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Sommario	Mutations in several genes are associated with epilepsy (e.g. SCN1A, MECP2, ARX). Identifying genetic causes in epileptic syndromes is crucial to avoid a complex diagnostic work up, to provide genetic counseling, to start a tailored treatment in some cases and to avoid drugs potentially worsening seizures in others. Next Generation Sequencing (NGS) technologies allow analyzing a large number of genes in a single experiment, shortening the time to reach a definite diagnosis, and saving costs. Aim of this research was to identify gene variants underlying epilepsies with a challenging etiological classification. DNA from 81 pediatric epileptic patients was analyzed with a gene panel set up by child epileptologists, neurophysiologists and geneticists. This included 55 genes, later extended to 91, associated or not to intellectual disability, additional neurological signs, and complex malformations. In 14 patients pathogenic mutations were individuated, with an overall mutational frequency of 17,2% (14/81). 90,5% of patients had previously undergone unrevealing cytogenetic or single-gene analyses, thus our population was highly selected at the time NGS was performed. It is essential to underline that NGS must not be considered a screening examination, and that it requires a multidisciplinary approach in patients' selection, and results interpretation.