Skin microbes

Human skin may not be the most ideal habitat for micro-organisms, but as **Mark Farrar** and **Richard Bojar** report, the skin microflora is more species-rich than we think.

As a microbial habitat, human skin is somewhat inhospitable. Resident micro-organisms must be able to withstand a much drier and nutritionally limited environment than that found, for example, in the gut. As a consequence, there are relatively few microbial groups capable of colonizing human skin. The dominant micro-organisms belong to the genera *Staphylococcus*, *Propionibacterium* and *Corynebacterium*. Skin commensals can colonize both the skin surface and hair follicles. The distribution and density of these micro-organisms varies greatly over the body and is influenced mainly by nutrition and humidity. For example, total bacterial numbers per cm^2 of skin in the armpit or on the face can reach 10^7, whereas on the forearm numbers may only reach 10^2. On the whole our resident microflora exists without any detriment to human health and may actually play a protective role in preventing colonization by pathogens. However, occasionally our microflora can cause problems, some of which will be addressed in this article.

Staphylococci

Over 40 species of *Staphylococcus* are currently recognized, of which at least ten can be found on human skin. *Staphylococcus epidermidis* is the most prevalent member of the human skin microflora on most body sites. Other common skin residents belonging to this genus include *S. hominis*, *S. haemolyticus* and *S. capitis*. These are all coagulase-negative staphylococci. The coagulase-positive and more infamous *S. aureus* is not usually considered a resident of human skin but is found in the nose of approximately 30 % of the population. When found on skin it is most likely to be a transient colonization. Staphylococci are found in the highest numbers on the face and chest, and in some individuals in the armpit.

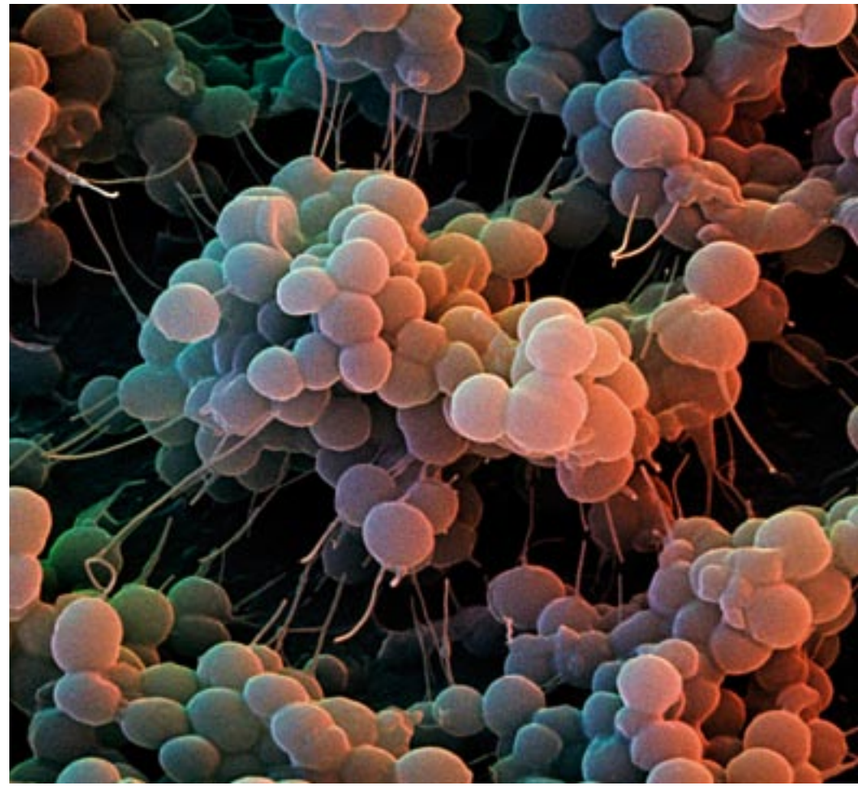
As pathogens, cutaneous staphylococci are most commonly associated with infections of catheters and prosthetic implants. *S. epidermidis* is by far the most common cause of such infections. The most significant virulence factor of coagulase-negative staphylococci is the production of extracellular polysaccharide or 'slime'. This is produced in large amounts by around 50 % of *S. epidermidis* isolates and enables the bacteria to adhere to and colonize medical devices. It also contributes to antibiotic resistance and interferes with removal of invading bacteria by the immune system. Consequently, staphylococcal infections of medical devices are difficult to treat.

Propionibacteria

Propionibacteria are most prevalent and found in the greatest numbers in lipid-rich areas of human skin, i.e. the face, chest and back. In the laboratory, propionibacteria are routinely isolated under anaerobic conditions. However, they are aerotolerant and growth has been shown to be increased in the presence of low concentrations of air, making them microaerophilic. Propionibacterial numbers on the face and back can reach 10^7 per cm^2 of skin. *Propionibacterium acnes*

▼ Inflammatory acne vulgaris on the back. *M.D. Farrar*

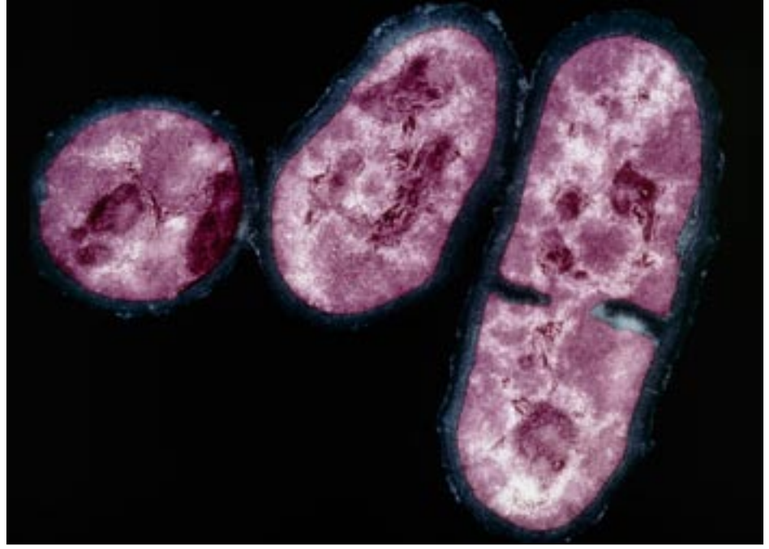
► Coloured scanning electron micrograph of clusters of *Staphylococcus epidermidis* bacteria. *David Scharf / Science Photo Library*

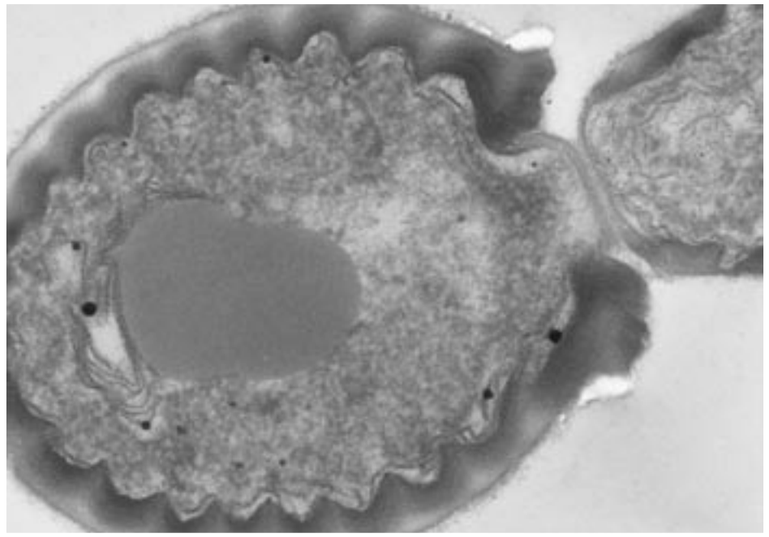


is the dominant member of the genus on skin. Other members of cutaneous propionibacteria include *P. granulosum*, *P. avidum* which is found in more humid areas such as the armpit, *P. propionicum* and *P. lymphophilum*. Propionibacteria have been associated with the common skin disease acne vulgaris for over 100 years. Although propionibacteria do not cause this disease, they are thought to be a significant factor in the development of inflammation. *P. acnes* has been the main focus of research into propionibacteria and acne due to its higher densities, but involvement of other propionibacteria and even members of other genera cannot be discounted. Skin propionibacteria are becoming an increasing cause of infections in immunocompromised individuals, particularly following surgical procedures. Endocarditis, eye infections and tissue infections have all been reported. Publication of the genome sequence of *P. acnes* in 2004 has helped to accelerate research, but the actual role of this organism in acne and the factors involved in the transition from harmless commensal to inflammatory stimulus are still unknown.

Corynebacteria

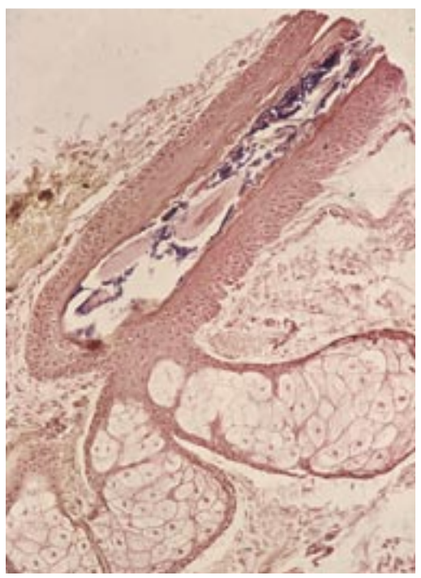
Corynebacteria are related to propionibacteria, but grow under aerobic conditions. This genus is less well characterized than *Staphylococcus* or *Propionibacterium*, but ribosomal RNA typing is helping to distinguish species. Skin residents include





▲ Coloured transmission electron micrograph of a section through *Propionibacterium acnes* bacteria. *Kwangshin Kim / Science Photo Library*

▲ Transmission electron micrograph of a budding *Malassezia* cell. *M.D. Farrar*



▶ Biopsy section of a human hair follicle showing Gram-positive micro-organisms within the follicle. *M.D. Farrar*

Molecular typing has shown there to be many more bacterial species present on human skin than previously thought

Corynebacterium bovis, *C. jeikeium* and *C. xerosis*. Corynebacteria are also found in lipid-rich areas and many are lipophilic. Recent sequencing of the genome of *C. jeikeium* has shown it to have a nutritional requirement for monounsaturated fatty acids, which it cannot synthesize. Corynebacteria are of great interest to the personal hygiene industry as they are thought to be major contributors to underarm body odour. Secretions from sweat and other skin glands can be metabolized to odorous compounds by this group of organisms. Many deodorant products contain antibacterial agents that aim to reduce bacterial numbers and therefore reduce the potential for odour formation. Corynebacteria may also cause opportunistic infections. *C. jeikeium* is recognized as a significant nosocomial pathogen and is resistant to several antibiotics, including erythromycin, tetracycline, kanamycin and chloramphenicol.

Malassezia spp.

From there being just one recognized species several years ago, molecular typing has led to the description of 13 species in this genus, 11 of which have been found on human skin. As with some of the bacterial groups already described, *Malassezia* spp. are also lipophilic. Members of this genus, in particular *M. globosa* and *M. restricta*, are thought to be involved in the pathogenesis of seborrheic dermatitis, a severe form of dandruff. Although their role is not exactly clear, disease is believed to develop due to an inappropriate immune response to the organism.

Other skin residents

Other micro-organisms are found on human skin and are recognized as commensals, although they are found in much lower numbers than the groups described above. True commensals include members of the genera *Micrococcus*, *Brevibacterium*, *Kytococcus* and *Dermacoccus* (both formerly classified as micrococci), and the Gram-negative *Acinetobacter*. All these can be regularly isolated, albeit in low numbers, from human skin. Less prevalent and probably considered transients rather than true commensals are species of *Streptococcus* and *Peptostreptococcus*.

Is the skin microflora more diverse than we thought?

With advances in molecular typing and classification of micro-organisms through the use of ribosomal RNA sequencing, the microbial diversity of numerous habitats has been shown to be greatly underestimated. Recently, such techniques have been applied to human skin. This has shown there to be many more bacterial species present on human skin than previously thought. This is mostly due to previous studies relying solely on culture techniques. However, a note of caution should be applied; to date, molecular studies have looked at samples at only a single point in time. This makes it difficult to distinguish those organisms that are true residents from transiently colonizing micro-organisms and environmental contaminants. If we are to truly understand the diversity of the human skin microflora, more long-term studies are required where multiple samples are taken from individuals over a period of time. However, those studies carried out to date are important as they have shown the skin to be a potential habitat for a diverse range of micro-organisms.

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