Codon 72 polymorphism of the TP53 gene

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Previous studies revealed that the human TP53 gene has a single-base difference in amino acid residue 72 among several cDNA and genomic clones (1, 2). The single-base change causes alteration of amino acid residue 72 from arginine to proline. Here we report that the variation at position 72 is caused by a polymorphism and not by mutation, and this polymorphism can be easily analyzed using polymerase chain reaction (PCR).

PCR Primers:
Sense oligo: 5'-TTGCCGTCCCAAGCAATGGATGA-3'
Antisense oligo: 5'-TCTGGGAAGGGACAGAAGATGAC-3'

Polymorphism: *Acc*II digest of the amplified fragment identifies two alleles: A1 = ~199 bp and A2 = ~113 bp + ~86 bp.

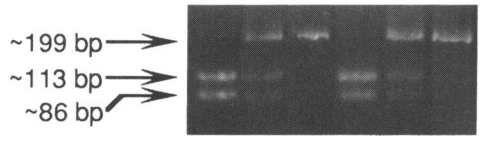
Frequency: Estimated from 50 unrelated individuals.
A1 = 0.36 A2 = 0.64

Chromosomal Localization: The polymorphic *Acc*II site occurs in the 4th exon (amino acid residue 72) of the human TP53 gene, which is localized to the short arm of chromosome 17 (17p13).

Mendelian Inheritance: Co-dominant segregation of the *Acc*II alleles observed in two families.

PCR Conditions: Target sequences are amplified in a 100-μl reaction volume containing 500 ng of genomic DNA, 1.25 mM dNTPs, 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 0.01% gelatin, 0.5 μg of each primer and 2.5 units of recombinant *Taq* DNA polymerase (Perkin Elmer Cetus, Norwalk, CT). The amplification is performed for 35 cycles with an annealing temperature of 60°C. The PCR product is digested with *Acc*II for 2 hr at 37°C. The DNA fragments are separated by electrophoresis on 4% NuSieve agarose gel.

References: 1) Harris,N., Brill,E., Shohat,O., Prokocimer,M., Wolf,D., Arai,N. and Rotter,V. (1986) *Mol. Cell. Biol.* **6**, 4650–4656. 2) Matlashewski,G.J., Tuck,S., Pim,D., Lamb,P., Schneider,J. and Crawford,L.V. (1987) *Mol. Cell. Biol.* **7**, 961–963.



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RsaI polymorphism in von Willebrand factor (vWF) at codon 789

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Source/Description: The sequence of vWF (Mancuso *et al.*) showed a potential DNA dimorphism of the first base in codon 789 (Thr/Ala). An RsaI site is present (+) when the sequence is ACC and absent (−) when it is GCC.

Polymorphism: Using two 20 base primers starting 200 bp 5' and 122 bp 3' to the dimorphic site, genomic DNA was amplified 35 cycles as described in Graham *et al.* under these conditions: 30'' at 90°C, 2' at 60°C, 4 mM $MgCl_2$, electrophoresis in 4% agarose. RsaI (−/−) persons show one 322 bp band, (+/+) show two (200 and 122 bp), and (+/−) show three bands.

Primers:
Primer 1: TGG GCA ACT CTG AGT CTC TT
Primer 2: AGA AAA CTG AAG GGC AGG CA

Chromosomal Location: 12pter-p12. Codon 789 of vWF gene.

Mendelian Inheritance: Autosomal co-dominant in one family.

Population Genetics: The (+:−) allele frequencies in 7 ethnic groups were: Anglo-Americans (100 chromosomes) .65: .35; Swedes (46) .56: .44; Basques (46) .56: .44; East Indians (46) .80: .20; Malays (42) .86: .14; Chinese (48) .94: .06; African-Americans: (74): .46: .54.

Heterozygosity: (expected/observed): Anglo-Americans .46/ .54; Swedes .49/.50: Basques .49/.43; East Indians .32/.39; Malays .23/.19; Chinese .11/.04; African-Americans: .50/.49.

References: 1) Mancuso,D.J. *et al.* (1989) *J. Biol. Chem.* **264**, 19514–19527. 2) Graham,J.B. *et al.* (1989) *Blood* **73**, 2104–2107.