MINIREVIEW

Classification of *Bacteria* and *Archaea*: Past, present and future ☆

Karl Heinz Schleifer[*]

Department of Microbiology, Technical University Munich, Am Hochanger 4, D-85350 Freising, Germany

Abstract

The late 19th century was the beginning of bacterial taxonomy and bacteria were classified on the basis of phenotypic markers. The distinction of prokaryotes and eukaryotes was introduced in the 1960s. Numerical taxonomy improved phenotypic identification but provided little information on the phylogenetic relationships of prokaryotes. Later on, chemotaxonomic and genotypic methods were widely used for a more satisfactory classification. *Archaea* were first classified as a separate group of prokaryotes in 1977. The current classification of *Bacteria* and *Archaea* is based on an operational-based model, the so-called polyphasic approach, comprised of phenotypic, chemotaxonomic and genotypic data, as well as phylogenetic information. The provisional status *Candidatus* has been established for describing uncultured prokaryotic cells for which their phylogenetic relationship has been determined and their authenticity revealed by *in situ* probing.

The ultimate goal is to achieve a theory-based classification system based on a phylogenetic/evolutionary concept. However, there are currently two contradictory opinions about the future classification of *Bacteria* and *Archaea*. A group of mostly molecular biologists posits that the yet-unclear effect of gene flow, in particular lateral gene transfer, makes the line of descent difficult, if not impossible, to describe. However, even in the face of genomic fluidity it seems that the typical geno- and phenotypic characteristics of a taxon are still maintained, and are sufficient for reliable classification and identification of *Bacteria* and *Archaea*. There are many well-defined genotypic clusters that are congruent with known species delineated by polyphasic approaches. Comparative sequence analysis of certain core genes, including rRNA genes, may be useful for the characterization of higher taxa, whereas various character genes may be suitable as phylogenetic markers for the delineation of lower taxa. Nevertheless, there may still be a few organisms which escape a reliable classification.
© 2009 Elsevier GmbH. All rights reserved.

Keywords: Bacteria; Archaea; History; Numerical taxonomy; Chemotaxonomy; Genotypic characterization; Concepts of classification; Polyphasic approach; Candidatus; Genome structure

Introduction

A reliable classification system is a prerequisite for scientists and professionals dealing with microorganisms in order to keep track of their tremendous variety. The ultimate objective of biological classification is the

characterization and orderly arrangement of organisms into groups. Classification is often confused with identification but, as a matter of fact, classification is a prerequisite for identification.

Currently, there is no official classification of *Bacteria* and *Archaea* available. Many bacteriologists think that Bergey's Manual represents the official classification but this is a misunderstanding. The editors of Bergey's Manual try to provide a classification that is as accurate and up-to-date as possible but it is not official, in contrast to bacterial nomenclature where each taxon has one valid name. The closest to an official classification system is the one that is widely accepted by the community [5].

History of classification

The history of the classification of bacteria clearly demonstrates that changes were caused by the availability of new techniques (Table 1). The late 19th century was the beginning of bacterial taxonomy and Ferdinand Cohn in 1872 [11] was the first to classify six genera of bacteria (as members of the plants) mainly based on their morphology. However, at that time, the majority of scientists were interested in the description of pathogenic bacteria. Actually, many of the pathogenic bacteria known today were described between 1880 and 1900. At that time, besides morphology, growth requirements and pathogenic potential were the most important taxonomic markers [24].

At the beginning of the 20th century more and more physiological and biochemical data were used, in addition to morphology, as important markers for the classification and identification of microorganisms. Numerous biochemical and physiological properties of bacterial cultures were determined for their characterization and identification. Later, enzymes were studied and metabolic pathways were elucidated. The first

edition of Bergey's Manual of Determinative Bacteriology [3] classified the *Bacteria* in 1923 on the basis of these phenotypic properties as "typically unicellular plants", the so-called *Schizomycetes*. Even in the 7th edition of Bergey's Manual [4], published in 1957, *Bacteria* were still classified as members of plants (*Protophyta*, primitive plants). Based on the partial sequences of 16S ribosomal RNA (rRNA) genes, *Archaea* (originally named *Archaebacteria*) were first classified as a separate kingdom in 1977 [45].

The French protistologist Edouard Chatton, the mentor and long time colleague of A. Lwoff, mentioned for the first time in 1925 [9] the two categories prokaryotes and eukaryotes but only to distinguish prokaryotic from eukaryotic protists. However, his proposal did not become generally known. Later on, A. Lwoff propagated this distinction and finally convinced R. Stanier, together with C.B. van Niel in 1962, to describe a detailed and well-accepted division of prokaryotic (bacteria) and eukaryotic (animals, plants) organisms [42].

In the 8th edition of Bergey's Manual, which was published in 1974 [7], *Bacteria* were no longer considered as plants and were recognized as members of the kingdom *Procaryotae*. However, all former ideas about phylogeny and relationships were discarded and bacteria were arranged in groups based mainly on the Gram-stain, morphology and oxygen requirement. A typically bad example for the classification of phenotypically similar but genetically quite different bacteria is the treatment of the family *Micrococcaceae* in this 8th edition. The two genera of this family, *Micrococcus* and *Staphylococcus*, are definitely not related (see below).

Numerical taxonomy based on phenetic analyses

Numerical taxonomy improved phenotypic identification by increasing the number of tests used and by calculating the coefficients of phenetic similarities between strains and species [37]. For numerical studies, the results are tabulated in a table of t organisms versus n characters and the term OTU (operational taxonomic unit) is used for an individual strain. The characters are equally weighted and should come from the various different categories of properties (morphology, physiology, biochemistry, etc.). The number of common characteristics is considered as a quantitative measure of taxonomic relatedness, although this does not mean that the organisms are also phylogenetically related.

Chemotaxonomy

The chemical composition of cell constituents is a useful property for improving the classification and

Table 1. History of the classification of *Bacteria* and *Archaea*.

Time span	Classification mainly based on	References
Late 19th century	Morphology, Growth Requirements, Pathogenic potential	[11,24]
1900–1960	Morphology, Physiology, Biochemistry	[3,6]
1960–1980	Chemotaxonomy, Numerical Taxonomy, DNA–DNA Hybridization	[7,32,34,37]
1980–today	Genotypic Analyses, Multilocus Sequence Analyses, Average Nucleotide Identity, Whole Genome Analysis	[16,18,22,31, 39,44,46,47]