P2.08.

Global gene expression profile of identified neurogliaform interneurons in the neocortex

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Neurogliaform cells (NGFCs) are cortical GABAergic interneurons characterized by α-actinin 2, GABAAd receptor content and unitary volume transmission leading to slow GABAA and GABAB receptor mediated responses. Such functional distinction is expected to be based on the concerted action of several genes active specifically in NGFCs. We analyzed the global gene expression profile of NGFCs and applied a harvesting procedure standardized for single cell PCR. Combining whole cell recordings and post hoc light microscopic assessment to identify NGFCs (n=30) from rats (P22-40), RNA from harvested cytoplasms was amplified and hybridized onto a rat DNA-microarray. Out of 26209 genes, we identified 1143 transcripts that exhibited significantly (p<0.001) higher expression in NGFCs compared to controls. In addition, we tested the expression profile of 40 out of the 1143 NGFC specific transcripts with quantitative real-time PCR thus validating the gene chip analysis. Among the NGFC specific transcripts, we confirmed known markers for NGFCs (GABAAd, α-actinin 2), and in addition, neurotransmitter receptor subtypes undetected in NGFCs to date. Whole cell electrophysiological experiments and immunocytochemistry confirmed the action of dopamine receptor subtypes not reported previously in NGFCs.These initial results confirm that global gene expression profiling combined with functional characterization is routinely feasible in identified cortical interneurons.