

Comparison of Oily or Dry Dandruff scalp: Clinical, Instrumental and Targeted Metagenomic Data

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Introduction:

Oily dandruff is associated to high sebum production and inflammation, yellowish and flakes adherent to the scalp and hair, and dysbiosis microbiota. Dry dandruff is in the form of small, whitish flakes, not adherent to the scalp and can be associated with itching and dry scalp [1]. If Oily dandruff Microbiota is well characterized, nothing is published about dry dandruff microbiota. Scalp microbiota is characterized by the presence of *Malassezia*, *Cutibacterium* and *Staphylococcus* genus [2].
The aim of this study was to compare dry Dandruff scalps versus oily dandruff scalps by clinical, instrumental and targeted metagenomic data, in order to answer the question: Is dry dandruff microbiota dysbiosis have the same microorganism's actors than oily dandruff one? If microbiota is different between dry dandruff and oily dandruff scalp, it could justify the development of adapted product to each type of scalp dandruff.

Materials & Methods:

Clinical study:

33 subjects with mild to moderate Dandruff Clinical score ≥ 4 on 10 points scale



- For both populations:
- ✓ Dandruff clinical evaluation (10 points-scale)
 - ✓ Itching and discomfort sensation (autoevaluation)
 - ✓ Hydration (Dermalab®)
 - ✓ Lipid index (Sebumeter®)
 - ✓ pH (pH-meter®)
 - ✓ Trans Epidermal Water Loss (Aquaflux®)
 - ✓ Swab sampling for fungi and bacteria microbiota analysis
- Statistical analysis of clinical parameter were done by Student's test

Microbiota studies:

After DNA extraction by QIAamp DNA Investigator kit:

- ✓ Taxonomic identification of bacteria was based on the sequencing of the ribosomal RNA gene, which is present in all microbial genomes. V1-V3 region of 16S ribosomal RNA genes (prokaryotes) were amplified by PCR using oligonucleotides targeting conserved regions common to all bacteria.
- ✓ Fungi population study was based on the sequencing of the ITS1 region of the ribosomal RNA gene, which is present in all fungi genomes. ITS1 region of the ribosomal RNA genes (Eukaryotes) were amplified by PCR using oligonucleotides targeting conserved regions common to all fungi.

Alpha and beta diversity were compared after normalization by rarefaction. Observed, Chao1, Shannon and invSimpson indices were compared by an ANOVA analysis for Alpha diversity evaluation. Beta diversity was evaluated with Jaccard, Bray Curtis, Unifrac and weighted Unifrac indices. The pValue of the comparison was carry out by PERMANOVA analysis.

Differential analysis between the two dandruff scalp populations was carried out, after GMPR normalization and DEseq2 method to identify genus that were significantly more abundant in one group than the other.

At the species level, absolute quantitative evaluation of *Malassezia restricta*, *Malassezia globosa*, *Cutibacterium acnes* and *Staphylococcus epidermidis* was done by digital droplet PCR (ddPCR).

References:

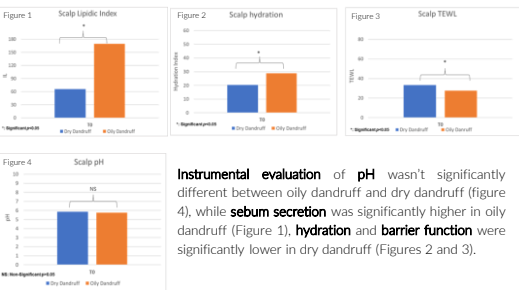
1. Ji-Seon Yoon et Al (2020) Biophysical characteristics of dandruff affected scalp categorized on basis of sebum levels. *Journal of cosmetic dermatology* 20(3) 1002-1008
2. Hee Kuk Park et Al (2012) Characterization of the Fungal Microbiota (Mycobiome) in Healthy and Dandruff-Affected Human Scalps. *Plos One*. 7(2):e32847
3. Li Wang et Al. 2022 Amplicon-based sequencing and co-occurrence network analysis reveals notable differences of microbial community structure in healthy and dandruff scalps. *BMC Genomics*. Apr 19;23(1):312.
4. K. Findley et Al (2013) Topographic diversity of fungal and bacterial communities in human skin *Nature* 20:498(7454):367-70

Results & Discussion:

Clinical and instrumental results

Clinical dandruff condition (dandruff state), itching and discomfort of scalp were not significantly different between oily and dry scalp (data not shown).

Instrumental results



Instrumental evaluation of pH wasn't significantly different between oily dandruff and dry dandruff (figure 4), while sebum secretion was significantly higher in oily dandruff (Figure 1), hydration and barrier function were significantly lower in dry dandruff (Figures 2 and 3).

Microbiota analysis

Microbiota biodiversity

Alpha and beta diversity analysis of bacteria and fungi population didn't show any significant differences between oily and dry dandruff.

Bacteria population

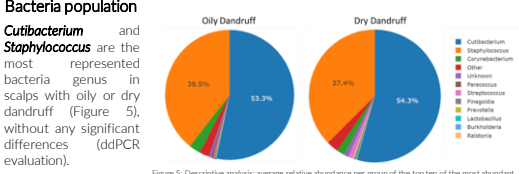


Figure 5: Descriptive analysis: average relative abundance per group of the top ten of the most abundant bacteria at the genus level

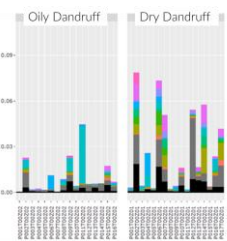


Figure 6: Histogram of genus of Actinobacteria of each subject with dry or oily dandruff.

Genus of the phylum **Actinobacteria** appeared to be more abundant and represented in dry dandruff (Figure 6). As example, differential analysis showed that *Pelomonas*, *Ralstonia*, *Nesteria*, were more abundant on the scalp of dry dandruff than on that of oily dandruff. One genus of this phylum was more abundant in oily dandruff : *Brachyobacterium*. Differential analysis also identified *Capnocytophaga* and *Streptococcus* as more abundant in dry than in oily dandruff.

Fungi population

Oily dandruff scalp was dominated by *Malasseziaceae* family (figure 7). This observation was confirmed by differential analysis and absolute quantification of *Malassezia restricta* and *globosa* by ddPCR. This result correlates with the significantly higher lipid index measurement on oily dandruff scalp than on dry dandruff scalps. Microbiota of dry dandruff scalp was composed of more unclassified fungi (figure 7 - unknown). Differential analysis highlighted the genus *Filobasidium* as being related to dry dandruff. This genus was published to be associated with dandruff by Hee Kuk Park et Al. in 2012 [2].

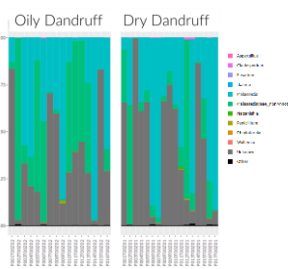


Figure 7: Histogram of fungi genus of each subject with dry or oily dandruff.

Conclusions:

According to published data, dehydration and low sebum production are characteristic of dry dandruff scalps whereas oily dandruff scalps display high sebum production and inflammation. Our results confirm the previous findings. Interestingly, the barrier function of the skin scalp seems to be more impaired in dry dandruff scalp. In addition, we have shown here that scalp microbiota of these two dandruff states are different. These results highlight the importance to address dry dandruff and oily dandruff scalps with specific scalp care products. This study is linked with the poster N°446: Effectiveness of Targeted Antidandruff Shampoos: Clinical, Instrumental and Metagenomic Analysis