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ABSTRACT BOOK



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Genome-Resolved Taxonomic and Functional Characterisation of the Genus *Limnospira*

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The cyanobacterial genus *Limnospira* comprises economically important species that are cultivated under the commercial name “Spirulina”. Despite being based on both single-marker gene and recent whole-genome analyses, the clear delineation of species and functions within the genus remains a matter of debate. This study presents the results of a taxonomic assessment and metabolic annotation of two new *L. platensis* and *L. maxima* genomes, compared to a selection of high-quality genomes obtained from the Genome Taxonomy Database and GenBank. Average nucleotide and amino acid identities (ANI and AAI) and digital DNA–DNA hybridisation values (dDDH) revealed distinct differences between the two species, which were further confirmed by phylogenomic and pangenomic analyses. While the two species shared a broadly similar core cyanobacterial metabolism, striking differences were related to the exclusive enrichment of dispensable genes associated, among others, with defence mechanisms, transposons, prophage-derived genes, and signal transduction systems, indicating different evolutionary pathways. Analyses carried out using liquid chromatography–mass spectrometry (LC-MS) on the two *Limnospira* strains confirmed the absence of the main legacy cyanotoxins, including several microcystin congeners, nodularin-R, anabaenopeptin-A, anatoxin-a, homoanatoxin-a, dihydroanatoxin-a, cylindrospermopsins and saxitoxins. Annotation of all the *Limnospira* species included in the analysis confirmed the absence of biosynthetic gene clusters (BGCs) encoding legacy cyanotoxins. Conversely, a few other classes of BGCs, including cyanobactins, were identified across the entire genome set. Furthermore, annotation revealed the presence of metabolic pathways associated with the biosynthesis of many bioactive compounds and nutraceuticals, including several vitamins, antioxidants, photosynthetic pigments (such as phycocyanin) and quinones, among others. Comparative genomics supports *L. platensis* and *L. maxima* as distinct species with conserved core metabolism, while species-specific enrichments in defence, mobile elements and signalling indicate divergent evolution. The absence of cyanotoxins, combined with the presence of widespread vitamin, antioxidant and pigment biosynthetic pathways, underscores their high nutraceutical potential and safety.

Keywords: *Limnospira*; Metagenomics; Metabolomics; Phylogenomics; Pangenomics.