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Characterizing the Alopecia Areata Microbiome

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Background: Alopecia areata (AA) is an inflammatory, non-scarring hair loss resulting from autoimmune attack of the hair follicle, affecting as much as 2% of the population. Researchers have not determined the exact pathogenesis of AA, but hypotheses include imbalances in innate immunity, environmental insults, and genetic predisposition. The microbiome is a community of commensal and pathogenic microorganisms that live on and within our bodies. With growing evidence that the microbiome plays a significant role in inflammatory skin conditions such as atopic dermatitis and psoriasis, recent cases postulate that the gut microbiome plays a role in AA development.

Methods: In this pilot study, we aim to characterize the local (scalp) and global (gut) microbiome of AA patients and determine if there are significant differences when compared to healthy controls. Microbiome samples were collected from 25 subjects with AA and 25 healthy controls living in Southern California at a single, academic medical center; controls were age, gender and race-matched to alopecia patients. At the time of sample collection, all subjects were required to have no active gastrointestinal disease. Scalp swabs and stool samples were obtained from each subject. After DNA was isolated from each sample, 16s RNA and internal transcribed spacer (ITS) libraries

were created to identify bacterial and fungal taxonomy, respectively. Multi-variant analysis comparing the alopecia to control microbiomes was performed.

Results: AA subjects were 40.3 ± 14.7 years old, female (72%) and identified as Caucasian (60%). There were no significant differences noted in the demographic make-up of the alopecia and control groups. Significant differences were noted in both the scalp and gut microbiome of alopecia patients compared to controls. Alopecia patients' scalp samples had significantly decreased *Firmicutes* ($p < 0.05$) and increased *Actinobacteria* trending to significance, while their gut microbiome was significant for decreased *Bacteroides* ($p < 0.05$) and increased *Firmicutes* trending to significance.

Conclusion: Microbiome dysbiosis may cause inappropriate systemic immune response and inflammation leading to autoimmune alopecia in predisposed patients. It is our hope that this preliminary data may be used in the future to characterize changes in the scalp and gut microbiome that may be related to AA disease severity, patient dietary practices, and even predict prognosis and/or therapeutic response.

References:

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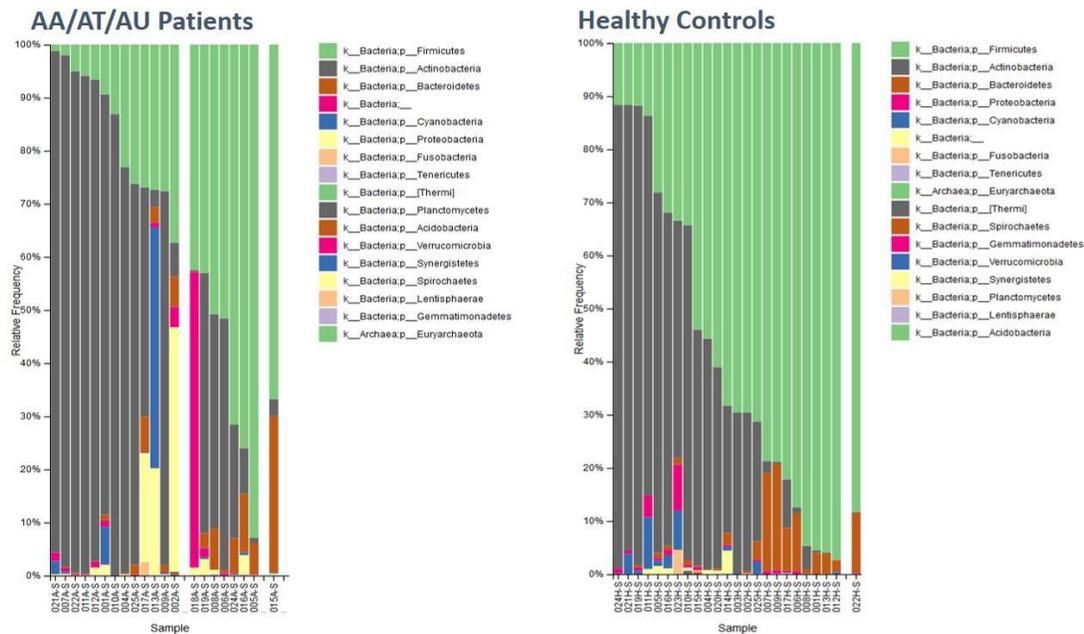


Figure 1: Comparison of the scalp bacterial microbiome from alopecia patients to healthy controls reveals significantly decreased *Firmicutes* ($p=0.00063$) in alopecia samples.