P37. ANALYSIS OF CORTICAL GENE EXPRESSION VARIABILITY IN A MOUSE MODEL OF X-LINKED INFANTILE SPAMS SYNDROME

L. Verrillo\textsuperscript{1,2}, M. Tuccillo\textsuperscript{1}, D. Drongitis\textsuperscript{3}, E. Mangano\textsuperscript{3}, C. Franco\textsuperscript{4}, G. Terrone\textsuperscript{5}, L.M.T. Canzoniero\textsuperscript{4}, E. Del Giudice\textsuperscript{5}, R. Bordoni\textsuperscript{3}, L. Poeta\textsuperscript{1}, and M.G. Miano\textsuperscript{1}

\textsuperscript{1}Institute of Genetics and Biophysics “Adriano Buzzati-Traverso”, CNR, Naples, Italy; \textsuperscript{2}University of Campania “Luigi Vanvitelli”, Caserta, Italy
\textsuperscript{3}Institute of Biomedical Technologies, CNR, Segrate (MI), Italy; \textsuperscript{4}Department of Science and Technology, University of Sannio, Benevento, Italy; \textsuperscript{5}Department of Translational Medicine, University of Naples Federico II, Naples, Italy

Background: Infantile Spasms Syndrome (ISS) is an early-onset epileptic encephalopathy characterized by epileptic spasms during early infancy and severe global developmental delay. A GCG triplet repeat expansion in X-linked Aristaless-related homeobox gene (ARX) is the most commonly inherited error found in patients with X-linked ISS. Although a growing number of studies have been done on the identification of the complete subset of ARX targets, the effect of repeat instability remains unknown.

Objectives: Here we describe a single-cell RNA sequencing study design aimed to identify transcriptome landscapes in the epileptogenic cortex of the Arx mouse compared to the wild type one. The Arx model develops severe tonic-clonic seizures in a phenotype that well recapitulates the chronic epilepsy associated to the c.304ins(GCG)\textsuperscript{7} mutation in ISS children. We have isolated cortical Arx and wild type neurons from the developing brains and set up the experimental conditions to proceed with the scRNA-seq protocol. Our main objective is to define how the activity of the expanded-polyalanine ARX TF perturbs directly or indirectly transcriptome profiles in distinct inhibitory and excitatory sub-types. The generation of these datasets will constitute a valuable resource to probe cellular composition and molecular features of the epileptogenic cortex associated to ARX defects. Understanding all these aspects may help us to identify cell-specific epileptic-biomarkers linked to the disease-response that could be used as druggable targets in anti-epileptic drug discovery research.