



311 Ferst Drive ES&T, Room 3224
Atlanta, Georgia 30332
Office: 404.385.3628; Fax: 404.894.8266
Email: kostas@ce.gatech.edu
Lab: <http://enve-omics.gatech.edu/>

Kostas Konstantinidis, PhD

Assistant Professor

Department of Civil and Environmental Engineering,
Department of Biology (Adjunct),
Center for Bioinformatics and Computational Genomics

Microbial Taxonomy and Phylogeny: Extending from rRNAs to Genomes

Although the 16S rRNA gene has served successfully as the backbone of prokaryotic taxonomy to date, it has its limitations. The 16S rRNA gene does not offer robust resolution at the species level and it has occasionally undergone convergent evolution and (perhaps more rarely) horizontal gene transfer. In this presentation, I will summarize our efforts to develop new genomic approaches, such as the Average Nucleotide Identity (ANI), to evaluate the 16S rRNA-based phylogeny and replace the cumbersome techniques for classifying new organisms such as the DNA-DNA hybridization (DDH). Application of the ANI methodology to closely related organisms recovered from the same habitat revealed that natural microbial communities consist of discrete, sequence-defined populations of bacteria and archaea, with intra-population sequence relatedness of 95% ANI or higher, which corresponds to 70% DDH. The identification of discrete clusters, which may correspond to genuine species, contrasts with the notion that the processes driving diversification of bacteria do not necessarily produce sufficiently coherent groups of individuals (species). Extending the ANI approach to cover the whole bacterial domain revealed that the 16S rRNA-based phylogeny is robust but the higher ranks of taxonomy show, on average, 30% and up to \approx 50% overlap in terms of genetic relatedness, meaning that 30% of the pairs of organisms showing the exact same genetic distance to each other belong to different ranks. Further, only the 16S rRNA gene data clearly supports that the inter-phylum differences are larger than the inter-class differences. Improving such ambiguous taxonomic designations will require an international effort to re-evaluate these designations and the definition of phylum in light of the recent omics data. Only then will the promise for an advanced genomic taxonomy be realized.