1. INTRODUCTION

Bacterial taxonomy is the science that makes logical and rational communication possible among all scientists, microbiologists, physicians, biochemists, and others; indeed, all people who need to know and use microbiological information. Combining, as it does, the arts of classification and identification with stringent rules of nomenclature, there is much that remains subjective in the selection of limits allowed in defining each taxon. However, with the explosion of information that is accumulating regarding the chemical and genetic composition of bacterial cells, it is now becoming possible to approach the definition of limits so as to include in a taxon, at the level of either genus or species, only organisms that are truly closely related.

To classify bacteria into coherent units, as many properties as possible of pure cultures of the organisms must be determined and described. By selection of those characteristics that are stable and common to a group of organisms but that distinguish that group from other well-defined units, separate taxa can be constructed. Properties of new isolates can then be compared with those of accepted taxa and the new isolates identified. Where the new isolates are sufficiently unlike any that have been previously accepted, a new taxon must be described and an appropriate name assigned according to the International Code of Nomenclature of Bacteria prepared by Lapage et al. (1975).

For classification, a great deal of information must be gathered about the strains studied: morphological, biochemical, chemical, physiological, metabolic, genetic, etc. Much of this may never be needed again, but it should be available in the literature so that it can be related to as new

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information is developed. Where only one or a few strains are described, they should be tested several times under different conditions to determine any variations that might exist. For identification, as few properties as possible are selected that distinguish one organism from others that are closely related. These properties must be common to all strains, stable, and preferably easy to determine by simple, rapid, reliable, and inexpensive tests.

2. HISTORICAL REVIEW

The genus *Clostridium* was described originally by Prazmowski (1880). With the limited information available at that time, the genus was separated from the genus *Bacillus* to include those gram-positive rods that are obligately anaerobic in their metabolism with central or subterminal heat-resistant spores that swell the cell. As the numbers of presumably different species that fit that description proliferated, there have been numerous proposals, principally on morphological grounds (position of spores, motility, gram stain, possession of capsule), to split the genus into smaller units (Chester, 1901; Weinberg *et al.*, 1937; Handuroy *et al.*, 1937; Prévot, 1938, 1940). With current routine diagnostic techniques, there has been little or no advantage gained from splitting the genus into smaller genera for purposes of identification, although most recent genetic data indicate that several only distantly related groups are included in the genus as it is currently defined. The definition adopted by Bergey *et al.* (1923), a slightly expanded version of that of Prazmowski, is essentially that given today in *Bergey's Manual of Systematic Bacteriology*, Volume 2 (Cato *et al.*, 1986). For inclusion in the genus, there are few requirements: anaerobic or micro-aerophilic spore-forming rods that do not form spores in the presence of air, are usually gram-positive, and do not carry out a dissimilatory sulfate reduction.

During the first half of this century, many species of clostridia were named, often with a sketchy description of a single strain, which might differ in one or two reactions from species already described. Some inconsistencies were due to the use of impure substrates or less than optimal methods or growth conditions, and some to the particular interest, capability, or bias of the different investigators. Many original strains were lost; others became contaminated and results could not be confirmed. This situation was greatly alleviated by the publication of the 1980 "Approved Lists of Bacterial Names" (Skerman *et al.*, 1980), the subsequent list of nomenclatural changes between 1980 and 1985 (Moore *et al.*, 1985), and, later, "Validation Lists" published in the *International Journal of Systematic Bacteriology*. Only those species that were adequately described, and for which a type strain was available and deposited in a recognized and accessi-