**Epigenetic changes in the *hippocampus* of an epilepsy model.**

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**Introduction**: Epigenetic summarizes alterations to the chromatin template that collectively establish and propagate different patterns of gene expression without changes in DNA sequence. To better understanding the role of epigenetic changes in epilepsy, we determined the methylation profile of an animal model of temporal lobe epilepsy in comparison with control animals.

**Material and Methods**: We used laser capture microdissection to obtain tissue from the *hippocampus* of rats treated with pilocarpine (*n*=2) as well as control animals (*n*=2) and we performed two technical replicates. DNA was extracted using proteinase K protocol with modifications and it was converted by bisulfite with EZ DNA Methylation-Lightning™ Kit (Zymo Research). After conversion libraries were generated using TruSeq DNA Methylation and sequencing was performed in an Illumina HiSeq 2500.

**Results**:We found 51 differently methylated regions (DMR) along the 20 rat chromosomes. 21 DMR were found within known genes (in exons and/or introns). In these regions we identified several genes, including Scrib (scribbled planar cell polarity protein) involved in astrocyte cell migration; Cacna1d (calcium voltage-gated channel subunit alpha1 D) a divalent metal ion transport; Gabbr2 (gamma-aminobutyric acid type B receptor subunit 2) which inhibits high voltage activated calcium ion channels; Csnk1e (casein kinase 1, epsilon) which is involved in cellular response to nerve growth factor stimulus and others.

**Conclusion**: Although preliminary, our results show that the epileptogenic insult induced by pilocarpine injections in rats resulted in significant methylation changes when compared to control animals. These changes involve genes, which have been already recognized as implicated in epileptogenesis; however, as our data is further analyzed and validated we may find new molecular pathways contributing to the epileptogenic process.