

A New Type of Silent Butyrylcholinesterase Genotype found in Hyogo Prefecture

— a case of familial cholinesterasemia —

Kazuo HIDAKA*, Toshiko YAMASAKI* and Iwao IUCHI**

Department of Biochemistry, Kawasaki Medical School,

577 Matsushima, Kurashiki 701-01, Japan,*

Department of Medical Illustration and Designing,

Kawasaki College of Allied Health Professions,

*577 Matsushima, Kurashiki, 701-01, Japan***

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ABSTRACT

A point mutation that causes a silent phenotype for human serum butyrylcholinesterase(BChE) was identified in the DNA of a 47-year old Japanese woman visited the hospital for complaining hypertension.

The propositus had extremely low BChE activity, but her younger sister and her daughter had intermediate value of BChE activity and her elder sister showed normal level.

An immunological method revealed that the propositus showed the presence of usual amounts of BChE protein in serum. DNA sequence analysis of the propositus identified a point mutation at codon 199(GCA → GTA), resulting in a Ala → Val substitution. This alteration site is one amino acid downstream of the esteratic site(Ser, 198). A new PstI restriction site was introduced into the PCR product from the normal subject by PCR-primer introduced restriction analysis(PCR-PIRA) using a specific mismatched primer and the family analysis by digestion with PstI disclosed that her younger sister and her daughter had the same mutation.

Key Words : silent type hereditary serum cholinesterase deficiency ;
succinylcholine ; gene analysis ; point mutation

Introduction

Hereditary serum butyrylcholinesterase(BChE) deficiency is a rare autosomal recessive disease characterized by resistance to hydrolysis of several esteratic drug, particularly succinylcholine(SCC), a short acting muscle relaxant. When this drug is injected intravenously into individuals homozygous for this disease, a dangerous prolonged apnea occur as the result of muscle paralysis, but the carrier with this disease has no harmful disabilities in daily life. Recently, several genetic variants of BChE deficiency have been reported in Japanese population, such as BCHE ALU355¹⁾, BCHE365R^{2,3)}, BCHE FS315³⁾, BCHE418S, BCHE515C, BCHE210P and BCHE 465P⁴⁾. All these variants were characterized by silent type of BChE. In this paper, we show a new case of a point mutation of the silent type of BChE.

MATERIALS AND METHODS

The proband was a 47-year old Japanese woman who visited the hospital for complaining hypertension. Laboratory data revealed that the level of BChE was markedly decreased. Physical examination showed no abnormal findings except that her blood pressure was 160/92. She had no previous history of organophosphate compound poisoning. BChE activity measured on her family members indicated that her younger sister and her daughter were suspected of having the BChE deficiency.

BChE activity in serum was measured using butyrylthiocholine iodide as a substrate by the method of Iuchi et al⁵⁾ and phenotype was determined by measuring the inhibition numbers, dibucaine number(DN) and fluoride number(FN).

Sera of the proband and her three family members were electrophoresed on 8% polyacrylamide slab gel and stained with 2-amino-5-chlorotoluene azotate and α -naphthylacetate as substrates.

Antihuman BChE rabbit serum purchased from Dako (Glostrup, Denmark) was used as the first antibody and then with horseradish peroxidase conjugated swine antirabbit IgG as the second antibody for Western Blotting analysis(Hangaard et al⁶⁾ and Hirano⁷⁾).

Genomic DNAs were prepared from peripheral white blood cells according to the method of Maniatis et al⁸⁾ with slight modification and PCR was carried out according to the method of McGuire et al⁹⁾ with specific primers: sense 5'-CCTAAAAGTGTAACCTCTCTTTGGAGAACTG-3', which binds from codon 189 to the first base of codon 199 and contains a single base mismatch at the third position from the 3' end(asterisk), and antisense 5'-GGGACAACAAATGCTTCATTCAGAAGAATTTCTTGGGGA-3', which binds to codon 281-268. The amplified DNA fragments(278bp) were digested with Pst I restriction enzyme according to the manufacturer's instructions. The digests were separated by electrophoresis on 1.0% agarose gel.

The DNA of the four individuals was amplified by PCR with one pair of primers: sense 5'-CAAGCATCATATTTTAGGTAATTATCATCAATAAAG-3', which binds at 91 nucleotides upstream from the intron1/exon2 junction, antisense 5'-GGGACAACAAATGCTTCATTCAGAAGAATTTCTTGGGGA-3', which binds to codon 268-281 in exon2. The PCR products were directly sequenced by means of a cycle sequencing kit with an automated DNA sequencer(Applied Biosystems, 373 DNA Sequencer).

RESULTS AND DISCUSSION

The family tree of the proband is shown in figure 1.

The proband(I-2) had unusually low SChE activity. Her younger sister(I-3) and her daughter(II-1) had intermediate values for BChE activity, but her elder sister(I-1) showed normal level. Inhibition numbers of the proband could not be measured, but other three members of this family had dibucaine and fluoride numbers characteristic of the usual phenotype(data not shown).

Electrophoretically seen C₄ band was not identified for the serum of proband, but was identified for the serum of other family members. But intensity of the bands for the serum of her younger sister and her daughter were much weaker than that of her elder

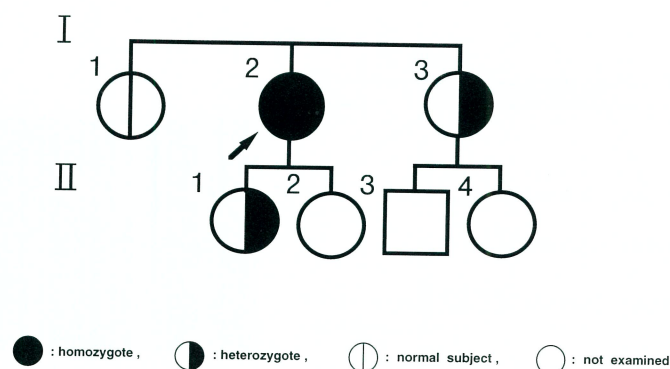


Fig. 1. Family tree. An arrow indicates the proband.

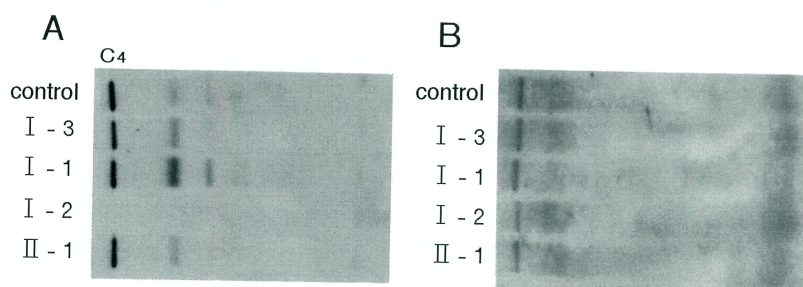


Fig. 2. A: BChE activity staining of the proband and her three family members. B: Peroxidase staining of immunoreactive BChE protein on nylon membrane. Note that the proband and other family members demonstrated immunoreactive BChE protein in their serum.

sister and normal subject (Fig. 2a). Immunoreactive BChE protein in serum of both the proband and three family members was detected by treatment of anti-BChE antibody after Western Blotting analysis (Fig. 2b).

The PCR product of 278 bp resulted from the elder sister (I-1) of proband created a new PstI restriction site and was completely digested into two fragments of 32 and 246 bp by Pst I. The PCR product from the proband was found to be resistant to Pst I digestion because of the absence of PstI site. Two other family members (I-3 and II-1) showed the two restriction fragments bands of 246 and 278 bp (Fig. 3). Sequence analysis revealed that BChE gene of the proband had a transition mutation of C to T in nucleotide 596, which converted codon 199 from GCA (Ala) to GTA (Val), who was homozygote of this mutation. Her younger sister and her daughter had two bases C and T on the same position in the nucleotide 596, suggesting heterozygous for this mutation and her elder sister showed only one base, C, in the nucleotide 596 (Fig. 4).

There are four genes recognized on the locus E_1 that participate in directing ChE

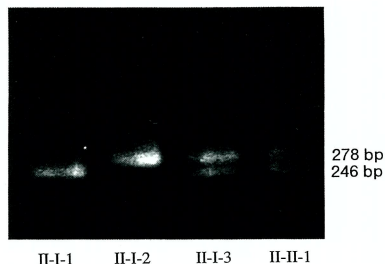
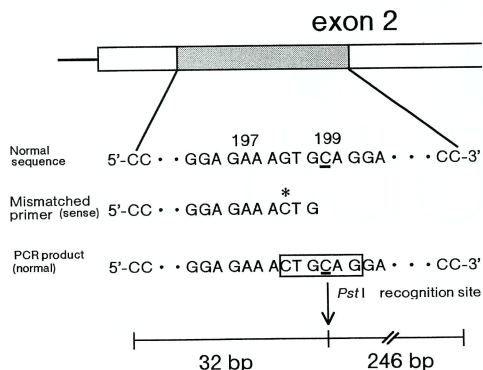


Fig. 3. Scheme for detection of Ala199Val mutation of BChE variant. Specific primer is composed of 31 mer and contains a mismatched single base(G → C) at the third position from the 3' end(asterisk). The pCR product of 278bp derived from the normal subject at codon 199(under bar) has a new PstI restriction site(square box) and is digested into two fragments of 32bp and 246bp.

Right: separation of PstI restriction fragments of four members(I-1, I-2, I-3 and II-1) on 4% agarose gel.

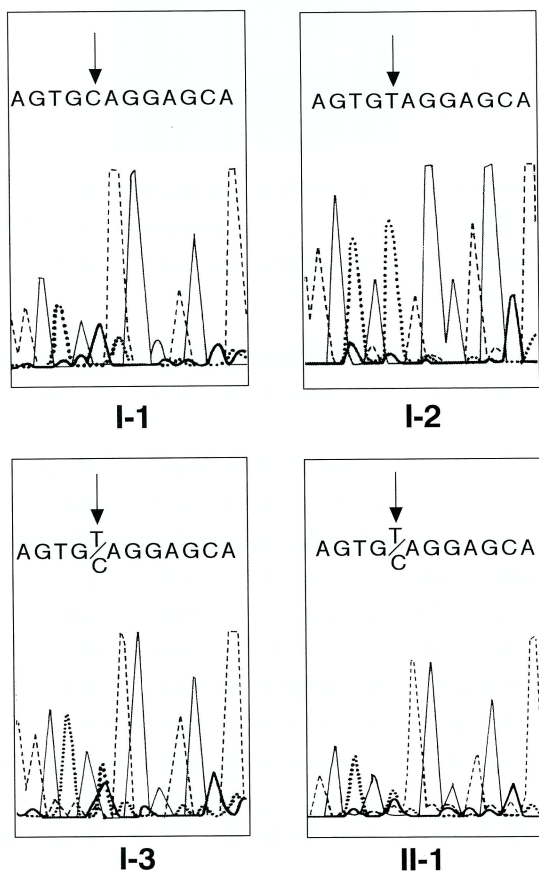


Fig. 4. Sequence analysis of the automated DNA sequencer for the region of the mutation. a) the propositus (I-2) is homozygous for the substitution GCA → GTA at codon 199(Ala → Val), b) the elder sister (I-1) and the younger sister(I-3) and daughter(II-1) had a normal and a heterozygous condition for the same mutation, respectively.

biosynthesis. They are E₁^u(usual : normal enzyme), E₁^a(atypical : dibucaine-resistant type), E₁^f(fluoride-resistant type) and E₁^s(silent type).

The E₁^s gene includes at least two BChE variants. One has zero activity and does not cross-react with antibody to normal human BChE(type I). The other has about 2 % of normal activity and is recognized as the presence of cross-reactive protein(type II). Our case is supported to be the latter type.. Recently, three BChE variants of silent type, which produce normal amounts of immunoreactive materials but enzymatically inactive BChE protein in the serum, have been reported by Primo-Parmo et al¹⁰, but this kinds of BChE variant have not been found in Japan. Therefore, the present case is the first one detected in Japan. In this investigation, we found a point mutation (GCA → GTA) at codon 199, resulting in a missense mutation from alanine to valine.. This alternation site is one amino acid downstream from esteratic region (Ser 198).

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