
عنوان مقاله:

A comprehensive study on SARS-CoV-۲ Through Gene Expression Meta-Analysis and Network Biology Approach

محل انتشار:

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خلاصه مقاله:

Introduction: Coronaviruses are significant pathogens of both human and animals and are globally distributed. Out of seven CoVs strains, the most lethal coronavirus strains being portrayed is SARS-CoV-۲. It can cause bronchial asthma, and severe pneumonia and acute respiratory disease. Due to its contagion in infants, adults, and immunocompromised patients which further results in making this a deadly disease, thus there is an urgent need to develop effective and safe therapeutics against it.Materials and Methods: Meta-analysis of publicly available gene expression datasets belonging to SARS-CoV-۲, SARS-CoV, MERS-CoV, and HCoV-۲۲۹E were carried out to identify the potential differentially expressed genes exclusively associated with SARS-CoV-۲, and then a network model was developed to decipher significant drug targets, associated pathways and drug candidates which can be repurposed for this infection.Results: The COVID-۱۹ infection mainly targets immune responses and regulatory processes. A novel role of Relaxin signaling pathway was identified in SARS-CoV-۲ infection. Anti-inflammatory, anti-tumor, nutraceutical and anthelmintic agents were found to be good prospective candidates for repurposing against COVID-۱۹.Conclusions: This theoretical study resulted in the identification of approved drug targets that may have the potential to be .repurposed for COVID ۱۹ treatment

کلمات کلیدی:

COVID-۱۹, Microarray Data, RNA-Seq Data, Systems biology, drug targets, Pathogenesis

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