Dinucleotide repeat polymorphism at the human gene of the light and heavy chains of myeloperoxidase glycoprotein (MPO)

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Source/Description: The polymorphic (AC)_n repeat begins at base pair 6304 of the human gene of light and heavy chains of myeloperoxidase glycoprotein (MPO) on chromosome 17q21–23 (1). The polymorphism can be typed using the polymerase chain reaction (PCR) as described previously (2). The predicted length of the amplified sequence was 110 bp.

Primer Sequences: TCCAGATCGCTCTACATGA (AC strand); CACAGCTTCAGAAGTCACAG (GT strand).

Frequency: Estimated from 50 chromosomes of unrelated individuals. Heterozygosity Index = 55%. PIC = 0.45.

Allele (bp)	Frequency
C1 110	0.40
C2 108	0.04
C3 106	0.02
C4 104	0.54

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

Chromosomal Localization: MPO has been assigned to chromosome 17q21–23 (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 (AC)₁₄ sequence.

References: 1)Johnson,K. *et al.* (1989) *Nucl. Acids Res.* **17**, 7985–7986. 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.

Dinucleotide repeat polymorphism at the human debrisoquine 4-hydroxylase (CYP2D) locus

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Source/Description: The polymorphic (GT)_n repeat begins at base pair 7882 of the human debrisoquine 4-hydroxylase (CYP2D) 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 100 bp.

Primer Sequences: CCTCTGGCTCTAACAGCAA (GT strand); AGCAAGACCCTGTCTCAAGA (CA strand).

Frequency: Estimated from 46 chromosomes of unrelated individuals. Observed heterozygosity = 80%. PIC = 0.78.

Allele (bp)	Frequency	Allele (bp)	Frequency
B1 116	0.02	B6 106	0.02
B2 114	0.17	B7 104	0.02
B3 112	0.07	B8 102	0.04
B4 110	0.05	B9 100	0.33
B5 108	0.06	B10 98	0.22

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

Chromosomal Localization: CYP2D has been assigned to chromosome 22q11.2-qter (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 (GT)₁₈ sequence.

References: 1)Mitchell *et al.* (1989) *Cytogenetics and Cell Gen.* **51**, 1045. 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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