Virginia Sedeño-Monge et al., J Clin Cell Immunol 2014, 5:5
http://dx.doi.org/10.4172/2155-9899.S1.018

Transcription level of the suppressors of cytokine signaling 1 and 3 in patients with multiple sclerosis

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Multiple sclerosis (MS) is an autoimmune disease characterized by a triad of inflammation, demyelination and gliosis. Some experimental observations suggest that IFN-γ and other proinflammatory cytokines have an important role in the pathogenesis of MS. The suppressors of cytokine signaling (SOCS) negatively regulate the proinflammatory cytokine-induced response, moderating consequently the immune response. The aim of the study was to quantify SOCS1 and SOCS3 transcription in peripheral blood leucocytes of patients with MS by quantitative real-time reverse transcription-PCR and analyze their correlation with disease progression. Values were analyzed by means of the comparative method $2^{-\Delta\Delta CT}$ (fold difference). Forty MS patients and twenty six healthy individuals were included; all persons were neurologically evaluated through the Expanded Disability Status Scale (EDSS). SOCS1 transcription decreased significantly in MS patients compared with neurologically healthy persons (0.08±0.02 vs. 1.02±0.23; $p=0.0001$); while SOCS3 transcription increased in MS patients compared with controls (2.76±0.66 vs. 1.03±0.27; $p=0.0008$). A weak correlation between the patients neurological status (EDSS values) and either SOCS1 or SOCS3 expression was found (for SOCS1 $r=-0.11$ $p= 0.5$; for SOCS3 $r= -0.2$ $p=0.2$) and slight negative correlation between SOCS3 and SOCS1 expression was found (Spearman's $r=-0.57$; $p=0.0003$) in MS patients. An important contribution of our study is that the ratio SOCS1:SOCS3 showed a strong and significant association between both genes in all samples, this can be a reflection of the fine balance between different members of SOCS family.

Biography

Virginia Sedeño Monge completed his PhD in Ciencias Microbiológicas in 2010 from Universidad Autónoma de Puebla. She is Professor of Physiology in the Universidad Popular Autónoma del Estado de Puebla School of Medicine. She is member of Sistema Nacional de investigadores (SNI) of México since 2012, and is currently working on transcription genes with real time PCR.

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