

BACTERIAL SKIN FLORA OF DIABETIC PATIENTS IN THE JOS UNIVERSITY TEACHING HOSPITAL, JOS.

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SUMMARY

Diabetics frequently are afflicted with bacterial skin infections because of the high circulating blood sugar. The frequent skin infections in these patients may be a result of change in normal skin flora. This study was carried out to find out the normal skin flora of these patients.

Ninety four (50 study and 44 control) consecutive subjects were studied for bacterial skin flora at the Jos University Teaching Hospital (JUTH). It was observed that Staphylococcus epidermidis was commonly isolated from the skin of diabetic subjects. Staphylococcus aureus ranked second for both groups. In the control group, Escherichia coli was the commonest organism isolated. Although, more organisms were isolated from study than from control subjects, there was no statistically significant difference in skin colonization. However the types of organisms colonizing the skin of the two groups were different.

One would, therefore, conclude that there is a change in bacterial skin flora of diabetic subjects from Escherichia coli which is the com-

monest in control subjects to Staphylococcus epidermidis which is the commonest in study subjects. This therefore may be the explanation for the increased prevalence of bacterial skin infection in the diabetics.

Key Words: Skin, flora, bacteria, diabetes.

INTRODUCTION

The human epithelium harbours a lot of microorganisms: bacteria, fungi and protozoa. These constitute the normal flora microorganisms[1]. Bacteria are the dominant organisms and these inhabit the epithelium of the skin, the nose, the mouth, upper respiratory surfaces, intestinal tracts and the genitourinary tracts[2,3]. Some of these normal flora microorganisms of the skin may be opportunistic pathogens and could cause infection if tissue injury occurs at specific sites or if the resistance of the body to infections is decreased. This is the case with prolonged antibiotic therapy, use of immunosuppressive drugs for the treatment of some diseases or diseases that cause immunosuppression [2]. Human immunodeficiency virus infection and diabetes mellitus are examples of such disease states.

In diabetes mellitus, there is paralysis of the cell mediated arm of the immune response. Diabetics therefore become prone to the development of bacterial skin infection. These bacteria also proliferate fast in these patients because of the excess sugar in their environment. This immune paralysis correlates well with the level of blood sugar, so that in poorly controlled diabetics, the immune paralysis is worse[4]. The study of bacterial skin flora of diabetic patients in JUTH, seeks to study the skin flora of both diabetics and non-diabetic controls. This is to determine whether there are differences in flora as diabetes mellitus has a lot of influence on the extracellular fluid of the body. This is also expected to influence the environment of the microorganism flora of the diabetic.

MATERIALS AND METHODS.

Patients with diabetes mellitus diagnosed and classified according to World Health Organisation guidelines [5,6] attending the diabetes clinic of the Jos University Teaching Hospital, Jos in Central Nigeria, were studied from July to December 2002. The study was approved by the hospital ethics committee.

Consecutive patients who consented to being part of the study after due explanation, were enrolled into the study. Patients who either did not consent to being part of the study or those that were on any kind of antibiotics: oral, parental, topical, as well as those who had other forms of immunosuppression like HIV/AIDS were excluded from the study.

The control subjects were similarly chosen from among patients from the endocrine clinic of the Jos University Teaching Hospital.

These subjects (study-diabetics and control-non-diabetics) had their armpits swabbed using swab sticks that had been soaked in a solution of normal saline. These swab sticks were cultured on media plates incubated at 37°C for a minimum of 18 hours. McConkey and Chocolate Agar media were used for aerobic and microaerophilic cultivation respectively. Resultant growths were identified by a set of cultural and biochemical characteristics including Gram's stain, oxidase, coagulase and catalase tests.

STATISTICAL ANALYSIS

Means were compared using the student's t-test and grouped frequencies were compared using chi-squared tests. The level of significance was determined by placing $P < 0.05$ in a two-tailed frequency distribution table.

RESULTS

There were 94 subjects in all: 50 were diabetics but only 44 non-diabetic controls agreed to participate in the study within the specified period. Of the 50 diabetics, 28 were females and 22 were males, and of the controls, 27 were females and 17 were males.

The mean(SD) age of the diabetic study subjects was 45.88(11.06) years while the mean(SD) age of the control non-diabetic subjects was 43.39(17.26) years. The study subjects seemed apparently older but there

Table 1: Distribution of Subjects by Organisms

| Organisms | Frequency Among Subjects | | Total | P-value |
|------------------------------------|--------------------------|-----------|------------|-------------------|
| | Study | Control | | |
| <u>Staph. epidermidis</u> | 27 | 7 | 34 | P=0.007173* |
| <u>Staph. aureus</u> | 13 | 10 | 23 | P=0.811906 |
| <u>Bacillus spp</u> | 13 | 9 | 22 | P=0.721644 |
| <u>Yersinia spp</u> | 1 | 0 | 1 | P=0 |
| <u>Klebsiella pneumoniae</u> | 3 | 5 | 8 | P=0.572 |
| <u>Streptococcus spp</u> | 3 | 0 | 3 | P=0 |
| <u>Serratia marcescens</u> | 0 | 3 | 3 | P=0 |
| <u>Corynebacterium diphtheriae</u> | 1 | 3 | 4 | P=0.479500 |
| <u>Escherichia coli</u> | 1 | 12 | 13 | P=0.000016* |
| <u>Pseudomonas aeruginosa</u> | 1 | 0 | 1 | P=0 |
| <u>Proteus mirabilis</u> | 1 | 0 | 1 | P=0 |
| <u>Enterobacter spp</u> | 0 | 1 | 1 | P=0 |
| Yeasts | 1 | 0 | 1 | P=0 |
| Total | 65 | 50 | 115 | P=0.169295 |

N.B. *statistically significant

was no statistically significant difference between the mean ages ($t=0.8328$, $P > 0.10$).

A total of 114 bacterial organisms with one yeast organism were isolated from these subjects. This was made up of 13 different organisms. Swabs from 10 (3 diabetic and 7 non-diabetic) subjects did not yield any bacterial growth after 48 hours of incubation. Thirty (30) cultures had mixed flora (i.e., more than one organism). Mixed flora were found more in the diabetics than in the controls (18 diabetics and 12 non-diabetics). Staphylococcus epidermidis was more frequent in diabetic patients than in controls. Staphylococcus aureus and Bacillus species were found in nearly equal frequencies in study and control subjects. The result of the frequency of bacterial culture is presented on Table 1.

There was a higher frequency of bacterial growth in diabetic patients than in controls although there was no statistically significant difference between diabetic and control subjects ($P=0.169$).

DISCUSSION

Generally, the bacterial organisms isolated from the skins of diabetics were similar to those recovered from non-diabetics but the frequencies of isolation from diabetics was higher than those from non-diabetics. This is probably due to the change in the environment of the diabetic skin flora, i.e., higher blood sugar leading to increase in the sustainability of normal flora and encouraging flora proliferation. The isolate, Staph. epidermidis was statistically significantly more frequent in the study than in the control subjects. The finding of Staph. epidermidis be-

ing the commonest bacterial microorganism in diabetics is different from that of Pelczar et al [2] who documented that Staph. epidermidis is the commonest bacterial microorganism found in the skin of normal non-diabetics. Kenneth Todar [7] has also documented that Staph. epidermidis is the commonest bacterial organism in normal skin flora. In our study, diabetics had more of Staph. epidermidis than control. This is a change, as one expects to find this organism more among the control. This change of organism is probably due to the fact that the high sugar levels in diabetics makes it conducive for the proliferation of normal skin flora. Consequently, diabetics are more prone to staphylococcal infections particularly in an abridged skin from whatever cause. Staph. epidermidis is, ordinarily not a pathogenic organism. Once its infection occurs in diabetics, it may lead to septicaemia, and as an opportunistic organism, proves difficult to treat. This occurs particularly after surgery.

Escherichia coli has been documented as part of normal flora of the skin, and in this study, it was the commonest microorganism isolated from non-diabetic control subjects. It was however, isolated from only one diabetic subject. This might suggest that the high sugar milieu of the skin of diabetic subjects may not be favourable for the proliferation and survival of E. coli.

From this study, with a change in the skin flora microorganisms from Escherichia coli to Staphylococcus epidermidis, one can infer that, this change explains the increased preva-

lence of staphylococcus infections in diabetic subjects than among any other group of subjects. Diabetics frequently have carbuncles or furuncles which are diseases caused by Staphylococcus particularly Staphylococcus aureus and when there is a septicaemia in diabetics, it is usually caused by Staphylococcus epidermidis. However, Staph. aureus is the next commonest bacterial organism found in our study and control subjects. Todar [7] has also documented that Staph. aureus is the second commonest bacterial organism of normal skin flora. Other organisms found were few. Klebsiella pneumoniae has been documented as part of normal skin flora and it was present more in controls than in study subjects though not to a statistically significant level ($P=0.572$). Overall finding of seeing more bacteria in diabetics than in control, though not statistically significant ($P=1693$), reveals that diabetics have a tendency to carry more organisms on their skin because of the high sugar level in circulation.

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