CURRENT VIEWS AND PROBLEMS RELATING TO THE
TAXONOMY OF THE MICROCOCCACEAE

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SUMMARY. Criteria currently in use lead to conclusion that in the family Micrococcaceae the two genera Micrococcus and Staphylococcus may be recognized. The genus Staphylococcus presently contains two rather homogeneous species, S. aureus and S. epidermidis, and the genus Micrococcus contains two recognizable species, M. luteus and M. roseus. Other species in these genera have not been characterized adequately.

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Present concepts of the taxonomy of the Micrococcaceae are based primarily on data obtained from applying a limited range of physiological tests to collections of bacteria heavily weighted toward a single species. Based on this level of information it appears that there are two valid genera (Staphylococcus and Micrococcus) and two recognizable species within each genus (S. aureus, S. epidermidis, M. luteus and M. roseus). Other reputed species lack the over-all homogeneity that should characterize valid species. From a purely taxonomic point of view these genera and species are delineated by their possession of groups of common properties. From a practical, or diagnostic, standpoint one or two representative tests are generally sufficient for their differentiation. For example, the anaerobic fermentation of glucose is the diagnostic test for separating the two genera and the coagulase test is the best single test for separating S. aureus from S. epidermidis.

We need to expand the range of characters studied for taxonomic purposes to include such items as cell structure and composition, metabolic pathways for obtaining energy and synthesizing cell constituents, antigenic components, genetic composition and compatibility, as well as environmental effects. This will require application of both the concepts and methods of modern cytochemistry, serology, genetics and molecular biology.

Both the philosophy and the techniques of numerical taxonomy should be considered as we look for and describe the natural species in this family. We should bear in mind that large numbers of supposedly representative strains should be studied, that each member of a species will differ to some extent from every other member of the same species, and that no single feature will necessarily be possessed by every member of the species.

After species have been described we should develop diagnostic tests that are stable characters, possessed by virtually all members of a species and absent from most members of closely related species. Whereas the tests for defining species should attempt to measure the phenotypic expression of comparable genetic units (e. g. the coding for a single enzyme), diagnostic tests may be better when based on larger units of genetic information. The anaerobic fermentation of glucose by staphylococci represents a diagnostic test for an intact glycolytic pathway. This system is essential for anaerobic growth of these organisms and may be of importance in aerobic biosynthetic pathways. It is unlikely that mutants lacking single steps in this pathway would become a significant part of a natural population. Serological tests and genetic compatibility tests may also be measures of relatively large blocks of genetic information. The basis for the stability and reliability of the coagulase test is obscure, but this does not detract from its proven value as a diagnostic test.

In conclusion, we need to study large and representative collections of cultures using a wide array of carefully standardized tests and examine the resulting data to detect valid new species and to better define our present species. This should be followed by the evaluation and standardization of diagnostic tests.

(Read at the meeting of the Subcommittee on Taxonomy of Staphylococci and Micrococci at Brno, 5-6 October 1964.)