Identification of novel immune and barrier genes in atopic dermatitis by means of laser capture microdissection

**Background:** The molecular signature of atopic dermatitis (AD) lesions is associated with T(H)2 and T(H)22 activation and epidermal alterations. However, the epidermal and dermal AD transcriptomes and their respective contributions to abnormalities in respective immune and barrier phenotypes are unknown. **Objective:** We sought to establish the genomic profile of the epidermal and dermal compartments of lesional and nonlesional AD skin compared with normal skin.

**Methods:** Laser capture microdissection was performed to separate the epidermis and dermis of lesional and nonlesional skin from patients with AD and normal skin from healthy volunteers, followed by gene expression (microarrays and real-time PCR) and immunostaining studies.

**Results:** Our study identified novel immune and barrier genes, including the IL-34 cytokine and claudins 4 and 8, and showed increased detection of key AD genes usually undetectable on arrays (ie, IL22, thymic stromal lymphopoietin [TSLP], CCL22, and CCL26). Overall, the combined epidermal and dermal transcriptomes enlarged the AD transcriptome, adding 674 upregulated and 405 downregulated differentially expressed genes between lesional and nonlesional skin to the AD transcriptome. We were also able to localize individual transcripts as primarily epidermal (defensin, beta 4A [DEFB4A]) or dermal (IL22, cytotoxic T-lymphocyte antigen 4 [CTLA4], and CCR7) and link their expressions to possible cellular sources. Conclusions: This is the first report that establishes robust epidermal and dermal genomic signatures of lesional and nonlesional AD skin and normal skin compared with whole tissues. These data establish the utility of laser capture microdissection to separate different compartments and cellular subsets in patients with AD, allowing localization of key barrier or immune molecules and enabling detection of gene products usually not detected on arrays.
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