ABSTRACT BOOK ABSTRACTS



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ATOPIC ECZEMA/DERMATITIS

IDENTIFICATION OF DIFFERENTIALLY EXPRESSED GENES IN LESIONAL VERSUS NONLESIONAL SKINS OF ATOPIC DERMATITIS USING RNA-SEQ

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Background: Atopic dermatitis(AD) is a common chronic inflammatory skin disease associated with heredity. The exact pathogenesis of AD has not been fully defined. The potential molecular recognition of AD is mostly based on gene chip or quantitative real-time PCR, but there is little studyusing the new generation of RNA sequencing (RNA-seq).

Methods: RNA-seq were performed to identify differentially expressed genes(DEGs) (criteria: fold change \geq 2.0; falsediscovery rate \leq 0.05) in lesional versus nonlesional skins from 5 patients with moderate-to-severe AD.

Results:10 samples were measuredwith an average of 10.96 GB sequence reads per sample. The analysis of the RNA-Seq data revealed 78 DEGs,comprising 69 upregulated and 11 downregulated genes. Among them, several genes with known roles in inflammatory (CXCL1/2/8,IL6/1β,MMP1,SERPINB4,S100A2,GZMB, OASL, OSM) and barrier (KRT16,FABP5)and keratinocyte differentiation (IL-20) are associated withAD.The KEGG pathway showed that the DEGs were co-enriched into 132 signaling pathways, of which 13were significantly enriched such as the IL-17, the NOD-like receptor, and the Toll-like receptor signaling pathways.

Conclusion: This study showed DEGs in lesional versus nonlesional skins ofpatients with AD, and suggested that the IL-17, NOD-like receptor, and Toll-like receptor signaling pathways may play an important role in the pathogenesis of AD.



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