

Title	Dinucleotide repeat polymorphism at the D17S518 locus
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Publication date	1991
Original Citation	Couch, F. J., McCarthy, T. V., Gregg, R. G. and Hogan, K. (1991) 'Dinucleotide repeat polymorphism at the D17S518 locus', Nucleic Acids Research, 19(18), p. 5093. doi: 10.1093/nar/19.18.5093
Type of publication	Other
Link to publisher's version	<a href="https://academic.oup.com/nar/article-lookup/doi/10.1093/nar/19.18.5093">https://academic.oup.com/nar/article-lookup/doi/10.1093/nar/19.18.5093</a> - 10.1093/nar/19.18.5093
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Download date	2025-03-20 15:03:21
Item downloaded from	<a href="https://hdl.handle.net/10468/5043">https://hdl.handle.net/10468/5043</a>



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**University College Cork, Ireland**  
 Coláiste na hOllscoile Corcaigh

## Dinucleotide repeat polymorphism at the D17S518 locus

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**Source/Description:** A human genomic Sau3AI/EcoRI fragment was cloned into pBluescript KS+ and selected by hybridisation to poly(dC-dA).poly(dG-dT). The cloned fragment was designated Wis3. Sequencing was performed to determine primer sequences for the polymerase chain reaction. The predicted length of the amplified fragment was 90 bp.

### Primer Sequences:

5' GATCCAGTGGAGACTCAGAG 3' (CA strand);  
5' TAGTCTCTGGGACACCCAGA 3' (GT strand).

**Frequency:** Estimated from 58 chromosomes of unrelated CEPH family members.

Observed heterozygosity = 0.76, PIC = 0.67

Allele (bp)	Frequency	Allele (bp)	Frequency
100	0.017	90	0.328
98	0.086	88	0.310
94	0.259		

**Chromosomal Localization:** Assigned to chromosome 17q11.2-qter by PCR of somatic cell hybrid DNA. Linkage analysis of four CEPH families gave maximum two point LOD scores of 9.82, at  $\theta = 0.023$  with NGFR and 6.25, at  $\theta = 0.036$  with D17S37.

**Mendelian Inheritance:** Co-dominant segregation was observed in four informative two generation CEPH families.

**PCR Conditions:** Amplification was as follows, denaturation at 94°C (3 min), 32 cycles of denaturation at 94°C (1 min), annealing at 54°C (1 min) and extension at 70°C (1 min) using 0.5 U AmpliTaq, 1×GeneAmp buffer and 200 μM dNTPs (Perkin Elmer-Cetus), 100 ng genomic DNA and 10 pmol of each primer in a volume of 15 μl. Allele sizes were determined by comparison to the cloned sequence on 8% denaturing polyacrylamide gels with autoradiography. The sequenced repeat was (GT)<sub>16</sub>. The sequence has been submitted to EMBL data Library. Accession number = X60690.

**Acknowledgements:** This work was supported by a grant from the Department of Veterans Affairs (K.H.), and by EOLAS, the Irish Science and Technology Agency (F.C., T.V.M.).

## Dinucleotide repeat polymorphism at the D8S161 locus

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**Source/Description:** A human genomic Sau3AI fragment was cloned into pBluescript KS+ and selected by hybridisation to poly(dC-dA).poly(dG-dT). The cloned fragment was designated Wis2. Sequencing was performed to determine primer sequences for the polymerase chain reaction. The predicted length of the amplified fragment was 157 bp.

### Primer Sequences:

5' GATCAAGGAGCATCACATCT 3' (CA strand);  
5' TAACATGTCCCCTCATTGG 3' (GT strand).

**Frequency:** Estimated from 56 chromosomes of unrelated CEPH family members.

Observed heterozygosity = 0.75, PIC = 0.77

Allele (bp)	Frequency	Allele (bp)	Frequency
165	0.125	157	0.320
163	0.055	155	0.160
161	0.055	153	0.070
159	0.215		

**Chromosomal Localization:** Assigned to 8q by linkage analysis of CEPH families 1331, 1333 and 1341 which gave maximum two point LOD scores of 12.34 at  $\theta = 0$  with D8S34 and 9.93 at  $\theta = 0$  with D8S28.

**Mendelian Inheritance:** Co-dominant segregation was observed in three CEPH families.

**PCR Conditions:** Amplification was as follows, denaturation at 94°C (3 min), 32 cycles of denaturation at 94°C (1 min), annealing at 51°C (45 sec.) and extension at 70°C (1 min) using 0.5 U AmpliTaq, 1×GeneAmp buffer and 200 μM dNTPs (Perkin Elmer-Cetus), 100 ng genomic DNA and 10 pmol of each primer in a volume of 15 μl. Allele sizes were determined by comparison to the cloned sequence on 8% denaturing polyacrylamide gels with autoradiography. The sequenced repeat was (CA)<sub>21</sub>. The sequence has been submitted to EMBL data Library. Accession number = X60689.

**Acknowledgements:** This work was supported by a grant from the Department of Veterans Affairs (K.H.), and by EOLAS, the Irish Science and Technology Agency (F.C., T.V.M.).

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