



Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.



Gene expression analysis of MCF7 cell lines of breast cancer treated with herbal extract of *Cissampelos pareira* revealed association with viral diseases

Emine Güven*

Department of Biomedical Engineering, Düzce University, Düzce, Turkey

ARTICLE INFO

Keywords:

MCF7 cell lines
Biomarker
IL-1R1
IL-13RA1
Viral and infectious diseases
COVID-19

ABSTRACT

Background: It is necessary to assess the cellular, molecular, and pathogenetic characteristics of COVID-19 and attention is required to understand highly effective gene targets and mechanisms. In this study, we suggest understandings into the fundamental pathogenesis of COVID-19 through gene expression analyses using the microarray data set GSE156445 publicly reachable at NIH/NCBI Gene Expression Omnibus database. The data set consists of MCF7 which is a human breast cancer cell line with estrogen, progesterone and glucocorticoid receptors. The cell lines treated with different quantities of *Cissampelos pareira* (Cipa). Cipa is a traditional medicinal plant which would possess an antiviral potency in preventing viral diseases such as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection.

Methods: Utilizing Biobase, GEOquery, gplots packages in R studio, the differentially expressed genes (DEGs) were identified. The gene ontology (GO) of pathway enrichments employed by utilizing DAVID and KEGG enrichment analyses were studied. We further constructed a human protein-protein interaction (PPI) network and performed, based upon that, a subnetwork module analysis for significant signaling pathways.

Results: The study identified 418 differentially expressed genes (DEGs) using bioinformatics tools. The gene ontology of pathway enrichments employed by GO and KEGG enrichment analyses of down-regulated and up-regulated DEGs were studied. Gene expression analysis utilizing gene ontology and KEGG results uncovered biological and signaling pathways such as “cell adhesion molecules”, “plasma membrane adhesion molecules”, “synapse assembly”, and “Interleukin-3-mediated signaling” which are mostly linked to COVID-19. Our results provide in silico evidence for candidate genes which are vital for the inhibition, adhesion, and encoding cytokine protein including LYN, IGFBP5, IL-1R1, and IL-13RA1 that may have strong biomarker potential for infectious diseases such as COVID-19 related therapy targets.

1. Introduction

COVID-19 originated from China and is the cause of SARS-CoV-2 related to the human respiratory system. As of February 2021, a total of 104 million confirmed cases and 2.27 million deaths were reported worldwide, according to World Health Organization (WHO) estimation. While vaccines are developed and implemented at breakneck speed, the timeline for large-scale production and vaccination of the world's enormous population stays vague (McCallum et al., 2021). Moreover, although the primary endpoints are the vaccine's effectiveness and safety against laboratory-approved COVID-19, vaccine trials have not been strengthened to definitively evaluate efficacy by subgroup of any

age with certain known or unknown medical conditions such as cancer, chronic kidney disease, COPD (chronic obstructive pulmonary disease), heart failure, coronary artery disease, or cardiomyopathies, sickle cell disease, smoking, type 2 diabetes (Garassino et al., 2020; Polack et al., 2020; Wu and McGoogan, 2020).

COVID-19 is the first global pandemic that humanity has encountered in this century, and the character of defensive immune responses is not fully established; it is still indefinite which vaccine strategy will be most effective (Jeyanathan et al., 2020). The success of any vaccine strategy on a population can only be observed if the vaccine is effective in high risk groups and is distributed extensively to the whole population (Hodgson et al., 2020). The above are all hazardous circumstances

Abbreviations: COVID-19, coronavirus disease 2019; MERS-CoV, Middle East respiratory syndrome coronavirus; SARS-CoV, severe acute respiratory syndrome coronavirus; GO, Gene Ontology; Cipa, *Cissampelos pareira*.

* Engineering Building B, Konuralp Campus, Konuralp, Yörtükler, Düzce, Turkey.

E-mail address: emine.guven@duzce.edu.tr.

<https://doi.org/10.1016/j.genrep.2021.101169>

Received 9 February 2021; Received in revised form 6 April 2021; Accepted 15 April 2021

Available online 23 April 2021

2452-0144/© 2021 Elsevier Inc. All rights reserved.