

## Two RFLPs near HOX2@/NGFR at locus D17S444E

J.L.Kennedy, W.G.Honer<sup>1</sup>, C.A.Kaufmann<sup>1</sup>, J.A.Martignetti<sup>2</sup>, J.Brosius<sup>2</sup> and K.K.Kidd<sup>3</sup>  
Clarke Institute of Psychiatry, 250 College St, Toronto, Ontario, M5T 1R8, Canada, <sup>1</sup>Department of Psychiatry, Columbia University, 722 West 168 St, New York, NY 10032, <sup>2</sup>Mount Sinai School of Medicine, One Gustave Levy Pl., New York, NY 10029 and <sup>3</sup>Department of Genetics, Yale University School of Medicine, 333 Cedar St, New Haven, CT 06510, USA

**Source/Description:** Probe WH4 is a 381 bp cDNA fragment isolated from a lambda gt11 expression library made from human brain (temporal cortex). The fusion protein expressed from this cDNA was detected by monoclonal antibody EP10 (1) directed against a synaptic vesicle protein (2).

**Polymorphism:** WH4 detects two RFLPs in genomic DNA digested with the enzymes BglII and MspI:

**BglII polymorphism:**

Allele	Size	Freq. (n = 64 chr.)
A1	6.5Kb	0.11
A2	4.0Kb	0.89

**MspI polymorphism:**

Allele	Size	Freq. (n = 38 chr.)
B1	2.0Kb	0.32
B2	1.0Kb	0.68

**Not Polymorphic For:** BglI, BstEII, BstNI, DraI, EcoRV, HindIII, TaqI, XpnI.

**Chromosomal Location:** 17q21-q22. PCR of a BIOS<sup>TM</sup> somatic cell panel mapped the locus to chromosome 17; linkage analysis gives lod scores > 11 for close linkage with HOX2@ markers.

**Mendelian Inheritance:** Co-dominant inheritance was observed in 7 informative Caucasian families.

**Availability:** Available from Dr.J.L.Kennedy

**Acknowledgements:** This work was supported by the National Alliance for Research in Schizophrenia and Depression (NARSAD) and grants MH30929, MH54212 and MH39239 from the National Institutes of Mental Health, USA.

**References:** 1) Honer, W.G. *et al.* (1989) *Brain Res.* **500**, 379–383. 2) Honer, W.G. *et al.* (1991) *Biol. Psychiatry* (in press).

## A dinucleotide repeat polymorphism at the HOX2B locus

A.S.Deinard, G.Ruano<sup>1</sup> and K.K.Kidd<sup>1</sup>  
Department of Anthropology, and <sup>1</sup>Department of Genetics, Yale University, New Haven, CT, USA

**Source/Description:** The sequence of a 792 bp PstI fragment (EMBL accession no.X57979) 4 kb upstream of HOX2.2 revealed a dinucleotide (CA)<sub>n</sub> repeat located between base pairs 629 and 681 (1). The dinucleotide repeats are interspersed with CC doublets located at positions 637–638, 642–643, 647–648. The repeat is immediately (194 bp) downstream from a 300 bp STS within the PstI fragment (2).

Primer Sequences:	Name	Location
GAAATTGGAAGCCTGGAC (CA strand)	Pyg 8	base pairs 592–610
AGTTCGGGAGTAAAATTCTT (GT strand)	Pyg 1	base pairs 708–728

**Frequency:** Estimated from 31 unrelated Caucasians. Heterozygosity index = 74%. PIC = 70%. The high PIC value of this polymorphism exceeds that of the haplotypes defined by RFLPs in HOX2 (3, 4, 5).

Allele	B1	B2	B3	B4	B5	B6
Size in bp	140	138	136	134	132	130
Frequency	0.016	0.081	0.145	0.290	0.371	0.097

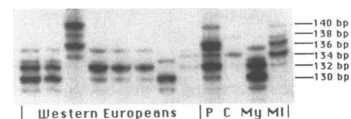
**Mendelian Inheritance:** Co-dominant segregation was observed in one informative (CEPH) family.

**Chromosomal Localization:** The human HOX2 has been mapped to 17q21-q22 (6). This cluster (CA)<sub>n</sub> repeat polymorphism is located ~2 kb downstream from the SacI polymorphism at HOX2B (3) and >20 kb upstream from the RFLPs at the HOX2F and HOX2G (4, 5).

**Other Comments:** The PCR reaction was performed with 1 µg genomic DNA, 0.1 µM each primer, 0.5 U Taq polymerase, 50 µM each nucleotide in 25 µl reaction buffer (50 mM KCl, 3.0 mM MgCl<sub>2</sub>, 10 mM Tris pH 8.4). Amplification was for 15 cycles with the following thermal profile: 1' at 94°C, 1' at 55°C, 1' at 72°C. Subsequently, 5 µCi of alpha-<sup>32</sup>PdCTP was added and amplification continued for an additional 10 cycles. The products were electrophoresed in a 6% acrylamide 8 M urea gel.

**Acknowledgements:** Supported by NIH grant HG 00365 and NSF grant BNS 8813234.

**References:** 1) Ferguson-Smith, A.C. (1989) PhD Thesis, Yale University. 2) Ruano, G. *et al.* (1990) *Nucleic Acids Res.* **18**, 1314. 3) Murphy, P. *et al.* (1987) *Nucleic Acids Res.* **15**, 6311–6312. 4) Ogura, T. *et al.* (1991a) *Nucleic Acids Res.* **19**, 1716. 5) Ogura, T. *et al.* (1991b) *Nucleic Acids Res.* **19**, 1716. 6) Solomon, E. and Barker, D. (1989) *Cytogenet. Cell Genet.* **51**, 319–337.



**Figure 1.** Western Europeans: Caucasians (mixed European ancestry); P: Biaka Pygmy (Central African Republic); C: Native Kampuchean; My: Mayan (Campeche, Mexico); MI: Nasioi Melanesian. Note: There is no example of the 138 bp allele in these 12 individuals.