

Session: OS087 The role of the microbiome in pathogenesis

**Category: 9b. Host-pathogen interaction**

23 April 2017, 15:06 - 15:16  
OS0454

### **Skin dysbiosis in hidradenitis suppurativa: a prospective metagenomic study**

Emeline Riverain-Gillet<sup>\*1</sup>, H el ene Guet-Revillet<sup>2</sup>, Jean-Philippe Jais<sup>3</sup>, Marie-Noelle Ungeheuer<sup>4</sup>, H el ene Coignard-Biehler<sup>2</sup>, Ma ia Delage<sup>4</sup>, Thitong Lam<sup>5</sup>, Sabine Duchatelet<sup>6</sup>, Alain Hovnanian<sup>6</sup>, Olivier Lortholary<sup>4</sup>, Xavier Nassif<sup>2</sup>, Aude Nassif<sup>4</sup>, Olivier Join-Lambert<sup>7</sup>

<sup>1</sup>*Ch Versailles; Biologie M edicale*

<sup>2</sup>*H opital Necker-Enfants Malades*

<sup>3</sup>*Universit  Paris Descartes, Inserm Umrs 1138 Team 22 and Aphp, H opital Necker Enfants Malades, Biostatistics Unit*

<sup>4</sup>*Institut Pasteur*

<sup>5</sup>*Hopital Necker*

<sup>6</sup>*Imagine Institute*

<sup>7</sup>*H opital Necker-Enfants Malades*

**Background:** Hidradenitis suppurativa (HS) is a chronic inflammatory disease of the hair follicle characterized by recurrent or chronic nodules, abscesses and suppurative lesions, typically localized in the axillar, inguinal and gluteal folds. We previously showed that *Staphylococcus lugdunensis* and particular anaerobic pathobionts (Prevotella, Porphyromonas and Fusobacterium) are associated with HS lesions but how these bacteria enter into the dermis and persist are unsolved issues. A recent study showed that keratinocytes isolated from HS patients display an intrinsic pro-inflammatory state with altered antimicrobial peptides production. These keratinocyte dysfunctions should likely induce skin dysbiosis in HS patients.

**Material/methods:** To demonstrate skin dysbiosis in HS, we obtained 142 patients' and 50 controls' skinfolds swab samples from 65 HS patients and 17 control subjects. All samples were analyzed by bacterial culture. The microbiomes of 79 HS and of 37 control subjects' samples were analyzed by 454 high throughput sequencing of 16S ribosomal RNA gene libraries.

**Results:** Patients and controls showed similar clinical characteristics, except for smoking (87% vs 6%, respectively,  $P < 10^{-3}$ ). Comparison of microbiomes alpha diversity showed no difference of richness, but demonstrated dissimilar relative bacterial abundances and dominance. A decreased abundance of *Staphylococcus epidermidis*, a major component of the normal skin microbiome was observed in HS patients, contrasting with an increased abundance of anaerobes by both methods. The relative abundance of Prevotella, an anaerobic commensal previously associated with HS lesions, was increased on HS skin. Skin dysbiosis did not depend on sex, body-mass index, clinical severity of the disease, or sample site.

**Conclusions:** This study demonstrates skin dysbiosis in pre-clinical HS, with a possible role for smoking. These modifications of the skin microbiome may predispose patients to skin infections associated with the disease.