

GENE 06583

# Rainbow trout mitochondrial DNA: sequence and structural characteristics of the non-coding control region and flanking tRNA genes

(Fish; *Oncorhynchus mykiss*; mitochondrial genome; displacement-loop; conserved sequence blocks; repeated sequences)

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## SUMMARY

We have determined the sequence of the 1003-bp control region (also referred to as the 'displacement-loop region') and flanking tRNA genes in the mitochondrial DNA (mtDNA) of the rainbow trout, *Oncorhynchus mykiss*. This region has the same overall structure (i.e., *trnT-trnP-control region-trnF*) as in mammalian and amphibian (*Xenopus laevis*) mitochondrial (mt)DNAs. The trout control region contains apparent homologues of the conserved sequence blocks (CSB) and termination-associated sequences identified in all other vertebrate mtDNA control regions; however, it is distinguished by having an imperfect direct repeat (68/73 bp; 77% positional identity) in the right domain (proximal to the phenylalanine tRNA gene), downstream from CSB-3 in the direction of heavy-strand transcription. Within the control region, rainbow trout mtDNA shares considerable sequence similarity with the mtDNAs of Atlantic cod, *Gadus morhua* (Johansen et al., Nucleic Acids Res. 18 (1990) 411-419) and white sturgeon, *Acipenser transmontanus* (Buroker et al., Genetics 124 (1990) 157-163). The highest level of identity in pairwise comparisons is 60-70% over about 80 bp in the right domain (encompassing CSB-2 and CSB-3). About 270 bp comprising the central domain of the control region (encompassing a polypyrimidine tract) are more moderately conserved (55-60% identity in pairwise comparisons), while the left domain is highly divergent. Comparison of five trout mitochondrial tRNA sequences with their human and *X. laevis* homologues emphasizes the strong A+T substitution bias shown by the human sequences.

## INTRODUCTION

A marvel of genetic economy, the vertebrate mitochondrial genome encodes 22 tRNAs, 13 mRNAs and two

rRNAs in a 16.5- to 17.5-kb closed circular molecule (Clayton, 1984; Attardi, 1985). Spacer nt between genes are minimal or absent and certain coding regions even overlap in different reading frames. There is only one substantial noncoding segment, the D-loop region, which encompasses the sites of initiation of heavy-strand replication and both heavy- and light-strand transcription (Chang et al., 1987; Clayton, 1991a,b).

The D-loop (control) region is the most rapidly evolving part of the animal mitochondrial genome (Brown, 1985), with only short stretches conserved among most vertebrates studied. These conserved motifs are of two types: (i) two or three CSB of <30 bp near the origin of replication, in the right domain (nearest the phenylalanine tRNA gene, *trnF*) (Walberg and Clayton, 1981); and (ii) se-

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Abbreviations: aa, amino acid(s); bp, base pair(s); CSB, conserved sequence block(s); D-loop, displacement-loop; kb, kilobase(s) or 1000 bp; mtDNA, mitochondrial DNA; nt, nucleotide(s); Myr, 10<sup>6</sup> years; ORF, open reading frame; *ori*, origin of DNA replication; PP, polypyrimidine tract; PRR, promoter-region repeat(s); TAS, termination-associated nt sequence(s); *tm*, tRNA-encoding gene; *X.*, *Xenopus*.