Chapter 2
Coagulase-negative Staphylococci: Classification and Problems

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The difficulties of classifying coagulase-negative staphylococci became evident to workers investigating the flora of the skin before most medical microbiologists were aware that a problem existed. The different staphylococci on the skin and the probable significance of this in ecological terms was realized, but the classifications available were of no practical use. Standard procedure was to identify all coagulase-negative staphylococci as Staphylococcus albus and to recognize coagulase-positive strains as the pathogen S. aureus.

What was to become widely accepted classification was proposed by Baird-Parker based on a few relatively simple biochemical tests, including the production of acid aerobically from arabinose, lactose, maltose, and mannitol and the production of coagulase, phosphatase, and acetoin. In this scheme the primary division between Staphylococcus and Micrococcus was made on the ability to ferment glucose under anaerobic conditions. The genus Staphylococcus was divided into six subgroups numbered SI–SVI, with subgroup SVI further subdivided into three types; and the genus Micrococcus was divided into eight subgroups, M1–M8. Later studies on the guanine-cytosine percentage composition of the DNA showed that at least the first four micrococcal subgroups were staphylococci, while M7 and M8 represented the genus Micrococcus. Baird-Parker amended his scheme so that the original subgroup SI became S. aureus; SII–SVI became S. epidermidis biotype 1–4 with biotype 1 including SII and SV; and M1–4 became S. saprophyticus biotypes 1–4. This definition of S. saprophyticus includes a wider set of strains than later classifications allow.

The original classification has been widely used in studies of skin flora and infections and permitted the recognition of differing pathogenicity among the subgroups. Subgroup II became associated with infected surgical prostheses and with diseased skin while subgroup M3 was associated with domiciliary urinary infection in young women, permitting the description of this newly differentiated disease. Studies of the normal skin flora also showed differences in proportions of the subgroups at different sites and in different environments.

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We found it necessary to extend the classification of Baird-Parker to include two additional groups, SY and MX, to allow for strains that produce acid from mannitol and produce phosphatase and acetoin. We also subdivide M3 in the same way that Baird-Parker subdivided SVI. Pelzer et al.\textsuperscript{21} found similar strains and added six further subgroups to the basic scheme.

Recently Kloos, Schleifer, and co-workers have described alternative classifications for both micrococi\textsuperscript{9} and staphylococci\textsuperscript{8} based on similar but not identical biochemical tests carried out by methods that differ from those of Baird-Parker. Their simplified scheme for staphylococci\textsuperscript{8} forms a dichotomous key with alternative pathways leading to 11 subdivisions, most of which are named, including \textit{S. aureus}, \textit{S. epidermidis}, and \textit{S. saprophyticus}. The definitions of \textit{S. aureus} and \textit{S. epidermidis} are compatible with the scheme of Baird-Parker, but the definition of \textit{S. saprophyticus} is narrower.

This scheme has been applied to infections\textsuperscript{19} and to normal human skin cocci.\textsuperscript{10,11} Navamar et al.\textsuperscript{16} have found the subdivision of Baird-Parker subgroup M3 by the classification of Kloos and Schleifer useful. For clinical work a scheme to identify \textit{S. aureus}, \textit{S. epidermidis}, and \textit{S. saprophyticus} while detecting the other species has been advanced as a compromise.\textsuperscript{25}

We studied 300 representative strains of catalase-positive gram-positive cocci by the methods of Baird-Parker and of Kloos and Schleifer. The collection included 96 strains from culture collections, 58 from animal sources, 16 from urinary infections, and 125 from human skin. For five strains the source was unknown. We then identified each strain by the two classifications.

Five biotypes gave very good correlation: \textit{S. aureus} and \textit{S. intermedius} equaled Baird-Parker SI; \textit{S. epidermidis} equaled SII; \textit{S. saprophyticus} equaled lactose positive M3; \textit{S. cohnii} equaled MX; and \textit{Micrococcus roseus} equaled M8. A minor redefinition of SIII to allow for maltose-positive strains made this subgroup equal \textit{S. simulans}; lower reliance on the OF test incorporated SVI(3) and M3(3) as \textit{S. capitis} and \textit{S. xylosus} included both M5 and M6 strains.

Correlation between the remaining three species of Kloos and Schleifer—\textit{S. haemolyticus}, \textit{S. warneri}, and \textit{S. hominis}—with the remaining staphylococcal biotypes of Baird-Parker was poor. Biotype M7 of Baird-Parker included the remaining \textit{Micrococcus} species, though some strains of \textit{M. kristinae} and \textit{M. varians} were misclassified into staphylococcal biotypes. Further work is needed to improve the identification schemes for these strains to assess the significance of the different weights given to acid production from lactose and mannitol in the two classifications.

While \textit{S. saprophyticus} is associated with urinary infection, the commonest biotype found in serious infections caused by coagulase-negative staphylococci is \textit{S. epidermidis} (SII). Of 223 strains associated with nonurinary infection received by us in 1977, 181 were identified as this biotype. For epidemiological studies, methods of subdividing this biotype are required. Phage-typing schemes have been developed;\textsuperscript{5} additional biochemical tests can be used.\textsuperscript{6} Antibiotic susceptibility testing and, in some