A *Bgl*III RFLP near the human neurofibromatosis type 1 (NF1) gene

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Source/Description: Cosmid 7G4 spans the *NotI* site distal to the NF1 translocation breakpoint t(17; 22) and is part of an overlapping series of cosmids identified by clone c11-1F10. An 8 kb *Bgl*III fragment (f7G4-GL.2) from cosmid 7G4 detects the *Bgl*III RFLP system.

Polymorphism: *Bgl*III identifies a two-allele polymorphism with fragment sizes of 4.1 (allele G1) and 3.3 kb (allele G2).

Frequency: 101 unrelated individuals typed from a panel of 60 CEPH families show allele frequencies of 0.36 (allele G1) and 0.64 (allele G2) and observed heterozygosity of 0.41 for the *Bgl*III system.

Not Polymorphic For: *Bam*HI, *Eco*RI, *Hind*III, *Pvu*II, *Pst*I, *Rsa*I, and *Taq*I using cosmid 7G4 to probe six unrelated individuals.

Chromosomal Location: The NF1 gene has been mapped to 17q11.2.

Mendelian Inheritance: Co-dominant Mendelian inheritance was observed in 60 reference families (717 individuals) from the CEPH collection.

Availability: The probe is available from L.B.Jorde.

Comments: *Msp*I identifies a 'plus-minus' polymorphism with a 3.6 kb fragment. This fragment was seen in 12 of 82 random individuals.

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References: 1) O'Connell, P. *et al.* (1990) *Genomics* **7**, 547–554. 2) Viskochil, D. *et al.* (1990) *Cell* **62**, 187–192.

Detection of four new *Taq*I alleles with probe St14-1

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The St14-1 probe is a 3 kb *Eco*RI fragment provided by Dr Mandel, derived from the original St14 (Laboratory acronym St14; designated DXS52 in the catalogue of cloned human DNA segments). The genetic locus defined by probe St14 has been located to the distal end of the X chromosome in Xq28 (1). *Taq*I digested human DNA revealed a polymorphic pattern showing 10 allelic fragments (2). We have studied *Taq*I restriction polymorphism with St14-1 probe in 27 females at risk for transmission of hemophilia A, 8 hemophilic males and 13 normal males belonging to 5 non related Spanish families. We have detected 4 new alleles which correspond to 5.0, 4.6, a combination of three fragments 4.6 + 3.6 + 1.2 kb (without the 5.5 kb constant fragment) and 4.3 kb of molecular sizes that we denominated 2B, 3A, 3B and 4A respectively (Table I). We used a non-isotopic hybridization technique employing dUTP-digoxigenine in the probe labelling by random primer and revealed by immunoassaying with a conjugated antibody.

References: 1) Oberlé, I., Camerino, G., Heilig, R., Grunebaum, M.D., Cazenave, J., Crapanzano, C., Mannucci, M. and Mandel, J. (1985) *New Engl. J. Med.* **312**, 682–685. 2) Oberlé, I., Drayna, D., Camerino, G. and Mandel, W. (1985) *Proc. Natl. Acad. Sci. USA* **82**, 2824–2828.

Table I. Molecular size of *Taq*I allelic fragments revealed by the St14 probe.

Alleles	Molecular size (kb)
1	6.6
2	5.4
2A	5.2
2B*	5.0
3	4.8
3A*	4.6
3B*	4.6 + 3.6 + 1.2
4	4.5
4A*	4.3
5	4.1
6	4.0
7	3.9
7A	3.6

(*) new alleles described in our study.

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