

Il microbiota del cuoio capelluto e dei capelli



**DERMOBIOTICA
MICROBIOTA E PELLE**

Modena, 29 Novembre 2018

Relatrice: Daniela Pinto, PhD



DISBIOSI del MICROBIOMA

DISBIOSI
ADATTAMENTO

EUBIOSI
RESILIENZA



**Patologie della cute e dello
scalpo**



PubMed

Ricerca per «SKIN» and «MICROBIOME»

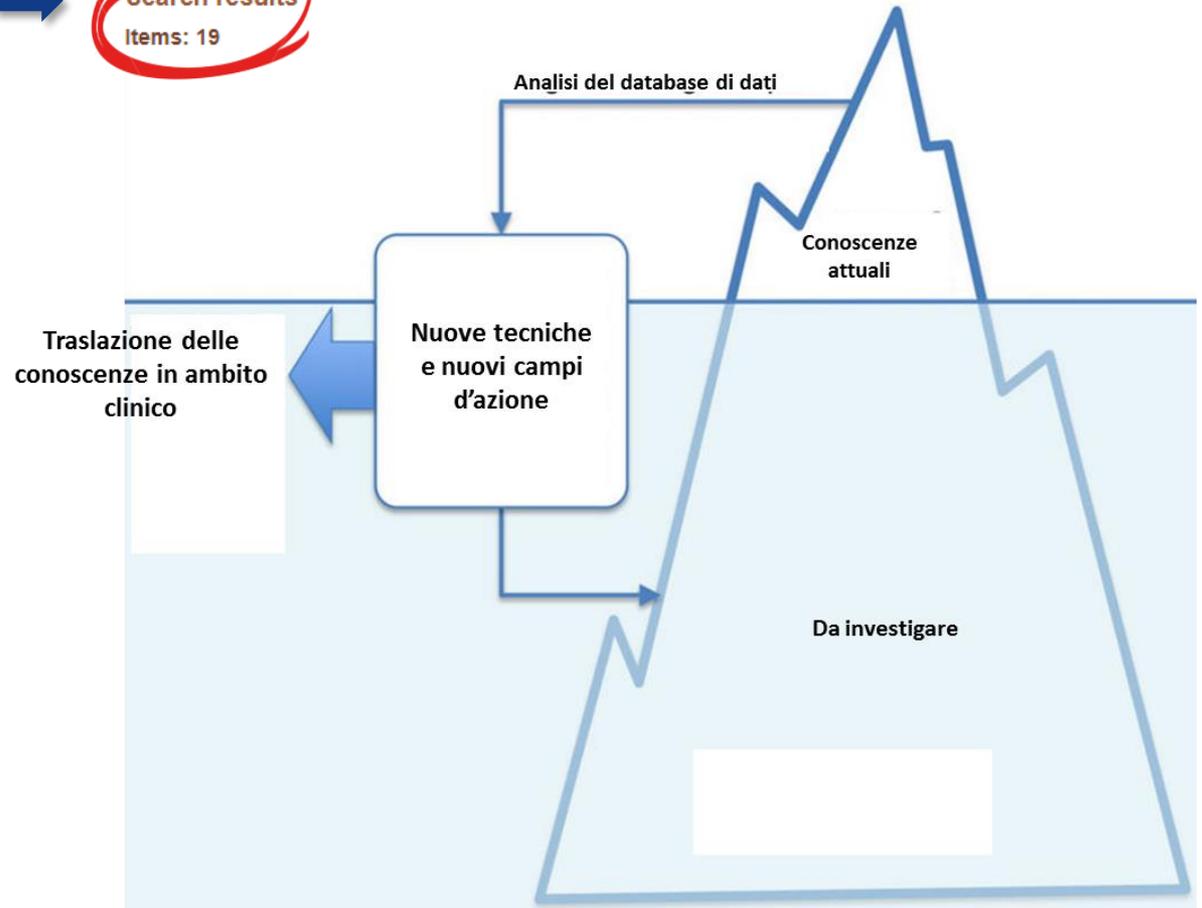


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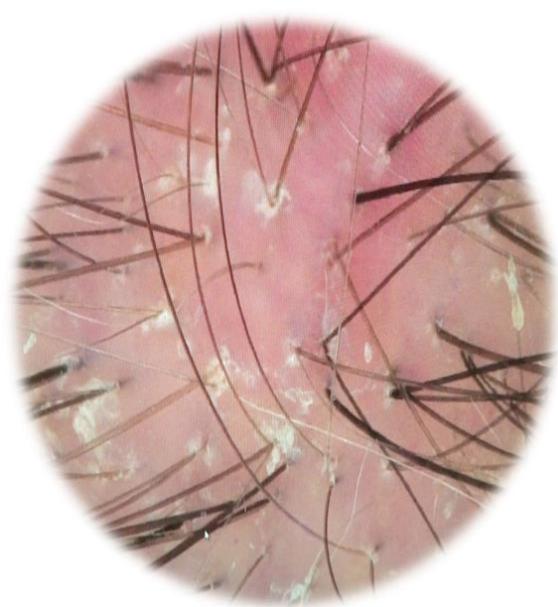
Ricerca per «SCALP» and «MICROBIOME»



Search results
Items: 19



La disbiosi del microbioma può essere causa di patologie dello scalpo?
L'esempio della dermatite seborroica



FORFORA e DERMATITE SEBORROICA

Experimental Dermatology

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LETTER TO THE EDITOR

Collapse of human scalp microbiome network in dandruff and seborrhoeic dermatitis

Taehun Park, Hye-Jin Kim, Nu Ri Myeong, Hyun Gee Lee, Ilyoung Kwack

Johnhwan Lee, Beom Joon Kim, Woo Jun Sul , Susun An 

First published: 11 April 2017 [Full publication history](#)

DOI: 10.1111/exd.13293 [View/save citation](#)



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Volume 26, Issue 9
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Pages 835-838

[European Journal of Dermatology](#)

June 2017, Volume 27, [Supplement 1](#), pp 4-7 | [Cite as](#)

New perspectives on dandruff and seborrhoeic dermatitis: lessons we learned from bacterial and fungal skin microbiota

Authors

[Authors and affiliations](#)

Luciana Campos Paulino 

 **frontiers**
in Cellular and Infection Microbiology

ORIGINAL RESEARCH
published: 04 October 2018
doi: 10.3389/fcimb.2018.00346



Comparison of Healthy and Dandruff Scalp Microbiome Reveals the Role of Commensals in Scalp Health

Rituja Saxena^{1†}, Parul Mittal^{1†}, Cecile Clavaud^{2†}, Darshan B. Dhakan¹, Prashant Hegde³, Mahesh M. Veeranagaiah³, Subarna Saha³, Luc Souverain², Nita Roy³, Lionel Breton², Namita Misra^{2,3*} and Vineet K. Sharma^{1*}

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- I cambiamenti nella **popolazione batterica** sono molto più evidenti rispetto ai cambiamenti nella **popolazione fungina** [2];
- Il rapporto **P. acnes/S. epidermidis** è riportato come più elevato nella popolazione sana;
- La *M. restricta* e in misura minore la *M. globosa* sono da considerarsi come le specie fungine maggiormente presenti sullo scalpo e una diminuzione del rapporto fra le due specie è stata associata ad una condizione di salute dello scalpo [3];
- “uncultured” *Malassezia* sp. (~25%) sullo scalpo di soggetti affetti da forfora rispetto alla popolazione sana (~14%) e di una correlazione significativamente positiva fra queste specie e i parametri associati alla forfora (TEWL, sebo, pH, prurito) [3];

[1]Gupta AK et al., 2001; [2] Clavaud C et al., 2013; [3] Saxena et al., 2018

Case Report

Is *Propionibacterium Acnes* Associated with Hair Casts and Alopecia?

Access this article online

Website:

www.ijtrichology.com

DOI:

10.4103/0974-7753.96907

Quick Response Code:



Etienne Wang, Joyce Siong-See Lee, Tan Hhok Hee

Department of Dermatology, National Skin Centre, 1 Mandalay Road, Singapore

ABSTRACT

We report a series of four patients who presented with complaints of diffuse non-scarring alopecia. They had similar clinical features of alopecia, hyperseborrhea, and distinct keratinaceous hair casts that encircled the hair shafts. *Propionibacterium acnes* was isolated from two of the patients' scalp, and Gram-positive, Giemsa-positive bacteria were seen in the hair follicles in the scalp biopsy of one of the patients. The patients' symptoms did not respond to standard treatment for seborrheic dermatitis, but responded to a course of systemic antibiotics targeting *P. acnes*. We propose a role for *P. acnes* colonization of the terminal hair follicles in the pathogenesis of hair casts, and possibly diffuse non-scarring alopecia. Possible mechanisms of pathogenesis are discussed with a literature review.

Key words: Hair casts, non-scarring alopecia, *Propionibacterium acnes*, systemic antibiotics

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DOI: 10.1111/1468-3083.2012.04591.x

ORIGINAL ARTICLE

First evidence of bacterial biofilms in the anaerobe part of scalp hair follicles: a pilot comparative study in folliculitis decalvans

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¹Centre Sabouraud, Hôpital Saint-Louis, Paris, France

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Abstract

Background The cause of folliculitis decalvans (FD) remains unknown. We hypothesized that a bacterial biofilm could be involved in its pathogenesis.

Objective To assess the presence or not of a bacterial biofilm in the hair roots of the scalp in FD.

Patients and methods Hairs plucked from four patients and three controls were examined by field emission scanning electron microscopy (FESEM) and confocal laser scanning microscopy (CLSM).

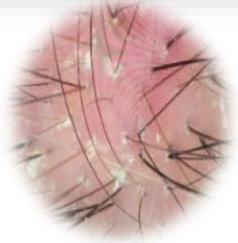
Results Bacterial communities organized as biofilms were observed both by FESEM and CLSM in the under infundibular part of hair follicles in all patients and in two of the three controls. In patients and controls, these biofilms were formed exclusively of bacilli of comparable shapes.

Conclusion This pilot study provides the first evidence of the presence of bacterial biofilms in the infra infundibular part of human scalp hair follicles. These biofilms were detected both in FD patients and controls, suggesting their ubiquity as a commensal biofilm with a possible pathogenic shift in FD.

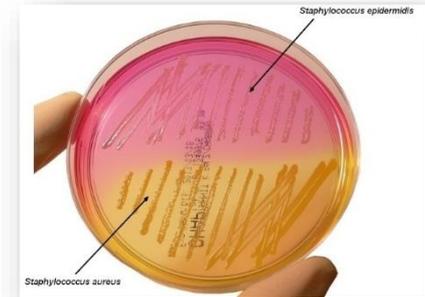
Received: 2 March 2012; Accepted: 3 May 2012

[4] Wang et al., 2012; [5] Matard et al., 2013;

IL MICROBIOMA DELLO SCALPO



Identificazione del sito
e collazionamento del
campione



Metodi coltura dipendenti

- *Malassezia*;
- *P. acnes*;
- *S. epidermidis*;
- *S. aureus*

Analisi genomica

Espressione genica
con qRT-PC
(cambiamento di
espressione di specifiche
classi microbiche)

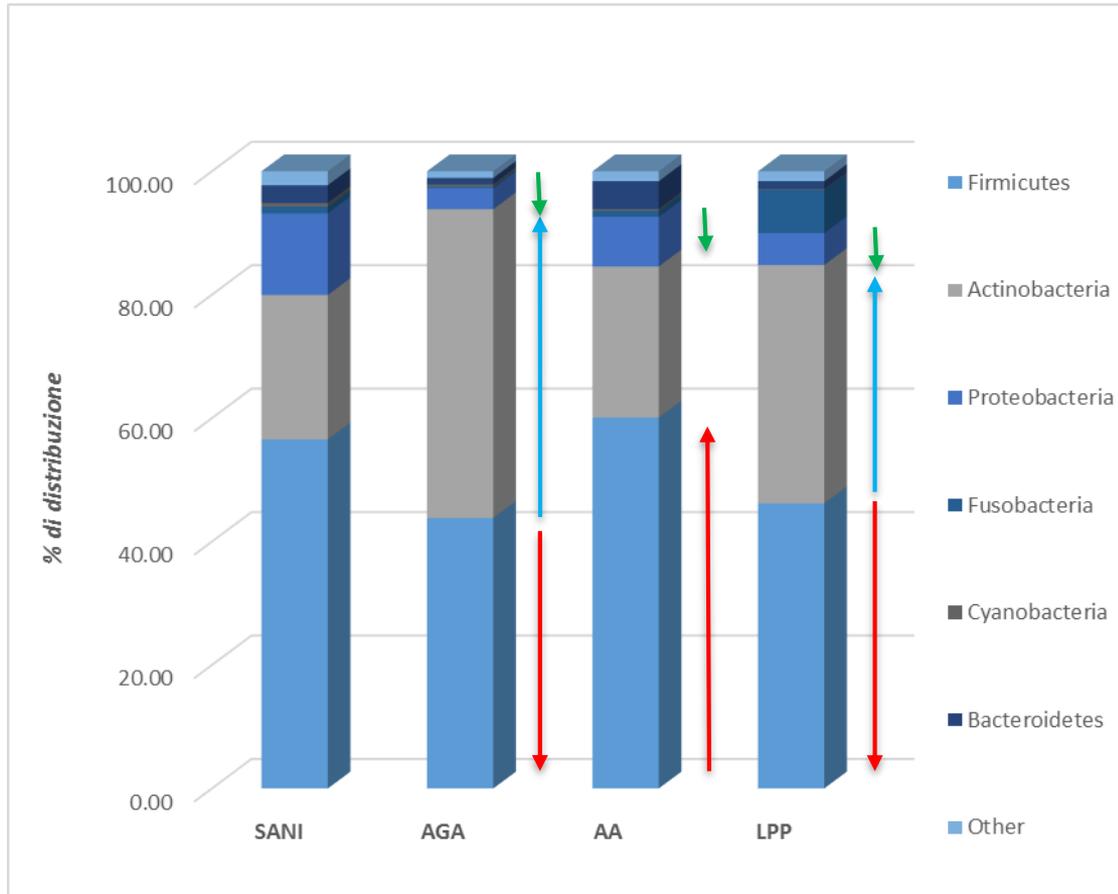
Sequenziamento
(mappatura completa)

- Proteomica
- Metatrascrittomica
- Metabolomica

Panel di 25 soggetti a patologia (Alopecia Androgenetica, Alopecia Areatata, Lichen Planopilaris, Dermatite Seborroica, Psoriasi)

I RISULTATI DELLA RICERCA

Distribuzione BATTERICA a livello di phylum



Firmicutes

Actinobacteria

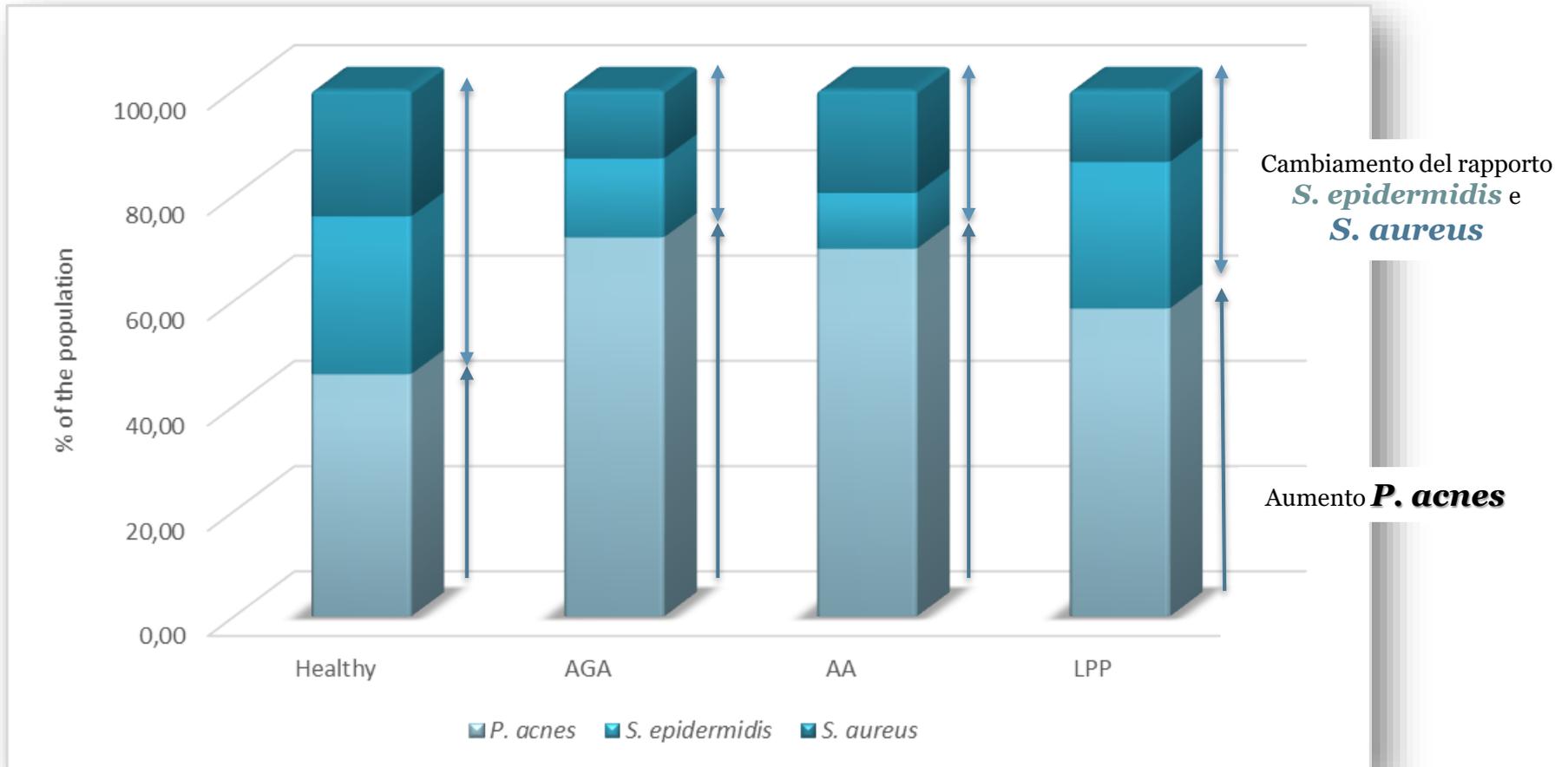
Proteobacteria
(*Roseomonas mucosa* example)

n≥15

*Sequenziamento 16S

I RISULTATI DELLA RICERCA

Distribuzione delle principali specie batteriche sullo scalpo



n \geq 15

*Dati di espressione genica (qRT-PCR)

I RISULTATI DELLA RICERCA

Distribuzione delle principali specie batteriche sullo scalpo

Journal of Translational Science

Mini-review

Human microbiome: what' s new in scalp disease

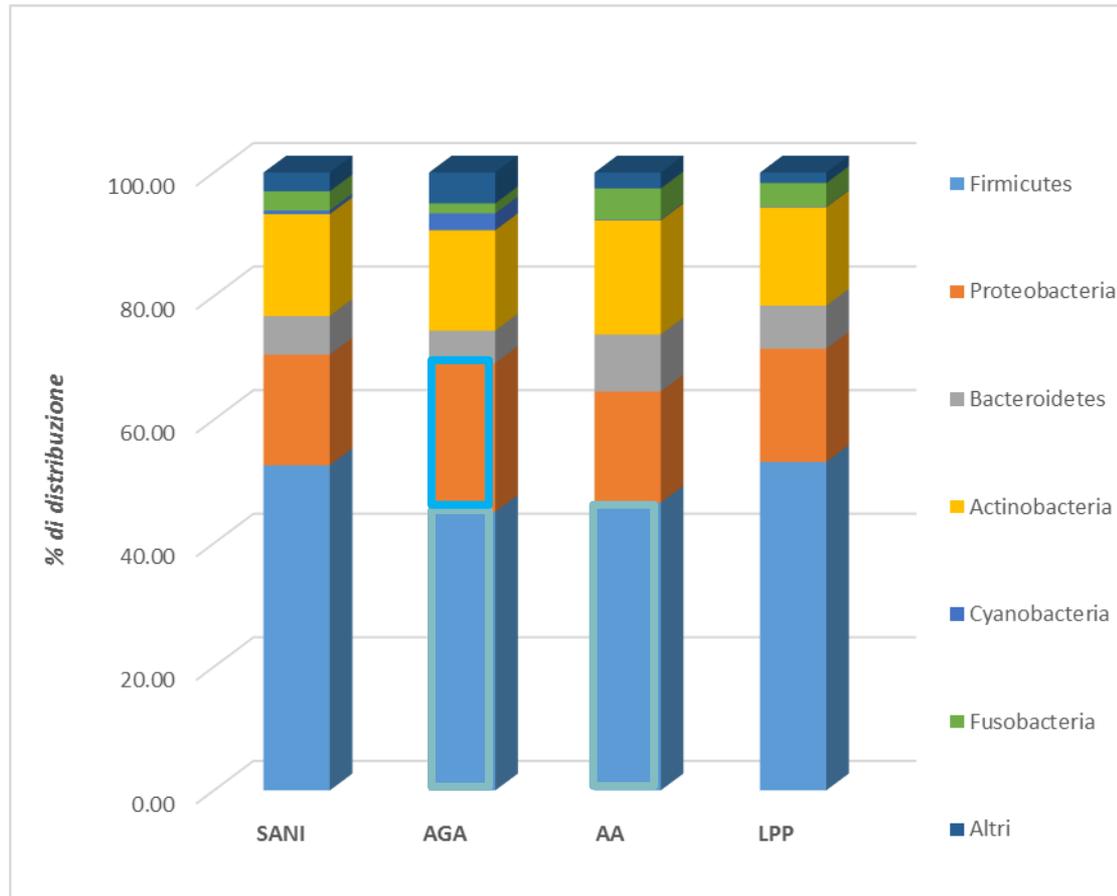
Rinaldi Fabio¹, Pinto Daniela¹, Marzani Barbara¹, Mariangela Rucco¹, Giammaria Giuliani²,
Sorbellini Elisabetta¹

¹ International Hair Research Foundation (IHRF), Milan, Italy

² Human Advanced Microbiome Project-HMAP

* Correspondence: fabio.rinaldi@studiorinaldi.com; Tel.: ++39-2-76006089

IL MICROBIOMA DEL CAVO ORALE NELLE PATOLOGIE DELLO SCALPO



<Firmicutes [1]

>Proteobacteria

Sequenziamento 16S (ILLUMINA seq, V3-V4)

[7] Singh et al., 2017; [8] Zhang et al., 2010; [9] Turnbaugh et al., 2008;

PARODONTITE?





HHS Public Access

Author manuscript

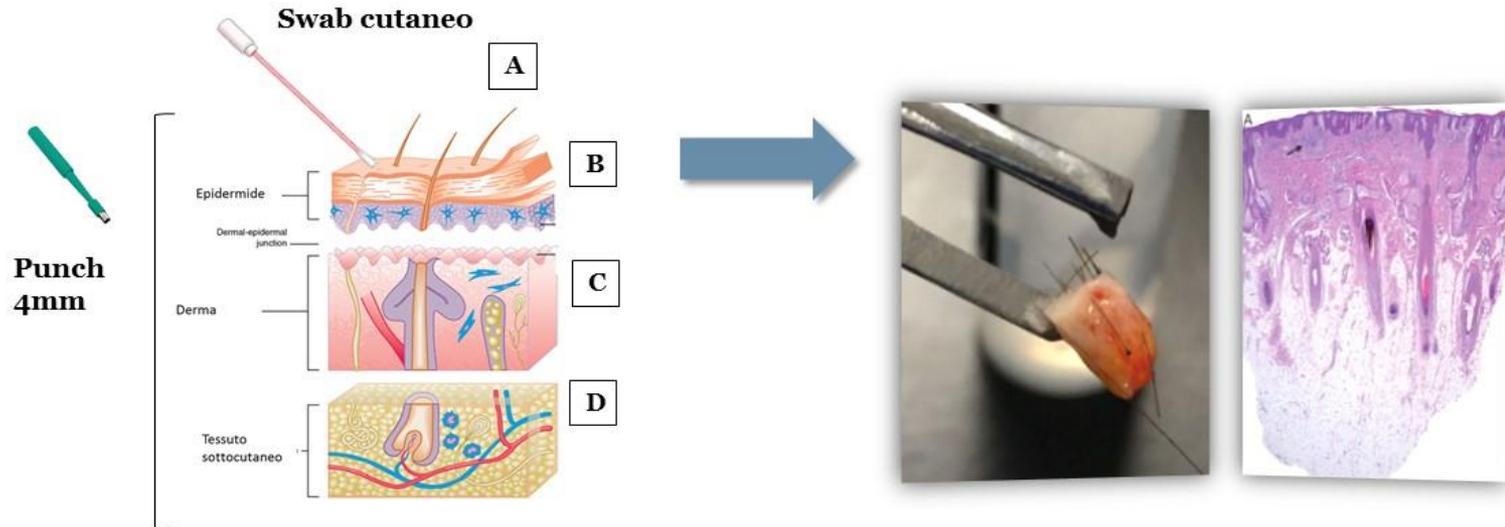
Nat Commun. Author manuscript; available in PMC 2013 July 01.

Published in final edited form as:

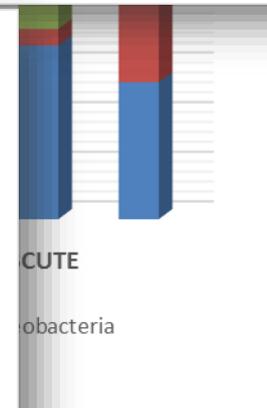
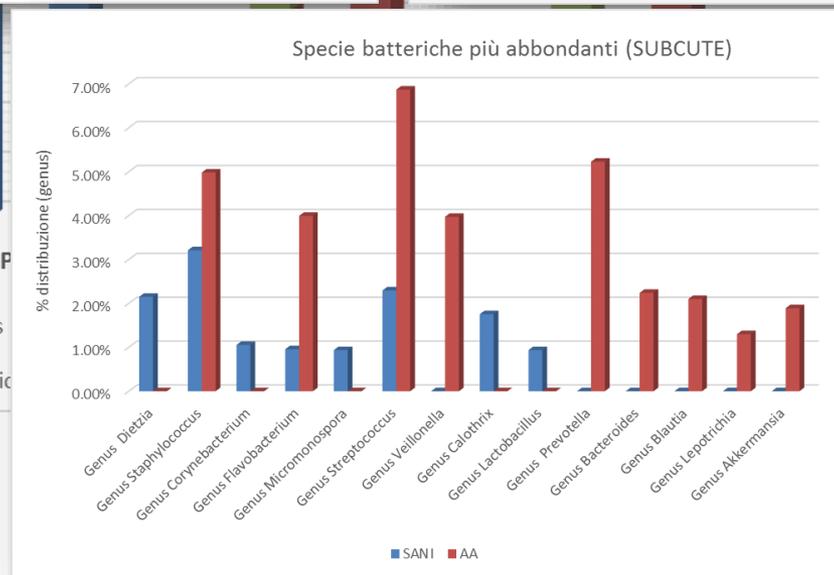
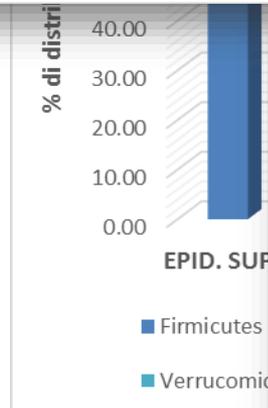
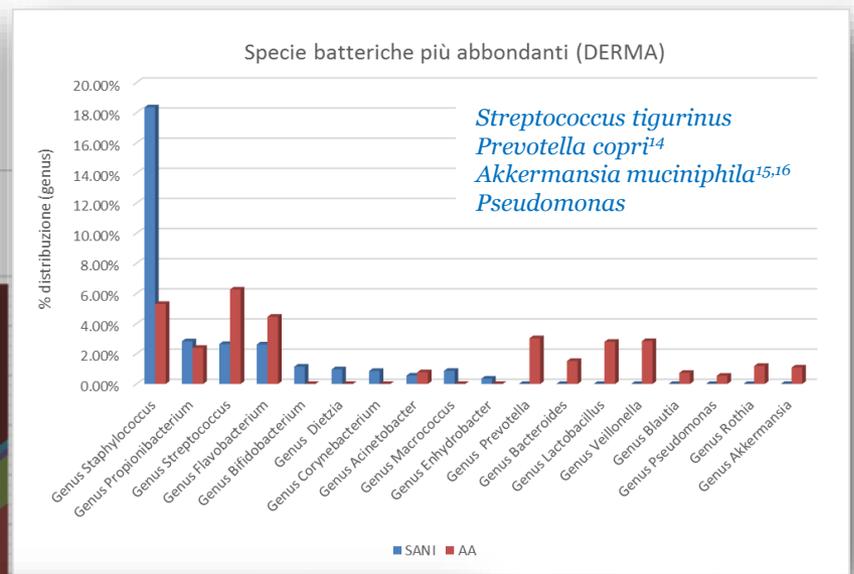
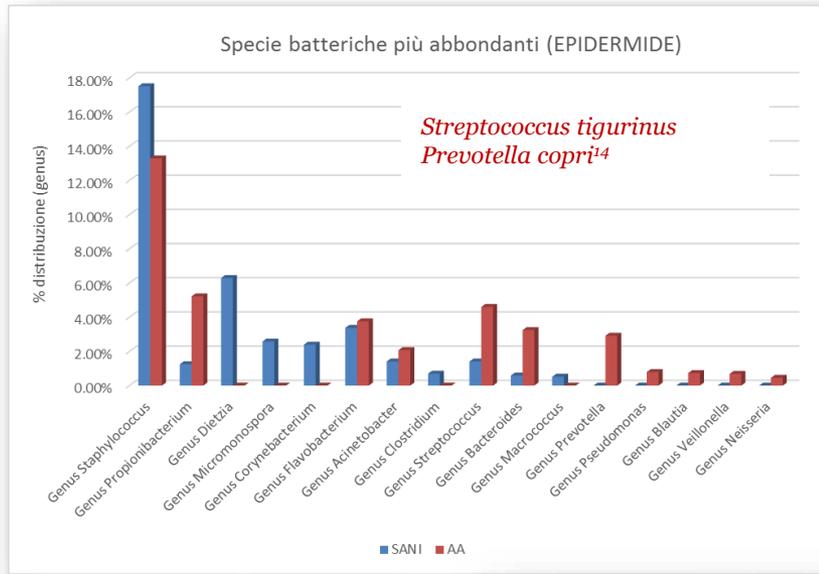
Nat Commun. 2013 ; 4: 1431. doi:10.1038/ncomms2441.

The microbiome extends to subepidermal compartments of normal skin

Teruaki Nakatsuji^{1,3}, Hsin-I Chiang^{2,4}, Shangi B. Jiang¹, Harish Nagarajan², Karsten Zengler², and Richard L. Gallo^{1,3,*}



ALOPECIA AREATA: distribuzione batterica nei compartimenti subepidermici

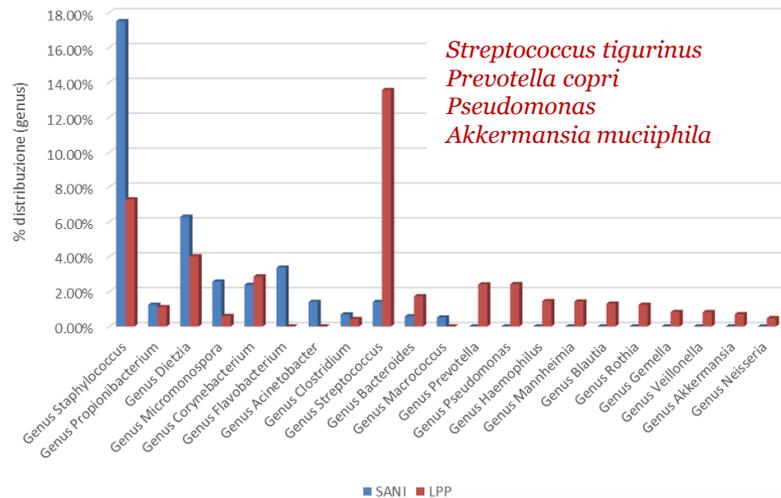


Streptococcus tigurinus
Prevotella copri¹⁴
Akkermansia muciniphila^{15,16}

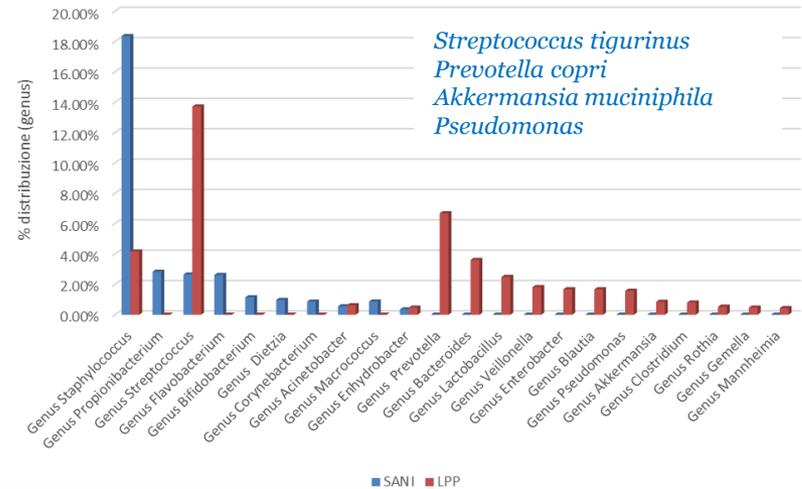
[14] Maeda et al., 2014; [15] Tan et al., 2017; [16] Alam et al., 2016;

LICHEN PLANOPILARIS: distribuzione batterica nei compartimenti subepidermici

Specie batteriche più abbondanti (EPIDERMIDE)

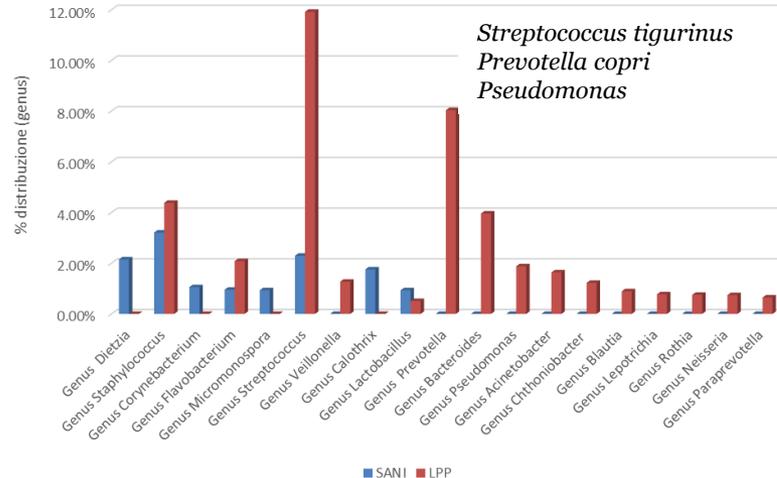


Specie batteriche più abbondanti (DERMA)



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EPID. S

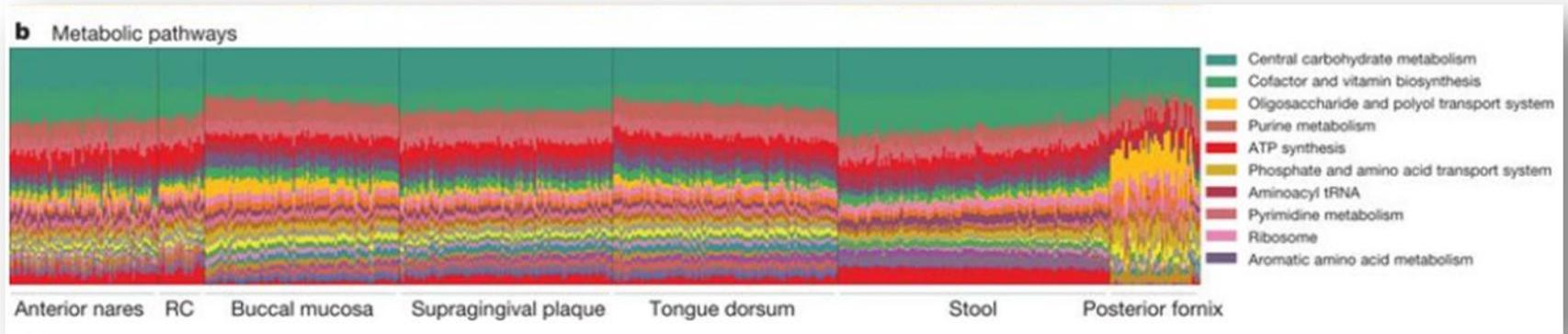
Specie batteriche più abbondanti (SUBCUTE)



SUBCUTE

proteobacteria

ltri

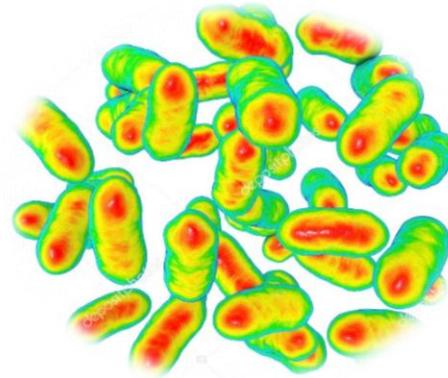


Propionibacterium acnes



- SCFA (con aumento dell'anaerobiosi)
- Acido propionico (fermentazione del glucosio)
- Porfirine

Prevotella copri



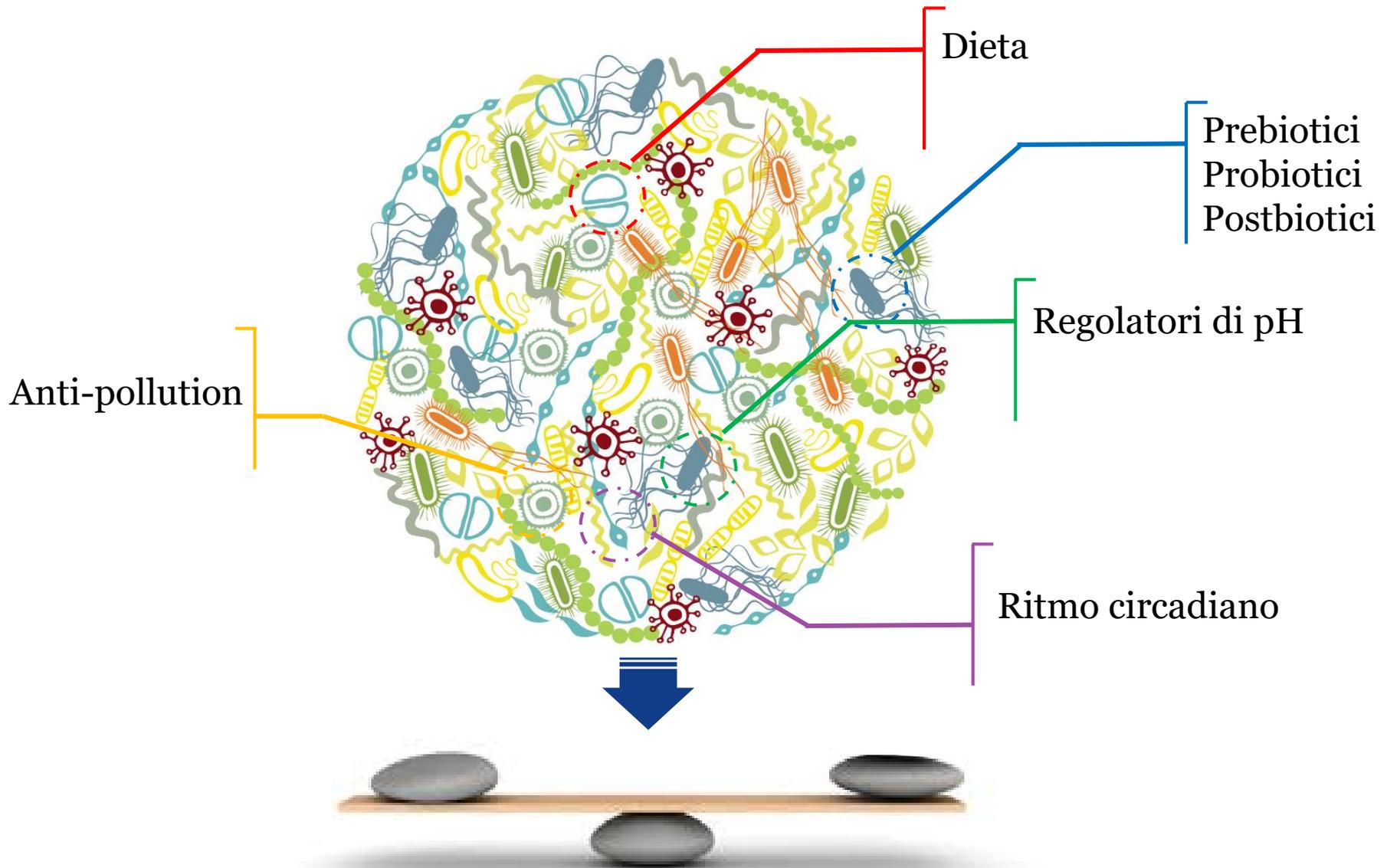
- Inibizione pathway delle purine
- Fosfoadenosina fosfosolfato reductasi (PAPS), ossidoreduttasi che induce la sintesi di tireodossina

Akkermansia muciniphila

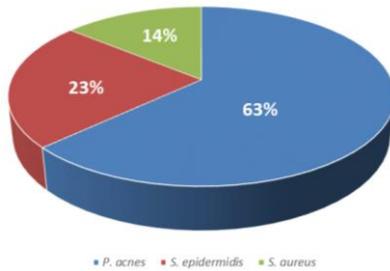


- Metabolismo lipidi
- Omeostasi metabolica
- Sintesi butirrato
- Biosintesi L-cisteina

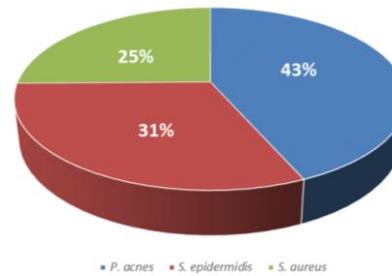
MICROBIOMA: possibili strategie di intervento



Case report: Donna, 47 anni (AA)



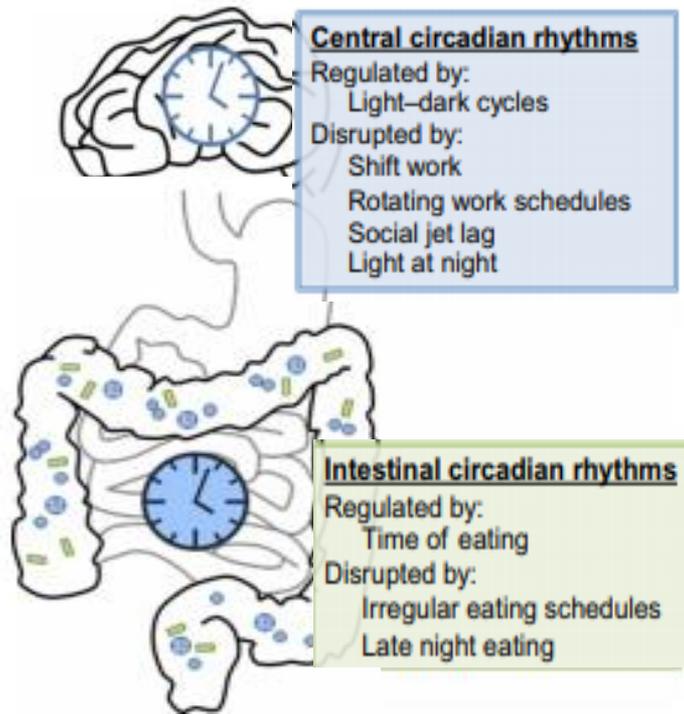
Before Gluten-free diet



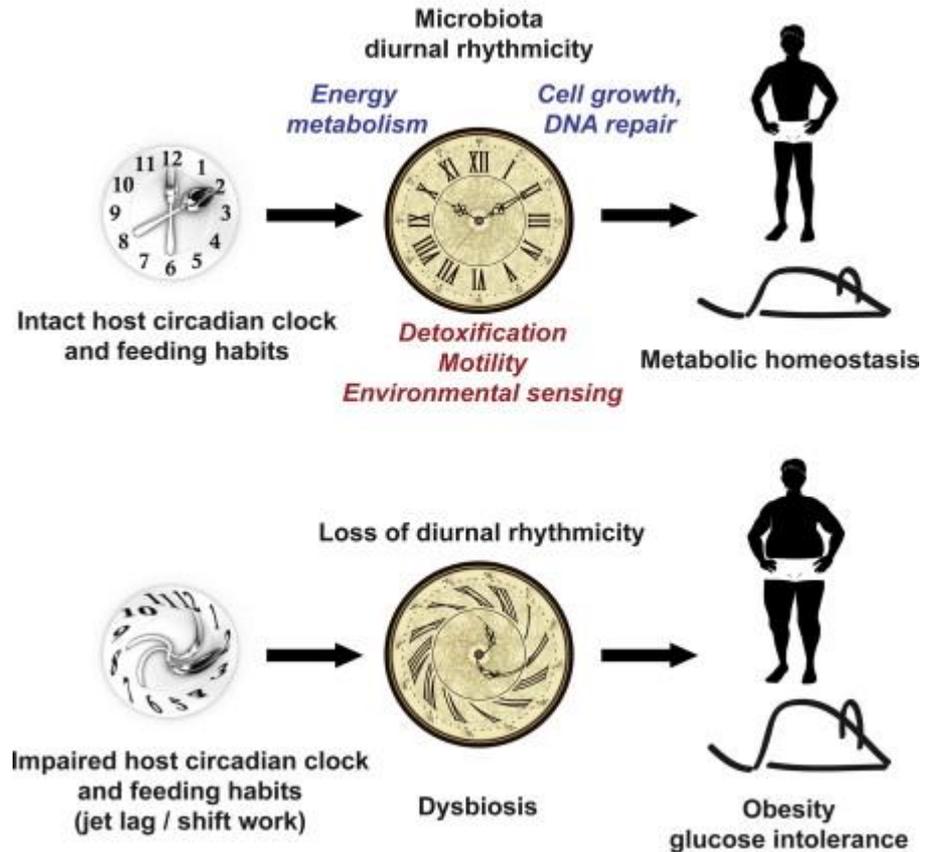
After Gluten-free diet



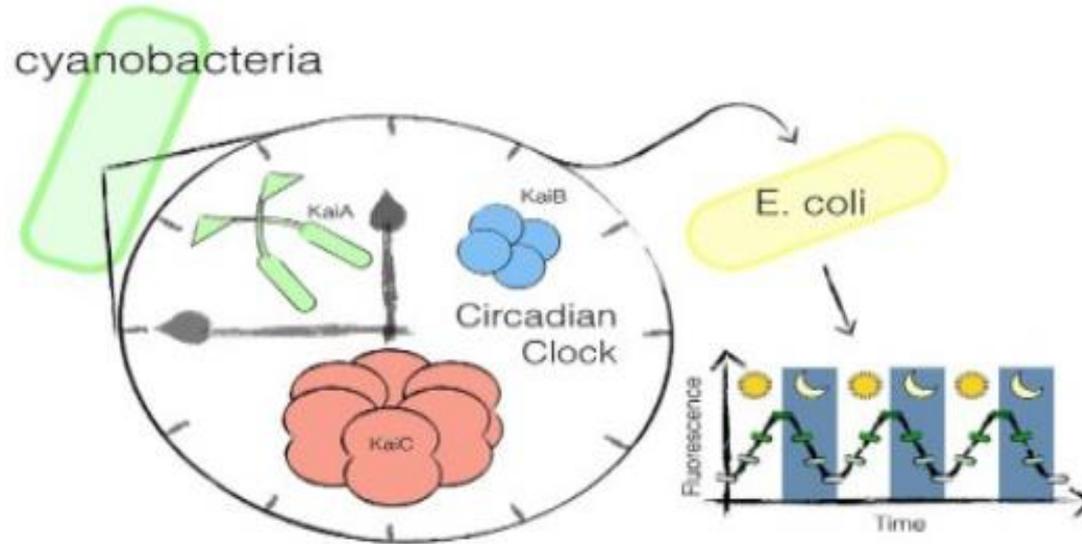
Microbioma e RITMO CIRCADIANO



Voigt et al., 2014, 2016; Thaiss, Zeevi, et al., 2014;
Liang, Bushman, et al., 2015; Zarrinpar et al., 2014



I microorganismi possiedono un loro RITMO CIRCADIANO?



E i microorganismi non
sensibili alla luce?

MICROBIOME as META-ORGANISM

Message in a Biota: Gut Microbes Signal to the Circadian Clock

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<http://dx.doi.org/10.1016/j.chom.2015.04.013>

Circadian rhythm involves diurnal oscillations in biological processes. In this issue of *Cell Host & Microbe*, Leone et al. (2015) show that the gut microbiota influences the circadian clock and undergoes circadian oscillations. Microbiota-produced metabolites change with host diet and may affect circadian rhythm, highlighting functional links between diet and physiology.

Gut Microbes 62, 137–142; March/April 2015; © 2015 Taylor & Francis Group, LLC

ARTICLE ADDENDUM

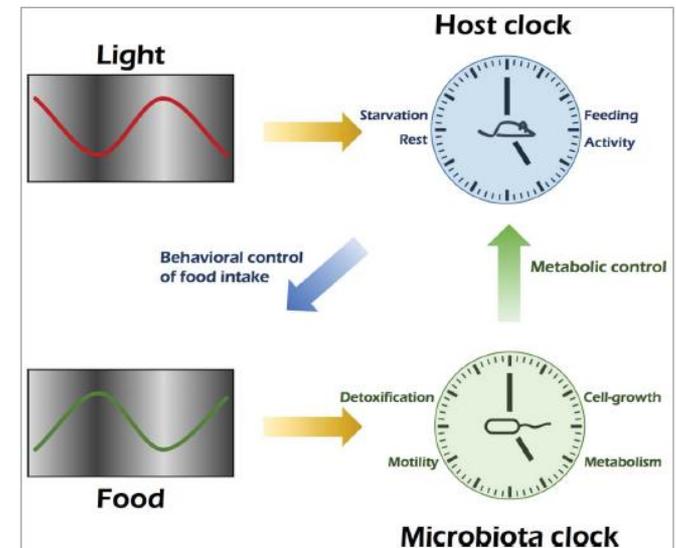
A day in the life of the meta-organism: diurnal rhythms of the intestinal microbiome and its host

Christoph A Thaiss^{1,†}, David Zeevi^{2,†}, Maayan Levy^{1,†}, Eran Segal^{2,†}, and Eran Elinav^{2,†,*}

¹Department of Immunology; Weizmann Institute of Science; Rehovot, Israel; ²Department of Computer Science and Applied Mathematics; Weizmann Institute of Science; Rehovot, Israel

[†]These authors contributed equally to this work.

^{*}These authors contributed equally to this work.



Bacterial circadian clocks set by metabolism, not only light

RESEARCH ARTICLE

Human Gut Bacteria Are Sensitive to Melatonin and Express Endogenous Circadian Rhythmicity

Jiffin K. Paulose, John M. Wright, Akrti G Patel, Vincent M. Cassone*

Department of Biology, University of Kentucky, Lexington, KY, 40506, United States of America

* Vincent.Cassone@uky.edu

Abstract

Circadian rhythms are fundamental properties of most eukaryotes, but evidence of biological clocks that drive these rhythms in prokaryotes has been restricted to Cyanobacteria. In vertebrates, the gastrointestinal system expresses circadian patterns of gene expression, motility and secretion *in vivo* and *in vitro*, and recent studies suggest that the enteric microbiome is regulated by the host's circadian clock. However, it is not clear how the host's clock regulates the microbiome. Here, we demonstrate at least one species of commensal bacterium from the human gastrointestinal system, *Enterobacter aerogenes*, is sensitive to the neurohormone melatonin, which is secreted into the gastrointestinal lumen, and expresses circadian patterns of swarming and motility. Melatonin specifically increases the magnitude of swarming in cultures of *E. aerogenes*, but not in *Escherichia coli* or *Klebsiella pneumoniae*. The swarming appears to occur daily, and transformation of *E. aerogenes* with a flagellar motor-protein driven lux plasmid confirms a temperature-compensated circadian rhythm of luciferase activity, which is synchronized in the presence of melatonin. Altogether, these data demonstrate a circadian clock in a non-cyanobacterial prokaryote and suggest the human circadian system may regulate its microbiome through the entrainment of bacterial clocks.



OPEN ACCESS

Citation: Paulose JK, Wright JM, Patel AG, Cassone VM (2016) Human Gut Bacteria Are Sensitive to Melatonin and Express Endogenous Circadian Rhythmicity. PLoS ONE 11(1): e0146643. doi:10.1371/journal.pone.0146643

Editor: Shin Yamazaki, University of Texas Southwestern Medical Center, UNITED STATES

Received: October 1, 2015

Accepted: December 21, 2015

Published: January 11, 2016

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*“The individual cells begin to communicate with each other and coordinate periods of **swimming** and **dividing** in a phenomenon known as **SWARMING**”.*

Alcuni microorganismi presenti a livello intestinale presentano un proprio «pattern circadiano» in quanto sono sensibili alla presenza della Melatonina



ORIGINAL CONTRIBUTION

Sensitive scalp is associated with excessive sebum and perturbed microbiome

Li Ma PhD¹ | Alexandre Guichard PhD¹ | Ying Cheng MSc¹ | Jie Li PhD² |
Ou Qin MSc¹ | Xuemin Wang MD, PhD^{1,‡} | Wei Liu MD, PhD^{1,3} | Yimei Tan MSc¹¹Skin and Cosmetic Research Department, Shanghai Skin Disease Hospital, Shanghai, China²Shanghai Measure Testing Technology Academe, Shanghai, China³Department of Dermatology, Air Force General Hospital, Beijing, China

Correspondence: Yimei Tan, Skin and Cosmetic Research Department, Shanghai Skin Disease Hospital, 1278 Baode Road, Shanghai 200443, China (amelt@163.com).

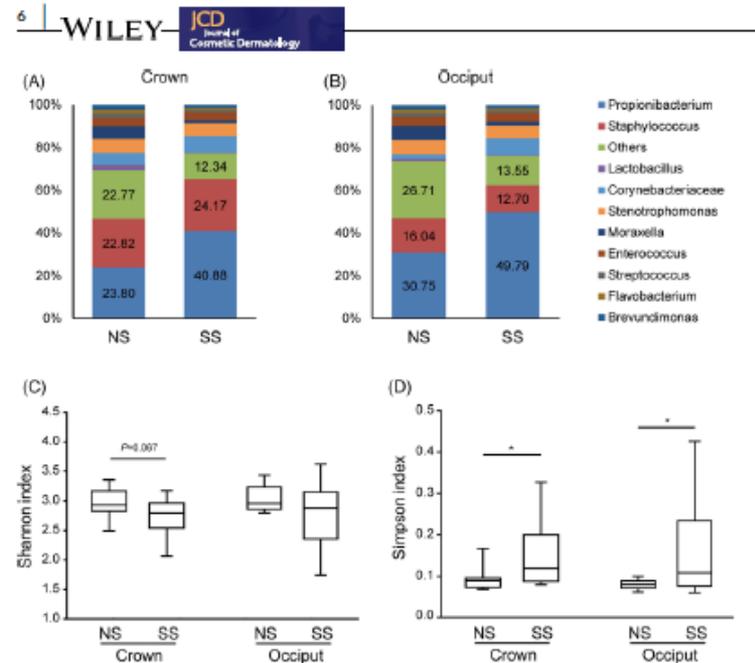
Funding information
Shanghai Skin Disease Hospital

Summary

Background: Sensitive scalp, one of the most frequent complaints among sensitive skin syndrome, has been described as abnormal and unpleasant sensory reactions of the scalp to environmental stimulus. However, the symptoms are usually objective and hard to diagnose.**Objective:** This study aimed to reveal the biophysical properties and etiology of sensitive scalp.**Methods:** Sixty-two healthy female subjects were enrolled and divided into nonsensitive scalp (NS) and sensitive scalp (SS) groups according to questionnaires. Noninvasive instruments were used to measure biophysical properties. Ultra-performance liquid chromatography-tandem mass spectrometry and gas chromatography mass spectrometry were introduced to quantify skin lipids profiles, and 16S rRNA sequencing was used to detect the composition of bacteria.**Results:** Sensitive scalp showed elevated pH level, more irritated skin, and more fluorescence of porphyrins. Increased sebum production was found in SS group at occiput, among which free fatty acids, cholesteryl ester, and squalene were significantly in higher amount compared with NS. SS also had significantly higher percentage of *Propionibacterium*, and lower bacterial diversity.**Conclusions:** Taken together, sensitive scalp showed disrupted barrier function, abnormal sebum amount and composition, as well as perturbed microbiome, which might be the direct cause. Products targeting these features could be helpful for the treatment of sensitive scalp.

KEYWORDS

biophysical properties, microbiome, sebum, sensitive scalp



Hair Growth in Two Alopecia Patients after Fecal Microbiota Transplant

Dionne Rebello, MD¹, Elaina Wang, BS¹, Eugene Yen, MD³, Peter A. Lio, MD⁴, and Colleen R. Kelly, MD, FACG^{1,2}



Figure 2. Hair regrowth on a 20-year-old patient's scalp after FMT. (A) The patient's scalp when he first started losing his hair at age 16. The patient's scalp (B) a few months and (C) 1.5 years after FMT.

Microbioma e PREBIOTICI, PROBIOTICI E POSTBIOTICI





Microbioma e PRP



REVIEW ARTICLE

Antimicrobial properties of platelet-rich preparations. A systematic review of the current pre-clinical evidence

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¹Dipartimento di Scienze Biomediche, Chirurgiche e Odontoiatriche, Università degli Studi di Milano, Milano, Italy, and ²Laboratory of Clinical Chemistry and Microbiology, IRCCS Istituto Ortopedico Galeazzi, Milano, Italy

Abstract

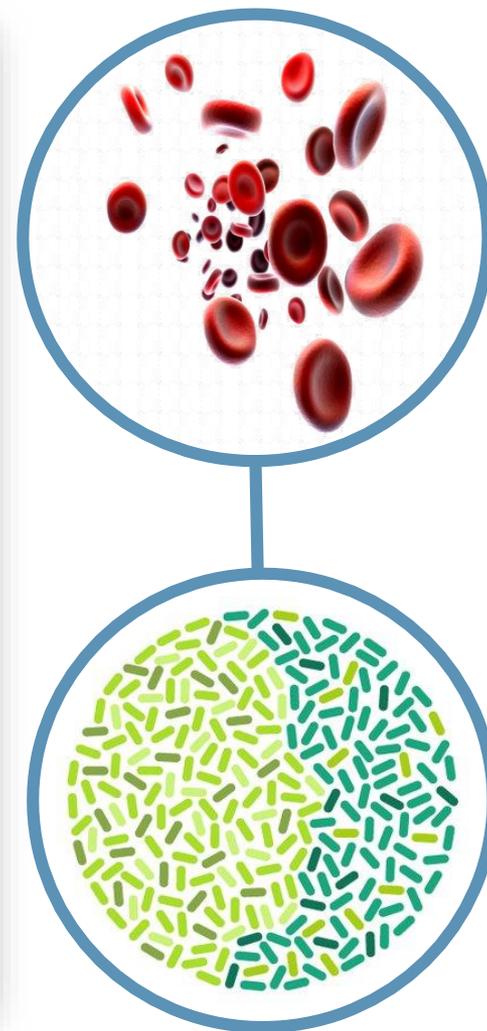
In recent years autologous platelet concentrates (APCs) have become popular in several medicine fields, representing a valuable adjunct to regenerative surgical procedures. Beneficial effects in the control of postsurgical discomfort and infection have also been frequently reported, suggesting that APC may possess anti-inflammatory and antimicrobial properties. The aim of the present review was to summarize the current evidence regarding the antimicrobial effects of platelet concentrates, investigated by *in vitro* and animal studies. This review was conducted following a systematic approach. An electronic search was performed on MEDLINE, EMBASE and Scopus databases using appropriate search terms, without language or time restrictions. Preclinical studies assessing the antimicrobial activity of APC were included and divided according to the experimental design. Twenty *in vitro* studies and four animal studies, investigating APC effects on a broad range of microorganisms, were included. In *in vitro* studies APC reduced the growth of microorganisms during the first hours of incubation, while they could not completely break down the microbial load. In fact, over time a recovery of bacterial growth was always observed, suggesting that APCs display a bacteriostatic rather than a microbicidal activity. All animal studies showed that APC administered by local injections were able to reduce the infection caused by different microorganisms, although to a lesser extent compared to antibiotics. In conclusion, although the exact action mechanisms of interaction with microbial pathogens need further investigation, platelet concentrates proved to have antimicrobial properties, and therefore could represent a useful natural substance for controlling postoperative infections at surgical sites.

Keywords

Autologous platelet concentrates, platelet-rich plasma, antimicrobial agents, systematic review

History

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Published online 14 January 2016



Platelet-released growth factors induce the antimicrobial peptide human beta-defensin-2 in primary keratinocytes

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Correspondence: Andreas Bayer, MD, Department of Heart- and Vascular Surgery, University Hospital Schleswig-Holstein, Campus Kiel, Arnold-Heller Straße 3, Haus 26, 24105 Kiel, Germany, Tel.: +49-431-597-4531, Fax: +49-431-597-5267, e-mail: andreas.bayer@uksh-kiel.de

*These authors contributed equally to this work.

Abstract Platelet-released growth factors (PRGF) and its related clinically used formulations [e.g. Vivostat platelet-rich fibrin (PRF[®])] are thrombocyte concentrate lysates that support healing of chronic, hard-to-heal and infected wounds. Human beta-defensin-2 (hBD-2) is an antimicrobial peptide expressed in human keratinocytes exhibiting potent antimicrobial activity against wound-related bacteria. In this study, we analysed the influence of PRGF on hBD-2 expression in human primary keratinocytes and the influence of Vivostat PRF[®] on hBD-2 expression in experimentally generated skin wounds *in vivo*. Treatment of primary keratinocytes with PRGF caused a significant increase in hBD-2 gene and protein expressions in a concentration- and time-dependent manner. The use of blocking antibodies revealed that the PRGF-mediated hBD-2 induction was

partially mediated by the epidermal growth factor receptor and the interleukin-6 receptor (IL-6R). Luciferase gene reporter assays indicated that the hBD-2 induction through PRGF required activation of the transcription factor activator protein 1 (AP-1), but not of NF-kappaB. In concordance with these cell culture data, Vivostat PRF[®] induced hBD-2 expression when applied to experimentally generated skin wounds. Together, our results indicate that the induction of hBD-2 by thrombocyte concentrate lysates can contribute to the observed beneficial effects in the treatment of chronic and infected wounds.

Key words: antimicrobial peptides – cutaneous innate defense – wound healing

Accepted for publication 29 January 2016

GRAZIE PER L'ATTENZIONE

