**Integrated analyses of zebrafish miRNA and mRNA expression profiles after pentylenetetrazole-induced seizures**

V. H. S. Zago1, R. A. Oliveira1, A. S. Vieira2, A. H. B. Matos2, W. Souza3, C. S. Rocha3, B. Carvalho3, I. T. Lopes-Cendes2, C. V. Maurer-Morelli1

1Zebrafish Laboratory, 2Molecular Genetics Laboratory, 3Bioinformatic Laboratory, Departament of Medical Genetics, School of Medical Sciences - UNICAMP

**Introduction:** MicroRNAs (miRNAs) have been accepted as key molecules underlying seizures as well as associated with epilepsy development. This study aimed to integrated miRNA and mRNA transcript profile by applying ultra-high-throughput sequencing system and bioinformatics approach in order to identify molecular mechanisms underlying seizures in the zebrafish seizure model.

**Materials and Methods:** Adult wild-type zebrafish and embryos were maintained according to standard procedures. Seven days post fertilization (7dpf) larvae were separated in three groups: controls (CTL, n=3), acute seizure (AS, n=2) and status epilepticus-*like* (SE-*like*, n=3). Larvae from groups AS and SE-*like* were exposed to PTZ 15mM for 20 minutes and 3 hours, respectively. MiRNA and mRNA libraries were achieved after RNA extraction using Illumina’s Sample Prep Kit according instructions. Validated and pooled libraries were sequenced in the Illumina HiSeq 2500 System. MiRNA and mRNAs differentially expressed (p<0.01) were determined and the target genes for miRNA investigated by *in silico* analysis.

**Results:** We identified three miRNAs (dre-miR-31, dre-miR-132-5p and dre-miR-459-3p) and 4622 mRNAs in the SE-*like* group compared to CTL group. In addition, we found two miRNAs (dre-miR-460-3p and dre-miR-725-3p) and 2897 mRNAs when comparisons were performed between AS and CTL groups. Comparisons between AS and SE-*like* groups showed that the time of exposition changed the expression pattern for the same miRNA. Our preliminary analysis for miRNA-mRNA integration data showed one putative miRNA-mRNA pair that was differential expressed in the AS group and seven for SE*-like* group.

**Discussion:** Animals from AS group presented an inverse correlation between dre-miR-460-3p (down-regulated) and its target, *inhbaa* gene that is related to cell survival, growth and differentiation. This gene participates of TGF-β signaling pathway, which has been associated with neurotransmission regulation in other animal models and humans. Furthermore, seven putative miRNA-gene target pairs were differently expressed in the SE-*like* group, among them, dre-miR-459-3p and its target *adar* and *grm2a* genes*,* previously associated with seizures and neuroactive ligand-receptor interaction, respectively. Additionally, we demonstrated a relationship between dre-miR-459-3p and *pcdh19* gene, which plays a role in early stages of brain morphogenesis during the zebrafish development.

**Conclusion:** To our knowledge, this is the first study investigating global integration between miRNA-mRNA transcript profile after seizures or SE-*like* states using the zebrafish as model. Besides, we have proposed a SE-*like* protocol for zebrafish. Our results showed that both, acute seizure and SE-*like* have distinct molecular profile. By integrating miRNA-mRNA data we hope to shed some light into the cellular pathways underlying seizure and SE.

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