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Ascidian Homologs of Mammalian Thyroid Transcription Factor-1 Gene Are Expressed in the Endostyle

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ABSTRACT—The endostyle is a special organ in the pharynx of urochordates, cephalochordates and cyclostomes. During evolution of the primitive chordates, the endostyle was organized in their common ancestor(s) with a shift to internal feeding for extracting suspended food from the water. In addition, the endostyle has an iodine-concentrating activity and is therefore thought to be functionally homologous to the vertebrate thyroid gland. Human \textit{TITF1} and mouse \textit{titf1} are members of the \textit{Nkx-2.1/TTF-1} gene subfamily, which encode an NK-2 type homeodomain transcription factor. The genes are expressed in the thyroid gland and are essential for thyroid-specific structural gene expression. In the present study, we isolated cDNA clones for ascidian homologs of \textit{titf1} from \textit{Halocynthia roretzi} and \textit{Ciona intestinalis}, and examined whether the genes are expressed in the ascidian endostyle. Results clearly indicated that both the \textit{H. roretzi} homolog \textit{Hrtitf1} and the \textit{C. intestinalis} homolog \textit{Cititf1} are expressed specifically in the endostyle. The present finding therefore provide molecular evidence for the functional relationship between the ascidian endostyle and vertebrate thyroid gland. However, the genes are expressed in the supporting element regions but not in the putative iodine-concentrating regions of the endostyle.

INTRODUCTION

We are interested in molecular developmental mechanisms underlying the evolution of chordate body plan. The phylum Chordata consists of the subphyla Urochordata (tunicates), Cephalochordata (amphioxus) and Vertebrata. Chordates are categorized as deuterostomes, together with two other non-chordate invertebrate groups, echinoderms and hemichordates, as supported by molecular phylogenetic studies (Wada and Satoh, 1994; Turbeville \textit{et al.}, 1994) as well as cladistic analysis (Schaeffer, 1987; Peterson, 1995). Chordates share several characteristic features including a notochord, a dorsal hollow nerve cord, and pharyngeal gill slits (e.g., Brusca and Brusca, 1990; Willmer, 1990; Nielsen, 1995; Gee, 1996). In addition, lower chordates including tunicates, amphioxus and larval lampreys share an endostyle. These are hallmarks of the chordate body plan. Therefore, investigations of molecular developmental mechanisms involved in the organization of these structures are of salient importance in attempts to understand the evolution of chordate body plan.

We have emphasized that these characteristic features of chordates seem to have evolved with the emergence of tadpole larva-like creatures (Satoh and Jeffery, 1995; Satoh, 1995). Coincidently with this change in the mode of larval locomotion, most of the primitive chordates or chordate ancestors shifted their feeding system to the use of the pharyngeal gill slits for extracting suspended food from the water and the endostyle for secreting mucus to catch the food particles. The ascidian endostyle forms a trough-shaped structure in the ventral wall of the pharynx which extends from the fore-part of pharynx to the esophagus (see Fig. 4C; Ogasawara \textit{et al.}, 1996 and references therein). The cells of this organ are differentiated into eight or nine strips or zones that run parallel to one another in longitudinal orientation. The cells of each zone are highly specialized in morphology and function (Barrington, 1957, 1958; Fujita and Nanba, 1971; Thorpe \textit{et al.}, 1972; Dunn, 1974, 1980). Because the cells of zones 7, 8 and 9 have an iodine-concentrating activity, as do the thyroid cells of higher vertebrates, the endostyle of lower chordates is commonly considered a homolog and primitive antecedent of the vertebrate thyroid gland (e.g., Barrington, 1957; Thorpe \textit{et al.}, 1972; Dunn, 1974, 1980).

In previous studies, to obtain insights into the molecular mechanisms responsible for the formation and function of the endostyle, we isolated cDNA clones for the endostyle-specific genes \textit{HrEnds1} and \textit{HrEnds2} from the ascidian \textit{Halocynthia roretzi} (Ogasawara \textit{et al.}, 1996) and \textit{CiEnds1}, \textit{CiEnds2}, and \textit{CiEnds3} from the ascidian \textit{Ciona intestinalis} (Ogasawara and Satoh, 1998). All of these genes encode
secreted proteins. Interestingly, \( Hr\text{Ends}2 \), \( Cl\text{Ends}1 \) and \( Cl\text{Ends}2 \) are expressed in zone 6 and encode similar secreted proteins, suggesting a molecular marker commonly used to monitor the ascidian endostyle differentiation. Because these genes encode structural proteins, we next focus on ascidian homologs of transcription factor genes that are expressed in the thyroid cells of higher vertebrates. The \( Nkx\text{-}2.1/\text{TTF-1} \) genes \( TITF1 \) (human) and \( titf1 \) (mouse) belong to the family of NK-2 type homeobox containing genes (Harvey, 1996). They are involved in the thyroid-specific gene expression (Civitareale et al., 1993) and organogenesis of the thyroid (Kimura et al., 1996). In the present study, we investigated whether ascidian homologs of the thyroid-specific transcriptional factor gene \( Nkx\text{-}2.1/\text{TTF-1} \) are expressed in the endostyle. Our results clearly indicated that the ascidian homologs of \( Nkx\text{-}2.1 \) are expressed specifically in the endostyle.

**MATERIALS AND METHODS**

**Biological materials**

Adults and juveniles of \( H. \text{roretzi} \) and \( C. \text{intestinalis} \) were collected near the Otsuchi Marine Research Center, Ocean Research Institute, University of Tokyo, Iwate, and the Marine BioSource Education Center of Tohoku University, Onagawa, Miyagi, Japan. After the dissection of adult specimens, tissues and organs were fixed for *in situ* hybridization or quickly frozen in liquid nitrogen and kept at -80°C until use.

**Isolation of RNAs**

Total RNA was extracted from various organs including the endostyle, pharyngeal gill, body wall muscle, intestine, gonad, and digestive gland of \( H. \text{roretzi} \) and \( C. \text{intestinalis} \) by the AGPC method (Chomczynski and Sacchi, 1987). Poly(A)^+ RNA was purified with oligotex dT30 beads (Roche Japan, Tokyo).

**RT-PCR amplification**

Reverse-transcription (RT) was carried out using \( H. \text{roretzi} \) endostyle Poly(A)^+ RNA with hexanucleotide mix (Boehringer Mannheim, Heidelberg, Germany). After purification of the cDNA, degenerated polymerase chain reaction (PCR) was performed using two degenerated primers. In order to amplify the DNA fragment of NK-2 type homeodomain, we screened the \( H. \text{roretzi} \) endostyle cDNA library with this DNA fragment as the probe, and obtained candidate cDNA clones. The PCR conditions were 30 cycles of 94°C for 1 min, 50°C for 2 min, and 72°C for 30 sec for both rounds.

**Isolation and sequencing of cDNA clones for an ascidian \( titf1 \) gene**

The DNA fragment isolated by RT-PCR was subcloned into the EcoRV site of the vector pBluescript II SK(-). cDNA clones for \( H. \text{roretzi} \) \( titf1 \) (Hrtitf1) were obtained by screening the \( H. \text{roretzi} \) endostyle cDNA library with this DNA fragment as the probe. Plaques which showed positive hybridization were selected and isolated by two rounds of screening. The specificity of the clones positive for the endostyle was confirmed by a Northern blot analysis. The clones were prepared for sequencing by controlled nested deletion from either the T3 or T7 side and sequenced using the ABI PRISM 377 DNA Sequencer (Perkin Elmer, Norwalk, CT, USA). The isolation and characterization of cDNA clones for \( C. \text{intestinalis} \) \( titf1 \) (Cititf1) were reported elsewhere (Ristoratore et al., submitted).

**Northern blot analysis**

The Northern blot hybridization was carried out by the standard procedure (Sambrook et al., 1989), and the filters were washed under high-stringency conditions. DNA probes for blot hybridizations were labeled with [\(^{32}\)P]-dCTP using a random primed labeling kit (Boehringer Mannheim).

**In situ hybridization**

Tissues of \( H. \text{roretzi} \) and \( C. \text{intestinalis} \) were fixed in 4% paraformaldehyde in 0.5 M NaCl, 0.1 M MOPS buffer at 4°C for 12 hr. For the young adult \( H. \text{roretzi} \), the tunic was stripped off with a razor-knife prior to fixation as above. In the case of young adult \( C. \text{intestinalis} \), the specimens were treated with L-menthol seawater to induce relaxation of the body-wall muscle, and then the tunic was stripped off with tungsten needles in the fixation buffer. Probes were synthesized by following the instructions from the kit supplier (DIG RNA Labeling Kit; Boehringer Mannheim). The *in situ* hybridization of whole-mount specimens was carried out basically as described previously (Ogasawara et al., 1996). For the *in situ* hybridization of sectioned specimens, samples were dehydrated with a graded series of alcohol, embedded in polyether wax (BDH) and sectioned at 10 μm.

**RESULTS**

**Isolation and characterization of cDNA for \( Hr\text{titf1} \) of \( Halocynthia roretzi \)**

With the aid of the conserved NK-2 type homeodomain sequence of \( Nkx\text{-}2.1/\text{TTF-1} \), we amplified a target fragment from the adult endostyle poly(A)^+ RNA by RT-PCR. After confirming that the fragment contained the predicted sequence of the NK-2 type homeodomain, we screened the \( H. \text{roretzi} \) endostyle cDNA library (Ogasawara et al., 1996) with the fragment as a probe, and obtained candidate cDNA clones.

Fig. 1 shows the nucleotide and predicted amino acid sequences of cDNA for the \( H. \text{roretzi} \) \( Hr\text{titf1} \) gene. The nucleotide sequence will appear in the DDBJ, EMBL, and GenBank Nucleotide Sequence Databases under Accession No. AB017704. The sequence of the cDNA encompassed 2,820 bp including 19 adenyl residues at the 3’ end. The ATG at the position 144-146 represented the putative start codon of the \( Hr\text{titf1} \)-encoding protein. The cDNA contained a single open reading frame, which predicted the \( Hr\text{TTF-1} \) protein of 557 amino acids. The molecular mass of \( Hr\text{TTF-1} \) was calculated to be 60,038. A data base search indicated that the polypeptide contained the TN domain at amino acid position 15-25, the homeodomain at 276-335, and the NK-2 domain at 415-432, respectively (Fig. 1).

**Characterization of \( Hr\text{TTF-1} \)**

The NK type homeobox genes were first cloned from *Drosophila* (Kim and Nirenberg, 1989), and four *Drosophila* genes so far isolated include \( NK1 \) (Dohrmann et al., 1990), \( NK2 \) (Jimenez et al., 1995), \( NK3 \) (Azpiazu and Frasch, 1993), and \( NK4 \) (Bodmer, 1993). The products of these genes were later classified into the two homeodomain protein classes, NK-1 (containing NK1) and NK-2 (containing NK2 to NK4) (Burglin, 1993). NK-2 homeobox genes were isolated from various organisms (Harvey, 1996). At least five members of this family were isolated from mouse, including *TTF-1/Nkx-2.1* (Oguchi
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et al., 1995), Nkx-2.2 (Price et al., 1992), and Nkx-2.5 (Lints et al., 1993). To identify subfamily to which HrTTF-1 belongs, we compared amino acid se-
quences of the HrTTF-1 TN domain (Fig. 2A) and homeodomain (Fig. 2B) with those of other Nkx-2 family mem-
ers. First, it was noted that NK-2 type homeodomains (those of mouse Nkx-2.1, Nkx-2.2, Nkx-2.3 and Nkx-2.5, and Droso-
phila NK2, NK3 and NK4) share a tyrosine residue at position 54 within this domain. As was evident in Fig. 2B, the amino
acid residue at position 54 of the HrTTF-1 homeodomain is tyrosine (arrow). This strongly suggests that HrTTF-1 is a
member of the NK-2 family.

The amino acid sequences of the TN domain of HrTTF-1
was identical to that of CiTTF-1 (TTF-1 of
C. intestinalis, see below; Fig. 2A; the Accession No. AJ009607). The grade of
identity of this domain was about 90% between the ascidian
(HrTTF-1 and CiTTF-1) and mammalian TTF-1/Nkx-2.1. How-
ever, the grade was relatively low between the ascidians and
mammalian Nkx-2.2, Nkx-2.3 and Nkx-2.5. This suggests that
HrTTF-1 is related to the Nkx-2.1 family.

A similar relationship was evident when we compared
the amino acid sequences of the homeodomain (Fig. 2B). Only
two amino acid residues were different between HrTTF-1 and
CiTTF-1, the identity being 97%. In addition, the degree of
identity of this domain was 90% between the ascidian
HrTTF-1 and mammalian TTF-1/Nkx-2.1 (Fig. 2B). However,
the identity decreased when compared between the ascidian
HrTTF-1 and mouse Nkx-2.2 (83%), Nkx-2.3 (82%) or Nkx-
2.5 (78%). Furthermore, the degree of identity of this domain
was about 82% between the ascidian HrTTF-1 and
Drosophila NK2, but the degree was relatively low when compared
with NK3 (65%), NK4 (65%), and NK1 (50%). This strongly
suggests that HrTTF-1 and CiTTF-1 are members of the Nkx-
2.1 family.

To test the above-mentioned results, we performed a mole-
cular phylogenetic analysis. Using 60 confidently aligned
sites of the homeodomain amino-acid residues, a molecular
phylogenetic tree was constructed by the neighbor-joining

Fig. 1. Nucleotide and predicted amino acid sequences of cDNA for Hrtitf1 of Halocynthia roretzi. The sequence of the cDNA encompasses 2,820 bp including 19 adenylyl residues at the 3' end. The ATG at the position 144-146 represents the putative start codon of the Hrtitf1-encoding protein. An asterisk indicates the termination codon. The TN domain at amino acid portion 15-25 is double-underlined, the homeo domain at 276-335 is boxed, and the NK-2 domain at 415-432 is underlined. The nucleotide sequence will appear in the DDBJ, EMBL, and GenBank Nucleotide Sequence Databases under Accession No. AB017704.
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As shown in Fig. 3, the ascidian HrTTF-1 and CiTTF-1 form a discrete group with vertebrate Nkx-2.1 (mouse TTF-1/Nkx-2.1, human TTF-1/Nkx-2.1 and dog Nkx-2.1). This grouping was supported by the bootstrapping value of 57%. In addition, this group was included in a larger clade with Drosophila NK2, mouse Nkx-2.2 and C. elegans CEH-22. This larger clade was supported by the bootstrapping value of 89%. From this data together with the results mentioned above, we concluded that HrTTF-1 and CiTTF-1 are members of the Nkx-2.1 family.

Hrtitf1 is expressed in the endostyle

The ascidian endostyle forms a trough-shaped structure in the ventral wall of the pharynx and extends from the forepart of the pharynx to the esophagus (Fig. 4C). The in situ hybridization of whole-mount specimens demonstrated that the Hrtitf1 signal was specific to the endostyle (Fig. 4A, B). No signal was detected in organs and tissues other than the endostyle. This was confirmed by Northern blot analysis. As shown in Fig. 4F, a distinct band of 2.8 kb was found in the endostyle. Although a very weak band was seen in the digestive gland (hepatopancreas), the signal was undetectable in the gonad, intestine, body-wall muscle and pharyngeal gill (Fig. 4F).

The endostyle cells are differentiated into eight or nine strips or zones and the cells of each zone are highly specialized in morphology and function (Fig. 4C; Barrington, 1957; Thorpe et al., 1972; Dunn, 1974, 1980). The cells of zones 7, 8 and 9 have an iodine-concentrating activity, as do the thy-
roid cells of higher vertebrates. The cells of zones 2, 4 and 6 have numerous secretory granules. These cells are believed to secrete the proteins or mucoprotein related to the digestion of food. The cells of zones 1, 3 and 5 are supporting elements and also as elements that might play a role in catching and transporting food. The \textit{in situ} hybridization of sectioned specimens demonstrated that the signal was not distributed over the entire area of the endostyle rather restricted to several zones (Fig. 4D, E). The \textit{Cititf1} transcript was evident in the entire region of zones 1, 3 and 5 (Fig. 4D), and in basement region of the zone 6 (Fig. 4D, E). No signal was detected in zones 2, 4, 7, 8, and 9 (Fig. 4D, E).

**\textit{Cititf1} is also expressed in the endostyle**

The isolation and characterization of a cDNA clone for \textit{Cititf1} of \textit{C. intestinalis} will be described in detail together with their expression pattern during \textit{Ciona} embryogenesis, and experiments to deduce its function (Ristoratore \textit{et al.}, submitted). The present analysis of CiTTF-1 (Figs. 2 and 3) clearly indicated that CiTTF-1 is also a member of the Nkx-2.1 family.

The \textit{in situ} hybridization of whole-mount specimens of a 1-month-old young adult \textit{C. intestinalis} demonstrated that the signal was evident in the endostyle (Fig. 5A). No signal was detected in organs and tissues other than the endostyle. The Northern blot analysis supported this result. As shown in Fig. 5D, a distinct band of 2.7 kb was found in the endostyle. The \textit{Cititf1} transcript was not found in the zones 7, 8, and 9 (Fig. 5B, C) with iodine-concentrating activity.

The \textit{in situ} hybridization of sectioned specimens demonstrated that the signal was restricted to several zones of the endostyle (Fig. 5B, C). The \textit{Cititf1} transcript was found in the entire region of zones 3 and 5 (Fig. 5B), and in part of the regions of zones 1, 2 and 6 (Fig. 5B, C). As was the case for \textit{Hrtitf1}, \textit{Cititf1} transcript was not found in the zones 7, 8, and 9 (Fig. 5B, C) with iodine-concentrating activity.
DISCUSSION

The present study investigated ascidian homologs of the transcription factor gene TTF-1/Nkx-2.1, which is expressed in the thyroid gland of higher vertebrates (human, Saiardi et al., 1995; mouse, Oguchi et al., 1998; dog, Van Renterghem et al., 1995; rat, Oguchi and Kimura, 1972; Dunn, 1974) and thyroperoxidase activity (Fujita and Kessel, 1998). We isolated cDNA clones for the H. roretzi gene Hrtitf1 and the C. intestinalis gene Cititf1. Both genes have a typical NK-2 type homeodomain (Fig. 2B) and are classified as members of the TTF-1/Nkx-2.1 family. The Northern blotting of adult tissues (Figs. 4F and 5D) and whole-mount in situ hybridization (Figs. 4A, 4B and 5A) clearly showed that the transcripts are present only in the endostyle. These results provide molecular evidence that the ascidian endostyle is homologous to the vertebrate thyroid gland.

The in situ hybridization of sectioned specimens showed that transcripts of Hrtitf1 are detected in the entire regions of zones 1, 3 and 5, and in part of the zone 6. The Cititf1 transcript is also expressed in the entire regions of zones 3 and 5, and in part of the zones 1, 2 and 6. As was mentioned above, zones 7, 8 and 9 are thought to be homologous to the thyroid cells of higher vertebrates, because the zones have an iodine concentrating activity (Thorpe et al., 1972; Dunn, 1974) and thyroperoxidase activity (Fujita and Sawano, 1979). Interestingly, both Hrtitf1 and Cititf1 were not expressed in these zones with iodine-concentrating activity. Instead, Hrtitf1 was expressed primarily in the supporting zones and mucus secretion zones.

During the evolution of chordates, their ancestor(s) may have obtained an internal feeding system, using the pharyngeal gill slits and endostyle for extracting suspended food from the water. The endostyle of ascidians and amphioxus consists of two different regions, a mucus-secretory region and an iodine-concentrating region. The endostyle of larvae of cyclostomate lamprey has several cell types including protein secretory cells and iodine-concentrating cells (Fujita and Honma, 1968). During metamorphosis, the endostyle loses the protein secretory cells and transforms into the thyroid gland (Wright and Youson, 1976). The endostyle is therefore a key structure for clarifying not only the origin of chordates, but also the evolution to the thyroid gland of higher vertebrates. As shown in this study, Hrtitf1 and Cititf1 were not expressed in the region with iodine-concentrating activity but rather were expressed primarily in the supporting region and mucus secretion region as well. Therefore, further examinations of the pattern of titf1 expression (e.g., during the transformation of the endostyle of larval lamprey) are required to understand the relationships between the titf1 expression and formation of the thyroid-like organs during chordate evolution.

In previous studies, we isolated genes specific to the endostyle (Ogasawara et al., 1996; Ogasawara and Satoh, 1998). The HrEnds1, HrEnds2, CiEnds1 and CiEnds2 genes are expressed in the whole region of zone 6, CiEnds3 in zone 2, and CiEnds4 or a cytoplasmic actin gene in zones 3, 5 and 7. Although the expression of the ascidian titf1 genes only partially overlap with that of these structural genes, it is an intriguing research subject to determine whether HrTTF-1 or CiTTF-1 regulates the expression of these structural genes.

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