

Report of the Ad Hoc Committee on Reconciliation of Approaches to Bacterial Systematics

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Bacterial taxonomy, which began as a largely intuitive process, has become increasingly objective with the advent of numerical taxonomy and techniques for the measurement of evolutionary divergence in the structure of semantides, i.e., large, information-bearing molecules such as nucleic acids and proteins. These developments have forced the adoption of changes in nomenclature, sometimes with disruptive or even perilous consequences (2). Since the present nomenclatural system evolved during a period when hierarchical taxonomic divisions were only vaguely defined, it has become important to reexamine that system in the light of newer taxonomic understanding. Accordingly, an ad hoc committee of the International Committee for Systematic Bacteriology was convened for a Workshop on Reconciliation of Approaches to Bacterial Systematics at the Institut Pasteur, Paris, on 14 to 16 May 1987.

Perspectives. To arrive at a common ground of understanding, the committee reviewed the current state of bacterial systematics from the following perspectives:

(i) **Phylogenetic.** Phylogenetic studies are directed at a basic understanding of pathways through which taxa have evolved from primordial and recent ancestors, calculated from analyses of evolutionary distances between selected semantides.

(ii) **Descriptive.** Descriptive research represents the bridge between semantide-based phylogenetic taxonomy and traditional phenotype-based bacterial systematics. Organisms are described in phenotypic terms, and the descriptions help define a taxonomic group that may also be recognized at the phylogenetic level.

(iii) **Diagnostic.** Diagnosis involves the selection of features from those in a phenotypic description, or of probes derived from phylogenetic analyses, in a way that permits the recognition of an unknown strain and the assignment of a label to it. The most useful labels for applied purposes are names at the genus, species, and subspecies levels; infrasubspecific categories that are not governed by the Bacteriological Code (1) may be useful for recognition of special attributes.

(iv) **Associative.** Associative studies use a name to evoke practical information about a strain, such as its medical, industrial, or ecologic significance.

The committee offers the following conclusions and recommendations.

HIERARCHICAL TAXONOMY

An ideal taxonomy would involve one system. A single formal overall system appears to be adequate, and a second system is not needed if vernacular grouping is retained for diagnostic purposes.

There was general agreement that the complete deoxyribonucleic acid (DNA) sequence would be the reference standard to determine phylogeny and that phylogeny should determine taxonomy. Furthermore, nomenclature should agree with (and reflect) genomic information.

The group agreed that hierarchical consistency is essential but recognized that the depth in a ribonucleic acid (RNA) dendrogram at which a given hierarchical line is to be drawn may vary along different major branches of the dendrogram and will be strongly influenced by phenotypic consistency at each level. This is a consequence of differences in ages of the different branches and the recognition that older branches will exhibit greater nucleic acid structural genetic drift, even as environmental constraints tend to limit phenotypic drift.

A cautionary note about hierarchical interpretation was expressed with the recommendation that active searches continue for additional powerful semantides independent of the ribosomal RNA cistrons.

The chemotaxonomic approach has two sets of derivative data: structural phenetic (including "signatures") and phylogenetic (evolutionary). There should not be further designation of hierarchical levels without substantial chemotaxonomic and sequence data to support the proposal.

Species, subspecies, and infrasubspecific categories. At present, the species is the only taxonomic unit that can be defined in phylogenetic terms. In practice, DNA reassociation approaches the sequence standard and represents the best applicable procedure at the present time. The phylogenetic definition of a species generally would include strains with approximately 70% or greater DNA-DNA relatedness and with 5°C or less ΔT_m . Both values must be considered. Phenotypic characteristics should agree with this definition and would be allowed to override the phylogenetic concept of species only in a few exceptional cases.

It is recommended that a distinct genospecies that cannot be differentiated from another genospecies on the basis of any known phenotypic property not be named until they can be differentiated by some phenotypic property.

Subspecies designations can be used for genetically close organisms that diverge in phenotype. There is some evi-

* Comments on the conclusions and recommendations included in this report are welcome and should be sent to Lawrence G. Wayne, Tuberculosis Research Laboratory(151), Veterans Administration Medical Center, 5901 East Seventh St., Long Beach, CA 90822.

dence, based on frequency distribution of ΔT_m values in DNA hybridization, that the subspecies concept is phylogenetically valid and can be distinguished from the infrasubspecific variety concept, which is based solely on selected "utility" attributes, but not demonstrable by DNA reassociation. *There is a need for further guidelines for designation of subspecies.*

Genera. Genera form the essential basis of bacterial systematics, and each genus must remain subject to continuing assessment. A degree of flexibility in circumscription is necessary. Unfortunately, there is currently no satisfactory phylogenetic definition of a genus. *The scope of the definition may differ among genera, as for any other higher taxa.*

Families. Families can be retained as long as they are consistent in terms of chemotaxonomic and hybridization or sequence data. Any other hierarchical level established between family and division must also be consistent in terms of supporting taxonomic data.

Divisions. It is clear that there are at least 15 clearly separated lineages of great antiquity in evolutionary terms at the level of division or greater.

Kingdom. There is no need at this time for more than one kingdom, but there may be need for a term to describe major primary lineages. A rank such as phylum may be needed in the future.

NOMENCLATURE

After a review of alternative approaches to the occasional conflict between binomials based on strict phylogenetic relationships at the species level and the practical application of the binomials, the following recommendations were made.

Nomenclature should reflect genomic relationships to the greatest extent possible. Rare exceptions are sanctioned under the emendation to Rule 56a embodied in Minute 7i of the Judicial Commission (Int. J. Syst. Bacteriol. 37:85-87, 1987), introducing the concept of a "nomen periculosum." It is anticipated that this concept need be applied in only a limited number of cases and hoped that this type of problem will disappear as new taxonomic methods and interpretations are more universally applied. *A mechanism is needed for broad dissemination of information about those cases where such nomenclatural discrepancies have been sanctioned.*

As needed, various vernacular appendices that pertain to needs for special purposes (medical, veterinary, agriculture, industry, etc.) including information about traits coded by plasmids, phages, and other extrachromosomal agents should be applied. These infrasubspecific "utility" categories are not governed by the Bacteriological Code. In certain medical situations, identification of the presence of certain virulence factors may be more important than the species name.

Regarding inadequate nomenclature, it is recommended that formal nomenclature is needed for the major divisional groupings. "Gram positives" should be Firmicutes as presently defined. The term "purple bacteria" causes confusion because it includes more than phototrophic bacteria, which is good reason for a formal name to be established.

OTHER CONCERNS

Special difficulties are expected in accomplishing the taxonomic reorganization of the major phylogenetic taxon

listed as "the purple photosynthetic bacteria and their relatives" (3), and this includes most of the classically defined gram-negative genera, both photosynthetic and chemosynthetic, in the alpha, beta, gamma, and delta groups of the purple bacteria. Thus, the major task of the greatest practical importance is the development of a taxonomic and nomenclatural approach to resolving the linked phylogenetic lineages of the remarkably diverse metabolic types of organisms within each of the groupings. Urgency is dictated by the large number of bacteria involved and by the many species that are crucial in ecological and diagnostic bacteriology. A number of genera must be reassessed, although many will persist in part, if not as a whole. There are gaps in our knowledge because the molecular/genetic surveys are incomplete. The first task is the definition and phylogenetic circumscription of the genera in this phylogenetic taxon, with inclusion of type strains of species in the genera. *It is recommended that this problem be assigned for special study by an ad hoc subcommittee of the International Committee on Systematic Bacteriology.*

Research should be directed toward solving the growth and diagnostic problems of noncultivable or hardly cultivable organisms, e.g., cholera somnificell, nongerminable endospores, and organisms not cultivable axenically but cultivable in multiorganism systems, such as representatives of consortia, *Pasteuria*, *Planctomyces*, etc. The Code may have to be emended to clarify the status of multiorganism cultures as type material; e.g., see Rule 18a and Advisory Note C, Chapter 4 (1).

A whole base line of bacterial taxonomy of various ecosystems is urgently needed, as is a broader knowledge of species distribution in ecosystems and improved knowledge of little known bacteria. ("Less than 20% of the bacteria are known.") Encouragement must be given to systematic studies and the search for new chemotaxonomic markers. Recognition of the importance of effective taxonomic understanding to all fields, basic and applied, and especially to biotechnology has been slow to develop, although the need is great. The group recognized, also, that ecologically relevant characterization of the members of complex bacterial populations requires the identification of these characters in a burgeoning field of biochemical/molecular/genetic research.

An overall concern of members of the Committee was that any phylogenetically based taxonomic schemes that result must also show phenotypic consistency.

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