Cyclosporine A changes the expression profile of genes and proteins related to the JAK/STAT signaling pathway in keratinocytes treated with lipopolysaccharide A

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Abstract

An important signaling pathway along which the signal transduction is abnormal in psoriasis is the JAK/STAT signaling cascade. This study aimed to analyze the influence of cyclosporine A on the JAK/STAT signaling pathway in keratinocytes treated with lipopolysaccharide A compared with the untreated cells. Human, adult, low-Calcium, high-Temperature keratinocytes (HaCaT) were first incubated in 1 μg/mL of bacterial lipopolysaccharide A (LPS) for eight hours to induce an inflammatory condition, and then cyclosporine A was added to the culture at a concentration of 100 ng/mL for 2 (H_2), 8 (H_8), and 24 hours (H_24). Untreated cells constituted the control group. Changes in the expression of genes were determined using the HG-U 133_A2 microarray technique. 37 mRNAs connected with the JAK/STAT signaling pathway were selected from the Affymetrix database from among 22283 mRNAs present on the HGU-133A_2 microarray plate. The number of mRNAs differentiating it from the control culture depending on the time of cell exposure to the drug was as follows H_2 vs. C = 8 mRNAs, H_8 vs. C = 3 mRNAs, H_24 vs. C = 1 mRNA. On the other hand, only one mRNA, namely *STAT3*, differentiated the drug-treated culture from the control independent of the time of exposure. During therapy with cyclosporin A, it was confirmed the activation of the

JAK/STAT cascade, and STAT3 might be a complementary molecular marker in monitoring the effectiveness of cyclospo therapy.

Keywords

cyclosporin A, microarray, molecular marker, LPS, keratinocytes, JAK/STAT path