

عنوان مقاله:

Assessment of the Microbiome Role in Skin Protection Against UV Irradiation Via Network Analysis

محل انتشار:

مجله لیزر در علوم پزشکی، دوره 11، شماره 3 (سال: 1399)

تعداد صفحات اصل مقاله: 5

نویسندگان:

Mohammad Hossein Heidari

Mohammad Reza Razzaghi

Alireza Akbarzadeh Baghban

Mohammad Rostami-Nejad

Mostafa Rezaei-Tavirani

Mona Zamanian Azodi

Alireza Zali

Alireza Ahmadzadeh

خلاصه مقاله:

Abstract Introduction: Diverse microbiotas which have some contributions to gene expression reside in human skin. To identify the protective role of the skin microbiome against UV exposure, protein-protein interaction (PPI) network analysis is used to assess gene expression alteration. **Methods:** A microarray dataset, GEO accession number GSE117359, was considered in this respect. Differentially expressed genes (DEGs) in the germ-free (GF) and specific pathogen-free (SPF) groups are analyzed by GEO2R. The top significant DEGs were assigned for network analysis via Cytoscape 3.7.2 and its applications. **Results:** A total of 28 genes were identified as significant DEGs and the centrality analysis of the network indicated that only one of the seven hub-bottlenecks was from queried genes. The gene ontology analysis of IL6, Cxcl2, Cxcl1, TNF, IL10, Cxcl10, and Mmp9 showed that the crucial genes were highly enriched in the immune system. **Conclusion:** The skin microbiome plays a significant role in the protection of the skin against UV irradiation and the role of TNF and IL6 is prominent in this regard. **Keywords:** Microbiome UV radiation Gene expression Protein-protein interaction network

کلمات کلیدی:

لینک ثابت مقاله در پایگاه سیویلیکا:

<https://civilica.com/doc/2051980>

