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Detection hub genes involving in celiac disease

Effat Noori[a], *Bahram Kazemi[b], Mojgan Bandehpour[a,b], *Hakimeh Zali[c]

aDepartment of Biotechnology School of Advanced Technologies in Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran

bCellular and Molecular Biology Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

cDepartment of Tissue Engineering and Applied Cell Sciences, School of Advanced Technologies in Medicine, Shahid Beheshti University of Medical Sciences,Tehran, Iran

**Corresponding Author's E-mail: hakimehzali@gmail.com*

bahram_14@yahoo.com

Abstract

Coeliac disease (CD) is a chronic autoimmune disease that is characterized by malabsorption in sensitive individuals. CD is triggered by the ingestion of grains containing gluten. It is a multifactorial disease with a worldwide prevalence of 1% .The advent of high throughput technologies has provided a massive wealth of data which are processed in various omics scale fields. bioinformatics analyses indicated that STAT1, ALB, IL10, IL2, IL4, IL17A, TGFB1, IL1B, IL6, TNF, IFNG hub genes significant roles in CD.

Keywords: Coeliac disease; bioinformatics; system biology

Introduction

CD exhibits a wide spectrum of clinical representations that can involve almost any organ of the body. Both innate and adaptive immune systems are involved in the pathogenesis of CD (Araya RE et al 2016) Undesirable immunological reactions could cause inflammation and villous atrophy of the small intestine (Pereyra L et al. 2013). CD is concomitant with several other disorders, including dermatitis herpetiformis, selective IgA deficiency, thyroid disorders, diabetes mellitus, various connective tissue disorders, inflammatory bowel disease, and rheumatoid arthritis (Ch'ng CL et al. 2007, Bibbo S et al. 2017, Assa A etal. 2017, Zubarik R et al. 2015) Investigations in the field of systems biology through bioinformatics tools have managed to integrate data from molecular, genomic, and biological connectivity studies (Zachariou M et al. 2018).

Materials and Methods

All data used in this study are collected from public databases. CD related data were extracted from CTD (http://ctdbase.org/), DISEASES (https://diseases.jensenlab.org/) and GeneCards (https:// www.genecards.org/). The common CD related genes from these 3 databases were obtained using the Venn Diagram software (http://bioinformatics. psb.ugent.be). All of these common genes were selected for further analysis by Enrichr database, WebGestalt, Cytoscape

Results

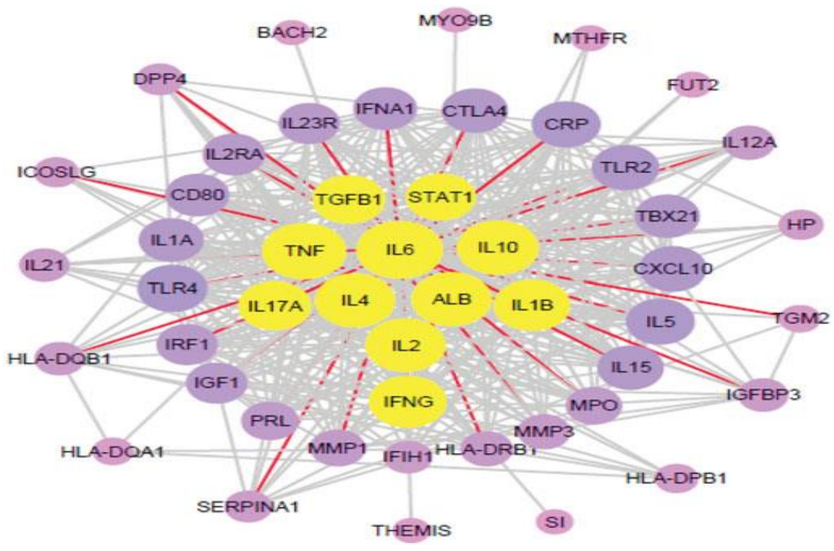

Figure 1. The network related to significant genes of CD is constructed by cytoscape software.

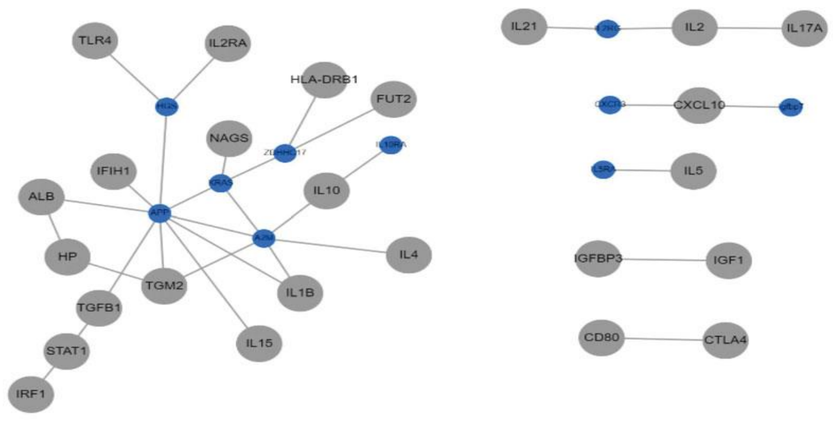

Figure 2. Protein-protein interaction of significant genes in WebGestalt that determined the sub- network of seed genes (big nodes) connected to first connected nodes (small nodes)

Discussion, Conclusion and Suggestions

Contemporary, biological data are vastly generated and stored in various databases; however, this data is not properly used for understanding and treatment of the diseases. This abundant amount of data and a large number of data storing databases require higher integration and deeper connection.

In the light these results, nine key genes, including IRF1, STAT1, IL17A, TGFB1, ALB, IL10, IL2, IL4, and IL1B, were identified to be associated with CD. These findings could be used to find novel diagnostic biomarkers, understand the pathology of disease, and devise more efficient treatments.

Table 1. Top 10 of OMIM disease related to CD.

Term	*p*-value	Z-score	Combined score	Genes
coeliac disease	4.65578E-08	−1.740014983	29.37592536	CTLA4;MYO9B;HLA-DQA1;HLA-DQB1
diabetes	0.001095052	−1.351522955	9.213269198	IL6;IL2RA;CTLA4
lung cancer	0.001453976	−0.329567694	2.153215141	IRF1;MPO
gastric cancer	0.000387452	−0.112766815	0.885887059	IL1B;IRF1
colorectal cancer	0.005226232	−0.142274214	0.747517936	TLR4;TLR2
rheumatoid arthritis	0.000547577	−0.087432695	0.65662026	IL10;IL6
anemia	0.011826604	−0.071132621	0.315644154	IFNG;IRF1
asthma	0.001745649	−0.005802229	0.036847805	TBX21;TNF
diabetes_mellitus,_type_1	0.002405147	0.081570202	−0.49188008	IL2RA;CTLA4
migraine	0.04235169	4.783613699	−15.12457599	TNF

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