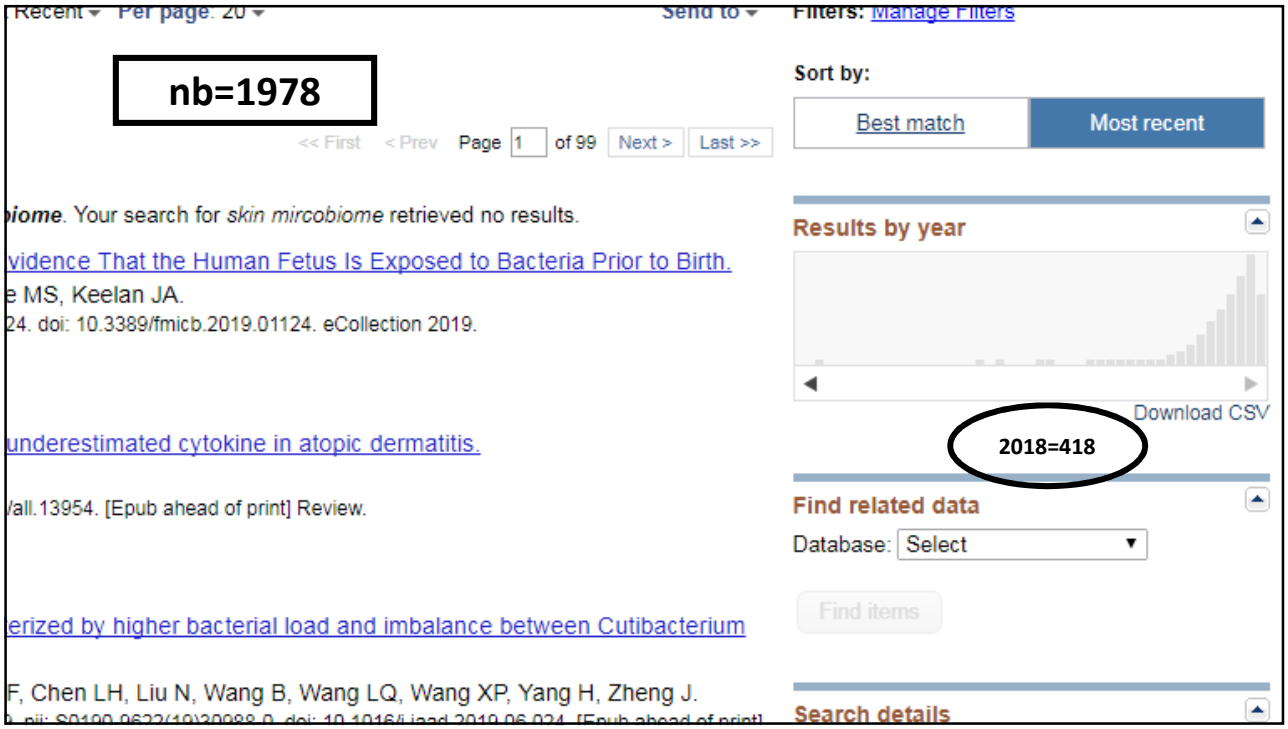
Microbiome cutané



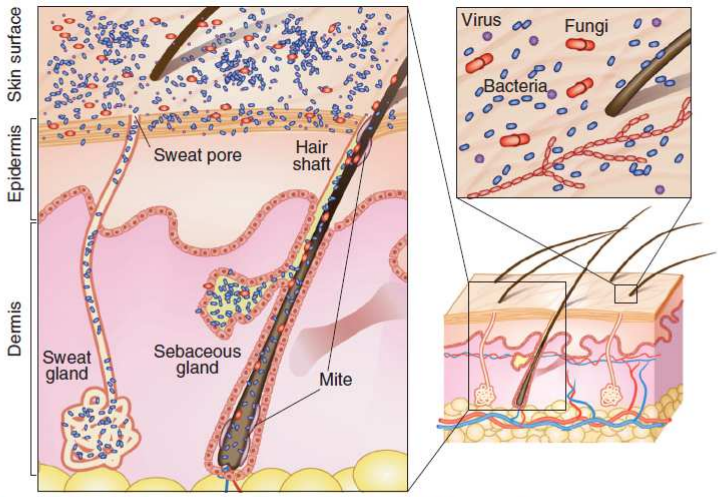
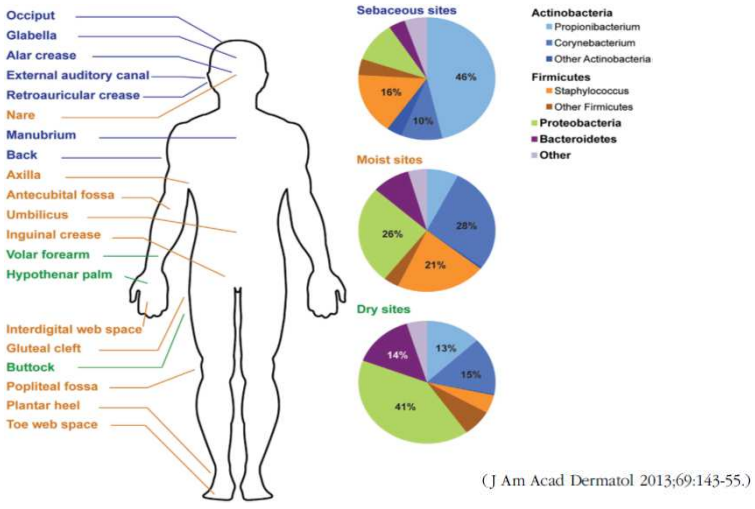


Figure 1. Schematic of skin histology viewed in cross-section with microorganisms and skin appendages. Microorganisms (viruses, bacteria and fungi, and mites) cover the surface of the skin and reside deep within the hair and glands.



(J Am Acad Dermatol 2013;69:143-55.)

Fig 3. Microbiome composition on normal-appearing human skin. Sebaceous (*blue text*), moist (*orange text*), and dry (*green text*) habitats are labeled anatomically. Microbial composition differs among habitats (pie charts at right). Four major phyla are shown: *Actinobacteria*, *Firmicutes*, *Proteobacteria*, and *Bacteroidetes*. Within these phyla, 3 most abundant genera are also shown: *Propionibacterium*, *Corynebacterium*, and *Staphylococcus*. Figure is compiled with data pooled from many metagenomes, from Grice et al.[31] Figure is adapted from Fig 3 in Grice and Segre[9] with permission from Nature Publishing Group.

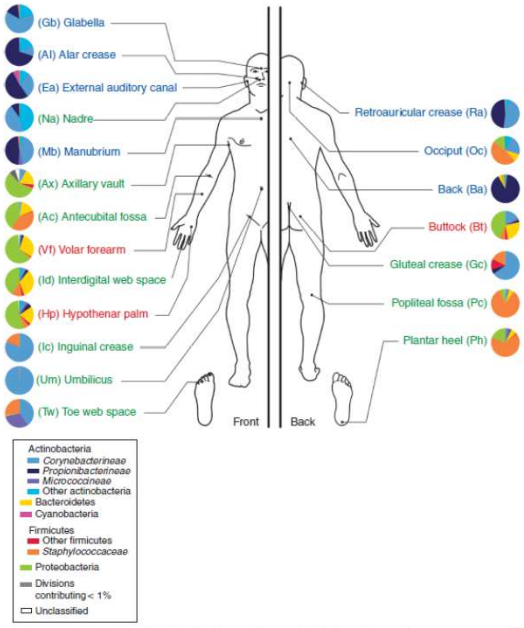


Figure 3. Topographical distribution of bacteria on skin sites. The skin microbiome is highly dependent on the microenvironment of the sampled site. Sebaceous sites are labeled in blue, moist sites are labeled in green, and dry surfaces are labeled in red. Family-level classification of bacteria colonizing an individual subject is shown. Data are from Grice *et al.* (2009).

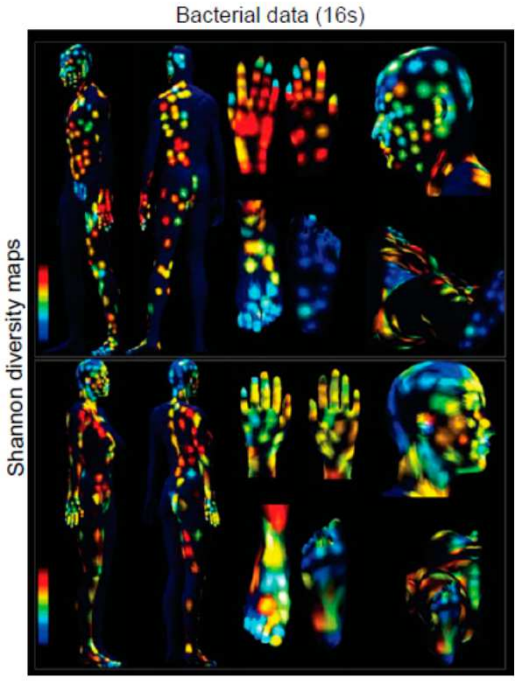
Journal of Investigative Dermatology (2012), Volume 132

PNAS

Molecular cartography of the human skin surface in 3D

Amina Bouslimani[a,1], Carla Porto[a,1], Christopher M. Rath[a,1], Mingxun Wang[b], Yurong Guo[c], Antonio Gonzalez[d,e], Donna Berg-Lyon[d,e], Gail Ackermann[d,e], Gitte Julie Moeller Christensen[a,f], Teruaki Nakatsuji[g], Lingjuan Zhang[g], Andrew W. Borkowski[g], Michael J. Meehan[a], Kathleen Dorrestein[a], Richard L. Gallo[g], Nuno Bandeira[a,b,h,i,2], Rob Knight[d,e,j,k,l,2], Theodore Alexandrov[a,i,h,i,2], and Pieter C. Dorrestein[a,m,n,o,2]

[a]Skaggs School of Pharmacy and Pharmaceutical Sciences, [b]School of Medicine, [c]Division of Dermatology, and Departments of [d]Biochemistry, [e]Pharmacology, and [f]Chemistry, University of California, San Diego, La Jolla, CA 92037; [g]Department of Computer Science and Engineering and [h]Center for Computational Mass Spectrometry, University of California, San Diego, La Jolla, CA 92093; [i]Department of Chemistry and Biochemistry, [j]BioFrontiers Institute, and [k]Howard Hughes Medical Institute, University of Colorado at Boulder, Boulder, CO 80309; [l]Department of Biomedicine, Aarhus University, DK-8000 Aarhus C, Denmark; [m]Center for Industrial Mathematics, University of Bremen, 28359 Bremen, Germany; [n]SCiLS GmbH, 28359 Bremen, Germany; and [o]European Molecular Biology Laboratory, Meyerhofstrasse 1, 69117 Heidelberg, Germany



REVIEW ARTICLE

Papulopustular rosacea, skin immunity and Demodex: pityriasis folliculorum as a missing link

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*Correspondence: F.M.N. Forton. E mail: fabienne.forton@skynet.be

CLINICAL AND LABORATORY INVESTIGATIONS

BJD
British Journal of Dermatology

Demodex-associated bacterial proteins induce neutrophil activation

N. O'Reilly,* D. Bergin,† E.P. Reeves,† N.G. McElvaney† and K. Kavanagh*

*Medical Mycology Unit, Department of Biology, National University of Ireland Maynooth, Co. Kildare, Ireland
†Respiratory Research Division, Department of Medicine, Royal College of Surgeons in Ireland, Beaumont Hospital, Dublin 9, Ireland

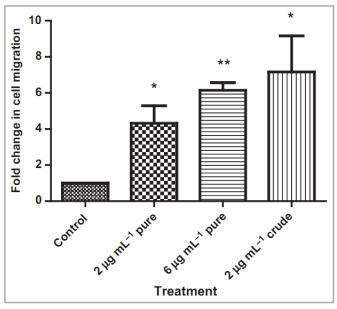

Fig 2. The effect of *B. oleronius* proteins on migration of human neutrophils through 3-μm porous inserts. The results are presented as a fold change in cell density compared with control, where a significant increase of $P < 0.05$ is denoted by * and $P < 0.01$ is denoted by **.

Journal of Infection 78 (2019) 119–126

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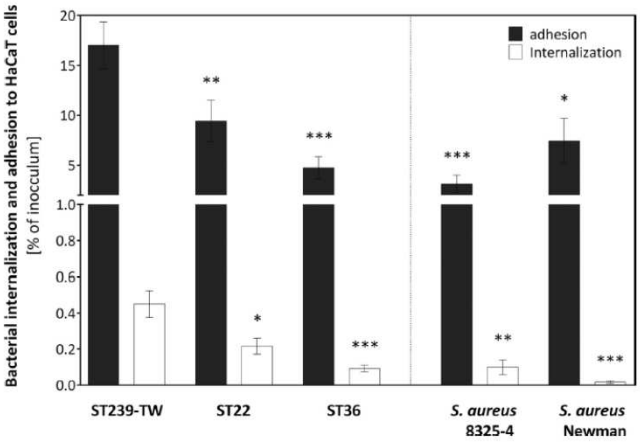
journal homepage: www.elsevier.com/locate/jinf

Tolerance of MRSA ST239-TW to chlorhexidine-based decolonization: Evidence for keratinocyte invasion as a mechanism of biocide evasion

Helene Marbach[a,1], Gema Vizcay-Barrena[b], Kaveh Memarzadeh[c], Jonathan A. Otter[d,2], Smriti Pathak[d], Robert P. Allaker[c], Richard D. Harvey[a,*], Jonathan D. Edgeworth[d]

[a] Faculty of Life Sciences and Medicine, Institute of Pharmaceutical Science,
[b] Centre for Ultrastructural Imaging, King's College London, Guy's Campus, L
[c] Barts and The London School of Medicine and Dentistry, Queen Mary Univ
[d] Department of Infectious Diseases, Centre for Clinical Infection and Diagno
Foundation Trust (GSTT), London, UK



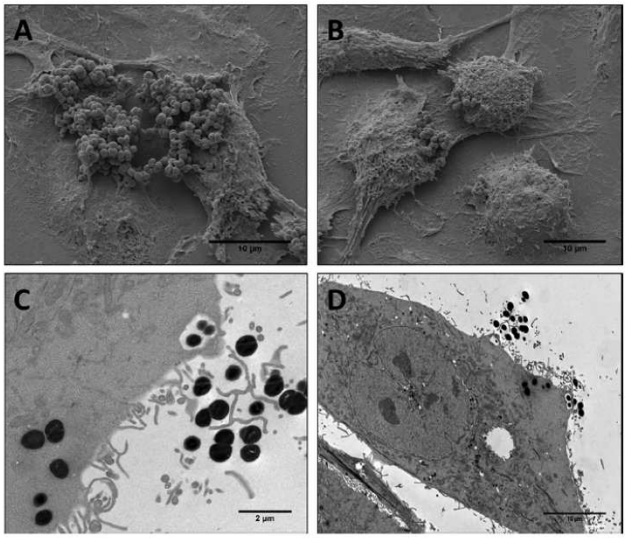


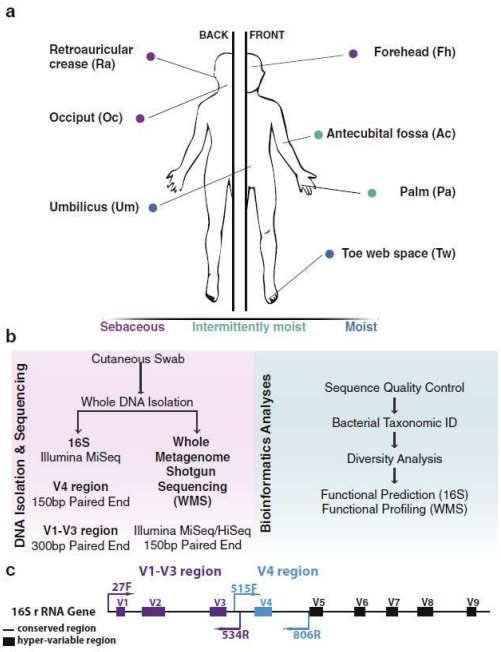
Fig. 3. Electron micrographs of HaCaT cells infected with MRSA ST239-TW strain (TW20)[20]. SEM (A, B) of adhered ST239-TW and TEM (C, D) of surrounding, and internalized ST239-TW, either presenting in vacuoles or embedded in the cell cytoplasm. SEM shows the top view and TEM a cross section of co-incubated HaCaT cells with ST239-TW (TW20) bacteria for one hour and a three time wash with PBS.

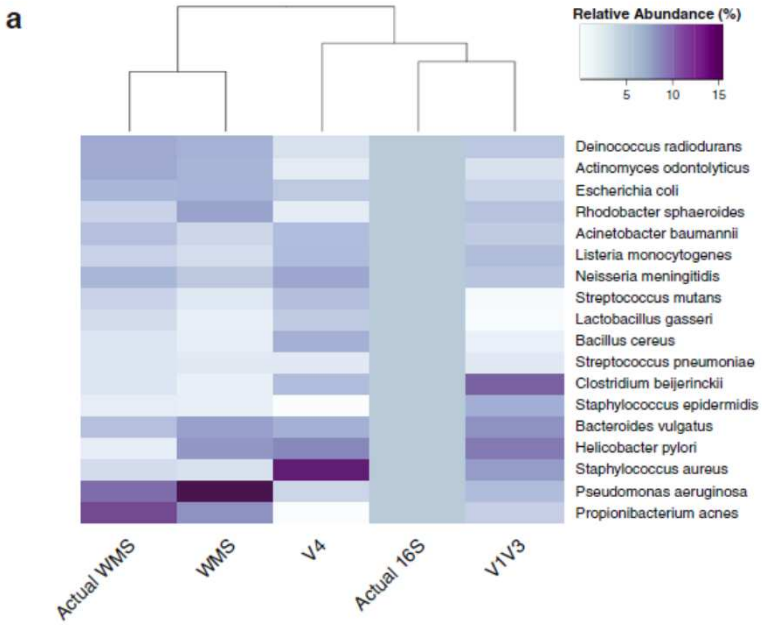
Microbiome change selon technique de recherche

Skin Microbiome Surveys Are Strongly Influenced by Experimental Design

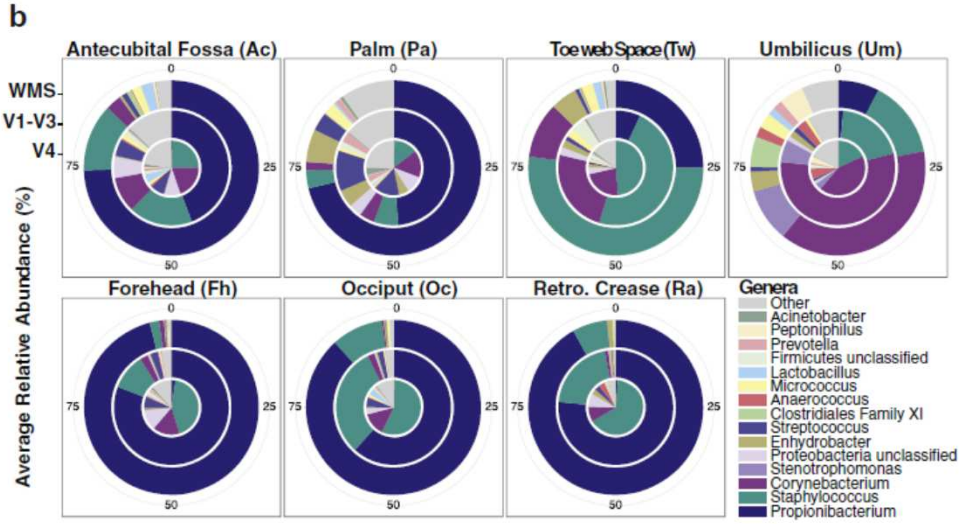
Jacquelyn S. Meisel[1], Geoffrey D. Hannigan[1], Amanda S. Tyldsley[1], Adam J. SanMiguel[1], Brendan P. Hodkinson[1], Qi Zheng[1] and Elizabeth A. Grice[1]

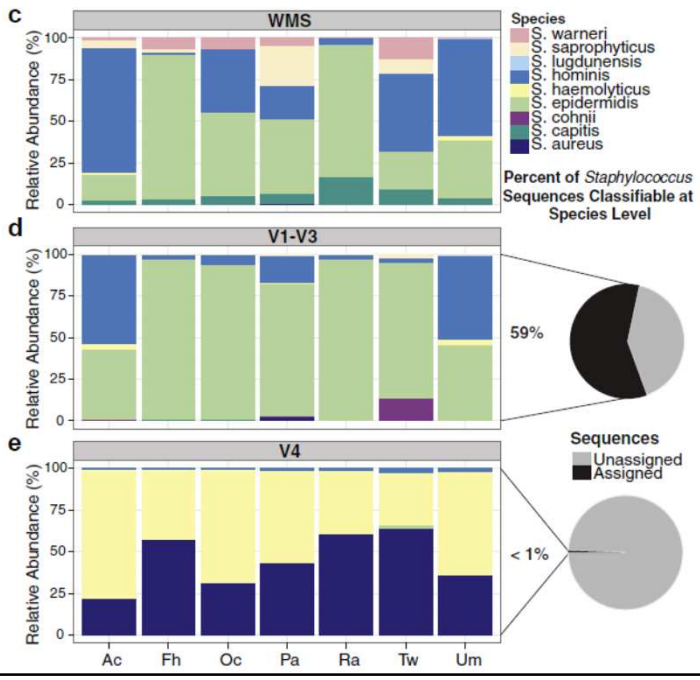
Culture-independent studies to characterize skin microbiota are increasingly common, due in part to affordable and accessible sequencing and analysis platforms. Compared to culture-based techniques, DNA sequencing of the bacterial 16S ribosomal RNA (rRNA) gene or whole metagenome shotgun (WMS) sequencing provides more precise microbial community characterizations. Most widely used protocols were developed to characterize microbiota of other habitats (i.e., gastrointestinal) and have not been systematically compared for their utility in skin microbiome surveys. Here we establish a resource for the cutaneous research community to


a
BACK
FRONT
Retroauricular crease (Ra)
Occiput (Oc)
Umbilicus (Um)
Forehead (Fh)
Antecubital fossa (Ac)
Palm (Pa)
Toe web space (Tw)
Sebaceous
Intermittently moist
Moist
b
DNA Isolation & Sequencing
Cutaneous Swab
Whole DNA Isolation
16S
Illumina MiSeq
V4 region
150bp Paired End
Whole Metagenome Shotgun Sequencing (WMS)
V1-V3 region
300bp Paired End
Illumina MiSeq/HiSeq
150bp Paired End
Bioinformatics Analyses
Sequence Quality Control
Bacterial Taxonomic ID
Diversity Analysis
Functional Prediction (16S)
Functional Profiling (WMS)
c
V1-V3 region
V4 region
27F
515F
16S r RNA Gene
V1
V2
V3
V4
V5
V6
V7
V8
V9
conserved region
hyper-variable region
534R
806R

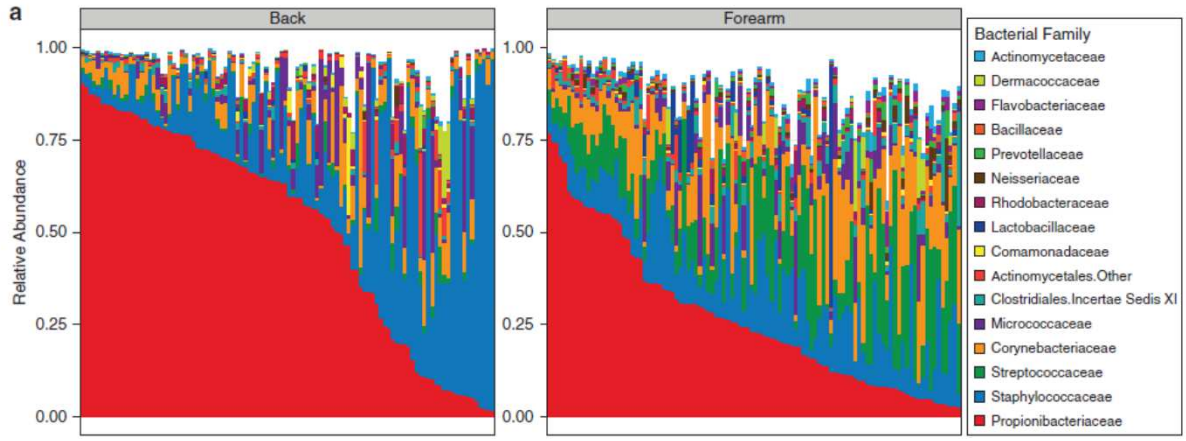

a
Relative Abundance (%)
5
10
15
Deinococcus radiodurans
Actinomyces odontolyticus
Escherichia coli
Rhodobacter sphaeroides
Acinetobacter baumannii
Listeria monocytogenes
Neisseria meningitidis
Streptococcus mutans
Lactobacillus gasseri
Bacillus cereus
Streptococcus pneumoniae
Clostridium beijerinckii
Staphylococcus epidermidis
Bacteroides vulgatus
Helicobacter pylori
Staphylococcus aureus
Pseudomonas aeruginosa
Propionibacterium acnes
Actual WMS
WMS
V4
Actual 16S
V1V3

Microbiome change selon site





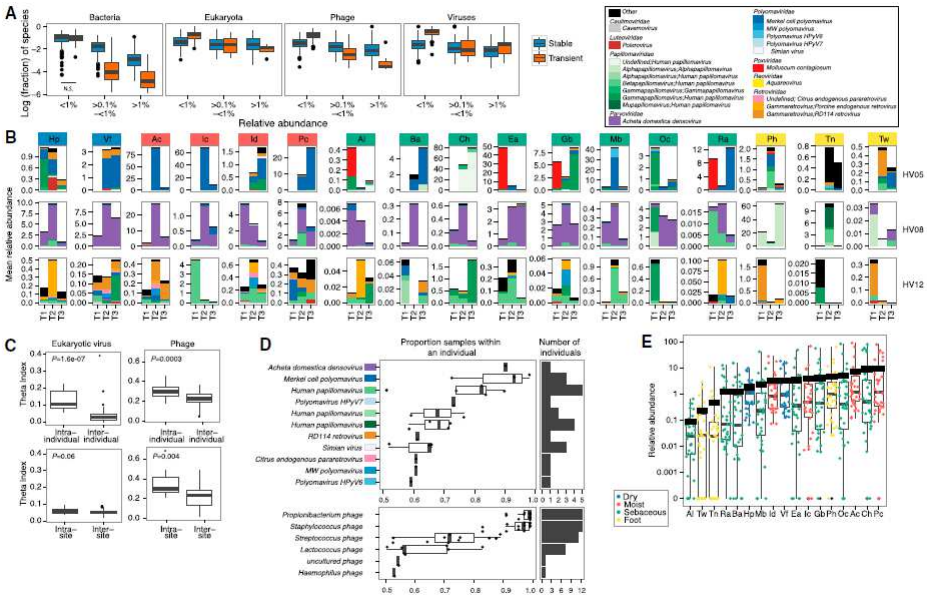
Microbiome change selon individus



Article

Cell

Temporal Stability of the Human Skin Microbiome

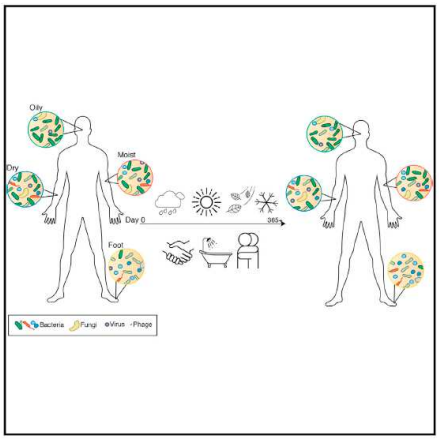


Article

Cell

Temporal Stability of the Human Skin Microbiome

Graphical Abstract



Authors

Julia Oh, Allyson L. Byrd, Morgan Park, NISC Comparative Sequencing Program, Heidi H. Kong, Julia A. Segre

Correspondence

konghe@mail.nih.gov (H.H.K.), jsegre@mail.nih.gov (J.A.S.)

In Brief

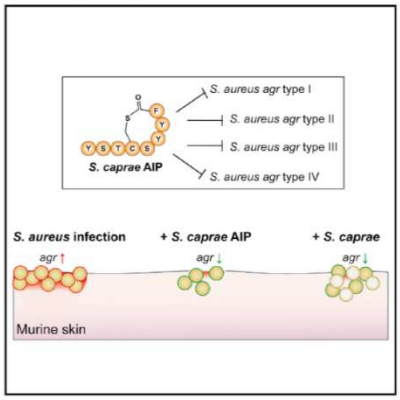
Healthy adults stably maintain their skin microbial communities over time at the kingdom, phylum, species, and even, strain level, despite constant exposure to the external environment and other individuals.

Article

Cell Host & Microbe

Coagulase-Negative Staphylococcal Strain Prevents *Staphylococcus aureus* Colonization and Skin Infection by Blocking Quorum Sensing

Graphical Abstract



Authors

Alexandra E. Paharik, Corey P. Parlet, Nadjali Chung, ..., Michael J. Van Dyke, Nadja B. Cech, Alexander R. Horswill

Correspondence

alexander.horswill@ucdenver.edu

In Brief

Paharik, Parlet, et al. demonstrate that the human commensal *Staphylococcus caprae* competes with *Staphylococcus aureus* by inhibiting quorum sensing. Through signal interference, *S. caprae* reduces methicillin-resistant *S. aureus* burden in both skin colonization and infection, highlighting the benefits of healthy skin flora and suggesting a new avenue for probiotic therapy.

TRANSLATIONAL RESEARCH

BJD
British Journal of Dermatology

Staphylococcus aureus colonization in atopic eczema and its association with filaggrin gene mutations

M.-L. Clausen,[1] S.M. Edslev,[2] P.S. Andersen,[2,3] K. Clemmensen,[1] K.A. Krogfelt[2] and T. Agner[1]

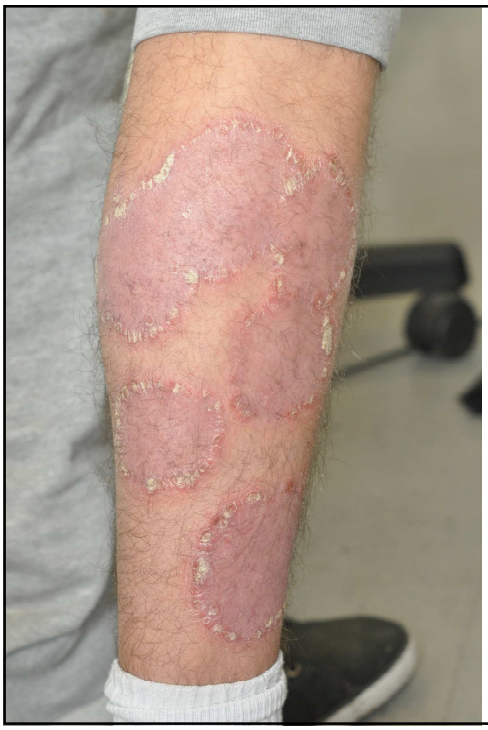
[1]Department of Dermatology, Bispebjerg University Hospital, Copenhagen, Denmark
[2]Department of Microbiology and Infection Control, Statens Serum Institut, Copenhagen, Denmark
[3]Institute of Veterinary Disease Biology, University of Copenhagen, Copenhagen, Denmark

LETTER

doi:10.1038/nature12655

Staphylococcus δ-toxin induces allergic skin disease by activating mast cells

Yuumi Nakamura[1], Jon Oscherwitz[2,3], Kemp B. Cease[2,3], Susana M. Chan[1], Raul Muñoz-Planillo[1], Mizuho Hasegawa[1], Amer E. Villaruz[4], Gordon Y. C. Cheung[4], Martin J. McGavin[5], Jeffrey B. Travers[6], Michael Otto[4], Naohiro Inohara[1] & Gabriel Núñez[1]



PLOS ONE

RESEARCH ARTICLE

IL-22/STAT3-Induced Increases in SLURP1 Expression within Psoriatic Lesions Exerts Antimicrobial Effects against *Staphylococcus aureus*

Yasuhiro Moriwaki[1]*, Kiyoko Takada[1], Toshinori Nagasaki[1], Natsuki Kubo[1], Tomohiro Ishii[1], Kazuaki Kose[1], Taihei Kageyama[2], Shoutaro Tsuji[2], Koichiro Kawashima[3], Hidemi Misawa[1]*

1 Department of Pharmacology, Faculty of Pharmacy, Keio University, Minato-ku, Tokyo 105–8512, Japan, 2 Molecular Diagnostics Project, Kanagawa Cancer Center Research Institute, Yokohama, Kanagawa, Japan, 3 Department of Molecular Pharmacology, Kitasato University School of Pharmacy, Minato-ku, Tokyo, Japan

RESEARCH ARTICLE

PSORIASIS

IL-29 Is Produced by T_H17 Cells and Mediates the Cutaneous Antiviral Competence in Psoriasis

Kerstin Wolk,[1,2,3,†] Katrin Witte,[1,2†] Ellen Witte,[1,2] Martin Raftery,[4] Georgios Kokolakis,[1,2] Sandra Philipp,[1,2] Günther Schönrich,[4] Katarzyna Warszawska,[1] Stefan Kirsch,[1] Susanna Prösch,[4†] Wolfram Sterry,[5] Hans-Dieter Volk,[6,7] Robert Sabat[1,2,7*]

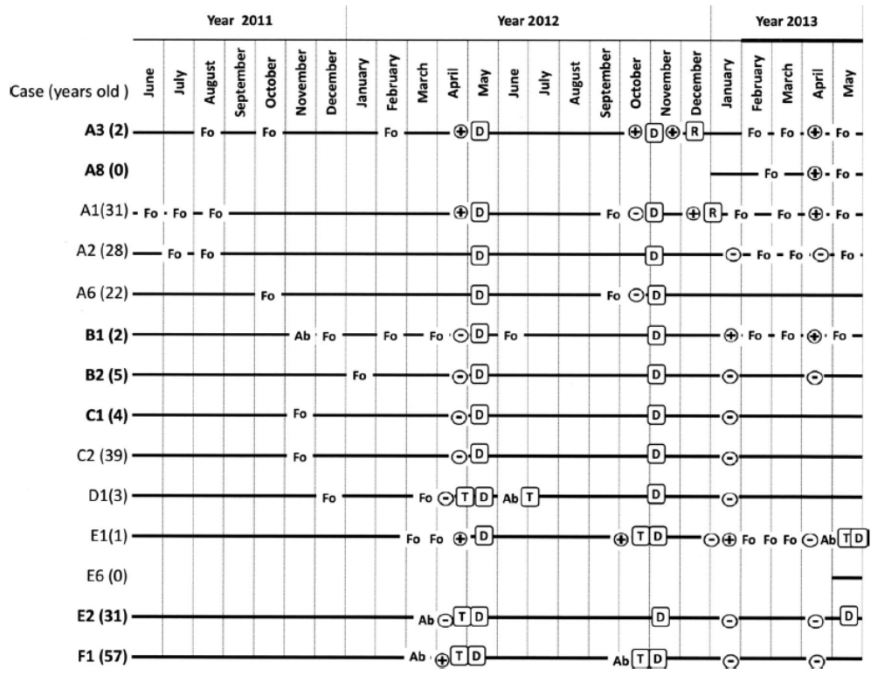
Psoriasis and atopic dermatitis (AD) are the most common chronic inflammatory skin diseases. Although both patient groups show strongly impaired skin barrier function, only AD patients frequently suffer from cutaneous viral infections. The mechanisms underlying the distinct susceptibilities to these pathogenetic and often life-threatening infections are unknown. We show that antiviral proteins (AVPs) such as MX1, BST2, ISG15, and OAS2 were strongly elevated in psoriatic compared to AD lesions and healthy skin. Of 30 individually quantified cytokines in psoriatic lesions, interleukin-29 (IL-29) was the only mediator whose expression correlated with the AVP levels. IL-29 was absent in AD lesions, and neutralization of IL-29 in psoriatic skin reduced AVP expression. Accordingly, IL-29 raised AVP levels in isolated keratinocytes, epidermis models, and human skin explants, but did not influence antibacterial protein production. AVP induction correlated with increased antiviral defense of IL-29–treated keratinocytes. Furthermore, IL-29 elevated the expression of signaling elements, resulting in increased sensitivity of keratinocytes toward its own action. We identified T helper 17 (T_H17) cells as IL-29 producers and demonstrated their ability to increase the antiviral competence of keratinocytes in an IL-29–dependent manner. Transforming growth factor-β and the activity of RORγt/RORα were most critical for the development of IL-29–producing T_H17 cells. IL-29 secretion by these cells was dependent on NFAT and c-Jun N-terminal kinase and was inhibited by IL-4. These data suggest that T_H17 cell–derived IL-29, which is absent in AD, mediates the robust antiviral state on psoriatic skin, and demonstrate a new function of T_H17 cells.

Eur J Clin Microbiol Infect Dis (2014) 33:1757–1762
DOI 10.1007/s10096-014-2127-6

ARTICLE

First outbreak of community-acquired MRSA USA300 in France: failure to suppress prolonged MRSA carriage despite decontamination procedures

O. Baud · S. Giron · C. Aumeran · D. Mouly · G. Bardon · M. Besson · J. Delmas · B. Coignard · A. Tristan · F. Vandenesch · G. Illes · O. Lesens


Year 2011
Year 2012
Year 2013
Case (years old)
June
July
August
September
October
November
December
January
February
March
April
May
June
July
August
September
October
November
December
January
February
March
April
May
A3 (2)
A8 (0)
A1(31)
A2 (28)
A6 (22)
B1 (2)
B2 (5)
C1 (4)
C2 (39)
D1(3)
E1(1)
E6 (0)
E2 (31)
F1 (57)