

Tytuł: „Genomics, phenotypic characterisation and microbiome analysis of edible cyanobacteria from *Arthrospira* genus”

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Dziedzina: Nauki Biologiczne

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Abstract

Introduction: Cyanobacteria are extremophilic, photosynthetic, cosmopolitan, pioneering organisms. *Arthrospira* is a member of cyanobacteria phylum, filamentous, free-floating or mat-making prokaryote typically inhabiting haloalkaline water-bodies in the tropical and subtropical climate. The possible industrial applications, e.g. consumption as supplement of a diet, production of edible pigments or various chemicals, made *Arthrospira* a subject of multiple studies. Thus far, based on the morphology and geographical origin criteria there has been over 20 species of *Arthrospira* described. The genetic studies conducted so far indicated the division of the genus into two or three clades. However, due to the turbulent history of cyanobacteria there has been no update in the taxonomy and nomenclature following those observations.

Aims: (1) Genomic characterisation of the *Arthrospira* genus based on the five introduced in the frame of this work and the eight publicly available genomes, (2) investigation of the change in the biomass of *Arthrospira* composition under the influence of chosen stress using phenomics approach, (3) analysis of the Arthrobiome: *Arthrospira*-associated bacteria diversity

Results and Conclusions: In the frame of this work five new *Arthrospira* genomes were sequenced, assembled and annotated. One of the genome sequences derived from the newly isolated Siberian strain - O9.13F possessing the mosaic structure of ITS sequence (I.B/III). Upon completing the genome sequences pool by missing genotypes (established based on ITS sequence) the phylogenetic analyses following the classical approach for cyanobacteria (based on sequences of 16S rRNA, ITS and *cpBA*-IGS) and phylogenomics were performed. The results of the single gene phylogeny were convergent with previous analyses and they indicated the division of *Arthrospira* genus into three clades. However, due to the observed possibility of recombination and horizontal gene transfer the results between different markers showed discrepancies. The whole genome-based phylogeny methods - ANI and *isDDH*, as well as, the phylogenetic tree constructed based on most conserved proteins, split the genus into two species corresponding to ITS clusters I+III (clade I) and II (clade II), with possible subspecies, abiding the thresholds (when applicable). This result was also supported by the pan-genome analysis revealing a higher level of similarities within the clades, rather than

between them. The fatty acids profiles of 15 *Arthrospira* strains were strain-specific and not showing any trend, which would allow for species distinction. Therefore the FA profiles did not complement the phylogenetic analyses. The change in temperature of cultivation did not influence the individual fatty acids ratio but the rise in the salinity of the medium caused a decrease in the percentage of γ -linolenic acid in favour of palmitic and cis-vaccenic acids. The study of the biodiversity of *Arthrospira*-associated bacteria, based on fresh, commercial and lyophilised biomass samples showed high convergence of the revealed bacteria with those found in the natural niche of this organism. From different laboratory cultures of *Arthrospira* five bacterial isolates were selected for genomes sequencing. One of those isolates was subjected to additional analyses and a proposal of the new genus - *Arthrospirobacter rubrum* gen. nov., sp. nov. was presented.