

Data reported over the last decade have revealed the importance of the environment to bacterial diversification and evolution. In particular, soil creates favorable conditions for bacteria diversification due to its heterogeneity in nutrients, particle size, pH, humidity, and microbiota. Meanwhile, soil is the primary niche for bacteria of the *Bacillus cereus* group, also named *Bacillus cereus sensu lato*. The group covers Gram-positive aerobic bacilli of which those of the highest economic, medical and ecological significance are *B. thuringiensis*, an entomopathogen, *B. cereus sensu stricto* (*B. cereus*) causing occasionally gastrointestinal infections and intoxications, and *B. anthracis*, the etiological agent of anthrax (not isolated by us in over a 15-year study). *B. cereus s.l.* contains also psychrotolerant *B. weihenstephanensis*, which can soil food products kept at low temperature, as well as *B. pseudomycooides* and *B. mycooides*, named together as *B. mycooides*, that form rhizoidal colonies on nutrient agar plates and produce metabolites that promote the growth of conifers. Recently, other two species have been separated from *B. cereus*: *B. cytotoxicus* causing severe infections and *B. toyenensis* used as probiotic in animal feed.

Whereas the main interest in these bacteria is focused on their pathogenicity or industrial applications, e.g. the extensive usage as an environmentally friendly biopesticides and probiotics, the ecological aspects have been poorly characterized. In this regards, highly significant and informative are our previous study, in which we demonstrated (i) on one hand a high genetic polymorphism of soil *B. cereus s.l.*, isolates as exemplified by the number of different sequencing types of house-keeping genes, and (ii) on the other hand a limited number of common genetic types between strains originating from distinct environments and classified into particular species. In this regard, of particular importance was the statistically significant abundance of distinct genetic types within bacilli from Białowieża National Park (BNP), when compared to those from Biebrza National Park and an agriculture soil. The scientific problem is whether there is any dependency between *B. cereus s.l.* complete genomes, metabolic properties and the environment. The explanation of this issue requires investigation of dynamics of pangenomes (genes present in all strains under study, e.g. one population or one *B. cereus s.l.* species) and proteomes of these bacilli originated from highly diverse environments, such as an area protected from human activity and an area anthropologically changed. For this reason we will study of *B. cereus s.l.* from organic soil of BNP, the last European natural forest with a primeval character and limited human activity, and the agricultural soil (mineral soil) in Jasienowka, a small village south of Podlasie province. The global objective of this project is to find a dependency(s) between the dynamics of pangenomes and proteomes of *B. cereus s.l.* and their environments. It is highly likely that the proportion of core genes (present in all bacteria) and other genes could be indicative of a correlation between strains origin (environmental habitat) and their metabolomes.

The proposal aimed to verify the following hypothesis: (H1) Pangenomes of *B. cereus s.l.* from the environments affected by human activity are less polymorphic than the pangenomes of bacteria isolated form environment of the primeval character. (H2) Within environmental *B. cereus s.l.* are present metabolic ecotypes, which are correlated with the level of nutrients and the physic-chemical properties of their habitat, and the ecotypes arise from the sum of properties encoded chromosomally and by plasmids. The hypotheses will be tested with *B. cereus*, *B. weihenstephanensis*, *B. thuringiensis*, and *Bacillus mycooides* already isolated and genetically typed during implementation of the previous project. At first stage we will select ~30-40 strains for pangenomic and proteomic analysis, representing different metabolic ecotypes. Then, we will determine their complete genomes using next generation sequencing (NGS) and plasmid profiles. The NGS results will be subjected to bioinformatics analysis in order to assess pangenome composition. From the perspective of the main goal of the project, special value will have the determination of the core genes (present in all isolates) and alternative genes. In order to have a boarder view on *B. cereus s.l.* pangenome composition, genomes available at sequence data bases be added into analysis. In parallel we will evaluate plasmid types by indicating metabolic, virulence, conjugative, and cryptic plasmids. The last stage of the project covers proteomic analysis of whole and extracellularly extracted proteins (secretomes) of *B. cereus s.l.* and response of the bacilli to environmental factors.

The project has a pioneering characteristic in attempting to define the ecology of the *B. cereus* group. Considering the importance of *these* bacilli in agriculture (biopesticides), medicine (food intoxication, intestinal infections), and food industries (probiotics; food spoilage), the results of the proposed project will influence many aspects of human life and will have societal impact. Among many others, the project may have impact in understanding the role of human on preservation of microbiological diversity and function of natural ecosystems. From a more global perspective, the project will not only transform the understanding of the *B. cereus s.l.* ecology, but will be relevant to different scientific fields, including Microbial Ecology, Landscape Ecology, Evolution and Development Biology.