The anonymous probe pDX15 (D15S91) detects an RFLP with MspI

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Source/Description: Probe pDX15 contains a unique 2 kb human DNA fragment subcloned into the EcoRI site of pBS+ (Stratagene Inc.). This subclone was derived from a λ library obtained from Los Alamos National Laboratory (LA15NS03).

Polymorphism: MspI identifies a 2-allele polymorphism:

A1: 5.71 kb

A2: 4.08 kb

Frequency: Estimated from 22 unrelated Caucasians:

A1: 0.82

A2: 0.18

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

Chromosome Localization: Localized to 15q11-q12 using a somatic cell hybrid regional mapping panel (Rich *et al.*, 1988), and by dosage analyses of a panel of chromosome 15-heteroploid cell lines.

Mendelian Inheritance: Co-dominant segregation of the MspI RFLP was observed in three generations of two families of 28 individuals

Probe Availability: Contact M.Rabin.

Other Comments: Identifies one allele: TaqI: 3.14 kb; RsaI: 1.89 kb; BamHI: 5.42 kb; HindIII: 2.91 kb; EcoRI: 2.5 kb.

Reference: Rich *et al.* (1988) *Nucl. Acids Res.* **16**, 8740.

Trinucleotide repeat polymorphism at the human intestinal fatty acid binding protein gene (FABP2)

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Source/Description: The polymorphic (TTA)_n repeat begins at base pair 3502 in intron B of the human intestinal fatty acid binding protein gene (FABP2) on chromosome 4q28-q31 (1). The polymorphism can be typed using the polymerase chain reaction (PCR) as described previously (2). The predicted length of the amplified sequence was 113 bp.

Primer Sequences: AACTCAGAACAGTGCCTGAC (TTA strand); ATTTCCCTCAAGGCTCCAGGT (AAT strand)

Frequency: Estimated from 50 chromosomes of unrelated individuals. Heterozygosity = 64%.

Allele (bp)	Frequency	Allele (bp)	Frequency
A1: 117	0.12	A4: 105	0.50
A2: 114	0.22	A5: 102	0.06
A3: 108	0.08	A6: 99	0.02

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

Chromosomal Localization: FABP2 gene has been assigned to chromosome 4q28-q31 (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 (TTA)₁₃ sequence.

References: 1) Sweetser, D. *et al.* (1987) *J. Biol. Chem.* **262**, 16060–16071. 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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