RESPONSE OF SKIN MICROBIOME TO EMOLLIENT TREATMENT IN PATIENTS WITH ATOPIC DERMATITIS

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INTRODUCTION

Changes in the composition of microbial communities that colonize skin have been linked to several diseases including atopic dermatitis. However, the dynamics of the associated bacterial communities and their responses to topical treatments remain poorly understood.
Using a high-throughput sequencing approach that targets part of the 16S rRNA gene is the best way to comprehensively characterize microbial communities associated with affected and unaffected atopic dermatitis skin. Furthermore, skin microbiota varies between individuals. This study was designed to characterize intra-individually specific microbiota associated with clinical symptoms of atopic dermatitis before and after a 3 month emollient treatment.

METHODS

This open label study was conducted between August and November 2012. Microbial communities of atopic dermatitis patients were characterized before (D1) and after (D84) a twice-daily treatment with an emollient containing Shea butter, thermal spring water, and niacinamide. Swabs were taken, under axenic conditions, from affected (AF) and proximal unaffected (UAF) skin and 16S rRNA bacterial gene was used to analyze the composition of bacterial communities.

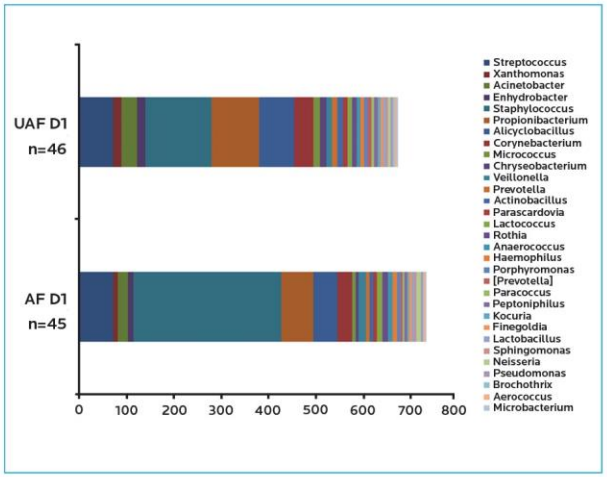
RESULTS

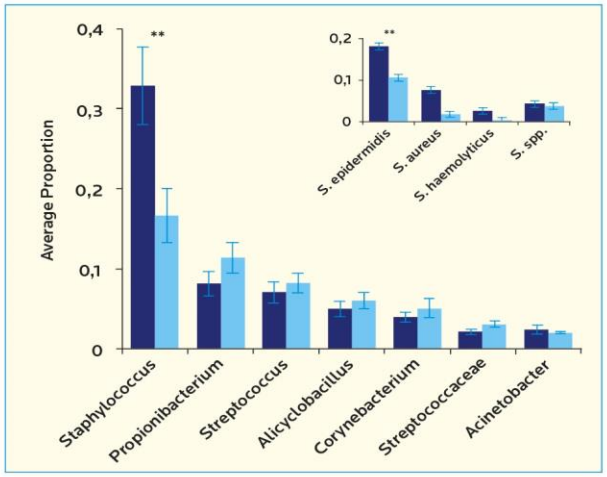
This study included 49 patients (17 male and 32 female) aged 12 ± 9 years (3 to 39 years) diagnosed with moderate atopic dermatitis. After eliminating individuals lacking paired samples from both time points, 36 individuals with 41-paired samples remained.

Microbiome of affected and unaffected skin prior to treatment with an emollient

The bacterial community dramatically differed in AD patients as opposed to healthy subjects for a given zone.
Using the Shannon diversity index, we found UAF skin sites had significantly more diverse microbial communities than adjacent AF skin for 28 of 41-paired samples (median AF = 5.93; median UAF = 6.32; p = 0.002). The bacterial diversity on AD skin was less on unaffected skin and more so on affected skin.

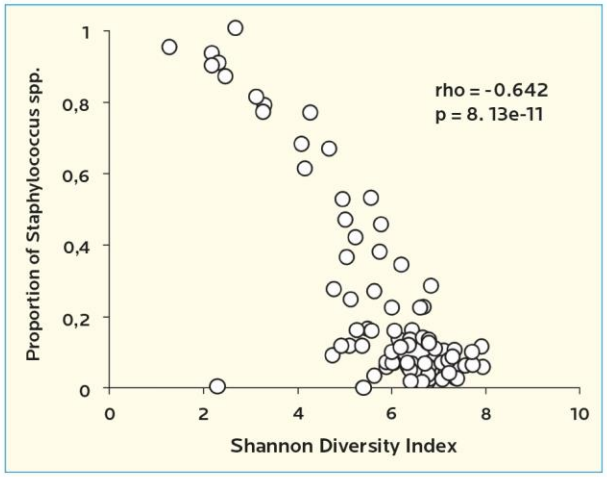
Although *Staphylococcus* was found to be the most abundant genus on AF and UAF skin areas, AF skin harbored a greater relative abundance of *staphylococci*. This confirmed, as published, a greater proportion of *Staphylococcus* during AD flares. Also of note, commensal *S. epidermidis* and *S. haemoliticus* (a recently characterized *Staphylococcus* species in AD), were also overrepresented in AF versus UAF skin areas.



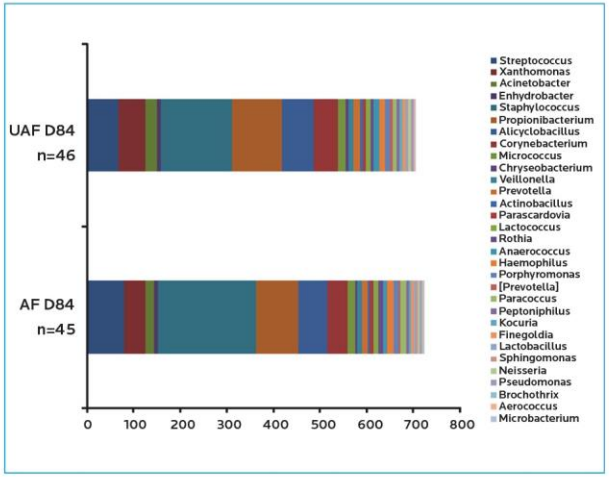


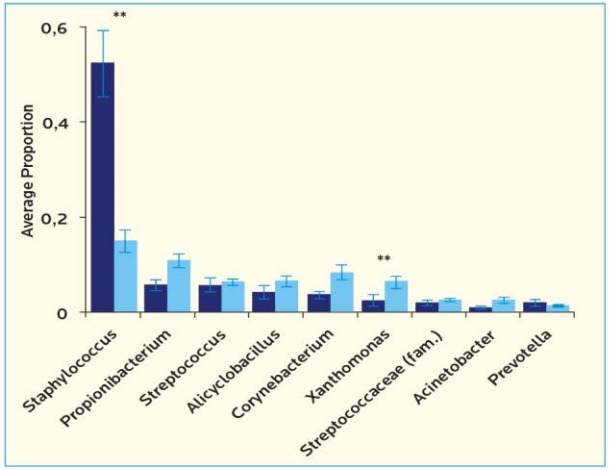
Dark blue bars are taxa associated with AF skin while light blue bars are from UAF skin. Asterisks denote statistical differences between AF and UAF ($p < 0.01$, Bonferroni corrected) based on Wilcoxon rank sum test for paired samples. Inset shows species of Staphylococcus. Error bars are ± SEM.

Staphylococcus abundance was inversely related to Shannon diversity



Results of Spearman rank correlations in top right of figure.





Dark blue bars are taxa associated with individuals that did not respond to treatment while light blue bars are from treatment responders. Asterisks denote statistical differences between groups ($p<0.01$, Bonferroni corrected) based on Wilcoxon rank sum test for unpaired samples. Error bars are ± SEM.

This confirms the capacity of the tested emollient to promote bacterial balance and diversity associated with clinical benefits. For the first time, our analysis identified a bacterium genus that seems to be linked to SCORAD decrease.

CONCLUSION

This study demonstrated that bacterial populations vary between adjacent affected and unaffected skin in atopic patient, providing an insight into AD associated skin dysbiosis. These data support the importance of emollients in managing atopic dermatitis and may lead to new antimicrobial and promicrobial therapies for atopic dermatitis and other chronic dermatoses.