Tetranucleotide repeat polymorphism at the human tyrosine hydroxylase gene (TH)

Mihael H.Polymeropoulos, Hong Xiao, Denise S.Rath and Carl R.Merril

National Institute of Mental Health Neuroscience Center, St Elizabeths Hospital, Room 131, 2700 Martin Luther King Avenue, Washington, DC 20032, USA

Source/Description: The polymorphic (TCAT)_n repeat begins at base pair 1170 in intron 1 of the human tyrosine hydroxylase gene on chromosome 11p15.5-p15 (1). The polymorphism can be typed using the polymerase chain reaction (PCR) as described previously (2). The predicted length of the amplified sequence was 254 bp.

Primer Sequences:

CAGCTGCCCTAGTCAGCAC (TCAT strand);
GCTTCCGAGTGCAGGTCACA (AGTA strand).

Frequency: Estimated from 70 chromosomes of unrelated individuals. Heterozygosity index = 78%. PIC = 0.75.

Allele (bp)	Frequency
K1 260	0.21
K2 256	0.26
K3 252	0.13
K4 248	0.14
K5 244	0.26

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

Chromosomal Localization: The human tyrosine hydroxylase gene has been assigned to chromosome 11p15.5 (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 tetranucleotide repeat was based on a (TCAT)₉ sequence.

References: 1) Kobayashi, K. *et al.* (1988) *J. Biochem.* **103**, 907–912. 2) Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396. 3) Jumen, C. and McBride, O.W. (1989) *Cytogenet. Cell Genet.* **51**, 226–258. 4) Weber, J.L. *et al.* (1990) *Nucl. Acids Res.* **18**, 4637.

Dinucleotide repeat polymorphism at the human non-histone chromosomal protein HMG14 gene

Mihael H.Polymeropoulos, Hong Xiao, Denise S.Rath and Carl R.Merril

National Institute of Mental Health Neuroscience Center, St Elizabeths Hospital, Room 131, 2700 Martin Luther King Avenue, Washington, DC 20032, USA

Source/Description: The polymorphic (GT)_n repeat begins at base pair 4829 in intron E of the human non-histone chromosomal protein HMG14 gene on chromosome 21q22.3 (1). The polymorphism can be typed using the polymerase chain reaction (PCR) as described previously (2). The predicted length of the amplified sequence was 82 bp.

Primer Sequences:

GAAGACTGAGGAGGTCAGAA (GT strand);
CTACTGTTTCAGAGTCAAAGC (CA strand).

Frequency: Estimated from 42 chromosomes of unrelated individuals. Heterozygosity index = 69%. PIC = 0.67.

Allele (bp)	Frequency	Allele (bp)	Frequency
B1 93	0.10	B6 83	0.05
B2 91	0.02	B7 77	0.03
B3 89	0.07	B8 73	0.12
B4 87	0.02	B9 71	0.02
B5 85	0.05	B10 69	0.52

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

Chromosomal Localization: The human non-histone chromosomal protein HMG14 gene has been assigned to chromosome 21 (1). Sub-localization to chromosomal band 21q22.3 was obtained by linkage analysis (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 (GT)₁₉ sequence.

References: 1) Landsman, D. *et al.* (1989) *J. Biol. Chem.* **264**, 3421–3427. 2) Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396. 3) Peterson, M.B. *et al.* (1990) *Genomics* **7**, 136–138. 4) Weber, J.L. *et al.* (1990) *Nucl. Acids Res.* **18**, 4637.