reduced Evenness, which was in turn mainly driven by *S. aureus* relative abundance, rather than to a reduced microbiome Richness. Finding associations between AD severity, the skin microbiome and patient's cofactors is a key aspect in developing new personalized AD treatments, particularly those targeting the AD microbiome.

11 | Skin microbiome and its association with host cofactors in determining atopic dermatitis severity

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Atopic dermatitis (AD) is a heterogeneous, chronic inflammatory skin disease linked to skin microbiome dysbiosis with reduced bacterial diversity and elevated relative abundance of Staphylococcus aureus (S.aureus). We aimed to characterize the yet-incompletely understood association between the skin microbiome and patients' demographic and clinical cofactors in relation to AD severity. The skin microbiome in 48 adult moderate-to-severe AD patients was investigated using next-generation deep sequencing (16S rRNA V1-V3) followed by denoising to obtain amplicon sequence variant (ASV) composition. AD severity was associated with S.aureus relative abundance (rS = 0.53, $p < 0.001$) and slightly better with the microbiome diversity measure Evenness (rS = –0.58, $p < 0.001$) in lesion. Multiple regression confirmed the association of AD severity with microbiome diversity, including Shannon (lesion, $p < 0.001$), Evenness (non-lesion, $p = 0.015$), or *S. aureus* relative abundance (<0.012), and with patient's IgE levels ($p < 0.001$), race ($p < 0.032$), age ($p < 0.034$) and sex ($p = 0.012$). Our results specify the frequently reported "reduced diversity" of the AD-related skin microbiome to