Diversity of Skin Bacteria Before and After Hand Wash

Talib J Kadium*   **Salwa Sh. Abdul-wahid****   **Sanna A. Abdul-wahab*****

*Prof. PhD. Veternary ; Dean of Diyala Medical College.

**MB;CHB.MSc.PhD. Community Medicine,Assist Prof./ Diyala Medical College.

*** PhD Microbiology / Assist Prof. College of Dendistry /Baghdad University.

Abstract

Back ground: The layers and structures of the skin serve as elaborate hosts to microbes, including a diversity of commensally and pathogenic bacteria that contribute to both human health and disease.

Aim: This study conducted to identify the microbes inhabiting the skin, and its density before and after hand washing.

Subjects &Methods: The study sample included 120 healthy undergraduate students from Diyala Medical College aged 20-22 years. Skin swabs from the hands before & after hand wash were taken. Detergent & disinfectants were used in hand washing.

Results: The results reveal that there were many types of bacteria inhabiting the skin, decreased in density after hand washing.

Key wards: Hand wash; skin bacteria; Detergent; Alcohol; Dettol**.**

التنوع البكتيري على الجلد قبل وبعد غسل اليدين

ا.د.طالب جواد كاظم وا.م.د.سلوى شلش عبد الواحد وا.م.د.سناء عبد السلام عبد الوهاب

الخلاصة

ان طبقات وهياكل الجلد تخدم المضيفين من الميكروبات، بما في ذلك مجموعة متنوعة من البكتيريا المتعايشة والبكتيريا المسببة للأمراض لدى الانسان وكذلك البكتيريا التي تساهم في صحة البشر . هذه الدراسة أجريت للتعرف على الميكروبات التي تعيش على الجلد، وكثافته قبل وبعد غسل اليدين. وشملت عينة الدراسة (120) طالبا من الاصحاء في المرحلة الجامعية من كلية الطب \ جامعة ديالى والذين تتراوح أعمارهم بين 20-22 عاما. أخذت مسحات الجلد من اليدين قبل وبعد

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غسل اليد. استخدمت المنظفات والمطهرات في غسل اليدين. أظهرت النتائج أن هناك العديد من أنواع البكتيريا التي تعيش على الجلد، ولوحظ انخفاض في كثافتها بعد غسل اليدين.

الكلمات المفتاحية : غسل اليدين ، بكتريا الجلد ، منظفات ، الكحول ،ديتول

Introduction

Bacteria thrive on and within the human body. One of the largest human-associated microbial habitats is the skin surface, which harbors large numbers of bacteria that can have important effects on health. Microorganisms play a central role in the regulation of ecosystem processes, and they comprise the vast majority of species on Earth. With recent developments in molecular methods, it has become tractable to quantify the extent of microbial diversity in natural environments (1). The skin surface is the largest human associated microbial habitats which harbors large numbers of bacteria that can have important effects on health. One of the largest human-associated microbial habitats is the skin surface, which harbors large numbers of bacteria that can have important effects on health (2, 3).Many of these bacteria are not simply passive or transient colonizers of the skin surface, but rather appear to be adapted to the specific rigors associated with living in different regions of the skin including frequent skin shedding, antimicrobial host defenses, exposure to soaps and detergents during washing, exposure to UV radiation, and low moisture availability (4, 5). Those bacterial communities that reside on the skin surface appear to be diverse, but the full extent of bacterial diversity has not been adequately determined (6). Currently, the factors driving this variability in skin bacterial community composition are not well understood (7,8). Hand wash & human skin microbiota will serve to direct future research addressing the role of skin microbiota in health and disease, and in projects addressing the complex physiological interactions between the skin and the microbes that inhabit this environment.(5).Skin hygiene, particularly of the hands, is a primary mechanism for reducing contact and fecal-oral transmission of infectious agents. Widespread use of antimicrobial products has prompted concern about emergence of resistance to antiseptics and damage to the skin barrier associated with frequent washing (8,9). Although bacteria are common on all skin surfaces, we focused on bacteria found on the palm because it is likely one of the more dynamic skin microbial habitats given the nearly constant and varied exposure to environmental surfaces and the frequency of perturbations caused by hand washing. In addition, pathogens may inhabit the palmar surface, and efforts to reduce disease

transmission by hand washing are a key public health concern (10,11). This study aims to identify various types of bacteria that inhibit the skin before & after hand wash with soap and disinfectants.

Subjects & Methods

Skin swabs were taken from different skin sites of (120) healthy, male & female volunteers who were students of Diyala Medical College. The researchers obtained (5) swabs from different sites of their hands' skin.   The skin bacteria were grown aerobically on agar at 37°C for 48 hours. All isolates were Gram-positive; they were characterized by macroscopic and microscopic analyses. They were plated on blood agar, nutrient agar, Mackonkey and selective agar plates (kanamycin and Mannitol salt).

Sample Collection.

From Diyala Medical College (120) undergraduate medical students were asked to participate in this study in November 2011 for specimen collection the students exited a room where they had all spent the previous hour taking an examination. Samples were collected from the palm surfaces of these students. Each subject provided information on their handedness and the time since last hand washing. The palm surfaces of both hands were swabbed separately with cotton tipped swabs moistened with distal water before using different antibacterial reagents. The entire palm surface was swabbed in 2 perpendicular directions to ensure that the maximum surface area of each palm was represented in the sample. Each individual washed his/her hands for 30 seconds with soap, followed by rinsing with tap water were swabbed in the exact same manner as described above. The same manner was followed with Dettol and heptane.

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Results

Table (1) Characteristics related to the study sample

Characteristics	Number	%
Gender		
Male	50	41.6
Female	70	58.4
Age		
19-21	82	68.3
22-24	38	31.7
Hands wash after		
After food intake	48	40.0
Before food intake	12	10.0
After WC	64	53.3
Before WC	10	8.3
Number of hands washIn home		
3+<	81	
>3	39	67.5
		32.5
Wash Materials used Soap	96	80.0
Dettol	4	3.3
Al-cohol	20	16.7
Time of wash		
60 second	88	73.3
➤ 60 second	32	36.7
Source of water used		
Tap water	120	100.0
Other	0	

Table (2) Distribution & types of skin bacteria according to disinfectant used.

Type of bacteria	Water 1m* 2m 5m	Alcohol 1m* 2m 5m	Dettol 1m* 2m 5m
E.coli	10% 40% 60%	1% 7% 10%	5% 10% 20%
Pseudomonas	5% 40% 60%	1% 5% 8%	5% 10% 25%
Staphylococci	2% 25% 45%	0% 2% 4%	2% 5% 15%
Streptococci	5% 20% 30%	0% 0% 1%	1% 7% 3%

*m = Minute

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Table (3) Distribution & types of skin bacteria according to detergent used.

Type of bacteria	Water			Soap		
	1m*	2m	5m	1m*	2m	5m
E.coli	4%	40%	60%	1%	20%	70%
Pseudomonas	5%	40%	16%	1%	20%	60%
Staphylococcus	2%	20%	40%	2%	10% 15%	40%
Streptococci	1%	15%	30%	2%	7%	30%

*m = Minute

Discussion

In the current study the researchers found a large numbers of bacteria in the student's swabs approximately for all samples, the researchers also explored the factors that contribute to the seemingly astounding numbers of microbial colonies found within individual samples. Nearly all samples contained hundreds of bacterial colonies. When personal features are taken into consideration, Many of the concepts developed to explain plant and animal diversity patterns can also be applied to microorganisms once we reconcile the scale of our analyses to the scale of the organisms being observed. Furthermore, knowledge from microbial systems may provide insight into the mechanisms that generate and maintain species richness in nonmicrobial systems. E-coli , pseudomonas ,which are Gram (-) bacteria are most prominent than Gram (+), when water used . While Al-cohol give an equal killing for all bacteria. Dettol affect Gram (+) bacteria . most than G(-) bacteria. Detergent (soap) shows a clear antibacterial activity also against the isolated bacteria.Noah Fierer et al. stated that the diversity of skin-associated bacterial communities was surprisingly high; a typical hand surface harbored >150 unique species-level bacterial phylotypes, and they identified a total of 4,742 unique phylotypes across all of the hands examined (1).The microbial communities of humans are characteristic and complex mixtures of microorganisms that have co-evolved with their human hosts. The species that make up these communities vary between hosts as a result of restricted migration of microorganisms between hosts and strong ecological interactions within hosts, as well as host

variability in terms of diet, genotype and colonization history(12,13). The result of current study showed antibacterial effect of alcohol   followed by soap, Dettol and water respectively. Colonization is driven by the ecology of the skin surface, which is highly variable depending on topographical location, endogenous host factors and exogenous environmental factors (5,14). For determination of the complexity of the microbes inhabiting the skin, Elizabeth A. Grice et al sequenced bacterial 16S small-subunit ribosomal RNA genes isolated from the inner elbow of five healthy human subjects. The study revealed 113 operational taxonomic units at the level of 97% similarity that belong to six bacterial divisions. The researchers using three methods: swab, scrape, and punch biopsy. Proteo -bacteria dominated the skin microbiota at all depths of sampling. Grice E.et al also stated that Interpersonal variation is approximately equal to intrapersonal variation when considering bacterial community membership and structure (7). To test whether an association exists between the intensity of chlorhexidine use and chlorhexidine susceptibility of micro-organisms isolated from patients in different clinical areas in an acute-care general hospital. Block C&, Furman M, in their study they stated that organisms frequently involved in nosocomial infections in the hospital were chosen for study over a six week period. The results of their study were Staphylococcus aureus (60 isolates), coagulase-negative staphylococci (48), Klebsiella pneumoniae (32), Pseudomonas aeruginosa (60), Acinetobacter baumannii (16) and Candida albicans (35). A statistically significant inverse correlation was shown between intensity of chlorhexidine use and the overall susceptibility of all study organisms taken together. There was no association when individual taxa were considered (15). To investigate the potential of *Salmonella enterica* and *Escherichia coli* O157 for adaptive resistance to commonly used biocides and to determine any cross-resistance to antibiotics Braoudaki M and Hilton AC conduct their study and concluded that adaptive resistance was readily achieved for both S. enterica and E. coli O157. Cross-resistance in adaptively resistant S. enterica varied with the serotype; Salmonella enterica serovar Enteritidis expressed cross-resistance to chloramphenicol, whereas Salmonella enterica serovar Typhimurium expressed cross-resistance to chlorhexidine. Benzalkonium chloride-resistant Salmonella enterica serovar Virchow showed elevated resistance to chlorhexidine; however, chlorhexidine-resistant Salmonella serovar Virchow did not demonstrate reciprocal cross-

resistance to benzalkonium chloride, suggesting specific rather than generic resistance mechanisms (16). Apparent differences in the bacterial response to soap & Dettol found which showed a decrease in susceptibility after exposure to these detergent and disinfectant.

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