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Identification of Significant Genes in Rheumatoid Arthritis, Melanoma Metastasis, Ulcerative Colitis and Crohn's Disease

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Abstract : Background: Our study aimed to identify common genes and potential targets across the four diseases, which include rheumatoid arthritis, melanoma metastasis, ulcerative colitis, and Crohn's disease. We used a network and systems biology approach to identify the hub gene, which can act as a potential target for all four disease conditions. The regulatory network was extracted from the PPI using the MCODE module present in Cytoscape. Our objective was to investigate the significance of hub genes in these diseases using gene ontology and KEGG pathway enrichment analysis. Methods: Our methodology involved collecting disease gene-related information from DisGeNET databases and performing protein-protein interaction (PPI) network and core genes screening. We then conducted gene ontology and KEGG pathway enrichment analysis. Results: We found that IL6 plays a critical role in all disease conditions and in different pathways that can be associated with the development of all four diseases. Conclusions: The theoretical importance of our research is that we employed various systems and structural biology techniques to identify a crucial protein that could serve as a promising target for treating multiple diseases. Our data collection and analysis procedures involved rigorous scrutiny, ensuring high-quality results. Our conclusion is that IL6 plays a significant role in all four diseases, and it can act as a potential target for treating them. Our findings may have important implications for the development of novel therapeutic interventions for these diseases.

Keywords : melanoma metastasis, rheumatoid arthritis, inflammatory bowel diseases, integrated bioinformatics analysis
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