



Detection of LDL receptor mutations by PCR, PCR-RFLP and Southern analysis of DNA from Oragene®/saliva samples[†]

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The Oragene® self-collection kit is a non-invasive method of collecting DNA from saliva and it gives the same results as DNA from blood for the analysis of mutations in the LDL receptor gene by PCR, PCR-RFLP and Southern analysis.

Introduction

Familial hypercholesterolemia (FH) is an autosomal dominant disorder that occurs about one in 500 individuals in Western populations. It is primarily caused by mutations in the LDL receptor (LDLR) gene and over 770 mutations have been described worldwide¹. Among French Canadians, the prevalence of FH heterozygotes has been estimated to be about one in 270². Due to a genetic founder effect, five mutations in the LDLR gene account for approximately 83% of FH diagnosed in French Canadians³. These mutations are gene deletions of >15 kb and 5 kb, and three missense mutations: Trp₆₆ → Gly (exon 3), Glu₂₀₇ → Lys (exon 4), and Cys₆₄₆ → Tyr (exon 14). Methods such as Southern blotting⁴, PCR-RFLP⁵, and PCR⁶ have been used to detect these mutations in DNA from blood. Unlike blood, the Oragene self-collection kit is a non-invasive method for collecting DNA from saliva. The purpose of this study was to compare the detection of these five LDLR gene mutations in DNA from blood and DNA from Oragene/saliva samples.

Materials and methods

DNA collection and purification

Blood and saliva samples were collected from nine healthy French-Canadian volunteers and five patients who had been previously diagnosed with FH due to various mutations in the LDLR gene. Saliva was collected using the Oragene self-collection kit (DNA Genotek) and DNA was purified according

to the prepIT™•L2P protocol⁷. Additional DNA was purified from 10 mL of whole blood using the QIAamp® DNA blood maxi kit (Qiagen). All of the samples were tested for five mutations: >15 kb and 5 kb deletions, and mutations in exons 3, 4, and 14.

>15 kb and 5 kb deletions

The >15 kb and 5 kb deletions in the LDLR gene were detected using two methods. First, 10 µg of genomic DNA from blood and Oragene were digested with the restriction enzymes XbaI and EcoRV, and analyzed with Southern blotting using the method of Ma et al. (1989). Second, the PCR assays described by Simard et al. (2004) were also used to test for both deletions.

Exon 3 and exon 4 mutations

Exons 3 and 4 were amplified by PCR, digested with BslI and MnlI respectively, and electrophoresed on 2.5% MetaPhor agarose gels (Cambrex) according to the method of Minnich et al. (1995).

Exon 14 mutation

Following the method of Vohl et al. (1995), mismatch primers were used to create a NlaIII restriction site in the exon 14 mutant but not in the normal allele. After digestion, the mutant allele gave two fragments of 163 and 33 bp in size, while the normal allele resulted in a 196 bp fragment. The fragments were separated by electrophoresis on 2.5% MetaPhor agarose gels.

Results

DNA yield

The average DNA yield was 159 µg from 2 mL of saliva collected with Oragene kits. The average A₂₆₀/A₂₈₀ ratio was 1.94.

[†] Saliva samples were collected with Oragene®•DNA or Oragene®•DISCOVER.

