Microbial Colonization Dynamics of the Axillae of an Individual over an Extended Period

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Sir,

The axilla supports one of the highest bacterial densities on the human body surface (1, 2). This site not only has hair follicles with sebaceous glands and eccrine sweat glands as found on the rest of the body, but also apocrine glands, which provide a further source of nutrition for the microflora. These factors combine to create a highly favourable site for bacterial multiplication (3). Due to the occluded nature of the axilla, this skin site is least prone to contamination from the environment and is therefore likely to support a microflora that is most representative of the indigenous cutaneous population (1). Axillary microorganisms have been implicated in the transformation of usually odourless apocrine secretions to compounds that give rise to the typical odour associated with the axilla (4, 5).

There have been numerous studies of the microflora of the axilla ranging from investigations into the 'normal' bacterial residents of this region to the effects of deodorants, antiperspirants, antibiotics and other compounds on the prevalence and population density of bacterial groups (1, 4, 5). Although many such studies have been quantitative, one common feature and significant shortcoming is that they have relied on single samples at the same site on groups of volunteers, and the data are expressed usually as the geometric mean of colony forming units (cfu) per cm^2. This approach is unsuitable for detecting any variations in the microflora of an individual over time.

MATERIALS AND METHODS

The study volunteer was a 24-year-old man who was in good health and had not received any antibiotic treatment for at least 1 year before commencing the study and did not receive any such treatment during the course of the study. He agreed to abstain from using antiperspirants and to use the same deodorant and soap products throughout the study period.

Samples were taken from both the left and right axilla every 2 weeks continuously for a total of 49 weeks (sample 1 was taken in week 1). Samples were taken on the same day of the week and 6 h after the subject had washed. The deodorant product was applied immediately after washing. Samples were taken using the scrub wash technique of Williamson & Kligman (6). Aliquots of dilution were spread plated onto selective and non-selective media.

Staphylococcus spp. were isolated using a selective agar (7). Aerobic coryneform (*Corynebacterium* spp.) selective agar consisted of 40 g l^{-1} blood agar base, 3 g l^{-1} yeast extract, 2 g l^{-1} glucose, 0.2% (v/v) Tween 80, 5% (v/v) defibrinated horse blood and 6 mg l^{-1} furazolidone. *Propionibacterium* spp. and micrococci were selected on reinforced clostridial agar (Oxoid, Basingstoke, UK) supplemented with 0.1% (v/v) Tween 80 and 6 mg l^{-1} furazolidone. Gram-negative organisms were quantified as one group by plating on heated blood agar on which these organisms could be readily identified by colony morphology. Staphylococci, aerobic corynebacteria, micrococci and Gram-negative organisms were grown aerobically for 2 days at 37°C. Propionibacteria were grown anaerobically for 7 days at 34°C.

RESULTS

The variation in population density of each bacterial group in the left axilla is presented in Fig. 1. Each graph shows the $\log_{10}$ increase or decrease in cfu cm^{-2} of skin from the median at each sample point. Most notable was the general rise in the population density of each bacterial group in the summer period (sample weeks 37–49) in contrast to the winter weeks where the population density was generally below the median (sample weeks 5–19). A similar magnitude of variation was seen in the numbers of aerobic corynebacteria, micrococci and Gram-negative organisms with an approximate 3 log range, although actual numbers of these latter two groups were less than the aerobic corynebacteria. The staphylococci and, in particular, the propionibacteria exhibited less variation in population density over the study period.

The percentage composition of the microflora of the left axilla is presented in Fig. 2 and clearly demonstrates that

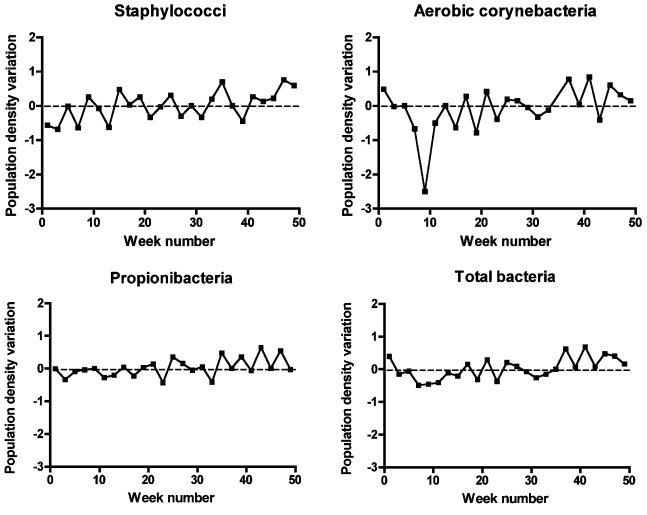

Fig. 1. Variation in population density of the main bacterial groups in the left axilla. Data points are the variation from the median of the $\log_{10}$ cfu cm^{-2} skin of each bacterial group: staphylococci, 5.447; aerobic corynebacteria, 6.301; propionibacteria, 5.756; total bacteria, 6.491. (Micrococci and Gram-negative organisms are not shown 2.279 and 3.556, respectively.)

overall, aerobic corynebacteria formed the dominant population in the left axilla. However, dominance did vary to some extent with propionibacteria forming the dominant bacterial group in weeks 7, 9, 35 and 43. In weeks 15 and 19 there was no dominant bacterial group.

Bacterial colonization of the right axilla exhibited greater variation in the population density of each bacterial group and in percentage composition of the axillary microflora compared with that of the left axilla (data not shown). A seasonal trend was again observed with the majority of samples in the winter being below the median and in summer above the median. Aerobic corynebacteria exhibited the greatest variation in numbers with a range of more than 4 logs. The population densities of the bacterial groups in the right axilla were found to be similar to those in the left axilla. Overall, bacterial densities in the right axilla were lower than those of the left axilla with medians of 1.2×10^6 cfu cm^{-2} skin and 3.1×10^6 cfu cm^{-2} skin, respectively, and maximums of 7.4×10^6 cfu cm^{-2} skin and 1.5×10^7 cfu cm^{-2} skin, respectively.

The dominant bacterial group in the right axilla changed more frequently from sample to sample between the three main bacterial groups (aerobic corynebacteria, staphylococci and propionibacteria). Propionibacteria and staphylococci tended to dominate more than aerobic corynebacteria.

DISCUSSION

The most significant findings of this study were that the microflora of the axilla was not stable and that no one group of organisms continuously dominated the population. Furthermore, this study found there to be differences between the colonization of the left and the right axilla of the study volunteer, in terms of both population density and group dominance. Overall, the left axilla was predominantly colonized by aerobic corynebacteria. Interestingly, the fluctuation in the population density of the aerobic corynebacteria was greater than that of the other bacterial groups and it was the changes in the numbers of this bacterial group that determined dominance, with the other groups remaining largely unchanged. The changes observed in the colonization of both axillae are most likely due to changes in nutrient availability and environmental conditions in the axilla, which in turn determine the growth rate of the organisms.

Cutaneous microorganisms have been shown to produce bacteriocins with inhibitory effects on the growth of other bacteria (8, 9) and such inhibition may occur between species residing on the skin. Conversely there may be interdependence between bacterial groups residing on human skin.

Sample weeks 37–49 were during the summer and corresponded to the highest bacterial numbers recovered from both axillae and also the greatest variation between samples. This may be a reflection of increased temperature and humidity in the axilla at this time of year. The magnitude of the variation in the total number of bacteria in each axilla was less than that for each individual group, which may indicate a limit to the total biomass that can be sustained by the axilla.

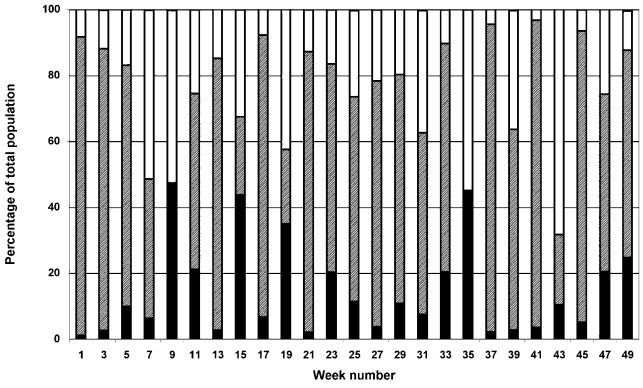

Fig. 2. Percentage composition of the microflora of the left axilla: staphylococci (black bars), aerobic corynebacteria (hatched bars), propionibacteria (open bars). The proportion of micrococci and Gram-negative organisms is too small to be seen in this figure.

ACKNOWLEDGEMENT

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