**Investigating the genetic landscape of childhood epileptic encephalopathies in Latin America**

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**Introduction and Hypothesis:** Childhood epileptic encephalopathies (CEEs) are severe cerebral disorder in which the epileptic activity itself may contribute to progressive development of psychomotor dysfunction. Recent advances in molecular genetics have led to the discovery of several genes for CEEs. However, the etiology in most patients remains unknown, and important population groups such as Latin American have not yet been well studied, which increases the possibility of the identification of new candidate genes for different forms of CEEs.

**Objective:** This study aims to characterize the genetic bases of CEEs in patients from Latin America.

**Methods:** This is an effort done in conjunction with the International League Against Epilepsy (ILAE) by means of the Commission on Latin American Affairs. Data will be obtained from patients with CEEs (West, Lennox-Gastaut, Otahara, Dosse, Dravet syndrome and others), from neurology services of each collaborative center in different Latin American countries. A common clinical protocol has been defined to determine inclusion and exclusion criteria for patient enrolment. Initially, patients will be evaluated for mutations on *SCN1A*, for both sequence variants and structural alterations, and if negative whole exome sequence will be performed.

**Relevance:** The presence of genetic heterogeneity and clinical variability represents a major challenge when assessing the impact of genetic discoveries in clinical practice; nevertheless, the specific diagnosis can influence treatment decisions in some patients. A systematic evaluation of CEEs has never been performed in Latin America, since it is well known that allele frequency for rare variants may significantly vary across populations from different ethnic backgrounds, it is possible that frequency of mutations in CEE patients in Latin America differ from previously described in the literature. In addition, because genetic variability, due to admixture, is high in Latin America one will have the opportunity to describe additional mutations/candidate genes.

**References:** [1] Gonsales MC et al., Arq Neuropsiquiatr 73(11): 946-958, 2015; [2] Casals F et al., Science 337(6090): 39-40, 2012.

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