**Transcriptome profile of hippocampus CA3 in the pilocarpine model of temporal lobe epilepsy**

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**Background:** It is well known that gene expression profile of specific tissue provides relevant biological information about molecular mechanisms potentially involved in complex biological phenomena. Recently, it has been recognized that due to marked heterogeneity of gene expression in different subset of cells, it is important to take sub-regional specificities when studying gene expression, especially in the CNS. The aim of this study was to analyze gene expression profile using next generation sequencing technology in different sub-regions of the *Cornu Ammonis* 3 (CA3) in an animal model of temporal lobe epilepsy induced by pilocarpine.

**Methods:** Male Wistar rats were injected with methyl-scopolamine (1 mg/kg) thirty minutes before of the systemic injection of pilocarpine hydrochloride (320 mg/kg) to reduce peripheral cholinergic side effects. Four hours after the administration of pilocarpine diazepam was administrated (4 mg/kg) in order to stop seizures. Control rats were injected with saline after methyl-scopolamine injection. Fifteen days after induction, rats were euthanized (n=4) and brains were processed for laser microdissection. Dorsal, intermediate and ventral CA3 were collected from each rat. RNA sequencing was performed in an Illumina Hiseq® platform. Sequences were aligned and quantified with the TopHat/DESeq2 pipeline for total RNA. Gene ontologies and gene interactions were analyzed with the MetaCore® software.

**Results:** We found a total of 2624, 1731 and 1278 genes differentially expressed (p<0.05) when comparing control and pilocarpine rats for the dCA3, iCA3 and vCA3 respectively. Gene ontology analysis indicates genes related to cytoskeleton remodeling and cell cycle upregulate in dCA3. In iCA3 we identified upregulation of genes involved in oligodendrocyte differentiation in adult stem cells. In vCA3 there was downregulation of glutamatergic neurophysiological process, and upregulation of genes related to regulation of G1/S transition.

**Conclusion:** Our results indicate region specific molecular mechanisms taking place in the hippocampus sub-regions of an animal model of temporal lobe epilepsy induced by pilocarpine. The transcriptome data suggest an interaction among several molecular components leading to epileptogenesis in this animal model that displays widespread hippocampal damage.

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