

## BRIEF REPORT — POLYMORPHISM REPORT

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**A polymorphic CA repeat sequence at the human calcitonin locus**

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**Abstract** A polymorphic dinucleotide (CA) repeat sequence was isolated from a genomic clone containing the human calcitonin gene at 11p15.2–p15.1. This polymorphism will be a useful marker in the genetic study of disorders affecting calcium metabolism including hyperparathyroidism, hypoparathyroidism, and osteoporosis.

**Key words** CA repeat, Calcitonin gene · Calcium metabolism · Osteoporosis · Hyperparathyroidism

**Introduction**

Calcitonin, a calcium-regulating hormone, lowers the calcium levels in serum by inhibiting bone resorption, and is implicated in the pathogenesis of disorders of calcium metabolism (Jacobs et al. 1981; Rosenfeld et al. 1983). In order to understand the relationship between genetic variations at the calcitonin locus and disorders of calcium metabolism including hyperparathyroidism, hypoparathyroidism, and osteoporosis (Alevizaki et al. 1989; Nakamura 1996; Yanase 1997), we isolated and characterized a dinucleotide repeat polymorphism at this locus.

**Source and isolation of CA repeat sequence**

A human genomic clone containing the calcitonin gene was identified from a P1-derived artificial chromosome (PAC) library by polymerase chain reaction (PCR) 3-dimensional screening using primer sequences derived from the 3' portion of the gene. A fragment containing a CA repeat was identified by Southern blotting of a PAC DNA digested by

*Hae*III, *Sau*3A, or *Rsa*I with the (GT)<sub>20</sub> probe, subcloned, and sequenced (Fig. 1). PCR primers were designed to flank this repeat sequence for polymorphism analysis.

**PCR primers**

Forward (CT, 4F): 5' -GGA GAC AAA CAG GGA TGA CA- 3'

Reverse (CT, 4R): 5' -CAG AAA CAT GGT GTG CCA GC- 3'

**PCR conditions**

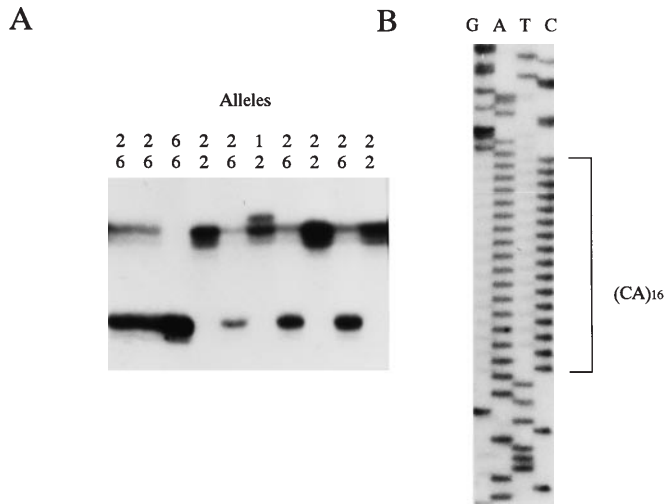
PCR was performed in a volume of 10 µl containing 20 ng genomic DNA, 10 mM Tris-HCl (pH 8.4), 50 mM KCl, 1.5 mM MgCl<sub>2</sub>, 0.01% gelatin, 200 µM dNTPs, 2.5 pmol of a [<sup>32</sup>P] end-labeled forward primer and an unlabeled reverse primer, and 0.25 units of *Taq* polymerase. Cycle conditions were 94°C for 4 min, then 30 cycles of 94°C for 30 s, 60°C for 30 s, and 72°C for 30 s, with a final extension step of 5 min at 72°C, in a Gene Amp PCR9600 System (Perkin Elmer Cetus, Norwalk, CT, USA) (Nakura et al. 1994). PCR products were electrophoresed in 0.3-mm-thick denaturing 6% polyacrylamide gels containing 36% formamide and 8 M urea, at 2000 V for 2–4 h. Gels were transferred to filter papers, dried at 80°C, and autoradiographed. The sizes of alleles were determined by comparison with a sequencing ladder of a control plasmid.

**Polymorphism and allele frequency**

Six alleles were detected in 192 chromosomes of unrelated Japanese individuals (Fig. 1A). The observed heterozygosity was 0.52. The size and frequency of the six alleles are shown in Table 1.

**Mendelian inheritance.** Codominant inheritance was observed in two three-generation families.

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**Fig. 1** **A** Autoradiogram showing a polymorphic CA repeat at the calcitonin locus in 10 unrelated individuals. **B** Nucleotide sequence of the CA repeat and the flanking regions at the calcitonin locus

**Table 1** Size and frequency of the alleles of the CA repeat polymorphism at the human calcitonin locus

Allele	Size (bp)	Frequency
A1	126	0.06
A2	124	0.61
A3	122	0.01
A4	114	0.01
A5	112	0.02
A6	110	0.29

**Chromosomal localization.** The human calcitonin gene was assigned to chromosome 11p15.1–p15.2 by fluorescence in situ hybridization (Hoovers et al. 1993).

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