Correlation between the modified expression of autophagy and endoplasmic reticulum stress markers and the continuous inflammation of the colon in ulcerative colitis

P-02.2-09

I. Samoila[I], S. Dinescu[I,II], M. Costache[I,II]

[I]University of Bucharest, Bucharest, Romania, [II]Research Institute of the University of Bucharest- ICUB, Bucharest, Romania

Ulcerative colitis (UC) is characterized by an unknown cause of chronic inflammation of the colon. Among the reasons that could trigger inflammation, an impaired autophagy process could further affect the endoplasmic reticulum stress (ERS) response, hence leading to unfolded protein response activation. The aim of this study was to evaluate gene and protein expression of specific autophagy and ERS markers, in order to correlate their level of expression with their possible implication in the inflammatory state of UC. In this study we used colon tissue samples isolated from 4 mice conditions: BALB/C, 2,4,6-trinitrobenzenesulfonic acid (TNBS)-induced UC BALB/C, STAT6 knockout and TNBS-induced UC STAT6 knockout. For gene expression evaluation, quantitative Real Time PCR was performed using primers for key autophagy and ERS genes, whereas protein expression evaluation was possible by immunohistochemistry, with specific autophagy and ERS antibodies. When analyzing gene expression of autophagy markers, we identified an increased *SQSTM1* and *ATG16L1* expression, but an inhibited *LC3-II* expression in TNBS-induced UC BALB/C mice when compared to BALB/C. Similar results were obtained for TNBS-induced colitis STAT6 mice, but with an even more exacerbated expression of *SQSTM1* and *ATG16L1* than in the case of TNBS-induced UC BALC/C. *XBP-1s*, *eIF2α* and *ATF6α* ERS markers investigation displayed an increased level of expression in colitis BALB/C mice in comparison to control group. Colitis STAT6 mice displayed higher values for ERS gene expression when compared to colitis BALB/C mice. Gene expression results were confirmed by protein expression antibodies staining. Our results indicated a modified expression of key intestinal homeostasis markers, which leads to epithelial barrier dysfunction, hence supporting the idea of an aggravated UC in STAT6 knockout mice. This work was supported by UEFISCDI PN-III-P1-1.2-PCCDI-2017-0407/INTELMAT.