
Partial nucleotide sequence of a 3.4kb fragment from the rat ribosomal DNA nontranscribed spacer

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Submitted 10 June 1986

Two recent papers have reported the sequence of a portion of the nontranscribed spacer (NTS) of rat rDNA (1,2). The region sequenced by both groups extends from the first Eco RI site upstream of the transcription initiation site to a Sau I site which lies ~2.5 kb downstream from that Eco RI site. The two sequences disagree from nucleotides 900 to ~2500. We have sequenced 3.4kb of the rat NTS starting at the same Eco RI site and extending to a Bam HI site at -287, relative to the transcription initiation site. Our sequence essentially agrees with that of Financsek et al.(2). The sequence of the region between nucleotides 900 and 2500 reported by Yavachev et al.(1) is the reverse complement of the consensus sequence derived from ours and that of Financsek et al.(2). Southern blots of rat genomic DNA agree with the restriction enzyme map generated by the consensus sequence, indicating that this sequence represents the major fraction of the rat ribosomal gene repeats. The sequence reported by Yavachev et al. (1) must represent a minor fraction of this gene family. This sequence extends our previous observations (3,4) that the 45S coding region is flanked by highly repetitive sequence elements such as identifier (5) and alu type 2 elements, as well as potential Z DNA sequences. Below is additional sequence, extending from the Sau I site (~2500) reported by Financsek et al.(2) to the Bam HI site. This region includes the site at which the variable region of rat rDNA is found (6) and allows for its placement in the rat ribosomal gene repeat (ca. nt 3145). The sequence is numbered relative to the Eco RI site which was the 5' end of the sequences reported (1,2).

Sau I .
 CCTGAGGGGGTTGGCCCGAGTCCATCCCGCTTCACTGTGTCCCGCGGACAAACCAGGACCSTTTGTGCCATTCGGAGAGGTGGTGGGTACCTG 2660
 CCCCTGTGTGCTGGGTGAGTGTCCCTGTGAGCTAGGGAGGCTCACTCTGGAGAGACGGAATGAGTGTGTGTGGCGCCGCGCGCCTGACAGTCTGTAT 2760
 GGTTTCTGTATCGAGATCGCTGTGCGGCGACACTAGTGGCGCACAGTTTCCGCAACGCTCTGTCCCGGTTGGTGCACAGGAGCGGGAGTGGCT 2860
 GTGGTGGCCCGCCAGGGTGGAGGGGTGACAGCGCAAGCGCGCGGTGCGCGACGAGACGCCCTGTGTCTGGGGACACTCTAGCTAGGAGGTTGTAC 2960
 CTGGAGACTTCAGGGAGGAGGGTGGCTGTACGACCTATTGGGACACAGGAGGGGTTGGTGGCAGCTGGAGAGGCTCGACGAGAGGCTTGGGCCCC 3060
 TCCCAGATTTTTTTTCCAAATTTTTTTTTTAAATTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 3160
 GAGCCATAGACACTTTTGGCCGAGAGGGTGTGTGTCCCGCGCTCGAGCCGAGGTGGCCCGGCTAGGGGGCCGACGAGATTTTTTTTTTTTTTT 3260
 TCTTTTCCAGGAGTCCCTTCGGTCCGAGCCAGCGGACCATAGACACTTTTGGGCGGAGAGGGTGTGTGTGTCCCGCGCTCGAGCCGAGGTGGCCCG 3360
 CTAGGGGGCGCTCCGAGACTTTATTTTTTCCAGG. .Bam HI

1. Yavachev et al. (1986) *Nucleic Acids Res.* 14, 2799-2810.
 2. Financsek et al. (1986) *Nucleic Acids Res.* 14, 3263-3277.
 3. Mroczka et al. (1984) *J. Mol. Biol.* 174, 141-162.
 4. Yang-Yen et al. (1985) *J. Mol. Biol.* 184, 389-398.
 5. Sutcliffe et al. (1984) *Nature*, 308, 237-241.
 6. Chikaraishi et al. (1983) *Nucleic Acids Res.* 11, 6437-6452.
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