

New wine in old skins: how flexible will bacterial taxonomy be in the (post)genomic era

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The history of bacterial systematics has witnessed a number of eras in which scientific achievements expanded the range of properties considered useful for identification and classification. Major phases of bacterial taxonomy were: from 1872 to 1900, influenced by botanists and medical microbiologists, resulting in the first descriptions of taxa based upon morphology; from 1900 to 1955 physiological properties were added, and taxonomic progress culminated in the seven editions of Bergey's Manual; from 1955-1980 numerical taxonomy, chemotaxonomy and the first DNA-based methods were applied, the term 'polyphasic taxonomy' was introduced; from 1980 the hierarchic system was revolutionized, species descriptions were standardized, and molecular methods allowed a glimpse into the evolution of the construct 'species'. At all times novel methods, designed for different purposes, were scrutinized for their usefulness for taxonomy. Enthusiastic novelties were often followed by periods of reluctant acceptance and at the end many new methods were implemented, improving identification and classification. Only at the end of the 1970s bacterial taxonomy almost lacked this flexibility when a reconciliation working group had to reunite opposite directions. As older methods were rarely abandoned, the range of properties increased, as will be exemplified on the genus *Vibrio*. With the availability of a hierarchic framework, due to the comparison of homologous molecules, the branching pattern of the phylogenetic tree was used to delineate higher taxa - still, however, subject to man's subjective decision as taxa and ranks are the construct of the mind. So far, results of the genomic era have not really been a challenge to bacterial systematics. The first larger sequencing approach, MLSA, could be easily accommodated to delineate various ranks between species and family, though not, however, for the intraspecies subdivision, namely the ecotype concept. Unless supported by accompanying phenotypic properties apt to discriminate the individual ecotypes from each other the concept, exciting as it is, will be left outside taxonomic considerations. Another recently introduced method is the determination of the average amino acid identity (AAI) and the average nucleotide identity (ANI), two parameters resulting from pairwise genome comparisons by averaging the sequence identities of shared orthologous genes (amino acid or nucleotide, respectively). Still to be applied to a higher number of genomes both methods appear to be powerful enough to replace the laborious (and scientifically unsatisfying) DNA-DNA reassociation method and eventually, depending on the genes selected, the circumscription of higher taxa. The main problem, however, is an old problem: by applying the AAI approach to prokaryotic taxonomy ranks above species will be defined numerically, hence the same way the taxon species is defined today. A system defined as such may be 'objective' but not less artificial than the one present today, ignoring the fact that tempo and mode differ vastly among Archaea and Bacteria. But genomes deserve and offer more than averages of amino acids and nucleotides. The presence of commonly shared core genes, defined individually for each genus individually, may offer another strategy - one that would deviate from today's practice to define the taxon 'species' and higher taxa by the same yardstick. Whatever the future will bring, the conservative nature of taxonomy will prevent any hasty, negligent and premature implementation of novel ideas and concepts. The skin is still sufficiently durable to tolerate a certain degree of fermentation process.