

RISING DERM STARS

The microbiome in preadolescent acne: assessment and prospective analysis on the influence of benzoyl peroxide

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Background/Objectives: The pathogenesis of preadolescent acne has not been well studied, and it is uncertain if *Propionibacterium acnes* is a predominant organism in the microbiome in this age group.¹⁻⁴ The aim of this study was to analyze the microbiome of preadolescent females, and to assess if benzoyl peroxide (BP) impacts the microbiome.

Methods: The study enrolled females, aged 7-12 years old, with evidence of at least six acneiform lesions who had not been previously treated with prescription acne products, BP, or had recently received oral antibiotics. Subjects' skin surface of forehead, cheeks, nose, chin, left retroauricular crease and extruded contents of a comedonal lesion were sampled at baseline. Subjects utilized BP 4% wash for 6 to 8 weeks and returned for skin surface sampling and extraction collection. Microbiome analysis was performed using 16S ribosomal RNA gene amplicon sequencing on all swab and lesional extraction samples.

Results: 51 subjects were enrolled with a median IgA score of 2 (mild). Changes in microbiome diversity were associated with increasing age and number of acneiform lesions ($p=0.001$) (Figure 1). *P. acnes* had higher abundances on forehead and nose, as opposed to cheeks and chin ($p=0.009$).

Bacterial diversity (alpha diversity) of the skin microbiome was comparable between preadolescent at baseline and after treatment with benzoyl peroxide (Figure 2).

Conclusion: This is the first large assessment characterizing female acne microbiome in early and late preadolescence. Results show that preadolescent acne can vary in its microbial profile, reflecting surrounding changes associated with the onset of puberty. Although benzoyl peroxide use was associated with decreased acne counts, its effect on microbial diversity was not demonstrated in our study.

Figure 1: Bar plot of Bacterial Species according to Number of Acne Lesions.

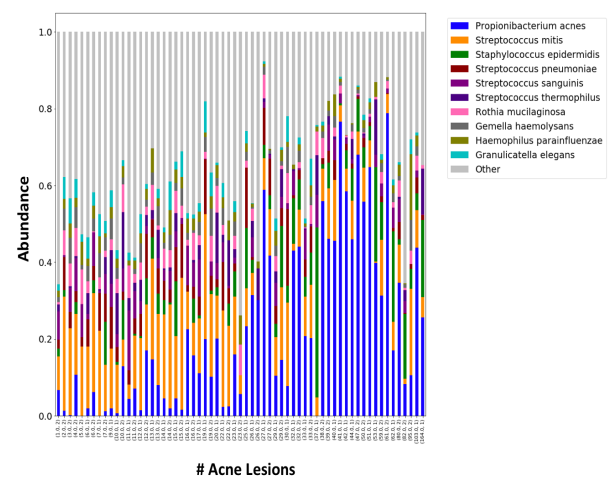
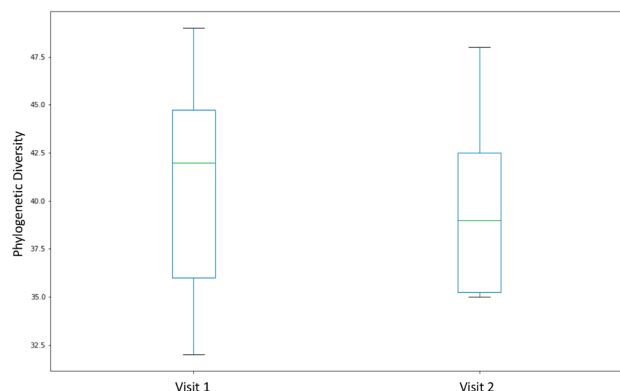


Figure 2: Phylogenetic Diversity in Visit 1 (pre-treatment) and Visit 2 (post-treatment). Boxes indicate the 25th percentile, median, and 75th percentile. Outliers are represented by open dots. Whiskers show the minimum and maximum ranges.



References:

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