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HAIR DISORDERS

CHARACTERIZING THE MRNA EXPRESSION PATTERN OF CENTRAL CENTRIFUGAL CICATRICIAL ALOPECIA USING GENE-CHIP MICROARRAY

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Introduction: Central Centrifugal Cicatricial Alopecia (CCCA) is the most common form of permanent scarring alopecia in women sub-Saharan African descent. The pathogenesis of this condition is unknown.

Objective: To characterize the transcriptional landscape of CCCA in hopes of gaining insight into the pathogenesis of CCCA.

Materials & Methods: We performed gene expression microarrays on paired samples of affected and unaffected scalp tissue to assess the transcriptional landscape of CCCA. We performed transcriptome-wide analysis of over 20,000 well-annotated human genes, interrogating all known exons and performed gene ontology to understand the functional significance of gene transcripts.

Results: Six of 50 genes that regulate fibroblast proliferation showed increased expression in CCCA tissue, including fibronectin 1 and PDGF receptor alpha and beta (p =0.024). Twelve of 39 genes associated with collagen fibril organization, including TGFß2, were preferentially expressed in diseased tissue (p <.0001). Peroxisome proliferator associated gene receptor gamma (PPAR-γ) was unchanged. In CCCA affected scalp, 66 of 856 genes that regulate the lipid metabolic process were downregulated (p <.0001). Out of all known canonical pathways, Ingenuity Pathway Analysis revealed greatest gene expression overlap between CCCA and both hepatic fibrosis (p <.0001) and atherosclerosis (p<.0001).

Conclusions: CCCA shows a molecular expression pattern that overlaps with conditions of aberrant fibroblast proliferation termed fibroproliferative disorders and shares an alteration of lipid metabolism genes seen in other cicatricial alopecias. Unlike lichen planopilaris, no change in PPAR-γ expression was noted. To the author's knowledge, this is the first study investigating the gene expression pattern of CCCA.

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