Tetranucleotide repeat polymorphism at the human prostatic acid phosphatase (ACPP) gene

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Source/Description: The polymorphic (AAAT)_n repeat begins at base pair 2342 of the human prostatic acid phosphatase gene on chromosome 3q21-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 275 bp.

Primer sequences:

GGGCAACATGGTGAAACCTT (AAAT strand);
CCTAGCCTATACTTCCTTTC (TTTA strand).

Frequency: Estimated from 70 chromosomes of unrelated individuals. Heterozygosity Index = 69%. PIC = 0.65.

Allele (bp)	Frequency	Allele (bp)	Frequency
C1 280	0.04	C4 268	0.27
C2 276	0.04	C5 264	0.06
C3 272	0.46	C6 260	0.13

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

Chromosomal Localization: The human prostatic acid phosphatase gene has been assigned to chromosome 3q21-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 (AAAT)₁₁ sequence.

References: 1) Sharief, F.S. *et al.* (1989) *Biochem. Biophys. Res. Commun.* **160**, 79–86. 2) Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396. 3) Winquist, R. *et al.* (1989) *Cytogenet. Cell Genet.* **52**, 68–71. 4) Weber, J.L. *et al.* (1990) *Nucl. Acids Res.* **18**, 4637.

Tetranucleotide repeat polymorphism at the human dihydrofolate reductase psi-2 pseudogene (DHFRP2)

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Source/Description: The polymorphic (AAAC)_n repeat begins at base pair 103 of the human dihydrofolate reductase psi-2 pseudogene (DHFRP2) on chromosome 6 (1). The polymorphism can be typed using the polymerase chain reaction (PCR) as described previously (2). The predicted length of the amplified sequence was 166 bp.

Primer Sequences:

GTAAGACTTTTGGAGCCATT (AAAC strand)
TTCAGGGAGAATGAGATGGG (TTTG strand).

Frequency: Estimated from 48 chromosomes of unrelated individuals.

Heterozygosity Index = 70%. PIC = 0.66.

Allele (bp)	Frequency
A1 173	0.12
A2 169	0.25
A3 165	0.15
A4 161	0.44
A5 157	0.04

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

Chromosomal Localization: DHFRP2 has been assigned to chromosome 6 (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 (AAAC)₇ sequence.

References: 1) Chen, M.J. *et al.* (1982) *Proc. Natl. Acad. Sci. USA* **79**, 7435–7439. 2) Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396. 3) Anagnou, N.P. *et al.* (1988) *Am. J. Hum. Genet.* **42**, 345–52. 4) Weber, J.L. *et al.* (1990) *Nucl. Acids Res.* **18**, 4637.