

ATOPIC ECZEMA/DERMATITIS

## EXAMINATION OF THE SKIN MICROBIOME ASSOCIATED WITH DRY AND NON-DRY SKIN

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**Introduction:** The application of next generation sequencing techniques to skin microbiology has in recent years greatly advanced our understanding of the composition of the human skin microbiome and how changes in microbiome composition correlate with skin condition. However, although differences in the skin microbiome have been described for dermatological conditions such as atopic dermatitis and psoriasis, the microbiome of dry skin remains understudied despite the much higher prevalence of this skin condition in the general population.

**Objective:** To characterize the cutaneous microbiome in geographically distinct population groups (Europe and N. America) with visually dry skin in comparison to those without dry skin.

**Materials and Methods:** Healthy, female subjects with either moderately dry skin or non-dry skin on their lower legs provided informed consent to participate in IRB-approved studies. Samples were collected and processed for bacterial metataxonomics assessment using 16S rRNA gene sequencing and analysis. Analyses of taxonomic microbiome composition, diversity and community associations were performed.

**Results:** Analysis of data across both studies consistent community associations when skin conditions were compared and demonstrated that *Staphylococcus*, *Cutibacterium* and *Corynebacterium* were the most abundant genera in both groups. No differences in alpha-diversity were observed however significant differences ( $p=0.04$ ) were identified in the beta-diversity.

**Conclusions:** Differences have been identified in the microbiome between visibly dry and non-dry. The differences found were consistent across both geographical locations and population groups.