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Atopic dermatitis (AD) manifests as a chronic skin disease with recurrent skin inflammation associated with microbiome dysbiosis and a complex interplay between a dysfunctional skin barrier, immune dysregulation, and genetic and environmental factors. AD prevalence is relatively high (20% of children, 10% of adults) and is linked to higher rates of allergic diseases. The detected microbial imbalance is associated with an elevated level of *Staphylococcus aureus*, but information is missing on the actual bacterial load on AD skin, which may affect the cell number driven release of pathogenic factors. Therefore, here we used two methods for skin microbiome analysis. Microbiome relative abundance was estimated using next-generation sequencing (NGS, 16S V1-V3) and the bacterial absolute abundance was obtained by targeted qPCR (total bacterial load = 16S gene, *S. aureus* = nuc gene). Lesional and non-lesional skin swabs were sampled cross-sectionally from 96 AD patients with different severity and from 20 healthy controls. *S. aureus* relative abundance and *S. aureus* cell numbers were highly inter-correlated across patients. In addition, differences between lesional and non-lesional skin were similarly reflected in both methods. Interestingly, compared to healthy controls, AD patients had a significantly higher total bacterial load in both lesional and nonlesional skin, as well as higher relative abundance and cell numbers of *S. aureus*. Furthermore, elevated *S. aureus* cell numbers were significantly associated with higher total bacterial load in AD lesional skin. Additionally, patients with severe AD presented significantly higher *S. aureus* and total bacterial load, in comparison to those with mild or moderate AD. Validation by skin type showed that, these associations were significant in dry and moist, but only a trend in sebaceous, bodysites. These findings suggest that severe AD patients exhibit increased bacterial skin colonization that is driven by *S. aureus*. This study demonstrates that bacterial quantification provides important insights in addition to microbiome composition by sequencing.