*Acc*II polymorphism of the p53 gene

Oscar de la Calle-Martín*, Virginia Fabregat, Matilde Romero, Jesus Soler[1], Jordi Vives and Jordi Yagüe
Servei d'Immunologia, Hospital Clinic, Villarroel 170, 08036 Barcelona and [1]Servei d'Hematologia, Hospital de Sant Pau, Barcelona, Spain

Here we report a rapid and simple method to analyze an *Acc*II polymorphism within the human p53 gene using the polymerase chain reaction.

PCR Primers: The primer sequences corresponded to the 4th exon of the human p53 gene as described by Lamb (1).
Sense oligo 5'-AATGGATGATTTGATGCTGTCCC-3'
Antisense oligo 5'-CGTGCAAGTCACAGACTTGGC-3'

Polymorphism: *Acc*II (CGCG) digest of the amplified fragment identifies two alleles; A1 = 259 bp and A2 = 160 bp + 99 bp.

Frequency: Allele frequencies were calculated from 90 unrelated Caucasians.
A1 = 0.32 A2 = 0.68

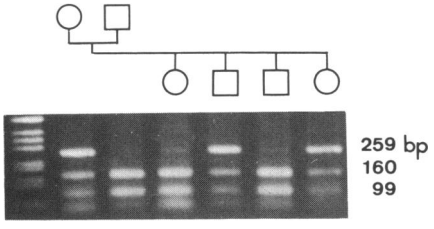
Chromosomal Localization: The polymorphic *Acc*II recognition site occurs within the 4th exon of the human p53 locus (17q13) (2).

Mendelian Inheritance: Co-dominant segregation demonstrated in 6 two-generation families.

PCR Conditions: PCRs were carried out in a total volume of 50 µl containing: 500 ng of genomic DNA, 50 pmoles of each primer, 2 mM $MgCl_2$, 200 µM dNTPs, 50 mM KCl, 20 mM Tris-pH 8.3 and 0.1% gelatine. The amplification is performed for 35 cycles with an annealing temperature of 62°C. The amplified DNA is digested overnight with a ten-fold excess of *Acc*II. DNA fragments are resolved by electrophoresis through a 2% agarose gel or a 7% polyacrylamide gel.

Acknowledgements: This work was supported by a CAICYT Grant # PB 86−0046 del Ministerio de Educación y Ciencia. O. de la Calle-Martín was supported by a Hospital Clinic grant.

References: 1) Lamb,P. and Crawford,L.V. (1986) *Mol. Cell. Biol.* **6**, 1379−1385. 2) Miller *et al.* (1986) *Nature* **319**, 783−784.



* To whom correspondence should be addressed

*Msp*I polymorphism of the human p53 gene

Oscar de la Calle-Martín, Matilde Romero, Virginia Fabregat, Guadalupe Ercilla, Jordi Vives and Jordi Yagüe
Servei d'Immunología, Hospital Clinic, Villarroel 170, 08036 Barcelona, Spain

Source and Description of Clone: p1A65 (pArgSP53) is a recombinant cDNA clone that codifies the entire coding region of the human p53 gene (1).

Polymorphism: *Msp*I (CCGG) identifies a two allele polymorphism.
A1 allele with bands of 900 bp, 700 bp, 500 bp and 330 bp.
A2 allele with bands of 900 bp, 700 bp, 500 bp, 330 bp and a varient band of 620 bp (Figure 1).

Frequency: Allele frequencies were calculated from 109 unrelated Caucasians.
A1 = 0.28 A2 = 0.72

Not Polymorphic For: BamHI, EcoRI, HindIII, PstI, PvuII, RsaI, TaqI and XbaI.

Chromosomal Localization: The human p53 locus has been localised to the short arm of chromosome 17 (17q13) (2).

Mendelian Inheritance: Co-dominant segregation demonstrated in 1 informative two-generation family.

Probe Availability: Request for probe to Dr. Crawford, Imperial Cancer Research Foundation, Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.

Other Comments: No problems on RFLP analysis under normal stringent conditions. This probe also detects a previously reported BglII polymorphism.

Acknowledgements: This work was supported by a CAICYT Grant # PB 86−0046 del Ministerio de Educación y Ciencia. O. de la Calle-Martín was supported by a Hospital Clinic grant.

References: 1) Matlashewski *et al.* (1987) *Mol. Cell. Biol.* **7**, 961−963. 2) Miller *et al.* (1986) *Nature* **319**, 783−784.