

Two common RFLPs of the human CYP2E gene

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Source and Description of Probe: The probe used, lhPD4, contains a sequence of 1.0 kb of the human cytochrome P450, subfamily IIE cDNA (Ref. 1).

Polymorphism: *DraI* (TTT/AAA) identifies two constant bands of 2.3 and 1.2 kb and a two-allele polymorphism of a third band of either 5.5 or 4.1 kb. *RsaI* (GT/AC) identifies two constant bands of 1.6 and 1.2 kb and a two-allele polymorphism of either 3.1 or 2.5 kb.

Frequency: *DraI* digestion of 26 unrelated individuals: 5.5-kb allele 0.29, 4.1-kb allele 0.71; *RsaI* digestion of 27 unrelated individuals: 3.1-kb allele 0.57, 2.5-kb allele 0.43.

Chromosomal Localization: 10 (Ref. 2).

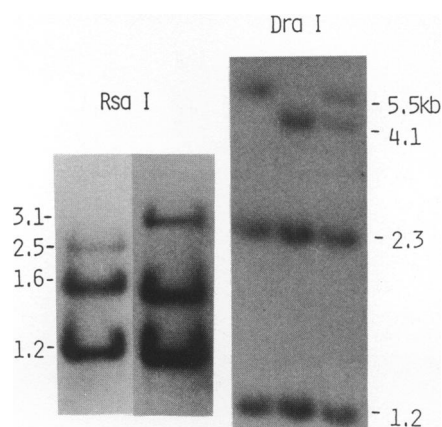
No Polymorphism Found For: *AluI*, *BanI*, *BanII*, *BstNI*, *EcoNI*, *Eco0109I*, *HaeIII*, *HinfI*, *PstI* and *PvuII* [14 individuals tested].

Mendelian Inheritance: Autosomal co-dominant for each polymorphism.

Probe Availability: Contact T.Kamataki.

Acknowledgement: This work was supported by Grants-in-Aid from the Ministry of Education, Science and Culture.

References: 1) Komori *et al.* (1989) *Arch. Biochem. Biophys.* **272**, 219–225. 2) McBride *et al.* (1987) *Nucl. Acids Res.* **15**, 10071.



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Dinucleotide repeat polymorphism at the human fms-related tyrosine kinase gene (FLT1)

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Source/Description: The polymorphic (TG)_n repeat begins at base pair 6973 of the human fms-related tyrosine kinase (FLT1) gene (1). The polymorphism can be typed using the polymerase chain reaction (PCR) as described previously (2). The predicted length of the amplified sequence was 180 bp.

Primer Sequences:

TTTGGCCGACAGTGGTGTAA (TG strand)
AGGACCAAACCATGTCTGTGTC (AC strand).

Frequency: Estimated from 50 chromosomes of unrelated individuals. Heterozygosity Index = 51%. PIC = 0.49.

Allele (bp)	Frequency	Allele (bp)	Frequency
A1 186	0.02	A5 172	0.06
A2 184	0.02	A6 170	0.02
A3 182	0.04	A7 166	0.68
A4 180	0.14	A8 164	0.02

Mendelian Inheritance: Co-dominant segregation was observed in two informative families.

Chromosomal Localization: FLT1 has been assigned to chromosome 13q12 (1).

Other Comments: The PCR reaction was performed on 80 ng of genomic DNA using 100 pmoles of each oligonucleotide primer. The samples were processed as described (3) except that the denaturation cycle at 94°C was extended to 1.4 minutes. The dinucleotide repeat was based on a (TG)₂₁ sequence.

References: 1)Shibuya,M. *et al.* (1990) *Oncogene* **5**, 519–524. 2)Weber,J.L. and May,P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396. 3)Weber,J.L. *et al.* (1990) *Nucl. Acids Res.* **18**, 4637.

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