TRAF6

- The up-regulated expression level of deubiquitinating enzyme USP46 induces the apoptosis of A549 cells by TRAF6
- Exploring the Role of TRAF6-TAK1 Pathway in Podocyte Pyroptosis and Its Implications for Primary Membranous Nephropathy Therapy
- Hepatocellular Carcinoma Cells in Humans Exhibit Resistance to Suberoylanilide Hydroxamic Acid (SAHA) Owing to the Diminished Level of Hsa-miR-125a-5p
- Interleukin-1 Receptor-Associated Kinase 1 in Cancer Metastasis and Therapeutic Resistance: Mechanistic Insights and Translational Advances
- NINJ1: A new player in multiple sclerosis pathogenesis and potential therapeutic target
- Inhibition of tumor necrosis factor receptor-associated factor 6 alleviates secondary brain injury by reducing neuronal pyroptosis after intracerebral hemorrhage
- Optical imaging detection of extracellular vesicles of miR-146 modified bone marrow mesenchymal stem cells promoting spinal cord injury repair
- PRMT6 facilitates EZH2 protein stability by inhibiting TRAF6-mediated ubiquitination degradation to promote glioblastoma cell invasion and migration

The study aimed to evaluate single nucleotide variants (SNVs) n.-411A > G (rs57095329) and n.60 G > C (rs2910164) in microRNA (miR)-146a, related to suppressing of TRAF6 with risk for epilepsy, as well as miR-146a and TRAF6 levels.

DNAs were extracted from epileptogenic tissues and blood leukocytes from drug-resistant epilepsy patients and healthy individuals, respectively. Genotypes were identified by real-time PCR. Hardy-Weinberg equilibrium (HWE) and Fisher or X2 tests evaluated the difference between groups. The disease risk was assessed by odds ratio (OR) with 95 % confidence interval (95 %CI). The prognostic impact on probability seizure-free survival (PSF) was evaluated by Kaplan-Meier and log-rank tests.

For rs57095329 both control and patient samples were not in HWE ($p < 0.05$) and the genotypes prevalence was similar in patients and controls ($p>0.05$). For rs2910164, control samples were in HWE ($p = 0.61$), contrasting with patients ($p = 0.03$), and similar frequencies of wild-type homozygous (GG) (43.4 % vs. 34.4 %, $p = 0.2$) and variant (CC) genotypes (8.0 % vs. 6.6 %, $p = 0.6$) were observed in patients and controls, respectively. However, an increased frequency of heterozygous (GC) was observed in patients compared to controls (59.0 % vs. 42.7 %, $p = 0.04$) with a 1.98 (95 %CI=1.09-3.57) risk for epilepsy. The miR-146a expression level in the epileptogenic tissues was lower in the GC ($p = 0.02$) and CC ($p = 0.09$) compared to GG genotype. The TRAF6 expression level was higher in CC than in the GG genotype ($p = 0.09$). Interestingly, there was an increased frequency of patients harboring GC genotype and less time until surgery compared to patients harboring GG or CC (36.06 % vs. 11.5 %, $p = 0.01$), confirmed by PSF ($p = 0.04$).

The GC genotype for SNV rs2910164 appears associated with susceptibility to drug-resistant epilepsy due to the decreased MIR146a expression, favoring NF-kB pathway through TRAF6 [1].

1)

Boschiero MN, Camporeze B, Santos JSD, Costa LBD, Bonafé GA, Queiroz LS, Van Roost D, Marson FAL, de Aguiar PHP, Ortega MM. The single nucleotide variant n.60G>C in the microRNA-146a associated with susceptibility to drug-resistant epilepsy. Epilepsy Res. 2020 Feb 29;162:106305. doi: 10.1016/j.eplepsyres.2020.106305. [Epub ahead of print] PubMed PMID: 32155539.