

Howard Maibach · Raza Aly

Skin Microbiology

Relevance to Clinical Infection



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Edited by
Howard I. Maibach and Raza Aly



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Preface

Not since the 1965 publication of *Skin Bacteria and Their Role in Infection* has our knowledge of clinical skin microbiology been reviewed and summarized. In the more than a decade and a half since that publication, we have seen a careful reevaluation of the ideas and information current in 1965 and the development of important new discoveries and information.

This volume, *Skin Microbiology: Relevance to Clinical Infection*, reviews developments in the field since 1965 and summarizes the current state of the art in thirty-six carefully prepared chapters. Emphasis is on the clinical perspective rather than straight microbiology, although we include enough of the latter to put the clinical aspects in a proper scientific context.

The authors contributing to this volume represent a cross section of authorities in the many specialty areas that contribute to our knowledge of skin microbiology. They include investigators in microbiology, infectious disease, epidemiology, surgery, pediatrics, and dermatology. Significant efforts have been made to minimize repetition and overlap in the various chapters. In some cases, however, information is deliberately repeated in order to provide for the reader a necessary frame of reference.

We hope that this volume will be of value to dermatologists, microbiologists, pediatricians, surgeons, public health workers, nurses, and others involved in the diagnosis and treatment of dermatologic problems caused by bacteria.

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Contents

Preface	v
Contributors	xi
 Part I The Cutaneous Flora and Its Control	
1. Identification of <i>Staphylococcus</i> and <i>Micrococcus</i> Species Isolated from Human Skin	
WESLEY E. KLOOS	3
2. Coagulase-negative Staphylococci: Classification and Problems	
RICHARD R. MARPLES	13
3. The Current Status of Aerobic Cutaneous Coryneform Bacteria	
DAVID G. PITCHER and PETER J. H. JACKMAN	19
4. Factors Controlling Skin Bacterial Flora	
RAZA ALY and HOWARD I. MAIBACH	29
5. Microbiology of Specialized Sites in Relation to Infection	
WILLIAM C. NOBLE	40
6. Newer Methods of Quantifying Skin Bacteria	
RICHARD R. MARPLES	45
7. Treatment of Nasal Carriers of Coagulase-positive Staphylococci	
L. JOSEPH WHEAT, RICHARD B. KOHLER, and ARTHUR WHITE	50
8. Practical Office Microbiology	
JOSEPH GREENBERG	59
9. Microbial Interactions and Antibiosis	
SYDNEY SELWYN	63
 Part II Topical Skin Antibacterials	
10. Clinical Trials of Topical Antimicrobials	
ALFRED M. ALLEN	77

11. Preoperative Shower Bath with 4% Chlorhexidine Detergent Solution. Reduction of <i>Staphylococcus aureus</i> in Skin Carriers and Practical Application	
STAFFAN SEEBERG, ANDERS LINDBERG, and BO R. BERGMAN	86
12. Preoperative Whole Body Disinfection by Shower-bath with Chlorhexidine Soap: Effect on Transmission of Bacteria from Skin Flora	
AKE BRANDBERG and INGRID ANDERSSON	92
13. Postoperative Wound Infections in Vascular Surgery: Effect of Preoperative Whole Body Disinfection by Shower-bath with Chlorhexidine Soap	
AKE BRANDBERG, JAN HOLM, JAN HAMMARSTEN, and TORE SCHERSTEN	98
14. Newer Germicides: What They Offer	
MARY BRUCH	103
15. Antibacterial Soaps: Chlorhexidine and Skin Infections	
DAVID TAPLIN	113
16. Antimicrobial Soaps: Benefits versus Risks	
FRANCIS N. MARZULLI and MARY BRUCH	125
17. Antimicrobials: Regulatory Aspects	
HEINZ J. EIERMANN	135
18. Antimicrobial Efficacy in the Presence of Organic Matter	
JOHN A. ULRICH	149
19. Topical Antimicrobials: Perspectives and Issues	
E. J. L. LOWBURY	158

Part III Bacterial Adherence and Factors

20. <i>Staphylococcus aureus</i> Adherence to Nasal Epithelial Cells: Studies of Some Parameters	
RAZA ALY, HENRY R. SHINEFIELD, and HOWARD. I MAIBACH	171

Part IV Infections and Epidemiology

21. Epidemiology of Skin Infections: Strategies Behind Recent Advances	
ALFRED M. ALLEN and DAVID TAPLIN	183
22. The Role of Hands in Nosocomial Gram-negative Infection	
M. W. CASEWELL	192
23. The Interaction of Fungi and Bacteria in the Pathogenesis of Athlete's Foot	
ALBERT M. KLIGMAN and JAMES LEYDEN	203
24. Experimentally Induced Cutaneous Infection in Man	
W. CHRISTOPHER DUNCAN, MOLLIE E. MCBRIDE, and JOHN M. KNOX	220

25. Exotic Infection: Its Relevance to Clinical Microbiology W. C. NOBLE	231
26. Dermatitis Skin: Microbiology and Treatment HOWARD I. MAIBACH and RAZA ALY	233
27. Staphylococcal Scaled Skin Syndrome: Clinical Features, Biology, and Pathogenesis PETER M. ELIAS and PETER FRITSCH	245
28. Means of Preventing Burn Wound Infection JOHN F. BURKE	265
29. Topical Antibiotic in the Prophylaxis of Experimental <i>S. aureus</i> and <i>S. pyogenes</i> Infections in Humans JAMES J. LEYDEN and ALBERT M. KLIGMAN	269
30. Current Concepts in Neonatal Bacterial Colonization WILLIAM T. SPECK, JANE O'NEILL, JOHN M. DRISCOLL, and HERBERT S. ROSENKRANZ	275

Part V Acne

31. <i>Propionibacterium acnes</i> : Present Status and Role in Acne Vulgaris S. M. PUHVEL	289
32. A Role for <i>Propionibacterium acnes</i> in the Production of Inflammatory Lesions in Acne Vulgaris GUY F. WEBSTER	298

Part VI Skin Infection: Treatment

33. Means of Preventing Bacterial Infection ALEXANDER S. D. SPIERS, SYLVIA F. DIAS, and JOSE A. LOPEZ	305
34. The Topical Treatment of Skin Infections SYDNEY SELWYN	317
35. Treatment of Serious Cutaneous Staphylococcal and Streptococcal Infections STEPHEN N. COHEN	329
36. The Role of Ketoconazole in the Management of Mucocutaneous Candidiasis Syndrome JOHN R. GRAYBILL and DAVID J. DRUTZ	333
Index	343

PART
ONE

THE CUTANEOUS FLORA
AND ITS CONTROL

Chapter 1

The Identification of *Staphylococcus* and *Micrococcus* Species Isolated from Human Skin

WESLEY E. KLOOS

Staphylococci and micrococci represent major groups of bacteria inhabiting human skin. The identity of each genus and currently recognized species offers a challenge to the skin microbiologist that should be rewarding in uncovering the population structure of cutaneous microbial communities and in providing a starting point from which to explore adaptive and evolutionary mechanisms. I believe that most human *Staphylococcus* and *Micrococcus* species have been discovered and given an appropriate taxonomic status. Perhaps others will be found, especially from unique niches or specially isolated human populations. Schleifer and coworkers²⁰ (K. H. Schleifer, personal communication) have shown that strains identified as *Peptococcus saccharolyticus* are actually anaerobic staphylococci which might constitute a new species. Preliminary ecological studies have indicated that the human forehead may carry rather large populations of this organism.¹⁴

In this paper, an attempt will be made to familiarize the reader with the current status of *Staphylococcus* and *Micrococcus* taxonomy including the choice of simple characters that may be tested in the routine laboratory for genus and species identification.

Separation of Staphylococci and Micrococci

Staphylococci and micrococci can be separated by several key tests easily performed in the routine laboratory. One such test proposed by Schleifer and Kloos⁴⁶ is based on the ability of staphylococci to produce acid, aerobically, from glycerol in the presence of 0.4 μg erythromycin per ml and on their susceptibility to lysostaphin at a concentration of 200 $\mu\text{g}/\text{ml}$. Curry and Borovian⁹ have shown that a nitrofurantoin-containing medium (FTO agar) permits the growth of micrococci but not staphylococci. Most *Staphylococcus* species produce detectable growth in a semisolid thioglycolate medium described by Evans and Kloos,¹⁶ whereas most *Micrococcus* species will not grow in this medium except near the surface.^{25,47} The

species usually not conforming to this test include *S. hominis*, some strains of *S. haemolyticus*, *S. cohnii*, and *S. xylosus*, and *M. kristinae*; however, the test provides more reliable results for the separation of these genera than the standard anaerobic glucose utilization test proposed by the International Subcommittee on Staphylococci and Micrococci (1965). Seidl and Schleifer⁵² introduced a serological test for separating staphylococci from micrococci based on different peptidoglycan types. Preliminary identification of these organisms can, in most instances, be accomplished on the basis of colony morphology and pigment and growth rate. Colonies of micrococci develop much slower than those of staphylococci (except for *Staphylococcus sciuri* subsp. *lentus*, which has been isolated from sheep and goats). Human *Staphylococcus* species produce detectable colonies (> 1 mm in diameter) on most nonselective plating agars, within 18 h at 34–37°C; whereas, micrococci require 36–48 h to produce detectable colonies. Most micrococci produce colonies typically more convex than staphylococcus colonies. Occasionally colonies of micrococci may be confused with those of corynebacteria, though these two groups can be resolved on the basis of cell morphology.

Micrococci and staphylococci are included currently in the family Micrococcaceae⁵ representing gram-positive, catalase-positive cocci; however, major differences in their DNA base composition^{1,6,25,30,33,44,47} and 16S ribosomal RNA sequences⁵³ indicate clearly that these organisms bear no special relationship to one another. It is expected that staphylococci and micrococci will be eventually separated and moved into other existing families.

Characterization of *Staphylococcus* Species Inhabiting Human Skin

Staphylococci are currently classified according to specific combinations of phenotypic characters^{10,19,25,31,47} and DNA relatedness.^{10,22,28,39,43,50} Extensive systematic and ecological studies have identified at least ten different *Staphylococcus* species living on human skin.^{8,11,12,15,18,23,24,25,26,31,47,50,57,58} These species include *S. aureus*, *S. epidermidis*, *S. hominis*, *S. haemolyticus*, *S. capitis*, *S. warneri*, *S. saprophyticus*, *S. cohnii*, *S. xylosus*, and *S. simulans*. In the routine laboratory, they can be identified with reasonably good accuracy (> 80 to > 95 percent, depending upon the species) using specific combinations of selected characters that are relatively simple to test and have a high predictive value in resolving DNA homology groups.^{24,27,32,55} The task of resolving at least ten different species is a relatively large one in any study. Here the investigator must determine whether or not it is important to resolve all species or only certain ones. The widely accepted Baird-Parker taxonomic schemes cannot identify most of the species inhabiting human skin, though they can identify with reasonable accuracy (> 70 percent) the more medically important species *S. aureus*

(*Staphylococcus* subgroup I), *S. epidermidis* (*S.* subgroup II or *S. epidermidis* biotype 1), and *S. saprophyticus* (*Micrococcus* subgroup 3 or *S. saprophyticus* biotype 3).^{2,3,4} Some microbiologists adhere to Baird-Parker's schemes, but in doing so, must realize that they are limiting their ability to recognize the variety of widely divergent populations present on skin, some of which demonstrate niche and host preferences.

S. aureus is considered the most potentially pathogenic species and for this reason has received the most attention. Several years ago, all coagulase-positive staphylococci were identified as belonging to this species. Today, we recognize the three coagulase-positive species *S. aureus*, *S. intermedius*, and *S. hyicus*; the latter two species are found primarily on lower mammals and birds.^{10,19,49} A moderate percentage of *S. hyicus* strains are coagulase-negative and were classified earlier as *Staphylococcus* subgroup III or *S. epidermidis* biotype 2 according to Baird-Parker's schemes. *S. intermedius* and *S. hyicus* are probably of minor concern to one studying the human cutaneous microflora, though they may be isolated on occasion from human skin if contact has been made with natural animal hosts (e.g. with pets or farm animals). Although these species may produce infections in a variety of animals and birds, it is not known if they are capable of producing infections in man. All three coagulase-positive species produce higher deoxyribonuclease activity than usually found with coagulase-negative species. Coagulase-positive staphylococci that produce weak, delayed acid or no acid, aerobically, from maltose are probably not *S. aureus*. *S. intermedius* strains isolated from carnivora (e.g. dogs, mink, raccoons, etc.) typically produce very weak acid from maltose in 48 to 72h and *S. hyicus* strains usually fail to produce acid from this carbohydrate. *S. intermedius* and *S. hyicus* do not produce acid from D-mannitol anaerobically and do not produce acetylmethylcarbinol (acetoin), except, perhaps, in small quantity. *S. aureus* on the other hand, is usually positive for these characters. Each of the coagulase-positive species are in different, widely divergent DNA homology groups exhibiting less than 20 percent relatedness under restrictive binding conditions.^{10,39,42}

The nine coagulase-negative species found living on human skin may be organized into three species groups.^{26,32} The major one of human skin is the *S. epidermidis* species group composed of the species *S. epidermidis*, *S. hominis*, *S. haemolyticus*, *S. warneri*, and *S. capitis*. These species are related slightly more to one another than to species in other groups. They exhibit a DNA relatedness of about 45 ± 6 percent at non-restrictive conditions and 15 ± 3 percent at restrictive conditions.^{22,28,50} *S. hominis* is more related to *S. haemolyticus*, and *S. epidermidis* is more related to *S. capitis* than to other species of this group.

S. epidermidis and *S. capitis* may be identified easily and with considerable accuracy (>95 percent). On a peptone-yeast extract-salt (P agar) medium,³⁰ colonies of *S. epidermidis* are small and are about 3.5 to 4 mm in diameter after incubation at 34°C for 3 days, followed by storage at room temperature for an additional 2 days. Colonies are slightly raised, rather sticky,