

Severe atopic dermatitis is associated with increased total skin bacterial load driven by staphylococcus aureus overgrowth

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Severe Atopic dermatitis (AD) is known to be associated with a Staphylococcus aureus driven microbiome dysbiosis. However, it is not yet clear how this dysbiosis is related to the actual bacterial load, in particular to the absolute Staphylococcus aureus load, on the skin. Here, we combined the relative abundance results obtained by next-generation sequencing (NGS, 16S V1-V3) with bacterial quantification by targeted qPCR (total bacterial load = 16S, S. aureus = nuc gene) to study the composition of absolute bacterial load in AD patients. Skin (lesional and non-lesional) swabs were sampled cross-sectionally in AD patients (n=135) and in healthy controls (n=20). AD patients, both in lesional and non-lesional skin, exhibited significantly higher total bacterial load, in addition to higher S. aureus relative abundance and S. aureus cell numbers, as compared to healthy controls. Moreover, significantly more severe AD patients had high total bacterial load in lesional skin as compared to moderate and mild AD patients. Furthermore, among AD patients with high total bacterial load, significantly more severe AD patients presented with higher S. aureus cell numbers and S. aureus relative abundance and total bacterial load, in correlation with the total bacterial load, as compared to patients with mild or moderate AD. Thus, indicating that severe AD patients exhibit an S. aureus driven increased bacterial skin colonization giving rise to higher total skin bacterial load. Our results warrant that, in addition to immune modulation treatment, severe AD patient could benefit also from therapy directed at suppressing skin bacterial overgrowth.