Dinucleotide repeat polymorphism at the human preproglucagon gene

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Source/Description: The polymorphic (GA)_n repeat begins at base pair 2771 in intron II of the human preproglucagon gene (GCG) on chromosome 2q36–37 (1). The polymorphism can be typed using the polymerase chain reaction (PCR) as described previously (2). The predicted length of the amplified sequence was 157 bp.

Primer Sequences: TTTGTCTGGATAGACTGGAG (GA strand); CCATCTTCCTGTGGCTGTA (CT strand).

Frequency: Estimated from 50 chromosomes of unrelated individuals. Observed heterozygosity = 88%.

Allele (bp)	Frequency	Allele (bp)	Frequency
A1 172	0.02	A7 156	0.02
A2 166	0.24	A8 154	0.02
A3 164	0.34	A9 152	0.02
A4 162	0.12	A10 148	0.02
A5 160	0.10	A11 142	0.02
A6 158	0.08		

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

Chromosomal Localization: The human preproglucagon gene has been assigned to chromosome 2q36–37 (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 dinucleotide repeat was based on a (GA)₁₉ sequence.

References: 1) Bell, G.I. *et al.* (1983) *Nature* **304**, 368–371. 2) Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396. 3) Schroeder, W.T. *et al.* (1984) *Cytogenet. Cell Genet.* **38**, 76–79. 4) Weber, J.L. *et al.* (1990) *Nucl. Acids Res.* **18**, 4637.

Dinucleotide repeat polymorphism at the human interleukin 9 gene

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Source/Description: The polymorphic (TG)_n repeat begins at base pair 3833 in intron D of the human interleukin 9 gene (IL-9) on chromosome 5 (1). The polymorphism can be typed using the polymerase chain reaction (PCR) as described previously (2). The predicted length of the amplified sequence was 127 bp.

Primer Sequences: CTAATGCAGAGATTTAGGGC (TG strand); GTGGTGTAAGACTGCATAG (AC strand).

Frequency: Estimated from 46 chromosomes of unrelated individuals. Observed heterozygosity = 62.5%.

Allele (bp)	Frequency	Allele (bp)	Frequency
A1 139	0.04	A5 131	0.15
A2 137	0.09	A6 129	0.09
A3 135	0.20	A7 127	0.07
A4 133	0.37		

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

Chromosomal Localization: IL-9 has been assigned to chromosome 5 (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 dinucleotide repeat was based on a (TG)₂₀ sequence.

References: 1) Renauld, J.C. *et al.* (1990) *J. Immunol.* **144**, 4235–4241. 2) Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396. 3) Mock, B.A. *et al.* (1990) *Immunogenetics* **31**, 265–270. 4) Weber, J.L. *et al.* (1990) *Nucl. Acids Res.* **18**, 4637.