Quand le métaséquençage révèle un déséquilibre du microbiote cutané au cours du vieillissement.

Mme Christine Grimaldi, PhD, Responsable du laboratoire Microbiologie Référent, SILAB

INTRODUCTION

Le microbiote cutané

- Sa composition et sa distribution sont influencées par la génétique et le mode de vie
- Le microbiote est responsable de l'immunité, de la nutrition et de la défense de la peau

OBJECTIF SILAB

Comparer la répartition du microbiote entre deux groupes d'âge différents de femmes Caucasiennes

Principalement étudié dans un contexte pathologique

Très peu de données sur une peau saine

METHODOLOGIE

1 2 3

Prélèvement sur le visage

- *Jeunes :* 17 volontaires Caucasiennes en bonne santé, âge moyen 28 ± 3 ans
- *Âgés :* 17 volontaires Caucasiennes en bonne santé, âge moyen 62 ± 5 ans

illumina®

Analyse des communautés bactériennes

- Amplification des régions V3-V4 de l'ADNr 16S
- Séquençage des amplicons sur Illumina MiSeq

FROGS pipeline

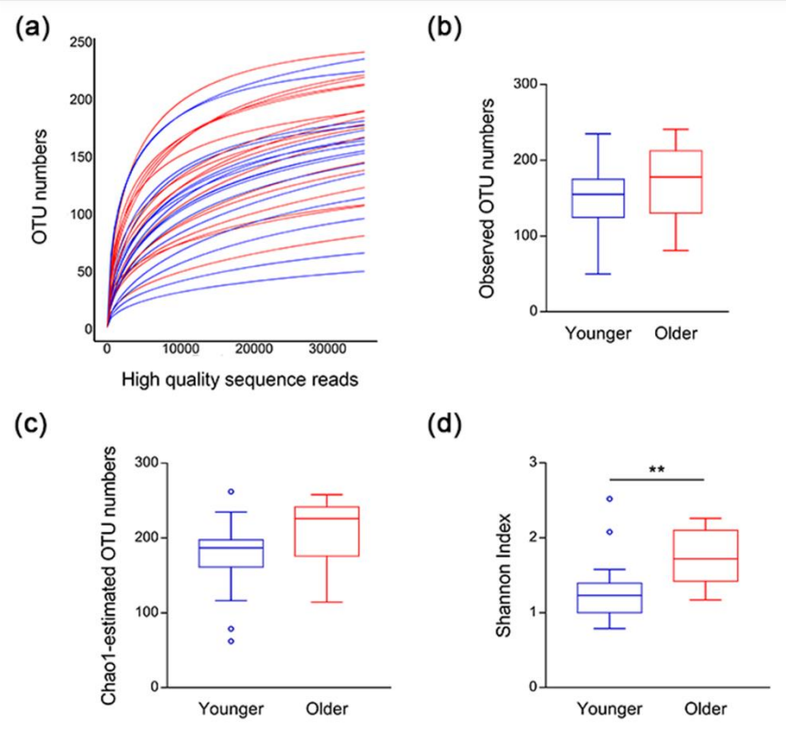
R software

Analyses bioinformatiques

- Traitement des données
- Validation de la méthode d'analyse
- Analyse des OTUs et classification taxonomique (FROGS)
- Analyse de l'α-diversité et de la β-diversité (sous R)

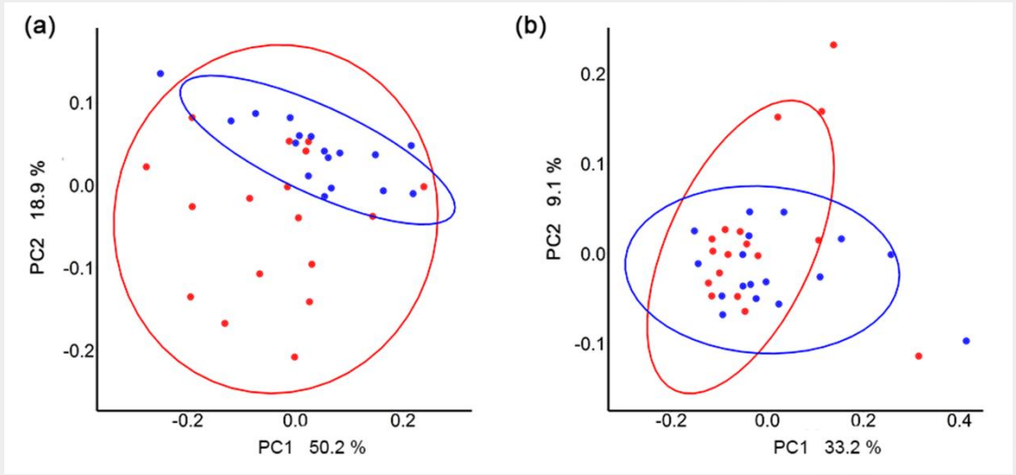
RESULTATS

Alpha diversité



➔ Impact du vieillissement sur la répartition mais pas sur la richesse du microbiote cutané

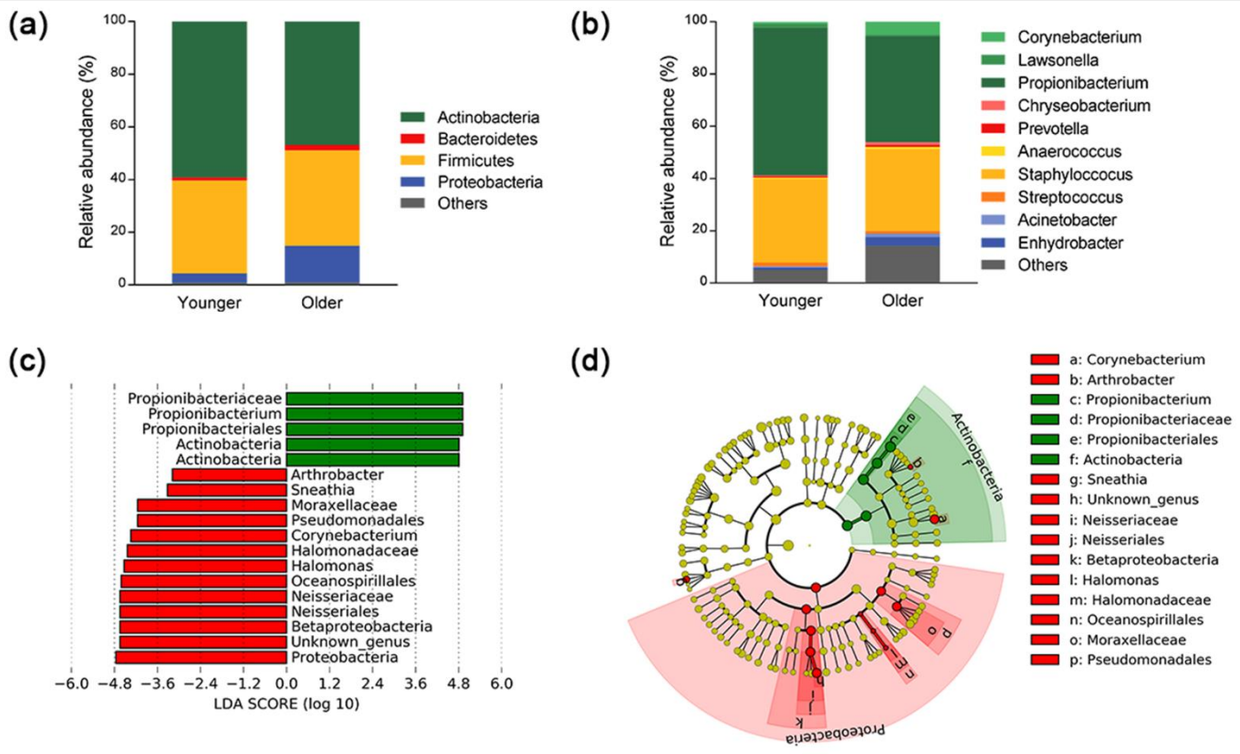
Beta diversité



➔ Impact du vieillissement sur l'abondance mais pas sur les membres du microbiote cutané

RESULTATS

Classification taxonomique



Etude taxonomique
(abondance relative)

Domaine
Phylum
Classe
Ordre
Famille
Genre
Espèce

Proteobactéries ↗
Actinobactéries ↘

Corynebactéries ↗
Propionibactéries ↘

➔ **Impact du vieillissement sur la classification taxonomique, au niveau du phylum et du genre, avec une augmentation de l'abondance relative des bactéries opportunistes**

CONCLUSION

WHEN METASEQUENCING REVEALED A MICROBIOTA IMBALANCE ACROSS AGING

C. Grimaldi, R. Jugé, P. Rouaud-Tinguely, D. Boudier, S. Bordes and B. Closs.

R&D Department, SILAB, Brive-la-Gaillarde, France
email: aclantifloom@silab.fr

INTRODUCTION

The skin hosts a real ecosystem composed of various microorganisms that are harmless and even beneficial[1]. Among the diversity of skin microbes, the bacterial flora represents the most studied community[2].

Inter-personal variations of skin microbiota have been largely reported. Indeed, the composition of human skin microbiota is influenced by multiple factors such as gender, environment, lifestyle, hygiene practices and aging[3].

While few studies give new insights in microbial diversity variations with aging, analyses are restricted to Asian skin[4-6].

To our knowledge, no study has identified potential age-related changes in cutaneous microbiota for Caucasian ethnicity.

AIM

In this context, the aim of our study was to compare the skin microbiota between two different age groups of Caucasian women.

METHODS

Swabbing from the forehead

- Young group: 17 healthy female Caucasian volunteers, mean age 29 ± 3 years
- Old group: healthy female Caucasian volonteers, mean age 62 ± 5 years

Bacterial communities analysis

- Amplification of 16S rDNA V3-V4 regions
- Sequencing of amplicons on Illumina MiSeq®

Bioinformatics analysis

- Data processing
- Validation of our analysis pipeline
- OTU analysis and Taxonomic classification through FROGS pipeline[7]
- Analyses through R software:
  - Bacterial richness: alpha diversity
  - Structural difference according to the phylogenetic distances: beta diversity

RESULTS

1. Impact of aging on alpha diversity

Figure 1. Comparison of forehead bacterial alpha diversity between younger and older age group.

- Rarefaction curves: tended to reach a plateau.
  → Sufficient number of OTUs analyzed for each sample to exhibit the full species diversity.
- Observed and chao1-estimated OTU numbers: no variation between two age groups.
  → No impact of aging on the richness of cutaneous microbiota.
- Shannon alpha diversity index: significant increase in older age group.
  → Impact of aging only on the evenness of cutaneous microbiota.

2. Impact of aging on beta diversity

Figure 2. Comparison of the bacterial community beta diversity between younger and older age group.

- Weighted UniFrac: distinct clustering of both age groups.
  → Change in abundance of bacterial communities across aging.
- Unweighted UniFrac: no clustering.
  → No change in membership of bacterial communities with age.

3. Impact of aging on taxonomic classification

Figure 3. Taxonomic analysis of forehead microbiota in younger and older subjects group.

- At phylum level, aging significantly decreased *Proteobacteria* relative abundance and significantly increased *Actinobacteria* relative abundance.
- At genus level, aging significantly decreased *Corynebacterium* relative abundance.

→ Impact of aging on taxonomic classification

CONCLUSION

- This study represents the first identification of skin microbiota shift during aging of Caucasian women.
- The modifications in pH level, sebum secretion or immune defenses that are characteristic of aged skin could lead to a lower selective pressure of commensal bacteria. Hence, opportunistic such as *Proteobacteria* and *Corynebacterium* can colonize the skin, leading to the different distribution of bacterial communities observed between young and aged volunteers.
- We hypothesize that the state of skin microbiota could become a readout predicting the progression of aging on skin.
- In the future, this study will support new approaches in order to rebalance the skin microbiota and prevent age-related skin disorders.

ACKNOWLEDGEMENTS

We thank all the volunteers for skin samples collection.

References:

- ➔ **1ère démonstration** d'une **modification du microbiote cutané** au cours du **vieillissement** chez la **femme Caucasienne**
- ➔ Dû à une **diminution des barrières mécaniques et immunes locales** au cours du vieillissement ?
- ➔ 1ère étape visant à **développer des approches pour rééquilibrer le microbiote cutané** et prévenir les désordres cutanés liés à l'âge.

MERCI POUR VOTRE ATTENTION !

J Appl Microbiol. 2018 May 23. doi: 10.1111/jam.13929. [Epub ahead of print]

Shift in skin microbiota of Western European women across aging.

Jugé R[1], Rouaud-Tinguely P[1], Breugnot J[1], Servaes K[1], Grimaldi C[1], Roth MP[2], Coppin H[2], Closs B[1].