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Validation of a prediction model for drug-response in mesial temporal lobe epilepsy based on genetic information

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Mesial temporal lobe epilepsy (MTLE) is the most common form of focal epilepsy in young adults. Approximately 40% of patients with MTLE are refractory to treatment with antiepileptic drugs (AEDs) and may be eligible for surgical treatment. Recently, we proposed an algorithm to predict whether a patient with MTLE will be refractory to AED with 0.8177 of accuracy based on SNPs located in pharmacogenetic genes. In this study, we aim to replicate and validate this algorithm in an independent cohort. The replication cohort contains 253 patients with MTLE classified into two groups: 38 AED-responsive and 215 AED-refractory, based on the ILAE criteria. We genotyped ten of the top 30 most significant SNPs identified in our previous study (rs2472306, rs12904742, rs12253253, rs12773342, rs2104161, rs2756104, rs9341244, rs9341263, rs28365067 and rs4086116), using TaqManTM and rhAmpTM real-time PCR system (Applied Biosystems, Foster City, CA, USA). We observed a 79.9% of accuracy to predict drug response based on the 10 SNPs selected for replication. Our results, which are in agreement with our initial findings show that molecular markers in pharmacogenetic genes can be used as predictors of AED response in patients with MTLE. We are currently working in a multicenter collaborative project to validate our results in other populations.

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