HAIR DISORDERS

THE MICROBIOME OF ALOPECIA AREATA - ELUCIDATING ITS ROLE IN DISEASE PATHOGENESIS

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Introduction: Approximately 2% of the population is affected by alopecia areata (AA). AA pathogenesis is believed to be multifactorial, including derangements in innate immunity, environment and genetic predisposition. Recent cases demonstrate that the gut microbiome plays a role in AA development.

Objective: To characterize the local (scalp) and global (gut) microbiome of AA patients and compare to healthy controls to determine significant differences.

Materials and Methods: 25 patients with AA and 25 healthy controls originating from Southern California were enrolled. At the time of microbiome collection, participants had no active gastrointestinal disease. Patients were age, gender and race-matched to controls. Scalp swabs and stool samples were obtained from each subject. Bacterial and fungal taxonomy was identified using operational taxonomic units in conjunction with appropriate databases. Comparison of the alopecia and control microbiomes was completed.

Results: There were no significant differences in the mean age, or distribution of gender and races/ethnicities between alopecia and control groups. A higher proportion of AA patients reported a history of atopy, thyroid disease or gastrointestinal disease than controls. Alopecia bacterial and fungal microbiomes, derived from both the skin and gut, demonstrate significant dysbiosis when compared to healthy individuals.

Conclusions: Preliminary data demonstrates significant changes in both the scalp and gut microbiome of alopecia patients compared to healthy controls. In predisposed patients, dysbiosis may lead to systemic inflammation and autoimmune attack of hair follicle. Future directions include characterizing microbiome changes as related to disease severity, prognosis, prediction of therapeutic response, and impact of dietary practices.