Tetranucleotide repeat polymorphism at the human c-fes/fps proto-oncogene (FES)

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Source/Description: The polymorphic $(ATTT)_n$ repeat begins at base pair 4713 in intron V of the human c-fes/fps proto-oncogene on chromosome 15q25-qter (1). The polymorphism can be typed using the polymerase chain reaction (PCR) as described previously (2). The predicted length of the amplified sequence was 154 bp.

Primer sequences:
GGAAGATGGAGTGGCTGTTA (ATTT strand); CTCCAGCCTGGCGAAAGAAT (TAAA strand).

Frequency: Estimated from 48 chromosomes of unrelated individuals.

Heterozygosity Index: = 75%. PIC = 0.70.

Allele (bp)	Frequency	Allele (bp)	Frequency
C1 163	0.04	C4 151	0.27
C2 159	0.23	C5 147	0.02
C3 155	0.33	C6 143	0.11

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

Chromosomal Localization: The human c-fes/fps proto-oncogene has been assigned to chromosome 15q25-qter (3).

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 (4) except that the denaturation cycle at 94°C was extended to 1.4 minutes. The tetranucleotide repeat was based on a $(ATTT)_{11}$ sequence.

References: 1) Roebroek,A.J.M. *et al.* (1985) *EMBO J.* **4**, 2897–2903. 2) Weber,J.L. and May,P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396. 3) Harper,M.E. *et al.* (1983) *Nature* **304**, 169–171. 4) Weber,J.L. *et al.* (1990) *Nucl. Acids Res.* **18**, 4637.

Dinucleotide repeat polymorphism at the human CTLA4 gene

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Source/Description: The polymorphic $(AT)_n$ repeat begins at base pair 642 of exon 3 of the human CTLA4 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 128 bp.

Primer sequences:
GCCAGTGATGCTAAAGGTTG (AT strand); AACATACGTGGCTCTATGCA (TA strand).

Frequency: Estimated from 38 chromosomes of unrelated individuals.

Heterozygosity Index = 92%. PIC = 0.91.

Allele (bp)	Frequency	Allele (bp)	Frequency
130	0.03	106	0.03
128	0.03	104	0.13
124	0.03	102	0.10
122	0.13	100	0.08
120	0.03	98	0.03
118	0.08	96	0.05
112	0.05	94	0.03
110	0.10	92	0.05
108	0.03		

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

Chromosomal Localization: CTLA4 has been assigned to chromosome 2q33 (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 $(AT)_{28}$ sequence.

References: 1) Dariavach,P. *et al.* (1988) *Eur. J. Immunol.* **18**, 1901–1905. 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.