

SKIN MICROBIOME IN PATIENTS WITH PSORIASIS BEFORE AND AFTER BALNEOTHERAPY AT THE THERMAL CARE CENTER OF LA ROCHE-POSAY

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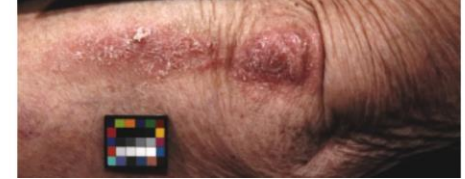
Conflict of interest: S. Seité and R. Martin are employees of La Roche-Posay Dermatological Laboratories, France and L'Oréal Research & Innovation, France

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INTRODUCTION

Changes in the composition of microbial communities that colonize skin have been linked to several diseases including psoriasis⁽¹⁾. Nevertheless, the intra-individual dynamics and how these communities respond to balneotherapy remain poorly understood.

The objective of this study was to comprehensively characterize microbial diversity and community structure associated with affected and unaffected skin of patients with psoriasis before and after balneotherapy treatment using selenium-rich thermal water.



MATERIALS AND METHODS

This open label study was conducted between July and September 2012. Microbial communities of patients with psoriasis vulgaris were characterized before and after a 3-week selenium-rich water balneotherapy treatment at the thermal care center La Roche-Posay (La Roche-Posay, France). Balneotherapy consisted of high pressure filiform showers, baths, facial and body spray treatments as well as La Roche-Posay thermal water consumption. Swabs were taken from affected (AF) and proximal unaffected skin (UAF) and the 16S rRNA bacterial gene was used to analyze the composition of bacterial communities.

RESULTS

This study included 54 patients (32 male and 22 female; aged 59 ± 13 years (25 to 86 years) diagnosed with moderate to severe form of psoriasis vulgaris (PASI before balneotherapy = 20 ± 14).

After eliminating individuals lacking paired samples from both visits, there were 30 paired samples corresponding to the 29 individuals showing a decreasing PASI at the end of the balneotherapy that were analyzed for their microbiome profile.

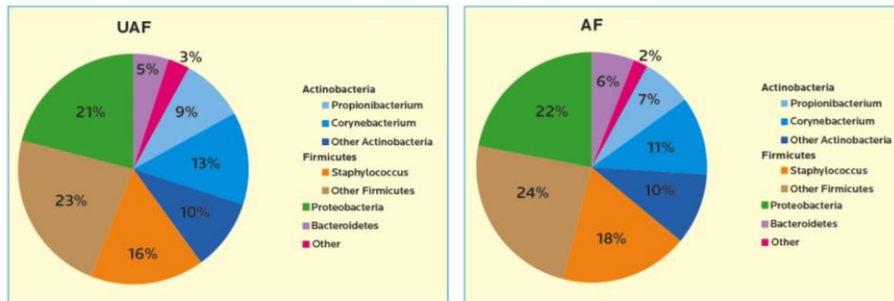
Microbiome of unaffected and affected skin prior to balneotherapy

We obtained a very low number of reads in our samples from psoriatic patients in comparison to those of healthy individuals or atopic ones analyzed with the same experimental conditions. Shannon Index indicates similar microbial communities on both unaffected and adjacent affected skin. A very poor biodiversity was also evidenced.

	Prior balneotherapy	
	UAF	AF
Richness (OTUs) (n=30)	152 ± 56	157 ± 56
Shannon Index (n=30)	3.76 ± 0.65	3.83 ± 0.77

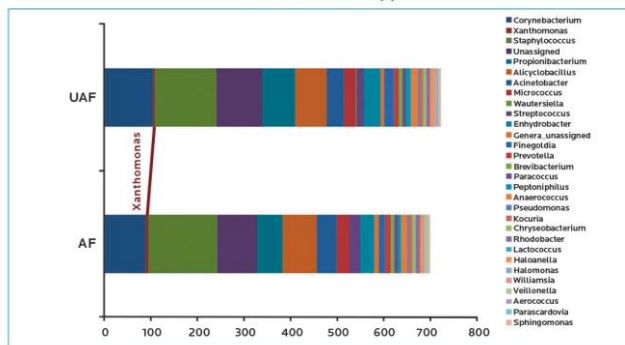
Analysis of bacterial phyla and families shows an abundance of Firmicutes phylum and a deficiency in Proteobacteria phylum as previously described^(1,2).

Prior balneotherapy



The global bacterial landscape was similar between both unaffected and affected skin.

Prior balneotherapy



Microbiome of unaffected and affected skin post balneotherapy

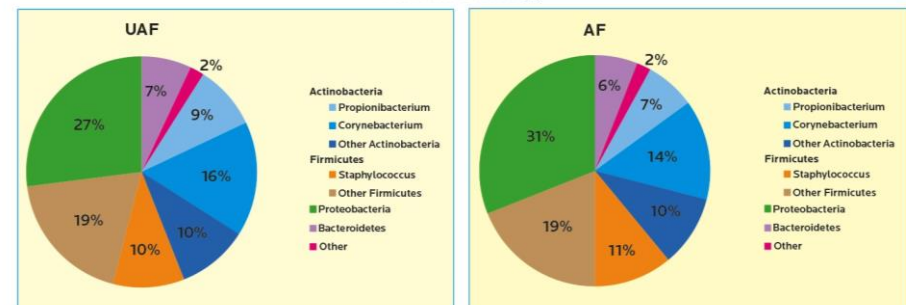
PASI values decreased after balneotherapy from 21 ± 10 to 8 ± 5 (-61%), implying improvement of disease symptoms.

No significant change in microbial communities and a very poor biodiversity were noticed at the end of the 3-week balneotherapy.

	Post balneotherapy	
	UAF	AF
Richness (OTUs) (n=30)	159 ± 59	153 ± 43
Shannon Index (n=30)	3.73 ± 0.75	3.65 ± 0.74

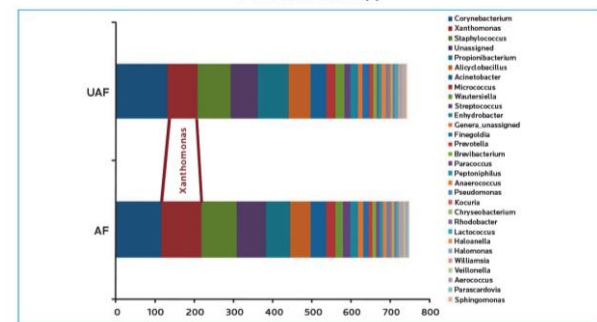
But analysis of bacterial phyla and families indicates a decrease of Firmicutes phylum (from 40 to 30%) and an increase of Proteobacteria phylum (from 20 to 30%).

Post balneotherapy



The average taxonomic composition of skin microbial communities associated with unaffected and affected skin of psoriatic patients after balneotherapy shows that treatment with La Roche-Posay thermal spring water significantly increased the level of *Xanthomonas* genus and, to a lesser extent, *Corynebacterium* genus associated with a reduced disease severity.

Post balneotherapy



CONCLUSION

We demonstrated that the comparison of affected and unaffected adjacent skin from the same psoriatic patient provides deeper insight into the bacterial communities involved in this skin dysbiosis. A very poor bacterial biodiversity in patients with psoriasis indicates that this pathology is associated with a poor skin microbiome barrier. Interestingly, the bacterial communities were similar on unaffected and affected adjacent skin, so a systemic alteration of the microbiome is perhaps implicated in this chronic skin disease. Family analysis identified, for the first time, *Xanthomonadaceae* belonging to Proteobacteria phylum and known to be keratolytic, associated with a clinical improvement (PASI decrease) observed after a 3-week balneotherapy with La Roche-Posay Thermal spring water.

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2. Hannigan GD, Grice EA. Microbial ecology of the skin in the era of metagenomics and molecular microbiology. *Cold Spring Harb Perspect Med* 2013, **3**: a015362