

Review Article

Lectin in Innate Immunity of Crustacea

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Abstract

Lectins are protein or glycoprotein with binding specificity to sugars and as pattern recognition molecule recognize glycosylated surface of pathogens. In crustacea, lectins are diverse and species specific and the mechanism of recognition by the lectin have an impact on immune response and immune regulation. The present review explains the evolutionary success of innate immunity based on the diversity of these recognition molecules.

Keywords: Crustacea; Lectins; Opsonin; Innate Immunity; Receptor

Introduction

The innate immunity of invertebrate appears to have evolved to a complex adaptive immune mechanism in vertebrates. The simple process of antigen or nonself recognition of innate immune response are transformed from a single step process to pathways or cascades involving receptor selection and regulatory process that target and attenuate adaptive immune responses [1]. The recognition and distinguishing of the nonself are based on recognition of cell surface glycoconjugate [2]. The modulations in carbohydrate molecules appear to be specific for species and are the basis of pathogen recognition. The glycosylated Pathogen Associated Molecular Pattern (PAMP) include, Lipopolysaccharide (LPS), Peptidoglycan (PGN), and diverse sugars including β 1-3 glucan and sialic acid, recognized by Pattern Recognition Receptors (PRR) that activate an immune response to eliminate the pathogen [3]. Lectins are molecules of ubiquitous occurrence and distinguish the nonself by binding specifically to the glycan of cell surface [4]. The report on the roles of lectins in enhancement of cellular immune responses also elaborates the function of lectin not only as recognition molecules but also as an opsonin [5]. The ability of lectin to bind to microbial glycosylated surface and induce a cascade of response leading to its elimination of invading pathogen was found to vary among the organisms [6]. The diverse ligand specificity and cell-cell interactions are the basis of multiple functions and pathways of immune response. In crustacea the structural and functional diversity of the lectins based on its sugar specificity appear to display diverse innate immune responses. The present review attempts to summarize the reported role of lectins in immunological functions in crustacea.

Carbohydrate Recognition Domain (CRD) in lectins

The Ca^{2+} -dependent carbohydrate-binding lectin are termed the C-type lectins are mediated by a compact module known as the 'Carbohydrate Recognition Domain' (CRD) present in all Ca^{2+} -dependent lectins but not in other types of animal lectins [7]. This domain, shows specific, but weak calcium-dependent binding to a variety of monosaccharides [8]. C-type lectin CRDs are found as building blocks in a variety of multi-domain proteins involved in organizing the extracellular matrix, endocytosis, the primary immune system and interactions of blood cells [9]. The CRD from various species of crustacea are summarized in (Table 1). The CRD with sequence QPD (Gln-Pro-Asp) motif was predicted with binding specificity for galactose and the CRD comprised of EPN (Glu-Pro-

Asn) motif for mannose [10]. The C-type lectins of the shrimps PmLT, *Penaeus monodon* [11], Fc-Lec2 *Fenneropenaeus chinensis* [12] and LvLT *Litopenaeus vannamei*, [13], had the two CRD with binding specificity for galactose and mannose. The lectins from shrimps possessed CRD with binding specificity for either one of the two sugars, the CRD for galactose QPD in Fc-Lec5 lectin from *F. chinensis* [14] and LvLectin 2 from *L. vannamei*, [15] and EPN CRD for mannose in, LvCTL of *L. vannamei* [16] and Fc-hsL of *F. chinensis* [16]. The phylogeny of the CRD for mannose and galactose from different species of shrimps appear conserved and despite the similarity in sugar binding specificity the amino acid sequence of the lectins appear divergent [13,18,19]. The evolutionary relationship of these CRDs in shrimp imply that the motif of amino acid sequence of the lectin protein though appear conserved differ with the binding glycan cluster [20]. The C-type lectin PtLP from the swimming crab *Portunus trituberculatus* contains a single CRD domain with six conserved cysteine residues does not contain a typical EPN or QPD motif in phylogenetic analysis was found in the a large cluster together with black tiger shrimp lectin PmAV [18]. The report of C-type lectins EsLecA and EsLecG from Chinese mitten crab, *Eriocheir sinensis* showed conserved CRD of QPD (Gln-Pro-Asp) motif for galactose in EsLecA, whereas the EsLecG had a key "EPE" (Glu-Pro-Glu) motif a mutated expression of mannose [21]. This clearly demonstrated the diversification of CRD by mutations and also explains convergence by retaining the conserved CRD. The CRD in lectin from different species of crustacea fail to explain the ligand specificity which appears to be determined either by multivalency of CRD developed within the primary structure of the protein or by clustering in cell surface glycans [22]. This amply describes the diversity in PAMP that enables the evolution under selection pressure of CRD in lectins.

Lectin as Pathogen Recognition Receptor (PRR)

Of the different types of PRR identified in crustacea the C-type lectins are found to vary in binding specificities and immune functions [23]. The purified recombinant lectin Fc-hsL [17], Fc-Lec2 [12], Fc-Lec5 [14] and rFcCTL [24] from the hepatopancreas of Chinese shrimp *F. chinensis* functions as PRR against Gram-positive and Gram-negative bacteria. However rFcCTL showed higher antimicrobial activity against Gram-positive bacteria than against Gram-negative bacteria and fungi. FcCTL expression was up-regulated in hepatopancreas and gills after White Spot Syndrome Virus (WSSV) challenge. The lectin Fc-Lec2 and Fc-hsL agglutinated some Gram-positive and

Table 1: Carbohydrate Recognition Domain in cDNA of lectins from crustacea.

S. No	Species in Crustacea	lectins	Amino acids	ORF*(bp)	CRD**	References
1	<i>Eriocheir sinensis</i>	EsLecA/EsLecG	159	480		[21]
		EsERGIC-53 EsVIP36,	501	465 1506 984		[33]
		EsLecF FC-L	327 220	477- 859	QPN" (Gln-Pro-Asn)	[70] [17]
2	<i>Fenneropenaeus chinensis</i>	FcCTL	333	1002	EPGD	[24]
		Fc-Lec2			EPN(Glu-Pro-Asn) mannose binding	[16]
		FcLec5		1,137	QPD(Gln-Pro-Asp) galactose binding	[24]
		Fc-hsL FmL	159	480	Gln-Pro-Asp (QPD) Glu-Pro-Gln (EPQ) EPN(Glu-Pro-Asn) mannose binding	[17] [71]
4	<i>Litopenaeus vannamei</i>	LvLec1	169	510	EPA' (Glu-Pro-Ala)	[26]
		LvCTL4	156	563	EPN (Glu(99)-Pro(100)-Asn(101)	[25]
		LvCTL1	156	638	EPN	[16]
		LvLectin-1		567	QPN (Gln122ePro123eAsn124)	[72]
		LvLectin-2 (LvLT)	345	625	QPD (Gln128ePro129eAsp13) EPN (mannose) QPD (galactose)0	[13]
5.	<i>Marsupenaeus japonicus</i>	MjLecA, MjLecB, and MjLecC)				[19]
6	<i>Marsupenaeus japonicus</i>	MjLectin	336	1011	rare mutant LPN (Leu ₁₃₄ -Pro ₁₃₅ -Asn ₁₃₆) in CRD1 EPN (Glu ₂₉₉ -Pro ₃₀₀ -Asn ₃₀₁) in CRD2, QPD	[73]
7	<i>Penaeus monodon</i>	PmLT			EPN	[11]
8	<i>Penaeus monodon</i>	PmLec	182	546		[74]
9	<i>Portunustrituberculatus</i>	PtLP	164	923	CTLD	[18]

CTLD- C-type lectin like-domain (CTLD)

*ORF-open reading frame

Gram-negative bacteria in a calcium-dependent manner and Fc-hsL exhibited antimicrobial activity against Gram-positive and Gram-negative bacteria [8,13]. C-type lectin from the shrimp *L. vannamei* (LvCTL1), showed activity against the WSSV [12] and LvCTL4 demonstrated antibacterial activity against *Vibrio parahaemolyticus* [25]. The cloned C-type lectin from hepatopancreasLvLec1 showed antibacterial activity against *Micrococcus lysodeikticus* and WSSV with sugar affinity to D-mannose, D-glucose, D-galactose and N-Acetyl-D-mannose [26]. The Pacific white shrimp, *Litopenaeus vannamei* and the Atlantic white shrimp, *Litopenaeus Setiferus*. RNA from the hemocytes and hepatopancreas expressed different immune functions [27]. A lectin from the hemolymph of the banana shrimp *Penaeus (Fenneropenaeus) merguensis* agglutinated *Vibrio harveyi* and *V. parahemolyticus*, which are pathogenic to *P. merguensis*, and to a lesser extent, *V. vulnificus*, but had no effect on the non-pathogenic *V. cholerae*, *Salmonella typhi* and *Escherichia coli* [28].

The mRNA transcript of C-type lectin PmLT from the shrimp *Penaeusmonodon* in hepatopancreas tissue appeared to decrease on WSSV infection initially and then gradually increased. The antibody of the recombinant lectin anti-rPmLT antibody, detected PmLT only in the Hepatopancreas Specific F cells (HPF). The lectin showed anti-viral response against WSSV to clearly indicate its role as PRR and activated anti-bacterial immune responses. Moreover, rPmLT coated agarose beads appeared to enhance encapsulation by the hemocytes [11]. Reports of C-type lectin, PmLec from the serum of the shrimp *Penaeus monodon* with PRR and opsonc function. The lectin was specific for bacterial LPS and the binding was mediated through the O-antigen. It had strong hemagglutinating and bacterial-agglutinating activity and by its binding affinity served as opsonin by enhancing hemocyte phagocytosis [29].

The C-type lectin, PcLT, from the red swamp crayfish *Procambarusclarkii* contained a Carbohydrate Recognition Domain

(CRD) with the ability to bind to *Vibrio alginolyticus* and WSSV [30]. Expressions of Pc-Lec1 from *P. clarkii* were up-regulated in the hepatopancreas and gills of crayfish challenged with *Vibrio anguillarum*, *Staphylococcus aureus*, or WSSV [31]; however expression of PcLec4 appeared upregulated after challenge with the bacteria *V. anguillarum* [32]. The lectin PcLec 5 from *P. clarkia* showed binding affinity to PGN, lipoteichoic acid and highest affinity to LPS of bacteria and selectively facilitated the clearance of injected bacteria [33].

The C-type lectins from mud crab *Scylla paramamosain* SpLec1 and SpLec2 mRNA in the megalopa a stage was first increased and were expressed mainly in haemocytes, muscle and hepatopancreas, with the highest expression level found in hepatopancreas [34]. In *Marsupenaeus japonicus*, three lectins, MjLecA, MjLecB, and MjLecC interact with WSSV and reduce the viral infection rate *in vitro*. Sequence analysis indicated MjLecA and MjLecB are likely to belong to the same lectin sub-family, while MjLecC belongs to another sub-family [19]. A C-Type Lectin Like-Domain (CTLD)-containing protein (PtLP) from the swimming crab *Portunus trituberculatus* contains a single CRD domain with six conserved cysteine residues with amino acid sequence identity to fleshy prawn *F. chinensis* C-type lectin [18].

Opsonin function of lectin

The cellular immune mechanism of phagocytosis appears conserved in invertebrates and vertebrates. The process of antigen recognition, internalization and elimination in innate immune response of invertebrates show increase in complexity in adaptive immunity of vertebrates. Opsonins are molecules that recognize pathogens and bind to the receptors on the surface of phagocytes to enhance phagocytosis. The lectins as carbohydrate binding molecules serve as opsonins for hemocytes in several species of crustacea. The lectin from the shrimp *P. monodon* PmLec [29], the red swamp crayfish and *Procambarus clarkia*, Pc-Lec1 [31], serve as opsonin to interact with hemocytes in clearance of bacteria. The C-type lectin FcLec4 from Chinese white shrimp *F. chinensis* functions as an opsonin to facilitate bacterial clearance. The purified FcLec4 protein confirmed its opsonic activity by interaction with β -integrin on phagocyte of kuruma shrimp *M. japonicas* for phagocytosis of *V. anguillarum*. The interaction between FcLec4 and β -integrin did not rely on the carbohydrate recognition domain but on the N-terminus of FcLec4 [35]. In *Penaeus japonicus*, N-acetylglucosamine (GlcNAc) specific lectin was shown to have opsonic activity [36].

The lectin with O-acetyl neuraminic acid specificity was isolated from the hemolymph of the freshwater crab *Paratelphusa jacquemontii* and served as an opsonin in the phagocytosis of rabbit erythrocyte. The desialylated rabbit erythrocyte failed to bind to opsonin or the hemocyte for phagocytosis and revealed that sugar specificity of the lectin was essential for immune function [37]. In *Macrobrachium rosenbergii* the phagocytic mechanism of hemocyte are mediated by recognition of nonself cells in the hemocyte membrane by two independent mechanisms: specific, via O-acetylsialic acid, as well as N-acetylated sugars on recognized cells and a nonspecific one [32]. The carcinolectins 5, CL5a and CL5b (counterparts of TL5a and TL5b, respectively) in the horseshoe crab *C. rotundicauda*, are the major lectin proteins that bind all representative microbes and

initiate the activation of a novel complement-like system, leading to the phagocytosis of pathogens [39].

Diversity in lectin function

Lectins often bind to natural polysaccharides with much higher affinity than to simple monosaccharides and it has been attributed to extended binding sites, where the terminal sugar bind to the lectin and other sugars of the oligosaccharide bind specifically or non-specifically to the protein. The binding affinity also appears to be enhanced to an extended oligosaccharide by multiple binding in a cluster of several identical binding sites, often achieved through protein oligomerization [40]. The review demonstrate the increase in binding sites or diversified structure, for multiple binding sites of the lectin are essential for its role as Pattern Recognition Receptors (PRR) in innate immunity of crustacean. As a living fossil with more than 500 million years of survival, the horseshoe crab *Tachypleus tridentatus* shows a repertoire of lectins with diverse ligand specificities having undefined function [41,42]. Tachylectins (TL) 1-4, which exhibit diverse *in vitro* ligand specificities, are confined to the hemocytes and their functions remains unknown. The activity was also inhibited more strongly by bacterial S-type LPS but not by R-type LPS lacking O-antigen. There is no significant sequence similarity to any other known LPS-binding lectins, whereas tachylectin-4 is homologous to the NH₂-terminal domain with unknown functions of *Xenopus laevis* pentraxin 1 [43]. The recombinant protein of TPL-1 and -2 showed specific PGN and LPS-binding activity suggesting a role in trapping Gram-positive and Gram-negative bacteria respectively in innate immunity [44].

Tachylectin-1 and 3 from amoebocytes are nonglycosylated proteins and exist as dimer of a glycoprotein of molecular mass 36 kDa and 29 kDa respectively. The deduced amino acid sequence of TPL-2 with an N-glycosylation site, Asn-Cys-Thr, at positions 3-5 shared sequence identity with tachylectin-3. However the reported TPL-2 also a dimer of a glycoprotein with an apparent molecular mass of 36 kDa showed functional similarity with TPL-1 to bind and entrap Gram-positive and Gram-negative bacteria or any other invading organisms [45]. TLs and TPLs have different properties. TPL-1 and -2 found in plasma with completely different ligand specificities also found in Carbohydrate Reactive Proteins (CRP) consist of closely related family-of proteins with polymorphic ligand-specificity have sequence identities encoded by multiple genes [41]. The multiple form of proteins enable PAMP recognition by diverse ligand specificity encoded in the different forms of the proteins that serve as PRR of the host [46]. Two lectins, tachylectins 5A and 5B (TL-5A and TL-5B) were identified in the hemolymph plasma of *T. tridentatus*. TLs-5 agglutinated Gram-negative and Gram-positive bacteria, and the activity was more efficient for Gram-negative than for Gram-positive bacteria however had no antimicrobial activity against these bacteria. The fibrinogen-like domain of mammalian ficolins sequence identity of up to 51%, in TL-5A and TL-5B. Interestingly, a collagenous domain found in ficolins was found missing in the corresponding regions of TLs-5, which are conserved in TL-5A (Asp-198 and Asp-200) and TL-5B (Asp-215 and Asp-217). The horseshoe crab with a unique functional homologue of vertebrate fibrinogen, coagulogen, as the target protein of the clotting cascade, implicated s fibrinogen-related molecules in hemolymph plasma. As a nonself-recognizing protein [47]. The lectin from demosponge *Suberites domuncula*,

termed Suberites lectin a transmembrane protein shared the highest sequence similarity with lectin from the horseshoe crab *Tachypleus trunculus* of 27 kDa size [48].

The lectin Dorin M from soft tick, *Ornithodoros moubata* revealed significant sequence similarity with lectins from *T. tridentatus* TL-5A, TL-5B and vertebrate ficolins [49]. However, the collagen-like domain found in ficolins was missing in Dorin M and likewise in the corresponding region of TL-5. The cysteines form two disulfide bridges in native TL-5A and TL-5B [50] and have analogues in the sequence of native Dorin M. This implied similar folds of the secondary structure and the related binding to glycan surface of pathogens. The protein sequence similarity of Dorin M with TL-5A lectin of *T. tridentatus* and mammalian ficolins suggested the evolutionary conservation among the effector proteins in both vertebrates and invertebrates with regards to their innate immunity. The carcinolectins 5, CL5a and CL5b, the CL5 isoforms of horseshoe crab, *Carcinoscorpius rotundicauda*, of molecular size 36 and 40 kDa, respectively are prominent plasma lectins that bind all representative microbes and pathogen-associated molecular pattern molecules [39].

The occurrence of multiple lectins in primitive horse shoe crabs explains the function of innate immune system dependent on the multiplicity or diversity of the pathogen recognition molecules to defend against the continuous diversification of invading pathogens in evolution. In vertebrates the adaptive immunity diversified the recognition mechanism by variable binding ability of immunoglobulin molecule. The multiple lectins BRA-1, BRA-2 and BRA-3 were identified and isolated from the coelomic fluid of the acorn barnacle, *Megabalanus rosa*. The BRA-3 lectin was composed of 4 identical subunits of 138 amino acids forming dimers cross-linked by 5 disulfide bridges with homology to *Sarcophaga* (flesh fly) lectin [51]. The BRA-2 lectin of six identical subunits consisting of 173 amino acids cross-linked by disulfide bonds formed a dimer with one intrachain and two interchain disulfide bonds identified as Cys-53, Cys-61, Cys-14, and Cys-50, Cys-14 respectively. The two intrachain disulfide bonds are conserved through all invertebrate lectins and calcium-dependent animal lectins. From the evolutionary stand point, the marked homology of the invertebrate lectins suggests that the gene for the lectin evolved by gene duplication from a common ancestral gene. The differential expressions arise by physiological modulation as explained from isolated cDNA clones of BRA-3. A polymorphism in the BRA-3 mRNA was revealed, with single-nucleotide differences at three positions within the coding region and cause conserved changes in the amino acid. The BRA-3 mRNA and BRA-3 protein levels increased during early summer in a similar fashion, indicating that BRA-3 production is regulated mainly at the level of transcription [52].

The serum lectins in the freshwater prawn, *Macrobrachium rosenbergii* specific to N-acetylated sugars and α 2,3, α 2,6 linked or 9-O-acetyl sialic acid residues agglutinated *Pseudomonas hemolytica* and *Pseudomonas multicoda* defining its role as recognition molecule [53]. A similar lectin on the surface of granular hemocytes with phagocytic function suggested variance in localization of the lectin. The predicted amino acid sequence of the sialic acid specific serum lectin Mrl (9.5 kDa) showed homology to hyperglycemic hormone from *M. rosenbergii* and to the variable region of the human immunoglobulin kappa and lambda light chains [54].

In another report lectin aggregates MrL circulating in the hemolymph of the prawn as high-molecular weight MrL aggregates (MrL-I) that lack hemagglutinating activity of 62.1, 67.1 and 81.4 kDa proteins and MrL-III, showed hemagglutinating activity of 9.6 kDa protein. Edman degradation indicated NH₂-terminal sequence of five amino acids for the 9.6 kDa MrL-III (DVPLL/A) and eleven for the main 81.4 kDa band identified in MrL-I (DVPLL/AXKQQD); analysis by MALDI-TOF indicated a different tryptic pattern for MrL-I and MrL-III. MrL-I was recognized by monoclonal antibodies against MrL-III. Circular dichroism indicated similarity in secondary structure and clearly indicated differential post translational processes to favor aggregations involved in regulation and activity of the lectins [55].

The multiplicity of the lectins as molecules of immune response apparently under continuous selective pressure, modulates its functions to enhance its efficiency at levels of post transcription or post translation though retaining nucleotide sequence of the gene or amino acid sequence of the protein at primary or secondary structure with changes in tertiary structure to bind to the glycosylated cell surface of the pathogen. Further studies on *M. rosenbergii* contend with the view on immune functions of lectins. About 20 lectins including C-type lectins [dual-Carbohydrate Recognition Domain (CRD) type and single-CRD type], L-type lectin, and lectin with Low-Density Lipoprotein Class A (LDLa) domain were identified under spiroplasma strain MR-1008 challenge and were found mainly distributed in the hepatopancreas, hemocytes, nerve, intestine, and heart. The lectin expression were upregulated at different times after the challenge (except Lectin 15) to indicate that lectins are variable and function in early or late immune responses against the recognized pathogen [56]. The gene expression for the lectin protein appears modulated at different levels of expression and controlled by factors that enhance immunity.

The existence of multiple lectins has been demonstrated in prawns and shrimps [19,11,17], also the lobsters *Homarus americanus* and species of *Jasus* have equipped the effector immune response by diverse forms of lectin [57, 58].

Sialic acid specific lectins

Sialic acids a family of 9-carbon carboxylated sugars with diverse forms arising by substitution or modification of its side chain and occupy the terminal position of glyconjugates on the cell surface of deuterostomes, developmental larval stages of protostomes [59] and some microbes [60]. The structural diversity of sialic acids and variation in binding affinity of lectins affected by structural modulations explains the diversity with an apparent evolutionary basis for host or pathogen recognition. The species in crustacea possess lectins with an ability to recognize diverse forms of sialic acid, N-acetyl neuraminic acid, Neu5Ac [61], N-glycolyl neuraminic acid, Neu5Gc [62], O-acetyl NeuAc [63, 64, 65]. The species in crustacea belong to protostomes and lack the enzymes for synthesis of sialic acid and the gene for sialic acid specific lectin was probably an event of lateral transfer among bacteria or vertebrate host or bacterial infection by vector and lead to convergent evolution [66]. Dorin M lectin from the tick *O. moubata* with binding specificity for sialic acids, recognize and bind to sialic acid on the cell wall of spirochete *Borreliaburgdorferi* and *B. duttoni*, the causative agent of relapsing

fever and transmitted by the vector tick [67]. The microbial transfer of the sialic acid specific lectin to microbes and even the host explains lateral transfer of genes [68]. The repertoire of sialic acid specific lectins in crustacea represents the evolutionary changes that occur in glycosylated surface of pathogens and their recognition. Further elucidation of lectin based innate responses probably explains pathogenesis with related glycosylated cell surface of the pathogen.

Conclusion

The innate immune response in invertebrates functions with an array of PRR to identify and recognize the diversification in the glycosylated surface of PAMP in pathogens. The lectins as effector molecules of innate response is involved in recognition and antibacterial activity, also as opsonin in cellular defense reactions of encapsulation and phagocytosis. The lectin molecule from crustacea in its structure has shown homology to the lectin from the simplest demosponge *Suberites domuncula* [48] to a complex variable region of the human immunoglobulin. However lectins from crustacea are variant forms with the amino acid sequence showing low identity or homology [54]. This diversity in C-type lectin is evident in crustacea though the CTLD in vertebrates occur with few modifications within the vertebrate lineage during evolution from fish to mammals [69]. The diversity in structural forms of lectin was probably directed to increase the binding sites and the specific binding affinity with more than one sugar. The evolution of the gene for lectin probably from multigene ancestors as of multi-segmental, multi-gene origin of immunoglobulin, probably explains the origin of diverse forms of lectin in a species. However, homology among the multiple forms of lectin in a species indicate the origin of the gene for lectin by duplication of a common ancestral gene, also oligomerization of protein increases the diversity in glycan binding affinity. Moreover the regulation of gene transcription and post- translation modulations are also factors that play an important role in the production of variant secondary or tertiary structures of lectin in response to the diversifying PAMP of pathogen. The crustacean lectins appear to have diversified against the challenge of mutating pathogens in the defensive process to survive and in the course of evolution the crustacean lectins are diverse with common function of PRR.

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