Tetranucleotide repeat polymorphism at the HPRT locus

C.M.Hearne and J.A.Todd*
Nuffield Department of Surgery, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK

Source/Description: A polymorphic $(TCTA)_{13}$ repeat is located at base 22928 of the human HPRT locus (1). The polymorphism can be typed using the polymerase chain reaction (PCR) and gel electrophoresis as described previously (2). The predicted length of the amplified sequence is 159 bp.

Primer Sequences:
Forward 5′TCTCTATTTCCATCTCTGTCTCC
Reverse 5′TCACCCCTGTCTATGGTCTCG

Frequency: Estimated from 48 chromosomes of unrelated individuals, PIC = 0.70.

Allele (bp)	Frequency	Allele (bp)	Frequency
D1 163	0.167	D3 155	0.292
D2 159	0.396	D4 151	0.104

Mendelian Inheritance: Co-dominant X-linked inheritance was observed in six two-generation families.

Chromosomal Localisation: The HPRT locus is located on chromosome Xq26 (3).

Other Comments: PCR was performed with 250 ng of genomic DNA and 125 ng of each oligonucleotide primer in a 25 μl volume as described previously (2).

References: 1) Edwards,A. *et al.* (1990) *Genomics* **6**, 593–608. 2) Love,J.M. *et al.* (1990) *Nucl. Acids Res.* **18**, 4123–4130. 3) Williamson,R. *et al.* (1990) *Cytogenet. Cell Genet.* **55**, 475–778.

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* To whom correspondence should be addressed

Trinucleotide repeat polymorphism at the CRYG1 locus

C.M.Hearne and J.A.Todd*
Nuffield Department of Surgery, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK

Source/Description: A polymorphic $(AAC)_9$ repeat is located at base 3021 of the human gamma B crystallin (HGM symbol CRYG1, EMBL Accession M19354). The polymorphism can be typed using the polymerase chain reaction (PCR) and gel electrophoresis as described previously (1). The predicted length of the amplified sequence was 182 bp.

Primer Sequences:
Forward 5′GCCTGGCGACAGAGTGAGAC
Reverse 5′AAGTGAGCTAATAGGTACTGACC

Frequency: Estimated from 48 chromosomes of unrelated individuals, PIC = 0.55.

Allele (bp)	Frequency
E1 191	0.266
E2 188	0.500
E3 182	0.234

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

Chromosomal Localisation: The CRYG1 is located on chromosome 2q33-q35 (2).

Other Comments: PCR was performed on 250 ng of genomic DNA using 125 ng each oligonucleotide primer in a volume of 25 μl, and the samples processed as described previously (1).

References: 1) Love,J.M. *et al.* (1990) *Nucl. Acids Res.* **18**, 4123–4130. 2) Williamson,R. *et al.* (1990) *Cytogenet. Cell Genet.* **55**, 475–778.

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