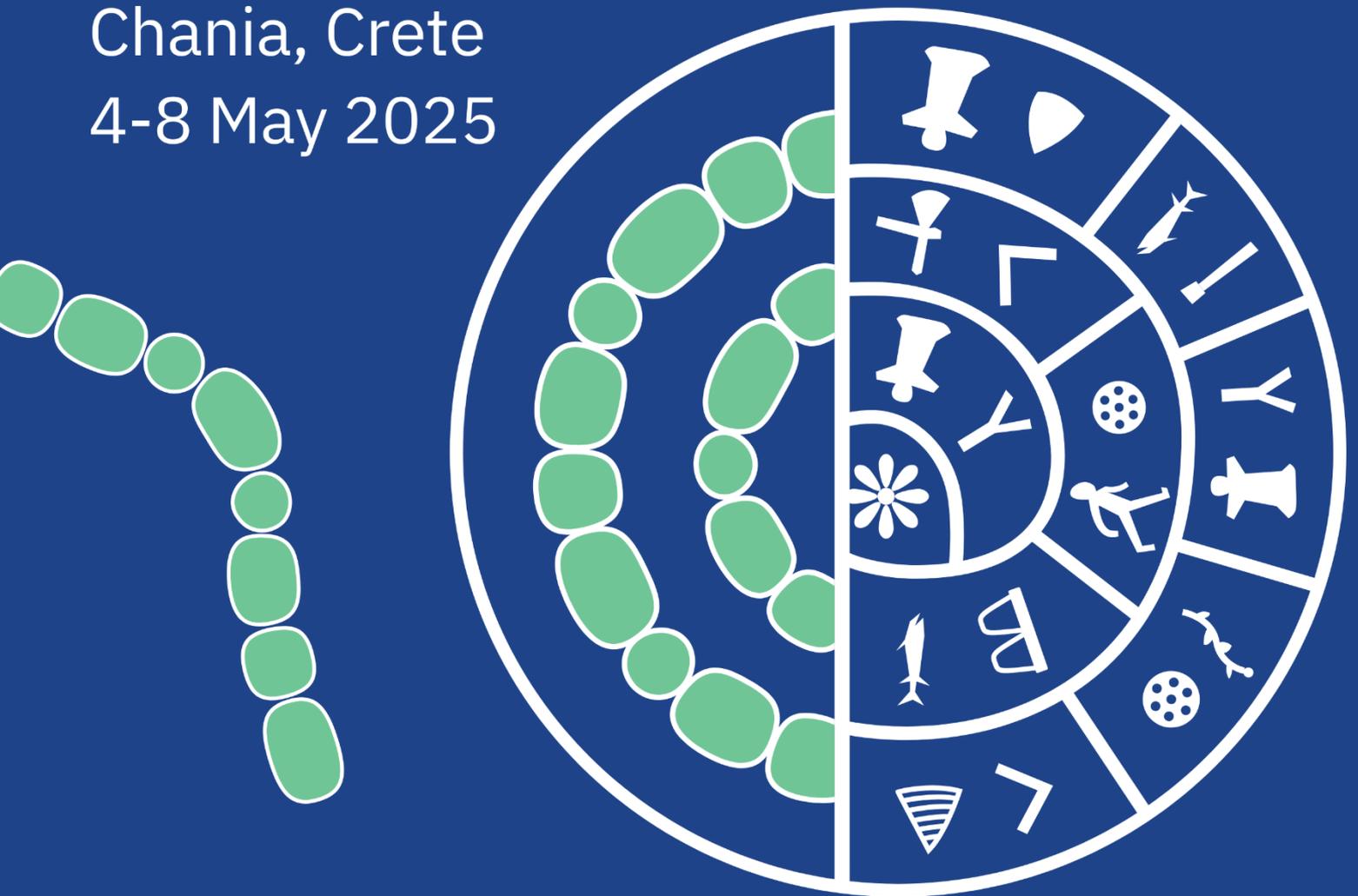# 13th International Conference on toxic cyanobacteria

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ABSTRACT BOOK

INVITED TALK

Taxonomic and functional metagenomic assessment of cyanobacteria

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The sequencing and use of single marker genes and the adoption of a polyphasic approach represented a major historical advance in the taxonomy and study of cyanobacteria. Currently, these approaches are still widely used and are helping to fill gaps in the taxonomy, geographic distribution and toxicity of cyanobacterial strains. However, these approaches have important bottlenecks that limit analyses to isolated and cultured specimens, single individuals or colonies, and monospecific environmental samples. In the last decade, the advent of innovative technological methods, particularly the increased use of high-throughput sequencing, has led to important advances in the study of microbial communities. The increasing use of amplicon sequencing approaches (metabarcoding) has paved the way for the study of microbial communities in environmental samples and has rapidly become a mature and de facto standard in many laboratories. However, metabarcoding for the identification of bacteria and cyanobacteria has several drawbacks, mainly due to the short length and resulting low taxonomic resolution of the 16S rRNA gene after bioinformatic processing (around 400 bp), which mostly limits classification to the genus level. Recent improvements in this approach (selection of non-ribosomal marker genes and sequencing of 16S rRNA long reads) have not broadened the scope of this approach, which remains limited to the taxonomic classification of microbial communities. A breakthrough has been the implementation of genomic and metagenomic methods, either based on short read assembly (whole genome shotgun sequencing) or long read assembly (Pacific Biosciences-PacBIO and Oxford Nanopore Technologies-ONT), which allow the reconstruction of draft or circular cyanobacterial genomes. These techniques are being applied to a wide range of samples (from isolates to complex microbial communities), providing information at the strain level and on species metabolic functions and community functioning following genome annotation. At the taxonomic level, the calculation of average nucleotide identity (ANI) and/or digital DNA-DNA hybridisation (dDDH) values, complemented by phylogenomic analyses based on the selection of single-copy marker genes or (from pangenomic analyses) single-copy core genes, represent an increasingly adopted approach for genome-based species delineation and evolutionary relationships among cyanobacteria. Overall, the study of cyanobacterial taxonomy and ecology is undergoing rapid and extensive development. These changes will be critically discussed by reporting on specific case studies from ongoing research and literature, highlighting the drawbacks and limitations as well as the prospects for development of the different approaches used in the modern study of cyanobacteria.

Keywords: metabarcoding, full shotgun sequencing, long-read sequencing, taxonomic classification, genome annotation