ANALYSIS OF PUTATIVE BETA-LACTAMASES FROM OPPORTUNISTIC PATHOGEN STENOTROPHOMONAS MALTOPHILIA

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In recent decades rapidly increasing bacteria resistance to commonly used antibiotics has become an urgent healthcare challenge, especially affecting individuals with compromised immune system [1]. Opportunistic multidrug-resistant gram-negative bacterium *Stenotrophomonas maltophilia* has gained prominence due to challenging infections and resistance to commonly used antibiotics. Although *S. maltophilia* resistance to clinically important beta-lactam antibiotics is well-observed, only two beta-lactamases L1 and L2 are currently documented and described [2]. Initial research of beta-lactam resistant *S. maltophilia* SM3 strain indicated that other previously undescribed genes might code beta-lactamases.

The aim of this study is to analyse putative *S. maltophilia* beta-lactamases and evaluate their enzymatic activity. Putative beta-lactamases were bioinformatically analysed using Beta-Lactamase DataBase [3]. In order to test selected putative beta-lactamases function, analysed genes will be cloned into expression plasmid, functional activity will be examined in *Escherichia coli* expression strain using beta-lactamase activity specific nitrocefin test.

The bioinformatic analysis showed that ten analysed proteins are homologous to known beta-lactamases, proteins identity reaching 24.8% to 29.5%. The methodology for detecting enzymatic beta-lactamase activity was successfully tested on a known beta-lactamase L1 and functional activity of remaining putative beta-lactamases will be evaluated using the same approach.

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[2] Lin et al. (2009). The role of AmpR in regulation of L1 and L2 beta-lactamases in Stenotrophomonas maltophilia. Research in Microbiology, 160(2), 152–158.

[3] Naas et al., Beta-Lactamase DataBase (BLDB) - Structure and Function. J. Enzyme Inhib. Med. Chem. 2017, 32, 917-919.