METABOLIC AND GENOMIC DISSIMILARITIES OF *PRIESTIA ENDOPHYTICA* STRAINS, FLUORESCENT PIGMENT PRODUCERS

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Bacteria within a single species may contain populations that have significant phenotypic variations even under the same culture conditions, and this is determined by genetic polymorphism. However, such genetic variability for certain species may be high (e.g., *Bacillus subtilis*) or low (e.g., *Mycobacterium bovis*). In previous works, we isolated 11 strains of aerobic spore-forming bacteria from different ecological niches and geographical areas. According to their physiological and biochemical characteristics and the ability to synthesize pink fluorescent pigments, they were similar to the 3 strains of *Priestia endophytica* (*Bacillus endophyticus*) from the Ukrainian Collection of Microorganisms of D.K. Zabolotny Institute of Microbiology and Virology of the NAS of Ukraine. This study aimed to determine metabolic and genetic dissimilarities between *Priestia endophytica* strains.

In our research, we used a number of classical and modern research methods: microbiological and biochemical methods, gas chromatography with mass detection, molecular genetic methods, and statistical data analysis. We found that the total fatty acid composition of all strains was almost identical, which indicated a high probability of them belonging to one species. Molecular genetic analysis of 16S rRNA gene fragments of *P. endophytica* UCM B-5715 typical strain and CHAES 2/3 strain showed that their sequences were identical. Nevertheless, we revealed quite a significant variability in colonies morphology between strains grown on one of the nutrient media (King A and LB). Moreover, the same strain expressed colonies of varying morphology on different media. Examining metabolic profiles, we noticed significant differences in the quantitative composition of metabolites. Furthermore, we observed a significant metabolic shift in different media for each strain. Orthogonal partial least squares analysis demonstrated that the metabolic dissimilarities between strains are partially due to the ecological niches from which they were isolated. To confirm the genome polymorphism of these strains, we performed ISSR-PCR analysis. According to the results, we found that only 1 of the 8 primers used gave a product that contained differences between strains. This outcome indicates a low level of strains' genetic variability. In respect of the results obtained, we hypothesize that significant differences in colony morphology, pigment synthesis, and metabolic profiles between strains are likely to stem from epigenetic mechanisms rather than genome polymorphism.