Volume 16 Number 2 1988 Nucleic Acids Research

Small cytoplasmic *Ro* RNA pseudogene and an *Alu* repeat in the human α-1 globin gene

Jerzy Jurka, Temple F.Smith[1] and Damian Labuda[2]

Bionet, 700 East El Camino Real, Mountain View, CA 94040, [1]Dana-Farber Cancer Institute, Harvard University, 44 Binney Street, Boston, MA 02115, USA and [2]Medical Genetica, Hopital Sainte-Justine, 3175 Cote Sainte-Catherine, Montreal, Quebec H3T 1C5, Canada
Submitted November 6, 1987

The 5'-end of the previously studied *Alu* repeat from the α1-globin gene (1) is flanked by a sequence 80% similar to one of the full length human small cytoplasmic *Ro* RNAs (Fig. 1a), denoted as HY3 (2). This is the first known example of a pseudogene for the *Ro* scRNA. Only a few such pseudogenes are expected to exist in the human genome (2). The pseudogene location next to the *Alu* sequence may suggest physical interactions between HY3-like RNA and the *Alu* RNA prior to the reverse transcription. The 3'-flanking region of the previously studied full size *Alu* repeat is another unreported *Alu* sequence truncated at the *Eco* RI restriction site (Fig. 1b). *In vitro* transcription of the region analysed (1) gave four RNA fragments. One of them, 86 nt long, is synthesized from the short class III transcriptional unit located on the 5'-side of the *Alu* repeat (3). This location coincides with the location of the HY3-like DNA sequence.

```
promoter?    GTGG-CNNAGTGG
HY3          GGCTGGTCCGAGTGCAGTGGTGTTTACAACTAATTGATCACAACCAGTTA    50
             *******| ********|* * *******|********** *********
3'-α1        GGCTGGTTGGAGTGCAGCGCTTTTTACAATTAATTGATCAGAACCAGTTA    52
                                                                    (a)
HY3          CAGATTTCTTTGTTCCTTCTCCACTCCCACTGCTTCACTTGACT-AGCCTTT  101
             |*|**** *|  ***************||******** ****** *****
3'-α1        TAAATTTATCÀTTTCCTTCTCCACTCCTGCTGCTTCAGTTGACTAAGCCTAA  104

promoter     GTGGCNNAGTGG
Alu          GGCCGGGCGCGGTGG-CTCACGCCTGTAATCCCAGCACTTTGGGAGGCCG    49
             **||****|*|**** ****************************|***|
3'-α1        GGTTGGGCACAGTGGCCTCACGCCTGTAATCCCAGCACTTTGGGAAGCCA   471
                                                                    (b)
promoter                                  GGGTTCGANNCC
Alu          AGGCGGGCGGATCACCTGAGGTCAGGAGTTC                       80
             ***|****|******   |*********|***
3'-α1        AGGTGGGCAGATCAC--AAGGTCAGGAATTC                      500
```

Fig. 1. (a) Sequence alignment between HY3 (2) and the corresponding 3'-α1-globin region (1). Putative polymerse III promoter is indicated. (b) Genomic *Alu* consensus (4), aligned to the 3'-α1-globin sequence at positions 423-500. Promoter boxes (5) are indicated. Sequences and numbering of the 3'-α1-globin region are identical to those in (1). Exact matches (*), purine-purine/pyrimidine-pyrimidine replacements (|), and gaps (-) are indicated in both alignments.

REFERENCES

(1) Shen, C.-K.J. and Maniatis, T. (1982) J. Mol. Appl. Gen. **1**, 343-360. (2) Wolin, S.L. and Steitz, J.A. (1983) Cell **32**, 735-744. (3) Hess, J., et al. (1985) J. Mol. Biol. **184**, 7-21. (4) Schmid, C.W. and Shen, C.-K.J. (1985) in Molecular Evolutionary Genetics (McIntyre, R.J. ed.), pp. 323-358. Plenum Publishing. New York. (5) Fowlkes, D.M. and Shenk, T. (1980) Cell **22**, 405-413.