

## Abstract

CD4<sup>+</sup> T cells play a critical role in allergic diseases, both in the affected tissue as well as systemically. Our objective was to investigate the *in vivo* activation state of peripheral blood CD4<sup>+</sup> T cells of atopic dermatitis (AD) patients, by analyzing gene expression profiles of unstimulated CD4<sup>+</sup> T cells.

mRNA samples from blood CD4<sup>+</sup> T cells, isolated from 5 AD patients, and 7 healthy controls (HCs) were analyzed using oligonucleotide arrays. Differentially regulated genes were validated by quantitative-PCR (Q-PCR) in a larger group of patients with AD, in a group of patients with allergic asthma (AA) and HC subjects. In addition, “typical” T<sub>H</sub>1 and T<sub>H</sub>2 related genes were analyzed by Q-PCR.

Microarray analysis revealed differential expression of 52 genes in AD patients. Q-PCR confirmed several differentially regulated genes in AD, including CCR10, CRTH2, C-JUN and NR4A2. Two groups of genes, with highly correlating gene expression levels, involved in tissue homing and proliferation or apoptosis respectively, were identified. No marked differences were found in gene expression levels of typical T<sub>H</sub>1 and T<sub>H</sub>2 genes in AD nor in AA patients.

This study demonstrates that peripheral blood, unstimulated CD4<sup>+</sup> T-cells in AD patients show differentially expressed genes involved in tissue homing, proliferation and apoptosis. No marked expression differences of “typical” atopy genes were found.