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Differentially Expressed Genes in Atopic Dermatitis: Bioinformatics Analysis Of Pooled Microarray Gene Expression Datasets In Gene Expression Omnibus

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Abstract : Background: Atopic dermatitis (AD) is a chronic and refractory inflammatory skin disease characterized by relapsing eczematous and pruritic skin lesions. The global prevalence of AD ranges from 1~ 20%, and its incidence rates are increasing. It affects individuals from infancy to adulthood, significantly impacting their daily lives and social activities. Despite its major health burden, the precise mechanisms underlying AD remain unknown. Understanding the genetic differences associated with AD is crucial for advancing diagnosis and targeted treatment development. This study aims to identify candidate genes of AD by using bioinformatics analysis. Methods: We conducted a comprehensive analysis of four pooled transcriptomic datasets (GSE16161, GSE32924, GSE130588, and GSE120721) obtained from the Gene Expression Omnibus (GEO) database. Differential gene expression analysis was performed using the R statistical language. The differentially expressed genes (DEGs) between AD patients and normal individuals were functionally analyzed using Gene Ontology (GO) and the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment. Furthermore, a protein-protein interaction (PPI) network was constructed to identify candidate genes. Results: Among the patient-level gene expression datasets, we identified 114 shared DEGs, consisting of 53 upregulated genes and 61 downregulated genes. Functional analysis using GO and KEGG revealed that the DEGs were mainly associated with the negative regulation of transcription from RNA polymerase II promoter, membrane-related functions, protein binding, and the Human papillomavirus infection pathway. Through the PPI network analysis, we identified eight core genes: CD44, STAT1, HMMR, AURKA, MKI67, and SMARCA4. Conclusion: This study elucidates key genes associated with AD, providing potential targets for diagnosis and treatment. The identified genes have the potential to contribute to the understanding and management of AD. The bioinformatics analysis conducted in this study offers new insights and directions for further research on AD. Future studies can focus on validating the functional roles of these genes and exploring their therapeutic potential in AD. While these findings will require further verification as achieved with experiments involving in vivo and in vitro models, these results provided some initial insights into dysfunctional inflammatory and immune responses associated with AD. Such information offers the potential to develop novel therapeutic targets for use in preventing and treating AD.

Keywords : atopic dermatitis, bioinformatics, biomarkers, genes
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