A Short-Form C-Type Lectin from Amphioxus Acts as a Direct Microbial Killing Protein via Interaction with Peptidoglycan and Glucan

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A Short-Form C-Type Lectin from Amphioxus Acts as a Direct Microbial Killing Protein via Interaction with Peptidoglycan and Glucan

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To investigate the evolution and immune function of C-type lectin in amphioxus, the primitive representative of the chordate phylum, we identified three C-type lectins consisting solely of a carbohydrate recognition domain and N-terminal signal peptide and found that they had distinct expression patterns in special tissues and immune response to stimulations analyzed by quantitative real-time PCR. We characterized the biochemical and biological properties of AmphiCTL1, which was dramatically up-regulated in amphioxus challenged with Staphylococcus aureus, Saccharomyces cerevisiae, and zymosan. Immunohistochemistry demonstrated that the localization of AmphiCTL1 protein was exclusively detected in the inner folding tissues of the hepatic diverticulum. Recombinant AmphiCTL1 was characterized as a typical Ca\(^{2+}\)-dependent carbohydrate-binding protein possessing hemagglutinating activity, preferentially bound to all examined four Gram-positive bacteria and two yeast strains, but had little binding activity toward four Gram-negative bacteria we tested. It aggregated calcium ions and specifically bound to insoluble peptidoglycan and glucan, but not to LPS, lipoteichoic acid, and mannan. Calcium increased the intensity of the interaction between AmphiCTL1 and those components, but was not essential. This lectin directly killed Staphylococcus aureus and Saccharomyces cerevisiae in a Ca\(^{2+}\)-independent fashion, and its binding to microorganism cell wall polysaccharides such as peptidoglycan and glucan preceded microbial killing activity. These findings suggested that AmphiCTL1 acted as a direct microbial killing C-type lectin through binding microbial targets via interaction with peptidoglycan and glucan. Thus, AmphiCTL1 may be an evolutionarily primitive form of antimicrobial protein involved in lectin-mediated innate immunity. The Journal of Immunology, 2007, 179: 8425–8434.
characteristic carbohydrate structures is considered as a universal and effective method of distinguishing self from nonself in invertebrates. The abundance of C-type lectins in invertebrates (such as Drosophila melanogaster and Caenorhabditis elegans) is a very effective repertoire for defending pathogens. C-type lectins from invertebrates such as the insect, starfish, and shrimp have been found to be involved in various biological responses, for instance, promotion of phagocytosis (9), activation of the prophenol oxidase system (10, 11), nodule formation (12), and antibacterial activity (13, 14).

CTLDs are found almost exclusively in Metazoa and are highly conserved in invertebrates but with considerable diversity among invertebrates. For example, the C-type lectin repertoire of C. elegans and D. melanogaster is drastically different from each other, and from the known vertebrate groups (6). The studies of CTLDs on those organisms that occupy crucial positions in the animal tree will give important implications for understanding the origin and evolution of the functional systems in which CTLDs are involved. Amphioxus is the most primitive representative of the chordate phylum, hence constitutes an important reference to the immunity evolution of CTLDs. There are >1000 C-type lectin gene models in the amphioxus genome based on our analysis, compared with 100~200 genes in other species such as human, fugu, and C. elegans (6, 15, 16) and most of them derive from lineages specific to amphioxus. Half of amphioxus CTLDs consist solely of a CRD domain (S. Huang, S. Yuan, Y. Yu, L. Gua, unpublished observation). In this study, we characterized three C-type lectins with a single CRD domain from the Chinese amphioxus, one of which possesses direct microbial killing activity by binding their microbial targets via interaction with peptidoglycan (PGN) and glucocarbohydrates.

Materials and Methods

Reagents

LPS from Escherichia coli 0111:B4, lipoteichoic acid (LTA) from Staphylococcus aureus, mannac from Saccharomyces cerevisiae, glucan from S. cerevisiae, zymosan from S. cerevisiae, maltose, mannanose, GlcNAc, BSA, DMSO, 3,3’-tetramethylbenzidine, and lactose Sepharose 4B were purchased from Sigma-Aldrich. PGN from S. aureus and Bacillus subtilis were purchased from Fluka Chemical. FITC (isomer I) and PHA were purchased from Amersco. Recombinant protein G agarose was purchased from Invitrogen Life Technologies. Sucrose, lactose, galactose, fructose, and glucose were obtained from Guangzhou Pure Chemical. Diaminobenzidine (DAB) and HRP-labeled IgG were purchased from Boster Chemical.

Preparation of microbial cells

Staphylococcus epidermidis and Enterococcus faecium were clinical strains isolated from the patients of the Third Affiliated Hospital of Sun Yat-Sen University (China). Vibrio vulnificus, Vibrio parahaemolyticus, Aequorans sovbia, and B. subtilis were isolated from amphioxus. They were characterized by using standard microbiological and biochemical procedures in the Medical Diagnostic Laboratory of the Third Affiliated Hospital, Sun Yat-Sen University. In addition to these strains, S. cerevisiae (American Type Culture Collection (ATCC) 9763), S. aureus (ATCC 12598), Pichia pastoris and E. coli DH5α were used. V. parahaemolyticus was cultured with a TCBS agar plate at 26°C while other bacteria separated from amphioxus were cultured at 26°C with aeration in Luria-Bertani (LB) medium prepared with fresh seawater. Other bacterial strains were cultured at 37°C in LB prepared with the distilled water. S. cerevisiae and P. pastoris were cultured with 2X YPD medium with 3% glucose (4% bactotryptone, 2% bacto-yeast extract (pH 5.8)) at 30°C. All microbial strains were harvested by centrifugation at 3500 x g for 10 min and resuspended in the buffer for an appropriate concentration. Quantification was performed by plating various bacteria dilutions on agar plates.

Cultivation and immune stimulation of amphioxus and preparation of tissue and embryo samples

Matured adults of Chinese amphioxus, Branchiostoma belcheri (genus Branchiostoma, family Branchiostomidae) were obtained from Xiamen (Fujian Province, China), and cultured at 25°C in a tank filled with air-pumped circulating sterilized seawater. Spawning females swimming up to lay eggs from the sand were caught with a net and immediately put into a large petri dish containing naturally inseminated seawater. The embryos at each period were collected and quickly frozen in liquid nitrogen. Adult amphioxus was not fed for 10 days before separating tissues under an optical microscope. For immune stimulations, a live microbial PBS suspension (15 μl/animal, 106 CFU/μl), component PBS suspension (15 μl/animal, 1 mg/ml), or PBS was injected into the coelom of amphioxus. Twenty random samples of each treatment were collected after injection and frozen by liquid nitrogen as experimental samples.

Full-length cDNA cloning and sequencing of amphioxus C-type lectins

Expressed sequence tags (EST) with sequence similarity to C-type lectin were identified from a series of EST libraries constructed by our laboratory. The 5’-RACE was performed using a GeneRACE kit (Invitrogen Life Technologies) according to the manufacturer’s instructions. Gene-specific primers were designed for amplifying the 5’ end sequence and the full-length sequence of amphioxus C-type lectins. In all PCR, total RNA of whole amphioxus was used as templates. And the amplified fragments were cloned into the pGEX-T easy vector (Promega) and sequenced by the PerkinElmer ABI Prism 3730 DNA sequencer.

Quantitative real-time PCR (Q-PCR) analysis of gene expression patterns for amphioxus C-type lectins

Q-PCRs were performed and analyzed as described (17). Total 40 cycles were performed with the primers 5’-GGGCTTACAGTACTGGTGTAAGCG-3’ (forward) and 5’-ATCGGATTGCCGAGAATTGTCG-3’ (reverse) for AmphitCTL1, 5’-AACGCTACGGGTCTCCACCAACGACT-3’ (forward) and 5’-GCTTGCTCTCTTGTTCTCG-3’ (reverse) for AmphitCTL2, and 5’-GGGAAACCGATACAAAGGGAAT-3’ (forward) and 5’-GGGAAACCGATACAAAGGGAAT-3’ (reverse) for AmphitCTL3. All samples were analyzed in three duplications and the results were expressed as relative fold of one sample in each experiment as mean ± SD.

Preparation of recombinant AmphitCTL1 proteins

Recombinant AmphitCTL1 proteins were expressed in two different systems. The nonfusion protein is expressed with pET21b system (Novagen) to prepare for the antiserum as the Ag. The coding region for mature AmphitCTL1 (Val24 to Ala153) was amplified by primers (forward primer: 5’-GGAAATTCCCATATGGTTACCCGATAGTAAACATGGTCG-3’; reverse primer: 5’-CCGGCTGCAGTTAGGCTGATGCATTGTTGCCTCT-3’) from the pGEM-T Easy vector (Promega) carrying AmphitCTL1 full-length cDNA. NdeI and Xhol endonuclease sites (underlined) were included at the 5’ end of the forward and reverse primer, respectively, while one strong stop codon was incorporated at the 5’ end of the reverse primer to produce native protein AmphitCTL1. The PCR products were digested with Ndel and Xhol, gel-purified, ligated to pET21b plasmid prepared in the same way, and confirmed by DNA sequencing to construct the expression vector pET-AmphitCTL1. The expression plasmids were introduced into E. coli BL21 (DE3) to express recombinant protein. The recombinant protein was purified from M urea and renatured by three dialysis steps as described (18), and each dialysis step was performed for at least 12 h at 4°C. Then, the soluble re- natural protein was purified with lactose Sepharose 4B.

To obtain the native soluble protein, we expressed recombinant Amphit CTL1 using a thioredoxin (TRX) fusion system containing a 6X His tag to facilitate the purification of fusion proteins on a Ni2+ -chelating Sepharose column. The recombinant protein was purified from the native solution by using a Ni2+ -chelating Sepharosecolumn. The recombinant protein was purified by Ni-NTA chromatography on a Ni2+ -chelating Sepharose column, pooled by elution with 150 mM imidazole.
The purified recombinant proteins were desalted to TBS (50 mM Tris - Cl (pH 7.5), 150 mM NaCl) with G-25 column, and concentrated by filtration through an Ultrafree centrifugal filter device (Millipore). Protein concentration was determined using a Bio-Rad Protein Assay dye reagent and BSA as a standard.

Preparation of AmphiCTL1 Ab

The inclusion body of AmphiCTL1 expressed by pET21b system was washed with 2 M urea, and the pellets were dissolved with the sample buffer and subjected to the SDS-PAGE. The specific band of AmphiCTL1 was detected by Western blot with an antihuman IgG HRP-labeled second antibody. The anti-AmphiCTL1 serum was collected at 4000 g for 10 min and washed with TBS, then resuspended with 500 μl of TBS and frozen-thawed for four times. Then, the mixture was quickly boiled at 100°C for 5 min to destroy the activity of the proteases. The cells were lysed by sonication for 10 min, incubated at 56°C for 30 min, and then mixed at 4°C with the 100 μl of serum for 12 h. Cell debris was removed by centrifugation. The IgG fraction was purified from bacteria-preabsorbed serum using recombinant protein G agarose (Invitrogen Life Technologies), and the preimmune serum was treated with the same methods.

Localization of AmphiCTL1 protein by immunohistochemistry

Amphioxus was severed into three to four pieces, and fixed in freshly prepared 4% (w/v) paraformaldehyde in 100 mM PBS (pH 7.3) with 24 mM CaCl2. After 60 min, the pieces were immersed in paraformaldehyde, and sections were cut at 5 μm. The sections were mounted on slides, and dried at 42°C for 6 h. They were dehydrated in xylene for 10 min (two changes for 5 min each) followed by immersion in absolute ethanol for 10 min (two changes for 5 min each), and then rehydrated in 95, 90, 80, and 70% ethanol (one change for 5 min) and brought to 100 mM PBS. After rinsing with distilled water for 5 min, the endogenous peroxidase activity in the sections was quenched with 3% hydrogen peroxide for 15 min, which was followed by a 5-min wash in redistilled water. Subsequently, the sections were preincubated with 5% BSA in 20 mM PBS (pH 7.3) at room temperature for 30 min, washed in 20 mM PBS for 5 min, and then incubated for 1 h with anti-AmphiCTL1 IgG diluted 1/1000 with 20 mM PBS containing 5% BSA in a humidified chamber at 37°C. The control sections were similarly incubated with preimmune rabbit Ab. Both experimental and control sections were washed three times for 3 min each in 20 mM PBS, and incubated further with HRP-labeled anti-rabbit IgG diluted 1/200 with PBS containing 5% BSA at room temperature for 1 h. The chromogenic reaction was achieved by addition of 0.015% (w/v) DAB containing 0.1% NiCl2 and 0.02% (v/v) H2O2 in 50 mM Tris/HCl buffer (pH 7.6) and 0.1% glutaraldehyde for 1 h. The sections were rinsed with 2 M urea, and the pellets were dissolved with the sample buffer quickly and denatured by heating at 100°C for 15 min. Protein binding was analyzed by Western blot, as follows. Proteins were fractionated by electrophoresis through 15% SDS-PAGE and electrophotoreti- cally transferred onto a nitrocellulose blot membrane (Pall Corporation). Membranes were blocked with 5% nonfat milk and PBST at room temperature for 2 h and washed three times with PBST. Anti-AmphiCTL1 Ab was diluted 1/5000 in PBST and incubated with the membranes overnight at 4°C. After washing three times with PBST, membranes were incubated for 1 h with HRP-labeled anti-rabbit IgG Ab diluted 1/1000 in PBST. The membranes were washed three times with PBS and detected with DAB. In this experiment, Sepharose 4B was treated with the same method as negative control. In some experiment, EDTA was added to eliminate calcium activity.

Microbial aggregation assays

For FITC labeling of the microbes, microbes collected from plate or liquid cultures were suspended in 1 ml of buffer at pH 9.0 containing 50 mM Na2CO3 and 10 mM NaCl and were mixed with 50 μl of FITC solution (10 mg/ml in DMSO). The reaction was incubated at room temperature in the dark for 1 h with gentle agitation and washed four times with TBS. FITC-labeled microbes and 10 μg of recombinant proteins were mixed and incubated 1 h at room temperature in the presence of 10 mM CaCl2. The agglutinating reaction was examined under fluorescence microscopy.

Binding assay of AmphiCTL1 with the components of microorganisms

A total of 20 μg of LPS, LTA, PGN, glucan (PGN and glucan are ultrasonically solubilized), and mannan were used to coat a 96-well microtiter plate (TPP) in 100 mM PBS (pH 7.3) overnight at 4°C. Nonspecific binding to the wells was prevented by the addition of PBS containing 3% BSA overnight at 4°C. Several concentrations of AmphiCTL1 protein were then added to the wells and incubated for 1 h at room temperature. Bound AmphiCTL1 was detected with anti-AmphiCTL1 Ab diluted 50,000-fold for 1 h at room temperature, followed by a 30-min incubation with a 1/1000 dilution of HRP-labeled IgG. Between each incubation step, unbound protein, Ab, or HRP-labeled anti-mouse IgG was washed off five times. Color was developed by adding 3,3',5,5'-tetramethylbenzidine liquid substrate, and the absorbance was read at 450 nm. The assay was repeated five more times with similar procedures.

The PGN and glucan-binding activities of AmphiCTL1 were also detected by pull-down assays. Insoluble PGN or glucan was incubated at 4°C for 1 h with 5 μg of AmphiCTL1 in TBS in the presence or absence of 10 mM CaCl2. The samples were centrifuged at 15,000 × g for 10 min and PGN or glucan pellets fractions were washed with the same buffer, centrifuged, and dissolved in reducing sample buffer. Pellets were analyzed on 15% SDS-PAGE and then transferred to the nitrocellulose membrane and detected by the anti-AmphiCTL1 Ab.

Antimicrobial activity assays

Antimicrobial activities against S. aureus and S. cerevisiae were performed on a petri dish. Thirty milliliters of warm nutrient agar (1.0%) mixed with microbes were poured into a 90-mm plate. The pores are 0.5 cm in diameter perforated with perforex. Then, the targeted protein or antibiotic in 100 μl of TBS was added to the pores at the final concentration of 1 μg/ml. The plates were incubated at suitable temperature for 16 or 40 h. A transparent ring around the pores indicated antibacterial activity.

The growth curves of S. aureus and S. cerevisiae cultured with Amphi CTL1 were tested as follows. Two single colonies were picked up and transferred into 1 ml of LB or 2X YPD broth. A volume of 50 μl of cell suspension was added to an equal volume of TBS or purified various concentrations of AmphiCTL1 with or without 10 mM CaCl2 in TBS. Each sample was incubated with aeration at 200 rpm and the OD at 600 nm (OD600) was measured every 1 h. An inhibition assay was performed by preincubating protein for 10 min with soluble PGN or glucan before the addition of microbes.

Electron microscopy

For electron microscopy, mid-log phase cultures of S. aureus were washed and resuspended in 1 ml of TBS. A total of 500 μl of resuspended bacteria was added to each of two reactions containing either buffer with 100 μg of TRX, or 100 μg of TRX-AmphiCTL1. Reactions were incubated for 2 h at 37°C. The bacterial pellets were washed three times with TBS, and then fixed overnight at 4°C in 4% paraformaldehyde, 0.1% glutaraldehyde in 100 mM PBS. Tissues were dehydrated in an ethanol gradient at decreasing temperatures (0 to −35°C), then embedded in KM4 under UV illumination for 2 days. Embedded tissues were then sectioned using a microtome.
floated onto grids, visualized using the JEOL electron cryomicroscope, and imaged on Kodak SO163 films.

Results

Cloning and sequence analysis of amphioxus C-type lectins

ESTs with sequence similarity to C-type lectin were identified from a series of EST libraries established in our laboratory. The full-length cDNA sequences of these ESTs were obtained by 5’-RACE and three of them encoded a sole CRD domain and N-terminal secreted signal. They encoded 153-, 157-, and 127-aa putative proteins composed of a 23-, 28-, and 17-aa signal peptides and CRD domains in C-terminal, named as AmphiCTL1, AmphiCTL2, and AmphiCTL3, respectively. These amphioxus C-type lectins shared 30–33% identity with each other, also with other species C-type lectins, such as mice reg|γ. Alignment analysis was conducted for these amphioxus C-type lectins and mice reg|γ, and several signature sequences of the C-type lectin family were found to be conserved (Fig. 1). The WIGL and WND motifs conserved in the classical C-type lectins also existed in amphioxus C-type lectins with a little variation, such as the WIGM for AmphiCTL3 and WDD for AmphiCTL2/3. The four cysteine residues, which are important to form the CRD internal disulfide bridges, were completely conserved. But two unconserved cysteine residues existing in some CRDs were not found in AmphiCTL1 and AmphiCTL3. The EPN, the key motif in forming coordinates with mannose/glucose in C-type lectins (21), was also found in AmphiCTL1 and AmphiCTL2, but was replaced by EPS in AmphiCTL3.

Expression patterns of amphioxus C-type lectins

Q-PCR analysis of amphioxus C-type lectins transcripts revealed that each had a distinct temporal- and spatial-specific expression pattern (Fig. 2, A and B). Amphioxus C-type lectins were expressed during the entire embryonic development, with a high expression level at 4 h (blastula stage) and 5.5 h (gastrulae stage), consistent with our previous results that most development and immune-related genes were increased in gastrulae stage because of the changing from multiple cell organization into organ formation in this period (17). These lectins had a relatively high expression at 16 h stage, especially for AmphiCTL3 (Fig. 2A). At the adult stage, AmphiCTL1 and AmphiCTL2 transcripts were detected in all tissues with the highest levels in the hepatic diverticulum for AmphiCTL1 and intestine for AmphiCTL2. The AmphiCTL3 transcript was abundant in the skin, ovary, intestine, and muscle, weak in the gill, notochord, and hepatic diverticulum (Fig. 2B).

FIGURE 1. Multiple alignment of amphioxus C-type lectins with mice reg|γ (NP_035390). Residues identical with the threshold of 60% in all sequences were shaded. Residues in black background indicate higher levels of amino acid similarity. The conserved cysteine residues and motif in character were listed in the last line.

FIGURE 2. Q-PCR analysis of the expression patterns of amphioxus C-type lectins. A, The relative level of amphioxus C-type lectin mRNA during the embryogenesis. Data were expressed as a ratio to AmphiCTL1 mRNA expression in adult. B, The relative level of amphioxus C-type lectins mRNA in different tissues. Data were expressed as a ratio to AmphiCTL1 mRNA expression in muscle. C, The relative level of amphioxus C-type lectin mRNA at 24 h after different immune stimulation. Data are expressed as a ratio to AmphiCTL1 mRNA expression in samples injecting with PBS. D, The time course of AmphiCTL1 mRNA expression at 4, 8, 12, 24, and 48 h after S. aureus challenge (□) compared with injection with V. parahaemolyticus (■). Data were expressed as an increasing ratio of AmphiCTL1 mRNA expression to unchallenged naive animals. In each experiment, values were normalized to the cytoplasmic actin expression, and mean ± SD is plotted.
70/H11011
400-fold compared with the injection with PBS. Additional
with Coomassie brilliant blue (lane 1 and 2), and detected anti-
AmphiCTL1 Ab (lane 4) or preimmune rabbit Ab (lane 5) by Western
blot. Purified AmphiCTL1 recombinant protein was also subjected to
the 12% SDS-PAGE and staining with Coomassie brilliant blue (lane 6)
and detected by anti-AmphiCTL1 Ab, as positive control. A polyclonal Ab raised against recombinant AmphiCTL1 was able to rec-
ognize AmphiCTL1 in the hepatic diverticulum (h) of amphioxus (a and
b). Preimmune rabbit Ab (c and d) could not stain those tissues. The
bar: 200 μm.

To determine whether these lectins were differentially regulated upon infection, Q-PCR analysis was also used to examine the relative expression of these lectins in amphioxus after challenged with different microbes and their cell wall components 24 h later (Fig. 2C). The results revealed 5–20-fold increased expression of AmphiCTL2 and AmphiCTL3 in all stimulated amphioxus, while the increased expression of AmphiCTL1 was specific for the stim-
ation of zymosan, S. cerevisiae and S. aureus, and up to 70–400-fold compared with the injection with PBS. Additional experiments of the infection time-course analysis revealed 130.2-
dependent manner. The competition inhibition of
HA was tested with AmphiCTL1 fusion protein on rabbit erythrocytes. AmphiCTL1 proteins at 20 nM with 10 mM CaCl2 could induce the hemagglu-
tination of the erythrocytes, while the addition of EDTA inhibited
the HA (Table I), indicating that the lectin activity of AmphiCTL1
was in a Ca2+-dependent manner. The competition inhibition of
HA was seen in the presence of at least 125 mM lactose, 200 mM maltose, sucrose, galactose, mannose, and GlcNAc, 250 mM glu-
cose (Table II). Up to 250 mM fructose and 1 mg/ml LPS, LTA, and mannose did not inhibit the HA induced by AmphiCTL1.

Binding and aggregating of AmphiCTL1 to microbes

The above-mentioned experiments demonstrated that AmphiCTL1
was mainly synthesized in the hepatic diverticulum, which had
long been considered as the precursor of vertebrate liver (22), and the high expression of AmphiCTL1 in this tissue was induced by

To study it. To identify the biological properties of AmphiCTL1,
we used the pET21b system to express it, but recombinant protein
was insoluble. The inclusion bodies washed with the urea and separated by SDS-PAGE were injected into the rabbit to prepare for the immune serum. The specificity of anti-
AmphiCTL1 polyclonal Ab purified with protein G agarose was examined by Western blot of amphioxus total protein. A single band, which corresponded well with the deduced mature AmphiCTL1 protein, was detected by the anti-AmphiCTL1 Ab, but not by the preimmune Ab (Fig. 3A), indicating that the anti-AmphiCTL1 Ab specifically recognized the native protein in amphioxus. The localization of AmphiCTL1 in amphioxus was then examined by immunohistochemistry using this Ab (Fig. 3B). The anti-AmphiCTL1 Ab specifically stained in the inner folding tissues of the hepatic diverticulum, consistent with the tissue expression patterns analyzed by Q-PCR. No spec-
IFIC staining was observed with the preimmune serum.

**Determination of sugar-binding specificity by HA**

To obtain the soluble protein, TRX fusion system was used to express soluble fusion AmphiCTL1 protein, which can be purified with a Ni2+-chelating Sepharose column. The HA was tested with AmphiCTL1 fusion protein on rabbit erythrocytes. AmphiCTL1 proteins at 20 nM with 10 mM CaCl2 could induce the hemagglutination of the erythrocytes, while the addition of EDTA inhibited the HA (Table I), indicating that the lectin activity of AmphiCTL1
was in a Ca2+-dependent manner. The competition inhibition of
HA was seen in the presence of at least 125 mM lactose, 200 mM maltose, sucrose, galactose, mannose, and GlcNAc, 250 mM glu-
cose (Table II). Up to 250 mM fructose and 1 mg/ml LPS, LTA, and mannose did not inhibit the HA induced by AmphiCTL1.

**Localization of AmphiCTL1 protein by immunohistochemistry**

The specific expression patterns of AmphiCTL1 in the tissues and immune response to stimulations prompted us to further study it. To identify the biological properties of AmphiCTL1,

**Table I. HA of AmphiCTL1 on erythrocytes**

<table>
<thead>
<tr>
<th>Samples</th>
<th>Minimal Agglutinating Concentration (nM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TRX plus CaCl2</td>
<td>ND*</td>
</tr>
<tr>
<td>PHA</td>
<td>2.5</td>
</tr>
<tr>
<td>TRX-AmphiCTL1 plus CaCl2</td>
<td>20</td>
</tr>
<tr>
<td>TRX-AmphiCTL1 plus CaCl2 plus EDTA</td>
<td>ND*</td>
</tr>
</tbody>
</table>

* ND, Not detected.

**Table II. Effects of saccharides on HA of AmphiCTL1**

<table>
<thead>
<tr>
<th>Saccharides</th>
<th>Minimal Inhibitory Concentration (mM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maltose</td>
<td>200 mM</td>
</tr>
<tr>
<td>α-glucose</td>
<td>250 mM</td>
</tr>
<tr>
<td>Lactose</td>
<td>125 mM</td>
</tr>
<tr>
<td>Galactose</td>
<td>250 mM</td>
</tr>
<tr>
<td>Sucrose</td>
<td>200 mM</td>
</tr>
<tr>
<td>α-mannose</td>
<td>200 mM</td>
</tr>
<tr>
<td>Fructose</td>
<td>&gt;250 mM</td>
</tr>
<tr>
<td>N-acetyl-α-glucosamine</td>
<td>200 mM</td>
</tr>
<tr>
<td>LPS from E. coli 0111:B4</td>
<td>&gt;1 mg/ml</td>
</tr>
<tr>
<td>LTA from S. aureus</td>
<td>&gt;1 mg/ml</td>
</tr>
<tr>
<td>Mannan from S. cerevisiae</td>
<td>&gt;1 mg/ml</td>
</tr>
</tbody>
</table>

**FIGURE 3.** Immunohistochemical staining of AmphiCTL1 in amphioxus. A. Detection of AmphiCTL1 proteins in the total amphioxus extracts with affinity purified serum. Total proteins were extracted from amphioxus with the lysed buffer (10 mM Tris · Cl (pH 8.0), 100 mM
NaCl, 1 mM EDTA) and subjected to the 12% SDS-PAGE and staining with Coomassie brilliant blue (lanes 1 and 2), and detected anti-AmphiCTL1 Ab (lane 4) or preimmune rabbit Ab (lane 5) by Western blot. Purified AmphiCTL1 recombinant protein was also subjected to
the 12% SDS-PAGE and staining with Coomassie brilliant blue (lane 3) and detected by anti-AmphiCTL1 Ab (lane 6) as positive control. B. Serial sections of amphioxus were stained with affinity purified Ab. A polyclonal Ab raised against recombinant AmphiCTL1 was able to rec-
ognize AmphiCTL1 in the hepatic diverticulum (h) of amphioxus (a and
b). Preimmune rabbit Ab (c and d) could not stain those tissues. The
bar: 200 μm.
the absence of calcium, the nonfusion AmphiCTL1 could also bind with these microorganisms, suggesting that the extra part had no effect on interaction between AmphiCTL1 and microbes (Fig. 4D).

To determine whether the binding activity of AmphiCTL1 could induce the aggregation of those microbial pathogens, we incubated FITC-labeled S. aureus and S. cerevisiae with TRX-AmphiCTL1 fusion protein and assessed microorganism aggregation by fluorescence microscopy. The addition of AmphiCTL1 caused a strong aggregation of S. cerevisiae, and a weak aggregation of S. aureus. The addition of 10 mM EDTA inhibited the S. aureus aggregation induced by AmphiCTL1, but did not completely inhibit the aggregation of S. cerevisiae (Fig. 5). However, the addition of 10 mM EDTA inhibited absolutely the aggregation of S. cerevisiae in calcium free in the buffer solution. We also tested the effect of the TRX-His-tag part on the aggregation activity, and found that AmphiCTL1 itself could induce the aggregation of S. aureus and S. cerevisiae in the presence of calcium. These data indicated that the TRX-His-tag part had no extra effect on AmphiCTL1 function. Because we used the denaturing/renaturing method to obtain the nonfusion AmphiCTL1 protein from the inclusion body, AmphiCTL1 may not fold precisely to the natural form which may cause subtle functional change for the recombinant protein. Thus, we chose the fusion protein for conducting the following functional studies.

**Binding of AmphiCTL1 to the microbial components**

AmphiCTL1 binding directly to microorganisms may be dependent on recognizing the components of the microbial cell wall, especially the carbohydrate groups on these molecules. Then, we performed a plate ELISA to test the interaction between AmphiCTL1 and those microorganism components. Microtiter plates were coated with the microbial cell wall components and incubated with AmphiCTL1 followed by detecting with anti-AmphiCTL1 Ab. Notably, AmphiCTL1 protein interacted with soluble PGN from S. aureus and B. subtilis, glucan from S. cerevisiae, but not with LPS, LTA, and mannan (Fig. 6A).

The binding activities of AmphiCTL1 to the insoluble PGN and glucan were also tested by the co-pull down assay. PGN and glucan were incubated with AmphiCTL1 and the unbounded protein
was separated from pellets by centrifugation. From our results, AmphiCTL1 directly interacted with the PGN from S. aureus and B. subtilis, glucan from S. cerevisiae. The interacting intensity of the PGN/glucan with AmphiCTL1 was dependent on the dose of the saccharides. AmphiCTL1 had a higher affinity with the PGN/glucan, though the interaction intensity between PGN/glucan and AmphiCTL1 was reduced compared with that in the presence of calcium (Fig. 6B). These results demonstrated that AmphiCTL1 recognized microorganisms and directly interacted with the cell wall components on those microorganisms.

Antibacterial activity of AmphiCTL1 against S. aureus and S. cerevisiae

To determine the antimicrobial activity of AmphiCTL1, its inhibition effect on the growth of microbes was examined. Compared with the TBS and TRX, a transparent ring was found to be around the pores with AmphiCTL1 like the pores with ampicillin or kanamycin in the plates of S. aureus and S. cerevisiae (Fig. 7, A and B). We used transmission electron microscopy to visualize morphological changes in S. aureus cell after exposure to AmphiCTL1 (Fig. 7, C and D). The images revealed evidence of cell damage and cytoplasmic leakage remarkably similar to those obtained with the mouse Regll|γ and human HIP/PAP (8). These indicated that AmphiCTL1 directly killed the microorganisms by cell wall permeabilization. We also tested the effect of AmphiCTL1 concentration on the antimicrobial activity. The antimicrobial activity of AmphiCTL1 was dose-dependent with 200 μg/ml AmphiCTL1 strongly suppressing the microbial growth, but 20 μg/ml AmphiCTL1 suppressing it weakly. To test the effect of polysaccharides on the antimicrobial activity of AmphiCTL1, PGN or glucan was preincubated with the protein. AmphiCTL1 antimicrobial activity against S. aureus was inhibited with PGN from S. aureus, and...
antimicrobial activity against S. cerevisiae was also inhibited with glucan from S. cerevisiae, indicating that lectin binding to the polysaccharide carbohydrate preceded killing microbes. We also tested the calcium-dependent property on its antimicrobial activity, and found that the calcium had no significant effect on the antibacterial activity of AmphiCTL1 (Fig. 7, E and F).

Discussion
In invertebrates such as amphioxus, the innate immune system is particularly important, because they lack the vertebrate adaptive immune system. The recognition of infectious pathogens is an important process for animals to mount an immune response. C-type lectins are a main kind of pattern recognition molecule in the innate immune system (3). They encompass a large family of proteins found almost exclusively in Metazoa. More than 100~200 human or C. elegans proteins containing CTLD have been identified (15, 16). But an enormous expansion of CTLD-containing proteins is found in the amphioxus genome with >1000 gene models encoding the CTLD domain (S. Huang, S. Yuan, Y. Yu, Y. Guo, and A. Xu, unpublished observation). It is generally hypothesized that a relatively small number of these C-type lectins function as opsonin or activate the complement pathway in the innate immune system (3, 6). Consequently, the many-fold amplification of this gene family in the amphioxus genome suggests that it is likely to function as a part of a fundamentally different immune mechanism. Moreover, studies on the C-type lectins from cephalochordate amphioxus, which occupy a crucial position in the animal evolution tree, may find the important functional link between the vertebrate and invertebrate C-type lectin families, especially in the innate immune system. In this study, three C-type lectins consisting of a C-terminal CRD and an N-terminal secreted signal were identified from Chinese amphioxus. This is the first report of C-type lectins in protocordate to date. These amphioxus C-type lectins have distinct express patterns in special tissues and responding to stimulations, and AmphiCTL1 may be an evolutionarily primitive form of lectin-mediated immunity through direct microbial killing activity. This study may help us understand the defense mechanisms to the pathogens in the invertebrate such as amphioxus and the immune evolution of the C-type lectin families from invertebrates to vertebrates.

C-type lectins are divided further into 17 subgroups in vertebrates and 7 subgroups in invertebrates (6, 15). Both group VII C-type lectins consist of only one CRD and a short N-terminal secreted signal. Approximately 500 C-type lectin gene models possessing the same structure as the known group VII C-type lectins are found in the amphioxus genome, most of them cluster into a group outside the vertebrate clade (S. Huang, S. Yuan, Y. Yu, Y. Guo, and A. Xu, unpublished data), indicating that the group VII C-type lectins may have specific function in amphioxus. In this study, three of them were cloned from the Chinese amphioxus. Although all CRDs have sequence similarity, including conserved hydrophobic residues and four invariant cysteine residues, they can be divided into two types: a “short form” ~115 residues long with four invariant cysteine residues and a “long form” ~130 residues long, which includes two additional disulfide-bonded cysteine residues at the N-terminus (24, 25). AmphiCTL1 and AmphiCTL3 were short form because they had a CRD with four cysteine residues, while AmphiCTL2 was regarded as long form because it had a CRD with two additional cysteines. In our experiments, we found that the transcripts of these amphioxus C-type lectins had a distinct temporal- and spatial-specific expression pattern, and were elevated in amphioxus stimulated by different microorganisms and corresponding cell wall components (Fig. 2). These results indicated that they were related to the defense mechanisms. However, these C-type lectins consist of secreted CRDs that lack collagenous domains required for complement recruitment, so they might function as fundamentally different immune mechanisms such as possessing the direct antibacterial activity the same as the tunicate Polyandrocarpa lectin (13). This hypothesis was proven by the biological properties of recombinant AmphiCTL1 protein.

Calcium was required for carbohydrate binding in mammalian C-type lectins, such as mannose-binding protein, which was a direct ligand for sugars (21). In this study, we found that calcium was essential to the hemagglutinating and microbial aggregation activities of AmphiCTL1, but not to the microbial binding and growth suppression activities of this lectin. The microbial aggregation activity of AmphiCTL1 was also in Ca2+-dependent manner, though 10 mM EDTA did not completely inhibit the aggregation against S. cerevisiae. This phenomenon could be explained by the fact that S. cerevisiae is a eukaryote that can release calcium flux from its cells when the cell wall is damaged, which is consistent with the microbial killing activity of AmphiCTL1. This presumption was confirmed because the aggregation against S. cerevisiae was completely inhibited when the buffer solutions were absolutely absent of calcium (Fig. 5). Although the C-type lectin family includes members that bind their ligands in a calcium-dependent manner, many other C-type lectins show the same Ca2+-dependent or -independent activity as AmphiCTL1. A C-type lectin of Conger eel, conCL-s, with binding to sugar in a Ca2+-independent manner, showed Ca2+-independent activity in its yeast-binding (26). Immuelectin-2, the insect immuelectin family with sequence similarities to C-type lectins, did not require calcium for its binding activity (27). Mouse Reglll and its human counterpart HIP/PAP did not require calcium for binding peptidoglycan and chitin (8). It seems that C-type lectins may bind to ligands using an alternative mechanism different from the classical one used by mammalian C-type lectins. From our experimental results, we postulate that calcium is not a direct ligand or essential factor for binding, but it may affect the formation of dimers or oligomers, which are required for agglutinating activity.

Most C-type lectins are able to bind PAMPs and microorganisms themselves through recognizing carbohydrate, so as to directly be involved in innate defense mechanisms as part of the acute-phase response to infection. The expression of AmphiCTL1 was quickly up-regulated after challenged with zymosan, S. cerevisiae, and S. aureus, indicating that AmphiCTL1 was also an inducible acute-phase protein to play a crucial role in host defense, which was consistent with its binding and aggregating activity to the invading pathogens. AmphiCTL1 could bind with all examined Gram-positive bacteria and yeast, but not with the Gram-negative bacteria studied. The microbial-binding activity of AmphiCTL1 was exerted by the interaction with PGN and glucan, but not with LPS, LTA, and mannan, which are the PAMPs existing in the microbial cell wall. The component binding results were consistent with transcript levels of AmphiCTL1 in amphioxus after challenge with cell wall components. These results suggested that AmphiCTL1 was a pattern recognition protein that recognized the PAMPs by the extended glycan chains of PGN and glucan. Though AmphiCTL1 did not bind to the examined Gram-negative bacteria, it interacted with the PGN from B. subtilis, which has the same
structure as the PGN of Gram-negative bacteria. This phenomenon could be explained by three differences between Gram-positive and -negative bacterial PGN. First, the affinity of AmphiciCTL1 to Gram-negative PGN (B. subtilis) was lower than the Gram-positive PGN (S. aureus) (Fig. 6B). Second, PGN existing in the Gram-negative bacteria is only 10–20% of cell wall components, compared with up to 50–80% in Gram-positive bacteria. Third, the PGN of Gram-negative bacteria is buried in periplasmic space, while that of the Gram-positive bacteria is exposed on the surface. The capacity of C-type lectins to sense microorganisms is highly dependent on the density of the PAMP present on the microbial surface (28). Therefore, AmphiciCTL1 cannot interact and respond to the equal dose of Gram-negative bacteria compared with Gram-positive bacteria.

An important part of innate immunity is that a group of protein has antimicrobial activity in addition to immune recognition. These proteins all play essential roles in nonspecific host defenses by preventing or limiting infections by their ability to selectively recognize potential pathogens. Most proteins exert their antifungal or antibacterial effects by interacting with and destabilizing the microbial membrane, leading to cell death. Except the traditional antimicrobial protein, such as defensin (29) and lysozyme (30), several C-type lectins have been reported to have antibacterial activity. In invertebrates, the C-type lectin purified from tunicate *Polyandrocarpa misakiensis* displayed a strong antibacterial activity even at the concentration of 1 μg/ml (13). The recombinant protein of scallop CFLec-1 displayed a remarkable inhibiting effect on Gram-positive bacteria *Micrococcus luteus* and relatively weak lytic activity against Gram-negative bacteria *E. coli JM109* (14). In vertebrates, the conglutinin from rat demonstrated antibacterial activity against *E. coli* and *Salmonella typhimurium* in vitro (31). Mouse Regγ and its human counterpart HIP/PAP have direct bactericidal activity on Gram-positive bacteria (8). In these reports, only Regγ and HIP/PAP were demonstrated to kill the bacteria by cell wall permeabilization. In our study, we found that AmphiciCTL1 could directly kill the microorganisms such as *S. aureus* and lead its cell wall damage the same as Regγ and HIP/PAP, and had wide-range microorganism killing activity. AmphiciCTL1 had the same effect on the yeast as *S. cerevisiae* by interaction with glucan, while either Regγ or HIP/PAP reduced the viability of fungal microorganisms. These indicated that the primitive C-type lectin in amphioxus possessed the more wide-range microorganism recognition than its vertebrate homologs. It is an inducible microbial killing protein that seeks out its microbial targets via interaction with the bacterial PGN or yeast glucan and represents a new function for invertebrate lectin-mediated immunity.

Although AmphiciCTL1 has the ability to kill the Gram-positive bacteria and fungi, it is plausible that those C-type lectins with the same structure as AmphiciCTL1 may also interact with the microbes in a similar way. AmphiciCTL1, which is abundant in the hepatic diverticulum, may have suppressing effect on the restricted Gram-positive bacterial and yeast strains in the fluid flow, where the resident microflora consists mostly of Gram-positive bacteria in amphioxus (Y. Yu, M. Pen, and A. Xu, unpublished data). The other amphioxus C-type lectins, AmphiciCTL2 and AmphiciCTL3, consisted of the same structure as AmphiciCTL1, but had different expression patterns analyzed by Q-PCR. Though the Q-PCR may have possible pitfalls for measuring gene expression, this technique can still tell us the relative expression of this targeted gene. From the Q-PCR, we found that AmphiciCTL2 possessed the highest levels in the intestine and was up-regulated by the all stimulations, so it was deduced that AmphiciCTL2 might mainly defend against those pathogens invading the intestine. AmphiciCTL3 might be a skin mucosal lectin because its transcript was abundant in the skin and it has high expression in the larva stage of amphioxus. At 16 h stage, the ovum theca of amphioxus embryo functioning as the first defense line was shocked off and the embryo was exposed to the culture environment. Up-regulation of AmphiciCTL3 in this stage was consistent with the highest transcript level in the skin. AmphiciCTL3 might defend against those microorganisms exposed to the body surface, so AmphiciCTL3 was up-regulated by all the stimulations. Thus, the C-type lectin family in amphioxus may recognize and defend many strains of pathogens collectively.

Taken together, the results from this work indicate that the primitive form of lectin-mediated immunity also exists in amphioxus, as determined here by AmphiciCTL1 as an example. This finding contributes not only to understanding the complexity of immunity in amphioxus in general, but also to the interesting facts on the evolution of the lectin-mediated immune system in particular. Our studies on AmphiciCTL1 in amphioxus indicates that these animals can defend themselves against microbial invaders by a secreted microbial killing C-type lectin. Furthermore, we find that C-type lectins with a similar structure to AmphiciCTL1 are abundant in the amphioxus genome, which may represent the primitive immune recognition strategy and be a main immune defense mechanism against different microorganisms in different tissues. They may constitute a defense network against almost all possible invading microorganisms. In view of the fact that the bactericidal protein Regγ and HIP/ PAP exist in high vertebrate, it may be predicted that such a diversity of C-type lectins also occurs in other vertebrate and invertebrate species. In short, this finding sheds new light on the lectin-mediated immune system, particularly its functional evolution from invertebrates to vertebrates.

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**Disclosures**

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**References**


