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Authors: Ali abdi, Alireza Khabazi, Ebrahim Sakhinia, Shahriar Alipour, Mahsa Talei, Zohreh Babaloo

PII: S0165-2478(18)30167-6
DOI: https://doi.org/10.1016/j.imlet.2018.07.001
Reference: IMLET 6220

To appear in: *Immunology Letters*

Received date: 30-3-2018
Revised date: 26-6-2018
Accepted date: 6-7-2018

Please cite this article as: abdi A, Khabazi A, Sakhinia E, Alipour S, Talei M, Babaloo Z, Evaluation of SOCS1 Methylation in patients with Behcet's disease, *Immunology Letters* (2018), https://doi.org/10.1016/j.imlet.2018.07.001

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Ali abdi[1,2], Alireza Khabazi[3], Ebrahim Sakhinia[4], Shahriar Alipour[4,5], Mahsa Talei[1,2], Zohreh Babaloo[1,2*]

[1]. *Immunology Research Center, Tabriz University of Medical Sciences, Iran.*

[2]. *Department of Immunology Medicine faculty, Tabriz University of Medical Sciences, Iran.*

[3]. *Connective Tissue Disease Research Center, Tabriz University of medical science, Iran.*

[4]. *Dept. of Genetics, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran.*

[5]. *Molecular Medicine, Faculty of Advanced Medical Sciences, Tabriz university of Medical Sciences, Iran.*

[*]***Corresponding author Emails**:* Zbabaloo20@gmail.com

Abstract:

Introduction*:* Epigenetic discusses to inherited changes in mitosis and meiosis in the gene expression pattern which is independent of primary DNA sequence. Since, SOCS1 hyper-methylation can activate JAK / STAT signaling pathway and activation of this pathway can directly affect the impact of different cytokines on cell function and subsequently lead to pathophysiology of diseases, in particular autoimmune diseases that interact directly with the amount of cytokines and due to the fact that the cause and pathology of Behcet's disease (BD) have not ever been completely determined. So, the purpose of this study was to evaluate the methylation pattern of SOCS1 gene in patients with BD and compare them with healthy group.

Methodology*:* This study was a case-control study in which 50 patients with BD and 60 subjects as healthy group participated. Blood samples were collected from all participants and then Peripheral Blood Mononuclear Cells (PBMCs) were isolated through Ficoll method. After extraction of DNA by Salting out method and its analysis with Nano-drop, the methylation level of SOCS1 was examined using qMS-PCR technique.

Results*:* Findings about methylation and gene expression in SOCS1 gene showed that the level of SOCS1 methylation was increased in patient groups compared with healthy subjects (control group) which the increase was statistically significant (p-value<0.05). Also, the results of gene expression revealed that the fold change of SOCS1 gene expression was decreased in patient group compared with healthy subjects which the decrease was statistically significant (p-value<0.05).

Discussion and conclusion*:* According to the results of this study, it can be suggested that the DNA methylation of SOCS1 gene is likely to affect the gene expression and thereby contribute to the pathogenesis of Behcet's disease.