Available online at www.scholarsresearchlibrary.com

Scholars Research Library

Scholars Research Library

Journal of Annals of Experimental Biology, 2022, 10 (4):61

(http://www.scholarsresearchlibrary.com)

ISSN: 2348-1935

Gene Co-Expression Network Analysis Identified Prognostic Genes of Sepsis-Induced ARDS

Divya Singh*

Editorial office, Annals of Experimental Biology, Uxbridge, United Kingdom,

***Corresponding Author:** Dr. Divya Singh, Editorial office, Annals of Experimental Biology, Uxbridge, United Kingdom E-Mail: info@scholarsresearchlibrary*

*Received: 11 July, 2022, Manuscript no. aeb-22- 81923**; Editor assigned:** 13 July, 2022, Pre QC no aeb-22- 81923 (PQ)**; Reviewed:** 22 July, 2022, QC no aeb-22- 81923 (Q)**; Revised:** 24 July, 2022, Manuscript no. aeb-22- 81923 (R)**; Published:** 29 July, 2022*

ABSTRACT

Sepsis frequently leads to the deadly consequence known as Acute Respiratory Distress Syndrome (ARDS). Early recognition's molecular mechanisms still have several limitations. The study's goal was to pinpoint any potential genetic differences between sepsis on its own and sepsis-induced ARDS. For bioinformatic analysis, the gene expression profiles of GSE66890 were chosen from the Gene Expression Omnibus (GEO) database. A co-expression network was built using the Weight Gene Co-Expression Network Analysis (WGCNA) to study the relationships between gene sets and clinical features and to pinpoint prospective hub genes. Then, we used GSE10474 and GSE32707 to confirm our findings. In the context of looking for new molecular targets, our research offers a more effective knowledge of the significance of biological pathways and the interactions between key genes in sepsis-induced ARDS. For sepsis-induced ARDS, promising diagnostic biomarkers include TOP2A, CENPF, DLGAP5, and BIRC5.

Keywords: Gene, ARDS

INTRODUCTION

A serious issue with public health is sepsis, which is characterized by an aberrant immune response and results in life-threatening organ failure. Sepsis frequently leads to the deadly consequence known as Acute Respiratory Distress Syndrome (ARDS). In a sizable worldwide investigation, sepsis was the underlying cause of ARDS in almost 75% of patients. Additionally, about 210,000 cases of sepsis-induced ARDS are reported in the US each year, per the US report. Some researchers have established a clinical network to sign up patients with sepsis and other risk factors into clinical trials to early prevent and treat individuals with ARDS. We still don't fully understand why just a small percentage of sepsis patients can develop ARDS, despite our improving understanding of the mechanisms behind sepsis-induced ARDS. Therefore, it is crucial to create a reliable model to identify certain particular biomarkers for the early identification of sepsis with or without ARDS.

Co-expression analysis is a useful method for creating free-scale gene co-expression networks that describe the patterns of gene correlation and identify the hub genes linked to particular disorders. Numerous research that used WGCNA to identify putative biomarkers had successfully studied the potential regulatory relationship between gene sets and clinical characteristics. The goal of the current work was to explain the relationship between genes and clinical features by using WGCNA and to find new biomarkers linked to sepsis-induced ARDS.

Sepsis-induced ARDS has been a frequent and lethal cause of death in critically ill patients throughout the past few decades. Although sepsis-induced ARDS therapy has improved, there are still some individuals who cannot be successfully treated. Therefore, it is crucial to continue researching some biomarkers to offer some early diagnostic and therapeutic approaches. In this work, we screened potential indicators to find sepsis patients with ARDS using the GSE668890 from the GEO database.

By using WGCNA, we created a co-expression network between patients with sepsis and those who had ARDS due to sepsis. It was determined which clinically important module had the strongest correlation with sepsis-induced ARDS. The hub genes were then determined to be the genes TOP2A, CENPF, DLGAP5, and BIRC5 with substantial connection in the clinically important module. The ROC curve and logistic regression model showed good performance in differentiating sepsis from sepsis-induced ARDS. Between prediction and observation, the nomogram was able to accurately predict sepsis-induced ARDS. These genes may serve as possible biomarkers for the detection of ARDS brought on by sepsis.