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Summary of PhD thesis entitled: "Identification and differentiation of *Proteus mirabilis*, *Pseudomonas aeruginosa* strains and bacteria from selected environments by genetic and spectroscopic methods".

The research hypothesis of the presented dissertation assumes that the infrared spectra of bacterial cells contain information that would allow for the clonal differentiation of bacterial strains.

As a research model, a collection of laboratory and clinical *Proteus mirabilis* strains and an international panel *Pseudomonas aeruginosa* strains were selected.

The current state of knowledge on the use of infrared spectroscopy and selected molecular methods in microbiological diagnostics, the chemometric methods used in the analysis of spectroscopic data and the pathogenicity of *Proteus mirabilis* and *Pseudomonas aeruginosa* are described.

The chapter devoted to the results of own research is divided into subsections. The first one deals with the optimization of infrared spectra of bacterial colonies and the evaluation of the diversity of IR spectra of *Proteus mirabilis* strains based on the value of index D. In the second subsection there is a comparison of mathematical analysis of IR spectra of bacterial strains. Based on the results obtained, a range of 1200-900 $cm^{-1}$ wave numbers characteristic of sugars for further investigation was chosen. In the third subsection, the methodology developed was used to analyze IR spectra of 32 laboratory *Proteus mirabilis* strains. In the fourth, based on the mathematical modeling of laboratory strains, IR spectra of 14 clinical *P. mirabilis* strains, isolated from human urinary tract infection, were compared in order to a degree of phenotypic diversity. For comparison, different spectral analysis methods were used, such as hierarchical cluster analysis, D index, random forest method, and self-organizing Kohon maps. By at least three chemometric methods, eight *Proteus mirabilis* clinical strains (104, 144, 1685, 1995, 2108, 3950, 542, 670) have been classified in a specific serogroup of laboratory strains. Results for six clinical strains (1674, 1693, 4619, 852, 817, 853), two of the four techniques used were identical. Subsection 5 shows the use of infrared spectroscopy for the analysis of bacterial endotoxins. Subsection 6 presents the chemometric analysis of IR spectra of the *Pseudomonas aeruginosa* strains using hierarchical cluster analysis. In Sections 7 and 8, two independent molecular methods, RAPD PCR and MLST,

were used for the genotyping of *Pseudomonas aeruginosa* strains. Subsection 9 describes an attempt to differentiate *Pseudomonas aeruginosa* strains isolated from patients with CF from isolated strains from other sources (environmental strains and other clinical strains) using the random forest method and linear discriminant analysis. The best correlation of grouping *of P. aeruginosa* strains to their isolation sources was obtained by analyzing the entire range of IR spectrum by random forest method.

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