

## Dinucleotide repeat polymorphism at the D11S528 locus

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**Source and Description of Clone:** Cosmid 13,1 was from a human chromosome 11q-specific library (1). p13,1-1 a subclone of this cosmid, was sequenced and the sequences flanking a (AC)<sub>17</sub> repeat (EMBL accession number X56995) were used to design PCR primers.

### PCR Primers:

(#42026)-5'-AATGGTGTCCCCACACATGT-3'

(#42027)-5'-TCCTACCTACCGAGCTTAAA-3'

**Polymorphism:** Allelic fragments were detected on DNA sequencing gels. Lengths (nt) were: A1 = 91, A2 = 89, A3 = 87, A4 = 83, A5 = 81, A6 = 79, A7 = 77, A8 = 75, A9 = 73.

**Frequencies:** From 28 unrelated European Caucasians.

A1 = .02	A2 = .02
A3 = .02	A4 = .05
A5 = .02	A6 = .04
A7 = .23	A8 = .05
A9 = .55	

The PIC calculated from these frequencies is 0.60.

**Chromosomal Localization:** Linkage analysis with THY1 (localized to 11q22.3-q23 (2)) in 5 informative CEPH families gave a maximum lod score of 3.2 at  $\theta = .064$ .

**Mendelian Inheritance:** Mendelian inheritance was observed in 5 informative CEPH families with a total 39 children.

**PCR Conditions:** PCR was performed in a total volume of 25  $\mu$ l containing: 50 ng genomic DNA, 5 pmole of each primer, 1.5 mM MgCl<sub>2</sub>, 200  $\mu$ M dNTPs, 50 mM KCl, 10 mM Tris Cl, pH 8.3, 0.6 units of Taq polymerase (Perkin-Elmer/Cetus) and 0.01% gelatin. Primer #42026 was 5' end labeled with <sup>32</sup>P. Amplification was for 35 cycles with denaturation at 94°C for 1 min, annealing at 52°C for 1 min and extension at 74°C for 1 min. Amplified products were resolved on DNA sequencing gels and detected by autoradiography.

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**References:** 1) Lichter, P., Tang, C.C., Call, K., Hermanson, G., Evans, G.A., Housman, D. and Ward, D.C. (1990) *Science* **24**, 64-69. 2) Junien, C. and McBride, O.W. (1989) *Cytogenet Cell Genet* **51**, 226-258.

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## G to A polymorphism in the second exon of the BCL2 gene

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**Source/Description:** Direct sequencing of the PCR products (1) of the BCL2 proto-oncogene revealed a G to A polymorphism at nucleotide position 21 (relative to the start codon) (see Figure). This transition results in no amino acid substitution for threonine, #7 of the BCL2 protein. The region -40 to 221 bp of the BCL2 gene was amplified by PCR with the primers shown below from genomic DNA of 28 normal individuals, 9 lymphoma specimens with t(14;18) chromosomes, and 3 cell lines. To detect the G/A polymorphisms, chemical mismatch analysis (2) was performed using as a probe the PCR product of a plasmid DNA containing a BCL2 genomic insert with the G allele (p18-21H). PCR-mismatch analysis resulted in bands at 262 bp and 200 bp corresponding to the full-length and the cleaved (G-A<sub>21</sub> polymorphism) probes, respectively (see Figure). DNA from heterozygous individuals (A/G) produces a weaker intensity band at 200 bp and can be distinguished from homozygotes (A/A) by densitometry (not shown). All experiments were repeated at least twice with independently derived PCR products.

### Oligomers Used for PCR:

5' AGA GGT ACC GTT GGC CCC CGT TGC 3' (-40)

5' GTC TGC AGC GGC GAG GTC CT 3' (221)

**Frequency:** Estimated from 80 chromosomes:

G-allele 0.49

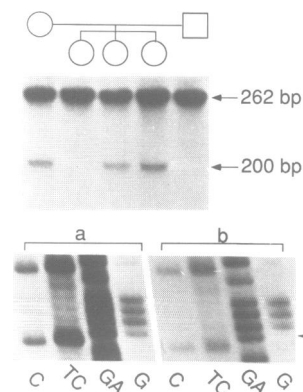
A-allele 0.51

**Chromosomal Localization:** 18q21.

**Other Comments:** Conditions for PCR: 40 cycles consisting of 1 minute at 95°C, 2 minutes at 55°C, and 2 minutes at 72°C.

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**References:** 1) Ohara, O. *et al.* (1989) *Proc. Natl. Acad. Sci. USA* **86**, 5673-5677. 2) Montandon, A.J. *et al.* (1989) *Nucl. Acids Res.* **17**, 3347-3358.



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