**Epigenetics in a model of temporal lobe epilepsy: what’s going on in *dentate gyrus*?**

Dogini DB1; Vieira AS1, Souza W1, Lopes–Cendes I1.

Departments of Medical Genetics1 and The Brazilian Institute of Neuroscience and Neurotechnology (BRAINN), School of Medical Sciences, University of Campinas – UNICAMP, Campinas, SP, BRAZIL.

**Introduction**: In order to improve the pathophysiology knowledge of temporal lobe epilepsy (TLE) *in vivo* animal models that present features similar to those seen in TLE patients have been developed. One of these models is based on the systemic administration of chemoconvulsants, like pilocarpine, to induce an initial precipitating injury (status epilepticus). Epigenetics 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 methylation pattern in animal models of TLE we performed whole genome bissulfite sequence (WGBS) in *dentate gyrus* samples of pilocarpine induced rats.

**Material and Methods**: We used laser capture microdissection (LCM) to obtain the *dentate gyrus* structure from hippocampus region of control rats (*n*=2) and pilocarpine induced rats (*n*=2). DNA was exctrasted using proteinase K protocol with modifications and the DNA was converted by bissulfite with EZ DNA Methylation-Lightning™ Kit (Zymo Research). After the conversion library was generated using TruSeq DNA Methylation kit then this material was sequenced in Illumina HiSeq 2500.

**Results**: Bioinformatics analysis found 18 different methylated regions (DMR) along the 20 chromosomes. In these regions we found several genes as Atp10d (ATPase, class V, type 10D) – involved with ATP binding, Puf60 (poly-U binding splicing factor 60) – involved with RNA/DNA binding.

**Conclusion**: The regions are still under analysis in order to find others genes that may be involved with TLE. We are going to increase the number of sample to improve our data