Dinucleotide repeat polymorphism in human GLUT2/liver facilitative glucose transporter gene on chromosome 3

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Primers/Description: Two primers (GLUT2−1, 5′-TCCGTCAGCAGCTATTCTAG-3′ and GLUT2−2, 5′-CAAATAGTCCTCATGCAGAA-3′) were used to amplify a 184−222 bp CA and TA repeat-rich region in intron 1 of the human GLUT2 gene.

Frequency: Fourteen alleles were observed in 68 unrelated Caucasians. The heterozygosity was 91%.

Allele	bp	Frequency	Allele	bp	Frequency
L1	222	0.02	L2	220	0.02
L3	218	0.06	L4	216	0.02
L5	214	0.06	L6	212	0.01
L7	202	0.01	L8	200	0.11
L9	198	0.18	L10	196	0.31
L11	194	0.05	L12	192	0.05
L13	186	0.04	L14	184	0.06

Chromosomal Localization: GLUT2 was assigned to chromosome 3q26.1-q26.3 (1).

Mendelian Inheritance: Co-dominant inheritance was observed in five nuclear families.

Other Comments: The PCR was preformed using ^{32}P-labeled GLUT2−1 and unlabeled GLUT2−2 for 30 cycles; denaturation at 94°C for 1 min; annealing at 55°C for 1 min and extension at 72°C for 2 min. The PCR products were analyzed on a 5% denaturing polyacrylamide gel (Figure 1). The dinucleotide repeat sequence in intron 1 was of the form $(TA)_{16}(CA)_6(TA)_5(CA)_9$; the complete sequence of this region is available from the authors.

References: 1) Fukumoto,H. *et al.* (1988) *Proc. Natl. Acad. Sci. USA* **85**, 5434.

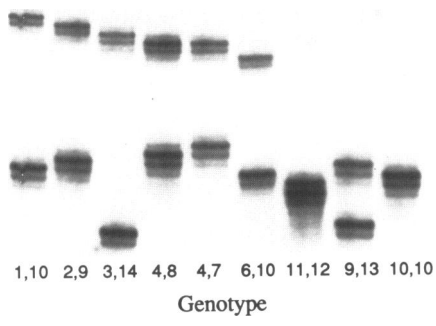

Figure 1. PCR amplification of dinucleotide repeat DNA polymorphism in human GLUT2 gene. The genotypes are noted at the bottom of the figure.

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Pentanucleotide repeat length polymorphism at the human CD4 locus

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Source and Description of Clone: Partial sequencing of an approximately 15 kb lambda insert (lambda hg1) containing exons 1−3 of the human CD4 gene revealed a tract of 12 CTTTT's. The sequences flanking the pentanucleotide repeat (CTTTT)n were then used to design PCR primers that amplified a 113 base pair fragment from lambda hg1.

Primer Sequences:
5′-TTGGAGTCGCAAGCTGAACTAGC-3′(CTTTT strand),
5′-GCCTGAGTGACAGAGTGAGAACC-3′(AAAAG strand)

Polymorphism: Allelic fragments in 5 bp intervals from 88 to 128 bp.

Frequencies: (a) in 100 unrelated Caucasians, (b) in 14 unrelated North American Blacks:

Allele	(bp)	Freq.(a)	Freq.(b)	Allele	(bp)	Freq.(a)	Freq.(b)
A8	88	0.365	0.286	A4	108	0.300	0.036
A7	93	0.295	0.214	A3	113	0.025	0.250
A6	98	0.005	0.107	A2	118	0.005	0.036
A5	103	0.005	0.036	A1	128	0.000	0.036

Mendelian Inheritance: Mendelian inheritance was observed in 4 three-generation families and 2 two-generation families.

Chromosomal Location: The human CD4 gene has been mapped to the short arm of chromosome 12 (1).

PCR Conditions: PCR was performed on 50 ng genomic DNA using 25 pmol of each primer. Thermocycling conditions were 94°C 5 mins then 94°C 30 secs, 55°C 30 secs and 68°C, 2 min. for 25 cycles in reaction conditions described (2).

Acknowledgements: Thanks to Dan Littman for supplying lambda clones containing the CD4 gene. Research supported in part by grants USPH U01 AI30243 and RR06404.

References: 1) Isobe,M. *et al.* (1986) *Proc. Natl. Acad. Sci. USA* **83**, 4399−4402. 2) Gibbs,R.A. *et al.* (1990) *Genomics* **7**, 235−244.

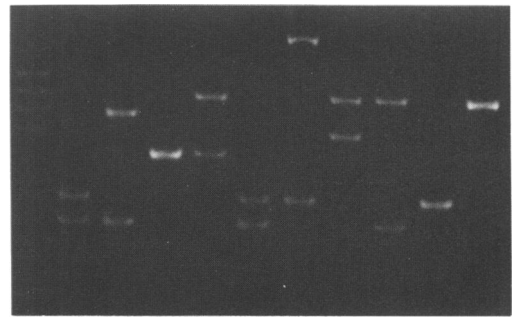

Figure. Alleles were detected by electrophoresis on 10% native acrylamide gels followed by ethidium bromide staining. The first lane shows size standards generated by a mixture of known alleles; other lanes show the patterns generated from individual DNA samples.