Volume 16 Number 1 1988 Nucleic Acids Research

Satellite II DNA of human lymphocytes: tandem repeats of a simple sequence element

Melvyn Hollis and John Hindley[1]

Department of Biochemistry and Molecular Biology, Harvard University, 7 Divinity Ave., Cambridge, MA 02138, USA and [1]Department of Biochemistry, University of Bristol, Medical School, University Walk, Bristol BS8 1TD, UK

Submitted November 10, 1987 Accession no. X06199

A 250bp fragment of satellite II DNA was cloned from sonicated and renatured (Cot=≈1) human lymphocyte DNA. This clone (AB6) was sequenced using standard methods (1). The sequence contains multiple Hinf1 and Taq1 restriction endonuclease sites and corresponds to the simple sequence component (satellite 2) of classical satellite II DNA (2).

```
        1
          C g T T t
G A T T C C A T T t G A T G t T  21
G A T T C C A T T C
G A g T C C A T T C G A T G A T  47
a A T T C C A T T C
G A T T C t t T g C G A T - - -  70
G A T T C C A T T C
c t T T C C A T T t G A - G A T  95
G A T T C C A T T C
G A g a C C A T T C G A T - - -  118
G A T T g C A T T C
a A T T C - A T T C G A T G A c  143
G A T T C g A T T C
a A T T C C g T T C a A T - - -  166
G A T T C C A T T C
G A T T C C A a T t G A T G A T  192
G A T T C C A T T C
G A T T C C A T T t G A T G A T  218
G A T T C C A T g C
G A T T C C A T T C G A T G A T  244
G A c T C C
          250

g a(n)t c       t c g a
 Hinf1           Taq1
```

The sequence presented here consists entirely of tandem repeats of a 26bp element which has been seen in other satellite II sequences such as the 48bp and 59bp genomic sequences of Prosser et al (2) and the pPD17 clone of Deininger et al (3). The 26bp repeating unit is formed from alternating 10bp and 16bp units which have common core consensus of (GATTCCATTC). This core is related to the 5bp repeat unit (ATTCC) of satellite 3 DNA and may be the original segment which was amplified to form the satellite II DNA.

The sequence shown is continuous and is aligned to show the repeating units. Highly conserved bases are indicated by capital letters and deleted bases are shown as hyphens. The Hinf1 and Taq1 sites are shown below the sequence and the numbering refers only to bases sequenced.

REFERENCES

1) Hindley,J. (1982) DNA Sequencing, Laboratory Techniques in Biochemistry and Molecular Biology 10.
2) Prosser,J., Frommer,M., Paul,C. and Vincent,P.C. (1986) J. Mol. Biol. 187, 145-155.
3) Deininger,P.L., Jolly,D.J., Rubin,C.M., Friedmann,T. and Schmid,C.W. (1981) J. Mol. Biol. 151, 17-33.