The Species Concept in the Genomic Era

Supported by the Bergey's Manual Trust and Organized by ICSP

12:30 - 14:25 Hall C

In the late 1980s, the International Committee on Systematic Bacteriology recommended that the complete DNA sequence of the genome would be the reference standard in bacterial taxonomy. It was further emphasized that phylogenetically-based taxonomic schemes must also show phenotypic consistency. At the time, genome sequencing was not yet feasible, and over the last two decades prokaryotic species were primarily based on DNA: DNA hybridization and 16S rRNA gene analysis supplemented with phenotypic characterization in a polyphasic approach. Recently, the prokaryotic species concept is being challenged by the development of whole genome sequencing, which enables other methodologies for determining DNA sequence similarity.

Four expert speakers will discuss these developments and the challenges and questions that bacterial taxonomists are facing today.

A broad spectrum of ideas will be presented on the problems related to the taxonomy of the specific organisms they study and means to solve the difficulties encountered in these groups.

Chairpersons: Milton S. Da Costa, Portugal
Lenie Dijkshoorn, Netherlands

Speakers:

- **Genome sequences as nomenclatural type material for novel taxa**
  William Whitman (USA)
- **Applying an evolution-based species concept for the delineation of bacterial species: The Pantoea example**
  Stephanus Venter (South Africa)
- **Towards a harmonized classification embracing cultured and uncultured taxa**
  Ramon Rosselló-Móra (Spain)
- **Type species in the genomic era of Mollicutes**
  Daniel Brown (USA)