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 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 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 and 84 days after twice-daily treatment with an emollient containing Shea butter, thermal spring water, and niacinamide. Swabs were taken, under axenic conditions, from lesions and proximal unaffected 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 lesional and non-lesional skin prior to treatment with an emollient

The bacterial community dramatically differed in AD patients as opposed to healthy subjects for a given zone internal data. Using the Shannon diversity index, we found non-lesional skin sites had significantly more diverse microbial communities than adjacent lesional skin for 28 of 41-paired samples (median lesional = 5.93; median non-lesional = 6.32; p = 0.002). The bacterial diversity on AD skin was less on unaffected skin and more so on lesions. Although Staphylococcus was found to be the most abundant genus on lesional and healthy skin areas, lesional skin harbored a greater relative proportion of Staphylococcus species in AD, were also overrepresented in lesions.

Microbiome of lesional and non-lesional skin post-application of emollient

SCORAD values decreased after treatment, implying disease symptoms improved for 72% of the study population (‘responders’). For the other individuals (‘non-responders’), SCORAD remained the same or increased after 84 days of treatment. A significant reduction of erythema, dryness and desquamation was noted on lesional skin areas sampled from an average global score of 4 ± 1 at day 0 to 2 ± 2 at day 84 (p < 0.0001). In contrary to prior treatment, for both ‘responders’ and ‘non-responders’, no differences were observed in diversity levels between lesional and non-lesional skin after treatment (responders, p = 0.10; non-responders, p = 0.20). The average taxonomic composition of skin microbial communities associated with lesional and non-lesional skin of patients with atopic dermatitis after emollient treatment shows that emollient treatment significantly reduced the level of all Staphylococcus species correlating with reduced disease severity, without any antibacterial therapy. The populations of other bacteria genera Propionibacterium, Streptococcus, Alicyclobacillus and Corynebacterium were similar after treatment than before.

CONCLUSION

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

This study demonstrated that bacterial populations vary between adjacent affected and unaffected skin from an 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 dermatosis.