Nucleotide sequence of a human 5S rRNA gene

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A gene for human 5S rRNA has been cloned and sequenced. The gene was isolated on a 638 bp fragment (Fig. 1) from human placenta DNA by digestion with BamHI and SacI and cloning into a Bluescript M13 plasmid. A ³²P-labelled SP6-transcript of a mouse pseudogene was used as a probe. The fragment has a restriction pattern identical to the pattern of the majority of human 5S rRNA genes, which are found in tandem repeats of 2.3 kb (unpublished results). The gene is transcribed in a HeLa cell extract. Comparative sequence analysis reveals only limited homologies to flanking regions of other eucaryotic 5S rRNA genes. In Fig. 2 is shown the comparison to position -1 to -60of a hamster 5S rRNA gene (1) and the Xenopus laevis somatic and oocyte 5S rRNA genes (2, 3). The A and G at positions -15and -14, which are conserved between human and Xenopus, is part of a Xenopus element suggested to bind an upstream stimulatory factor (4).

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Figure 1. Nucleotide sequence of the cloned fragment. The 5S rRNA gene is underlined.

	-60	-50) ·	-40	-30	-20	-1()
Hum	GCAATC	CGGCGGGGCA	CGGCCGGG	SCGGGGCTC	GGCTCTT	GGGGCAGC(CAGGCGCCT	CCTTCAGC
Ham	G C	Gecgege	6 C 6	6 G		66 (C G C	CC C C
Xls	GCA	6 6 GC	GGCC	66	6	66	AG C C	TC
Xlo	CA T		C G	CG G	G	GC	AG C	ttca c
Xlt	GCA T	A	C	CG	66 C	GGC	AG C	CTTCA C
Ham*	GC	Gecegec	G G	GC G	GGCTCTT	GEGEC GC	6CG C	C C 6C
	(-60)	(-50)	(-40)	(-3	0) (·	-20)	(-10)

Figure 2. Sequence homology between 5' flanking regions of the human 5S rRNA gene, a hamster 5S rRNA gene (1) and *Xenopus laevis* somatic, oocyte and trace oocyte 5S rRNA genes (2, 3). The asterisk indicates that the 5'-flanking region of the hamster sequence has been shifted four nucleotides relative to the human 5S rRNA gene sequence.