

**P119 | Targeted systemic treatment modulates the relative abundance of staphylococcus aureus in patients with atopic dermatitis**

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**Background:** Significant innovation has been achieved in treating inflammatory skin diseases like atopic dermatitis (AD) in recent years. However, the skin microbiome's role in the microbial-immunological interplay and its significance in the pathophysiological network AD still needs further elucidation.

**Methods:** To investigate the effect of local and systemic therapeutics on the human skin microbiome in patients with AD, we collected and analysed data and samples within the context of the ProRaD study at Augsburg and Bonn between 2017 and 2019. In total, 1077 skin microbiome swabs and medication data from 462 subjects were analysed and evaluated in the cross-sectional study design.

The patients' skin microbiome was assessed with amplicon-based 16S-rRNA nextgeneration sequencing of the V1-V3 region and bioinformatic annotation to species level with AnnotIEM. The current therapeutic regime was documented and the patients were clustered into treatment groups according to the recommendations of the EuroGuiDerm Guidelines.

**Results:** We could confirm a strong correlation between skin condition and the frequency of *Staphylococcus aureus* in skin lesions of AD patients. However, we observed no association between relative *S. aureus* frequency and age or sex.

In order to eliminate skin condition as a confounder, separate investigations of the skin microbiome were conducted for mild, moderate and severe disease courses. In patients with moderate AD, we found a significantly lower relative abundance of *S. aureus* in those receiving systemic treatment compared to those receiving topical treatment only.

Furthermore, in subjects undergoing systemic treatment, we found a trend towards differences in dependency on the active ingredient administered during systemic AD treatment. Specifically, the average relative frequency of *S. aureus* appeared to be lesser in participants receiving dupilumab than that of participants receiving conventional, systemic immunosuppressive therapy.

**Conclusion:** In our pilot study we observed and described potential correlations between AD treatment and microbiome changes within the patient collective of the ProRaD cohort. Our pilot study proves the relevance of specific immunological processes in the immunological microbial interplay in AD. However, exploring specific immunomodulatory substances and their influence on the skin barrier bears further potential for a more profound understanding of the host-immunity and skinmicrobiome interplay.