Towards a pragmatic and stable taxonomy of prokaryotes

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Abstract
The taxonomy of prokaryotes is facing a fascinating period in where the high-speed of molecular approaches and bioinformatic tools contrast with the apparent stagnation on the activities in classifying taxa. It is remarkable that the current sequencing capabilities and in silico data analysis allow the determination of single species genomes, in form of metagenome assembled genomes (MAGs) containing taxonomic information of almost the same quality as many published genomes of pure cultures [1]. Since the mid 1960’s genome comparisons had influenced how species are circumscribed, and phenotyping has been left as a residual, often non-informative part of the taxonomic classification [3]. These facts have brought taxonomists and molecular ecologists to advocate for a unified genome-based nomenclatural system, and therefore embracing both cultured and yet uncultured taxa by allowing DNA to become type material. This proposal was finally denied by the ICSP in April 1st [2]. We argue that a stable classification of prokaryotes with independence of pure cultures is feasible. We also argue that the genomic information retrieved from MAGs and Single Amplified Genomes (SAGs) is enough to classify cultivated and uncultured prokaryotes at the genus and species level. However, we believe that yet the most robust phylogenetic
framework to classify especially higher taxa is that based on the 16S rRNA gene. This approach has several advantages as (i) the unbeatable large collection of sequences (currently over 9 million), (ii) the highly informative and universal alignment based on the secondary structure (now improved up to ~100K positions); and (iii) the lack of problems derived from recognizing homology between distantly related taxa adding noise to the tree topology. We will present the latest novelties on the ARB-alignment, on the latest release of the LTP, as well as on the benefits and robustness of 16S rRNA approach. [1] Konstantinidis, K.T., Rossello-Mora, R., Amann, R. (2019) Advantages outweigh concerns about using genome sequence as type material for prokaryotic taxonomy. Environ. Microbiol. 22: 819-822 [2] Murray, A., Freudenstein, J., Gribaldo, S., Hatzenpichler, R., et al. (2020) Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiol. In Press.