

# Regulation of immune-modulatory genes in left superior temporal cortex of schizophrenia patients: A genome-wide microarray study

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**Objectives.** The role of neuroinflammation in schizophrenia has been an issue for long time. There are reports supporting the hypothesis of ongoing inflammation and others denying it. This may be partly ascribed to the origin of the materials (CSF, blood, brain tissue) or to the genes selected for the respective studies. Moreover, in some locations, inflammatory genes may be up-regulated, others may be down-regulated. **Methods.** Genome-wide microarrays have been used for expression profiling in post-mortem brains of schizophrenia patients. Array data have been analyzed by gene set enrichment analysis (GSEA) and further confirmed with selected genes by real-time PCR.

**Results.** In Brodman Area 22 of left superior temporal cortex, at least 70 genes (19%) out of 369 down-regulated genes ( $P < 0.05$ ) belonged to the immune system. 23 from those 70 genes were randomly selected for real-time PCR. Six reached significance level at  $P < 0.05$ . **Conclusions.** The present data support a brain-specific view