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T cell gene expression profiles

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Activated/resting T cells, microarray

Context

Understanding the differences in gene expression patterns between resting and activated T cells may give important information about the regulation of these cells in health and disease. Several techniques have been used previously including subtraction techniques, differential display and gene arrays using T cells cultured *ex vivo*. This study involves the use of microchip technology to determine the expression pattern of over 6300 genes encoding a broad range of activities. This technology allows quantitative assessment of the change in gene expression between resting and activated cells. To assess the differences in expression of 6300 genes in resting (0 h) and activated (8 and 48 h poststimulation) T cells.

Significant findings

The numbers of genes expressed at 0, 8 and 48 h were remarkably similar. Roughly 7% of the genes expressed at 0 h were upregulated by 8 h, with a similar percentage being downregulated. By 48 h the expression pattern was much closer to resting levels, with only 1.7% being increased and 0.7% decreased compared to resting cells. Many of the genes upregulated at 8 h poststimulation were involved in cell division (eg DNA polymerases and cyclin), whereas transcripts of several antimitotic genes were particularly abundant in resting T cells. In addition, major differences were found in levels of cytokine receptors, transcription factors and adhesion molecules.

Comments

The use of microarray technology has many potential uses in rheumatological research. It may be possible in future, for instance, to use this technology to examine gene profiles in arthroscopic samples from inflamed joints and perhaps give clues to diagnosis, prognosis or response to treatment. However

the generation of such a large amount of data on each sample will require the parallel developments in bioinformatics.

Methods

T cells were activated in C57BL/10 mice using a V?8 specific superantigen. Mice were sacrificed at 0 h, 8 h and 48 h and the T cells were purified from lymph nodes. RNA was isolated and cRNA prepared. This was passed over a microarray chip and the relative expression of each gene was compared at the three time points.

References

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