
Nucleotide sequences of 5S rRNAs from four jellyfishes

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ABSTRACT

The nucleotide sequences of 5S rRNAs from four jellyfishes, *Spirocodon saltatrix*, *Nemopsis dofleini*, *Aurelia aurita* and *Chrysaora quinquecirrha* have been determined. The sequences are highly similar to each other. A fairly high similarity was also found between these jellyfishes and a sea anemone, *Anthopleura japonica*.

INTRODUCTION

The Coelenterata, the phylum for the acceptance of jellyfishes and sea anemones, has been considered from anatomical evidence as a link of diblastic and triblastic animals. This phylum has been usually divided into three classes: the Hydrozoa containing primitive jellyfishes, the Scyphozoa containing more advanced jellyfishes, and the Anthozoa containing sea anemones. To deduce the phylogenic position of this phylum and to examine the validity of the above mentioned intraphylum classification, the 5S rRNA sequences from two hydrozoan jellyfishes and two scyphozoan jellyfishes have been determined and compared with those from a sea anemone and other eukaryotes as described previously (1).

MATERIALS AND METHODS

Two hydrozoan jellyfishes (*Spirocodon saltatrix* and *Nemopsis dofleini*) and two scyphozoan jellyfishes (*Aurelia aurita* and *Chrysaora quinquecirrha*) used in this study were collected at an area of the Seto Inland Sea near the Usimado Marine Laboratory, Okayama University. The 5S rRNAs were directly isolated from ovaries by the phenol method followed by gel electrophoresis as previously described (2). The sequence was analysed by the chemical method of Peattie (3) or the enzymatic method of Donis-Keller (4) and Delihias et al. (5) using 3' or 5'-end labeled 5S rRNAs. The 3'- and 5'-terminal bases were determined by the TLC plate analysis (2).

RESULTS

The nucleotide sequences were determined by the method involving chemical degradation of [3'-³²P] RNA (3). Three to 10 residues from the 5'-terminus were established or confirmed by the enzymatic methods using [5'-³²P] RNA (4, 5). The 5S rRNA primary sequences from the four jellyfishes so obtained are shown in Fig. 1, together with those from a sea anemone (2) and a sea urchin (6) for comparison.

The secondary structure of the *Chrysaora*, the *Spirocodon* and the *Nemopsis* 5S rRNAs was essentially the same as the previously proposed structure for the 5S rRNAs of other multicellular animals (2), where an A/C mismatch in the D-D' stem could be recognized (Fig. 1). However, the *Aurelia* 5S rRNA could have a bulge of one A, instead of the A/C mismatch, in the D-D' stem, which consisted of 9 base pairs (usually 8 in other multicellular animals).

DISCUSSION

The relatedness among the members of the Coelenterata deduced from the sequence similarity (Table 1) is consistent with the classification of this phylum with anatomical criteria. The jellyfish 5S rRNAs examined here are

	1			2			3			4			5		
	123456789	012345	678901	2345678	9012	345678901234	5678	90123456							
<i>Spirocodon</i>	GUCUACGGC	CAUACC	ACGAUG	AAUACAC	CGGU	UCUCGUCCGAUC	ACCG	AAGUUAAG							
<i>Nemopsis</i>	GUCUACGAC	CAUACC	ACAAUG	AACACAC	CGGU	UCUCGUCCGAUC	ACCG	AAGUUAAG							
<i>Aurelia</i>	GCCUACGAC	CAUACC	ACCAUG	AAUACAC	CGGU	UCUCGUCCGAUC	ACCG	AAGUUAAG							
<i>Chrysaora</i>	GCCUACGAC	CAUACC	ACCAUG	AGUAUAC	CGGU	UCUCGUCCGAUC	ACCG	GAGUCAAG							
Sea anemone	GUCUACGGC	CAUACC	ACCGGG	AAAAAAC	CGGU	UCUCGUCCGAUC	ACCG	AAGUCAAG							
Sea urchin	GCCUACGAC	CAUACC	AUGCUG	AAUAUAC	CGGU	UCUCGUCCGAUC	ACCG	AAGUCAAG							
	A	aLb	B	bLc	C	cLc'	C'	c'Lb							

	6		7		8		9		1		1		1	
	789012	345	6789012	34567	8901234567890123456789	012	3456789	012345678901	012	3456789	012345678901	012345678901	012345678901	012345678901
	CAUUGU	CGG	GCCAGGA	UAGUA	CUUGGAUGCGGGA	CCG	CCUGGG	AAC	UCCUGGU	GCCGUAGACUUU				
	CAUUGU	CGG	GCCAGGA	UAGUA	CUUGGAUGCGGGA	CCG	CCUGGG	AAC	GCCUGGU	GUCGUAGACUUU				
	CAUGGU	CAG	GCCGGGU	CAGUA	CCUGGAGUGGUGA	CCG	CCUGGG	AAC	ACCCGGU	GUUGUAGGCCU				
	CAUGGU	CGG	GCCGGGU	CAGUA	CCUGGAGUGGUGA	CCG	CCUGGG	AAC	ACCUGGU	GUUGUAGGCCU				
	CCCGGU	AGG	GCCAGGU	UAGUA	CUUGGAUGCGGUGA	CCG	CCUGGG	AAU	ACCUGGU	GCUGUAGACUU				
	CAGCAU	AGG	GCUCGGU	UAGUA	CUUGGAUGGGAGA	CCG	CCUGGG	AAU	ACCCGGU	GUUGUAGGCCU				
	B'		E	eLd	D	dLd'	D'		E'	A'				

Fig. 1. Comparison of the 5S rRNA sequences from four jellyfishes (*Spirocodon saltatrix*, *Nemopsis doyleini*, *Aurelia aurita* and *Chrysaora quinquecirrha*), sea anemone (2) and sea urchin (6). The squared off sequences (A, A', B, B', etc. in the lowest line) are possibly involved in base pairing in the secondary structural model (1, 2). The symbols aLb, bLc, etc. are for loop regions.

Table 1. Similarity matrix of the 5S rRNAs from eukaryotes.

SPI	DOF	AUR	CRY	SAN	SUR	LAN	NEM*	BPL	ART*	VER*	PRO*	FUN*	PLA*	
SPI	93	86	86	87	82	88	70	82	79	79	68	62	62	(<i>Spirocodon</i>)
DOF	93		86	86	84	82	87	82	77	77	67	63	64	(<i>Nemopsis</i>)
AUR	86	86		93	83	83	83	86	80	79	66	62	64	(<i>Aurelia</i>)
CRY	86	86	93		85	86	83	85	82	80	65	62	64	(<i>Chrysaora</i>)
SAN	87	84	83	85		84	87	80	77	80	65	64	65	(Sea anemone)
SUR	82	82	83	86	84		84	76	87	83	81	66	63	(Sea urchin)
LAN	88	87	83	83	87	84		76	89	83	80	66	63	(<i>Lingula</i>)
NEM*	70	71	71	71	68	76	76		79	71	73	62	60	(Nematodes)
BPL	82	82	86	85	80	87	89	79		83	79	63	63	(Rotifer)
ART*	79	77	80	82	77	83	83	71	83		76	64	59	(Arthropods)
VER*	79	77	79	80	80	81	80	73	79	76		64	60	(Vertebrates)
PRO*	68	67	66	65	65	66	66	62	63	64	64		58	(Protozoa)
FUN*	62	63	62	62	64	63	63	60	63	59	60	58		(Fungi)
PLA*	62	64	64	64	65	64	64	60	64	61	63	61	56	(Plants)

* The mean similarity values calculated from the sequences of 3 nematodes (NEM), 4 Arthropoda species (ART), 20 vertebrates (VER), 10 protozoans (PRO), 10 fungi (FUN) and 15 plants (PLA). For the sources of the sequences see ref. of (7) and (2).

highly similar to each other: 93% identity between *Spirocodon* and *Nemopsis* both belonging to the class Hydrozoa, 93% between *Aurelia* and *Chrysaora* both belonging to the class Scyphozoa, and 86% between the Hydrozoa and Scyphozoa. The jellyfish sequences examined here are also considerably similar (85%) to that of a sea anemone, *Anthopleura japonica*, that belongs to the Anthozoa, another class of the Coelenterata. The similarity between jellyfishes and the sea anemone is slightly less than that among the four jellyfishes.

The jellyfishes 5S rRNA sequences are related to a similar extent to the sequences of sea urchin (82-86% identity, 83% on average), the Arthropoda (72-86%, 77% on average) and the Vertebrata (73-83%, 79% on average), and are less to those of the Nematoda (70-71%), protozoa (67% on average), fungi and plants (63% on average). This would suggest that the ancestors of the Coelenterata, the Echinodermata, the Arthropoda and the Vertebrata emerged within a relatively short period after the emergence of protozoa, fungi and plants, and evolved to different directions.

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