Novel mutation of the notch3 gene in arabic family with CADASIL

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Abstract

Mutations in the NOTCH3 gene are responsible for cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL), an adult onset hereditary angiopathy leading to ischemic stroke, vascular dementia and psychiatric disorders. All mutations of NOTCH3 described so far are strikingly stereotyped leading to the gain or loss of cysteine residue in a given epidermal growth factor (EGF) repeat. We report an Arabic family affected with CADASIL mutation, G1790 C, in Exon 11 of the NOTCH3 gene. This is the first novel mutation reported in Arabic CADASIL patients. This finding confirms that mutations in NOTCH3 are associated with the pathogenesis of CADASIL across different ethnic background.

Introduction

CADASIL is an autosomal dominant vascular disorder clinically characterized by a variety of symptoms including migraine with aura, mood disorder, vascular dementia, ischemic stroke and premature death.1-3 The vascular lesions underlying CADASIL are non-arteriosclerotic, non-amyloid arteriopathy affecting small cerebral arteries with accumulating of granular and osmiophilic materials within the smooth muscles cell basement membrane.4,5 This initial thickening and expansion of the extracellular matrix can be found to a lesser extent in extra cerebral arteries such as skin arterioles.5

Mutation in the NOTCH3 gene is usually linked to CADASIL.6 NOTCH3 encodes a 300-kd transmembrane protein with a receptor and cell signal transduction function. Mutations are in majority mis-sense mutations causing the loss or gain of a cysteine residue and are detected in 95% of patients.7 All mutations are located within the epidermal growth factor (EGF) repeats in the extra cellular domain of the NOTCH3 gene and a strong clustering of the mutation were observed in Exon 3 and 4.8,9 Thus, there are more than 150 mutation have been identified. (The human gene mutation database www.hgmd.org), CADASIL is far more common than previously perceived and it may often be misdiagnosed because it can present under various guises.10 It also has been described in most ethnic groups from Western & Central Europe, Japan, Turkey, South Africa and South East Asia11,12 and only few reported families from Arabic origin.13,14 Hence, we described for a first time, a native Arabian family with CADASIL which harbor a novel mutation in NOTCH3 genes.

Materials and Methods

Genomic DNA was extracted from peripheral blood using an AutoGenFlex STAR automated DNA extractor (AutoGen, Inc.) Exons of the NOTCH3 gene reported to contain disease causing mutations (i.e., exons 2-5, 8, 11, 14, 18, 19, 22 and 23, were amplified by the polymerase chain reaction (PCR) and screened for mutations using dHPLC (WAVE; Transgenicom, Inc.) and Surveyor endonuclease digestion. Exons exhibiting altered elution were sequenced using a commercially available kit (A 1) and di-deoxy terminators. Sequences were analyzed on an automated DNA sequencer (ABI) and compared to normal sequence.

Discussion

The family described in this report showed various characteristics that are typical of CADASIL, an autosomal dominant pattern, recurrent ischemic stroke, migraine, cognitive impairment and premature death within 10 years after onset. One patient presented with late onset migraine with aura had an abnormal brain MRI, a feature along with family history is suggestive of this diagnosis.12 Positive brain MRI finding in asymptomatic individual indicate that NOTCH3 signaling may start up to a decade prior to clinical presentation.7

The C597S, NOTCH3 mutation in this family is likely the causative mutation as its co-segregate with the clinical phenotype and its absence in 120 ethnically related controls.
disturb the di-sulfate bond in EGF-like repeat at EGF-14 domain. In patients with suggestive clinical and MRI findings of CADASIL necessitate either genes testing and/or electron microscopy or immuno-histochemical examination of a skin biopsy. Mutation of a pathogenic NOTCH3 gene gives the definite diagnosis but the great number of different mutations (>150) makes the search for less common mutation cumbersome. The most efficient strategy in some populations will depend in the patient’s family history, founder mutations or the mutational background in patients ethnic group when certain mutations are prevalent as there is a variation in mutational spectrum between different ethnic group. The mutation hot-spots regions: Exons 3, 4, 5, & 8 of the NOTCH3 gene should be analyzed first, then Exons 6, 11 and 18 should be tested. The previous reported mutations in Arabs are located in Exon 3 & 4 of the NOTCH3 gene and had been reported previously in different ethnic groups. The finding of a noted novel mutation in Exon 11 in this family will further increase the spectrum of genetic finding in CADASIL.

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