

## VII BIENNIAL CONGRESS OF SESBE SEVILLE, 5-7 FEBRUARY 2020

**S5.O.4** 

## Progressive genome evolution in Cyanobacteria

Andrés Moya<sup>1;2;3</sup>; José L. Oliver<sup>4;5</sup>; Miguel Verdú<sup>6</sup>; Luis Delaye<sup>7</sup>; Vicente Arnau<sup>1</sup>; Pedro Bernaola-Galván<sup>8</sup>; Rebeca de la Fuente<sup>9</sup>; Wladimiro Díaz<sup>1</sup>; Francisco M. González<sup>7</sup>; Amparo Latorre<sup>1,2,3</sup>; Ricardo Lebrón<sup>4,5</sup>; Ramón Román-Roldán<sup>10</sup>; Sixto Santamaría<sup>1</sup>

(1) Institute of Integrative Systems Biology (I2Sysbio), University of València and Consejo Superior de Investigaciones Científicas (CSIC); (2) Foundation for the Promotion of Sanitary and Biomedical Research of Valencian Community (FISABIO); (3) CIBER in Epidemiology and Public Health; (4) Department of Genetics, Faculty of Sciences, University of Granada; (5) Laboratory of Bioinformatics, Institute of Biotechnology, Center of Biomedical Research; (6) Centro de Investigaciones sobre Desertificación, Consejo Superior de Investigaciones Científicas (CSIC), University of València and Generalitat Valenciana; (7) Department of Genetic Engineering, CINVESTAV, México; (8) Department of Applied Physics II and Institute Carlos I for Theoretical and Computational Physics, University of Málaga; (9) Institute for Cross-Disciplinary Physics and Complex Systems, University of Balearic Islands and CSIC; (10) Department of Applied Physics, University of Granada

andres.moya@uv.es

Progressive evolution, the tendency towards increasing complexity, is a controversial issue in Biology, whose resolution requires the proper measurement of complexity. To address this challenge, we consider that genomes are the best entities to measure complexity because they record the history and information gain of organisms in their ongoing biotic and environmental interactions. By recurring to six metrics that measure genome complexity, which are not primarily associated to functionality, we report the existence of progressive evolution towards higher genome complexity in the evolution of the *Cyanobacteria phylum*. We show that these complexity metrics plus three additional genome parameters present statistically significant phylogenetic signal in Cyanobacteria. Moreover, a ridge regression of genome complexity metrics against evolutionary age shows that three out of six present a positively driven evolutionary trend towards higher complexity. These findings support the existence of progressive genome evolution in this ancient and diverse group of organisms.