An integrated epigenetic and transcriptomic analysis reveals distinct tissue-specific patterns of DNA methylation associated with atopic dermatitis.

Abstract:
Epigenetic alterations are increasingly recognized as mechanisms for disease-associated changes in genome function and important risk factors for complex diseases. The epigenome differs between cell types and so far has been characterized in few human tissues only. In order to identify disease-associated DNA methylation differences for atopic dermatitis (AD), we investigated DNA from whole blood, T cells, B cells, as well as lesional and non-lesional epidermis from AD patients and healthy controls. To elicit functional links, we examined epidermal mRNA expression profiles. No genome-wide significant DNA methylation differences between AD cases and controls were observed in whole blood, T cells, and B cells, as well as lesional and non-lesional epidermis from AD patients and healthy controls. To elicit functional links, we examined epidermal mRNA expression profiles. No genome-wide significant DNA methylation differences between AD cases and controls were observed in whole blood, T cells, and B cells, and, in general, intra-individual differences in DNA methylation were larger than interindividual differences. However, striking methylation differences were observed between lesional epidermis from patients and healthy control epidermis for various CpG sites, which partly correlated with altered transcript levels of genes predominantly relevant for epidermal differentiation and innate immune response. Significant DNA
methylation differences were discordant in skin and blood samples, suggesting that blood is not an ideal surrogate for skin tissue. Our pilot study provides preliminary evidence for functionally relevant DNA methylation differences associated with AD, particularly in the epidermis, and represents a starting point for future investigations of epigenetic mechanisms in AD.

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