ABSTRACT BOOK
ABSTRACTS

24TH WORLD CONGRESS OF DERMATOLOGY MILAN 2019

A new ERA for global Dermatology
10 – 15 JUNE 2019
MILAN, ITALY

ACNE, ROSACEA, AND RELATED DISORDERS (INCLUDING HIDRADENITIS SUPPURATIVA)

CHARACTERIZATION AND ANALYSIS OF THE SKIN MICROBIOTA IN ROSACEA

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Introduction: The efficacy of antibiotics in rosacea treatment suggests a role for microorganisms in its pathogenesis. Growing concern over the adverse effects of antibiotic use presents a need for targeted antimicrobial treatment in rosacea.

Objective: We performed a case-control study to investigate the skin microbiota in rosacea patients compared to controls matched by age, sex, and race.

Materials and Methods: 19 participants with rosacea, erythematotelangiectatic (ETR), papulopustular (PPR), or both, were matched to 19 rosacea-free controls. DNA was extracted from skin swabs of the nose and bilateral cheeks of participants. Sequencing of the V3V4 region of the bacterial 16S rRNA gene was performed using Illumina MiSeq and analyzed using QIIME/Phyloseq softwares. The resulting 4,036,167 16S rRNA gene sequences were clustered into 1,593 species-level operational taxonomic units.

Results: Compared to controls, ETR was enriched in Salmonella enterica (p=0.04995) and depleted in Roseomonas mucosa (p=0.004). PPR was enriched in Campylobacter ureolyticus (p=0.001), Corynebacterium kroppenstedtii (p=0.008), and the oral flora Prevotella tannerae (p=0.001) and Prevotella intermedia (p=0.001) and depleted in Propionibacterium granulosum (p=0.005) and Acinetobacter johnsonii (p=0.046). The highest relative abundance of C. kroppenstedtii was observed in patients with both ETR and PPR (19.2%), followed by PPR (5.06%) and ETR (1.21%). C. kroppenstedtii was also associated with more extensive disease, with the highest relative abundance in rosacea affecting both cheeks and nose (2.82%), followed by rosacea sparing the nose (1.93%), and controls (0.19%). The relative abundance of Cutibacterium acnes, greater in male controls (57.5%) than female controls (29.7%), normalized between males (23.8%) and females (27.8%) with rosacea.

Conclusions: The skin microbiota in individuals with rosacea displays changes from that of healthy skin, including the enrichment and depletion of various bacterial taxa. These

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findings suggest a role for the skin microbiota in the pathogenesis of rosacea as well as potential targets for antimicrobial treatment.

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