INTRODUCTION

Generalized epilepsy with febrile seizure plus (GEFS+) has been described as an autosomal dominant inherited epilepsy disorder associated with febrile and afebrile seizures (Scheffer and Berkovic, 1997). Individuals with GEFS+ are characterized by febrile seizures in children and continue beyond 6 years of age (Escayg et al., 2000).

The common phenotypes of GEFS+ are tonic-clonic, myoclonic, atonic and heterogeneous afebrile seizures that may include global developmental delay, ataxia and behavioural concerns.

OBJECTIVE

To study the clinical presentations and to analyze the SCN1A gene associated with Malaysian GEFS+ patients.

GENETIC STUDY

Direct sequencing of SCN1A revealed seven sequence variants that associated with GEFS+ (Table 2). A base substitution c. 4765 A>G transition in exon 25 of SCN1A (Fig 1) was detected in the GEFS+ patient. The amino acid translation show the His1586Arg amino acid substitution.

RESULTS

Clinical features of GEFS+ patients (Table 1) with variety of seizure types and neurological deficits 6 clinically GEFS+ patients (Table 1) with variety of seizure types and neurological deficits, including global developmental delay, ataxia and behavioural concerns.

DISCUSSION

We report a comprehensive clinical and genetic study of GEFS+ patients, the clinical presentation is variable as the case of GEFS+ (Scheffer and Berkovic, 1997) with the affected individuals had a variable of phenotype including anxiety disorders and neuropsychiatric disease.

The clinical characterization of GEFS+ as an autosomal dominant disease (Scheffer and Berkovic, 1997) also lead to identification of mutation in SCN1A gene (Escayg et al., 2000). We identified a novel missense mutation in the SCN1A gene in Malaysian GEFS+ patient, the mutation leads to an amino acid change in a conserved region and was not found in healthy controls. This suggests that mutations in SCN1A gene cause of GEFS+ in Malaysia.

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