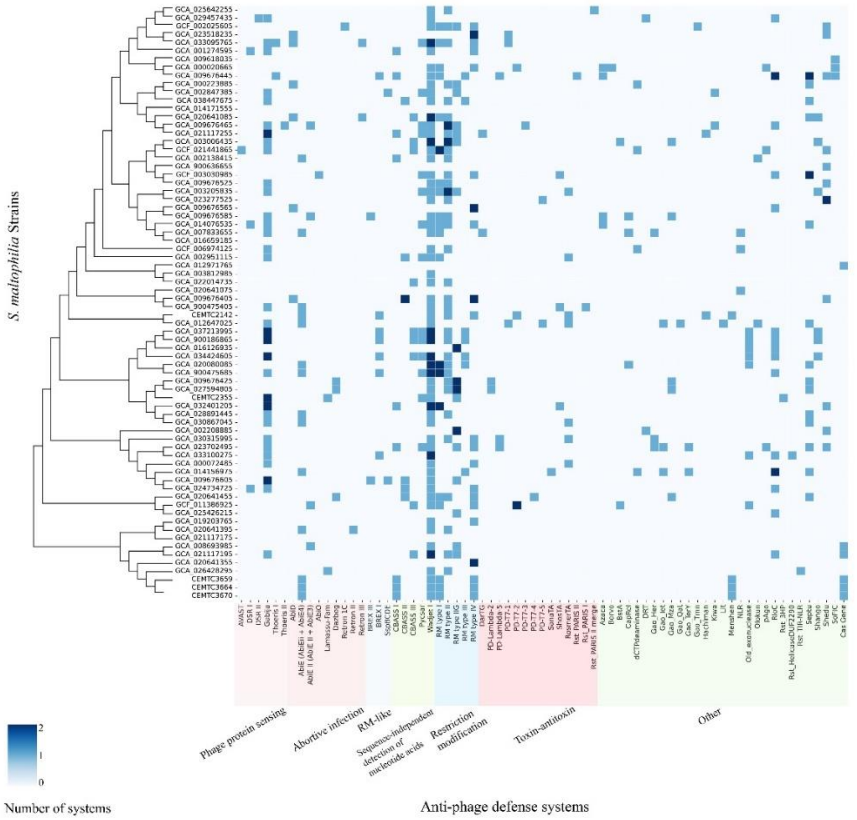

Fig. 1. Antiphage defense systems found in 71 *S. maltophilia* strains and their classification

Fig. 2. Conservation of *S. maltophilia* antiphage defense systems

Conclusion: Antiphage defense systems are widely variable among *S. maltophilia* strains, studying them helps determining one of the factors that determine the efficiency of utilizing phages in therapy.

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