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Genotype versus phenotype in the taxonomy of Prokaryotes – An example from the genus *Rhizobium* and the role of “Bergey’s Manual of Systematics of Bacteria and Archaea in modern Taxonomy”

Abstract:

Modern taxonomic approaches in microbiology aim at the establishment of a system that mirrors the evolution with the ultimate goal to describe the whole evolutionary order back to the origin of life. With the recognition of molecular markers present in all organisms (e.g. rRNAs, ssRNAs), this possibility has become more and more feasible and the generation of gene and increasing numbers of genome sequences allow now the generation of large amounts of data and a very detailed insight into the genetic potential of prokaryotes. The possibility to generate whole genome sequences leads to a strong tendency to base the taxonomic system more and more on sequence data, the genotype. However, the phenotype remains of major importance. Results of two *Rhizobium/Agrobacterium radiobacter* strains showing 99.8% average nucleotide identity with strong different ecological functions show this importance and point to the fact, that a comprehensive understanding of all the information behind sequence data is lagging far behind their accumulation. Genes and genomes may (or may not) function only in a given “environment”, with the cell as basic entity for the display of this potential.

A taxonomic encyclopedia like Bergey’s Manual of Systematics of Bacteria and Archaea may provide comprehensive informations not only for taxonomists but also for microbiology in general in this context.