The genes for U6 small nuclear RNA in *Tetrahymena* thermophila are repeated in tandem

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U6 RNA is the most highly conserved spliceosomal RNA involved in pre-mRNA splicing (1). The U6 RNA gene of fission yeast *Schizosaccharomyces pombe* was found to have an mRNA-type intron (2). A consideration of the origin of the U6 intron led to interesting possibility of a catalytic role of U6 RNA in pre-mRNA splicing (3, 4). To investigate whether there are U6 RNA genes which have an intron at the same site as the *S. pombe* U6 RNA gene does, we analyzed U6 RNA genes of 52 organisms by the polymerase chain reaction using primers corresponding to highly conserved regions of U6 RNA (4). In the course of this analysis, we observed two amplified products from the DNAs of *Tetrahymena thermophila*, horseshoe crab and *Drosophila melanogaster*. The size of the smaller amplified product (52 bp) detected in each DNA was identical to that of the amplified product from the U6 RNA gene with no intron (4).

Here, we report the complete nucleotide sequence of the larger amplified product (418 bp) observed in *Tetrahymena* DNA. The larger product contains two U6 RNA genes 264 bp apart from each other, showing that this amplified product was produced due to the tandem repetition of the genes. In a spacer region between two *Tetrahymena* U6 RNA genes, a TATA box-like sequence is found 22 bp upstream of the downstream U6 gene.

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10	2.0	30	40 GGCCCCTGCA	50	60
AAATTGAAAC	GATACAGAGA	AGATTAGCAT	GGCCCCTGCA	CAAGGATGAC	ACGCTCAAAG
***** ***	*******	*******	*******	*******	**** ****
AAAUUGGAAC	GAUACAGAGA		GCCCCUGCG	CAAGGAUGAC	ACGCACAAAU
U6 RNA gene 1					
70				110	
CAGAAGGATT * *	CCCCATTTTT ** * ****	TTTTCTAATT	TTTTATAATT	AGAATAAAAA	AGAAAATTAC
CGAGAAAUGG	UCCAAAUUUU				
130	140	150	160	170	180
ATTTAAATAA	AAATGATTAA	AATAATTTTA	AAGTTAAATT	AAACATTAAC	TATTAATAAA
190	200	210	220	230	240
GAATATAAAA	ТААААТАТАА	ATAAGTTTTC	AGTTAATTTT	ттстаааата	асааааатаа
250	260	270	280	290	300
AATAGATACA	CACTTGTTAG	AATTAAAATG	ATAATCTTTA	AGACCCATAA	AAAAAATATA
310	320	330	340 AATTTACATA	350	360
AGATAATTAA	ACTTCTTTAT	AAGCTTTAGT	AATTTACATA	GATTGGACAC	CCGAAGCTAT
				* *	** * **
				GUCCCU	UCGGGGACAU
270	280	300	¥ 400	410	
CCCTTRN 2 2 2	TECANCENTA	CACATA AGAT	400 TAGCATGGCC	CCTGCACAAG	GATGACAC
*** *****	*******	********	*********	***** ****	*******
CCGAUAAAAU	UGGAACGAUA	CAGAGAAGAU	UAGCAUGGCC	CCUGCGCAAG	GAUGACAC

The longer amplified product was subcloned into M13mpl8 and sequenced by the dideoxy method. The 5' and 3' ends of the *Tetrahymena* U6 RNA genes were tentatively assigned by a comparison with the tomato U6 RNA sequence (5). The upper line shows the non-coding strand sequence of the *Tetrahymena* U6 RNA gene. The lower line shows the sequence of the tomato U6 RNA. The TATA box-like sequence is boxed. The vertical arrowheads indicate the position of the intron present in the *S. pombe* U6 RNA gene. The regions corresponding to the primers used for PCR are represented by solid and dotted arrows over the sequence. The directions of the arrows coincide with that of primers (5' to 3'). The smaller product was amplified with primers represented by the solid and dotted arrows. The larger product was amplified with primers indicated by the solid arrows.

U6 RNA gene 2