# Chapter 4 Collectins: Innate Immune Pattern Recognition Molecules



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**Abstract** Collectins are collagen-containing C-type (calcium-dependent) lectins which are important pathogen pattern recognising innate immune molecules. Their primary structure is characterised by an N-terminal, triple-helical collagenous region made up of Gly-X-Y repeats, an a-helical coiled-coil trimerising neck region, and a Cterminal C-type lectin or carbohydrate recognition domain (CRD). Further oligomerisation of this primary structure can give rise to more complex and multimeric structures that can be seen under electron microscope. Collectins can be found in serum as well as in a range of tissues at the mucosal surfaces. Mannanbinding lectin can activate the complement system while other members of the collectin family are extremely versatile in recognising a diverse range of pathogens via their CRDs and bring about effector functions designed at the clearance of invading pathogens. These mechanisms include opsonisation, enhancement of phagocytosis, triggering superoxidative burst and nitric oxide production. Collectins can also potentiate the adaptive immune response via antigen presenting cells such as macrophages and dendritic cells through modulation of cytokines and chemokines, thus they can act as a link between innate and adaptive immunity. This chapter describes the structure-function relationships of collectins, their diverse functions, and their interaction with viruses, bacteria, fungi and parasites.

**Keywords** Collectins · Pathogens · Innate immunity · Phagocytes · Receptors

#### 4.1 Introduction

Collectins (collagen-containing C-type lectins) are soluble mammalian C-type lectins, which represent an important group of pattern-recognition molecules and serve multiple functions in the innate immune system. The term "collectin" was first

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used by Malhotra et al. (1992). They are known to mediate pathogen recognition through calcium-dependent carbohydrate recognition domains (CRDs). The following nine collectins have been identified to date: mannan-binding lectin (MBL), three bovine serum collectins, conglutinin, CL-43 and CL-46, lung surfactant proteins SP-A and SP-D, and more recently discovered collectins including, collectin kidney 1 (CL-K1, also called CL-11), collectin liver 1 (CL-L1, also called CL-10) and collectin placenta 1 (CL-P1 also called CL-12). The overall functions of collectins include microbial aggregation and neutralisation, opsonisation, complement activation, and modulation of inflammatory responses.

#### 4.2 Structure of Collectins

Collectins are oligomers of trimeric subunits, For most collectins, the subunits are homotrimers (made up of three identical polypeptides) but heterotrimers can be found for SP-A, which is made up of highly homologous SPA-1 and SPA-2 polypeptides. Hetrotrimers can also form in the case of CL-10 and CL-11 (Fig. 4.1). The subunit of each collectin is composed of (i) a short N-terminal (7-28 amino acid residues) cysteine-rich domain, involved in multimerisation (by disulphide bridging); (ii) a collagen-like domain composed of Gly-X-Y triplets repeats, where X and Y represent any amino acids; (iii) a short segment which can form coiled-coil helices, and (iv)

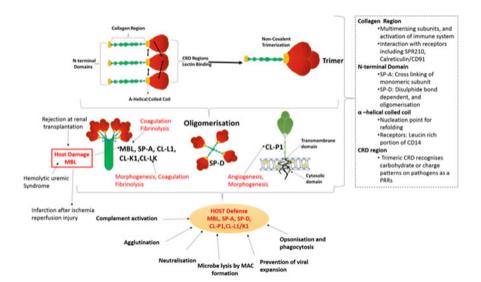
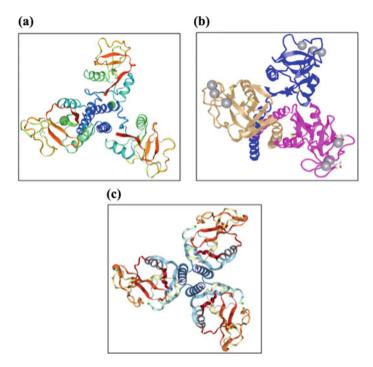


Fig. 4.1 Molecular structural representation and biological functions of human collectins. Collectins are shown as monomeric subunits, followed by trimeric subunits, composed of an N-terminal domain, collagen-like region,  $\alpha$ -helical coiled-coil neck region and C-terminal carbohydrate recognition domain (CRD). Biological functions of each domain are also briefly described



**Fig. 4.2** Three-dimensional structures of trimeric human SP-A (a), SP-D (b), and MBL (c). Representations of the trimeric "head" of collectins. These structures represent the 'neck', and the CRDs of three polypeptides which make up the trimeric subunit. The helix interacts with a neighbouring carbohydrate recognition domains (Kishore et al. 2006; Skjoedt et al 2012)

the C-terminal globular C-type lectin domain, also called the CRD (carbohydrate recognition domain) (Uemura et al. 2006) (Fig. 4.1).

The triple-helical collagen region provides significant rigidity and stability to the molecule (Colley and Baenziger 1987). Another structural feature of the collagen-like domain of collectins is that it can be O-glycosylated (Colley and Baenziger 1987). Both MBL and SP-A show an interruption of the Gly-X-Y triplet repeats, which introduces a bend in the otherwise straight triple helix. This enables the fully assembled multi-subunit structure to angle away from the central core, producing a structure resembling a bouquet of flowers (Fig. 4.2) (Voss et al. 1991). Several distinct functions of the collagen domain of collectins have been reported. The collagen domains of SP-A and MBL are involved in receptor-mediated properties. A GEKGEP specific motif found within the collagen domain of MBL is suggested to bind C1q receptor (Arora et al. 2001), and mediates the enhancement of phagocytosis through C1qR (Arora et al. 2001). A similar motif is within the collagen domain of SP-A (White et al. 1985), which is also involved in the interaction with C1q receptor (Malhotra et al. 1992; Malhotra et al. 1990), and mediates phagocytosis of *Staphylococcus aureus* by monocytes (Geertsma et al. 1994). Furthermore, the collagen

domain of MBL is shown to bind MBL-associated serum proteases, MASP1, 2 and 3, which mediate complement activation via the lectin pathway (Thiel et al. 1997; Tan et al. 1996). Additionally, the positively charged collagen region found in the membrane bound CL-P1 is involved in the uptake of oxidised LDL particles (Ohtani et al. 2001).

The cysteine residues found within the N-terminal domain (7-28 amino acids) form disulphide bonds between monomers, thereby, stabilising trimeric subunits as well as a larger multimers. It was believed that at least two cysteine residues are required at the N-terminal domain for the formation of multimers of trimeric subunits (Brown-Augsburger et al. 1996; McCormack et al. 1999; McCormack et al. 1997a, b). However, in the case of CL-43, it is secreted as a single trimeric subunit, despite having two cysteine residues (Rothmann et al. 1997; Lim et al. 1994a, b). Therefore, other factors contribute to oligomerisation of trimeric subunits, in addition to the of N-terminal cysteine residues.

The C-terminal region contains a coiled-coil trimerizing neck region (residues 112-130 in human MBL) (Fig. 4.1), and the CRD (residues 134-245 in human MBL) which folds up into an independent globular carbohydrate—binding structure for each polypeptide chain. Each subunit is held together covalently through disulphide bonds, or non-covalently structured into oligomers of up to six subunits. C-type CRDs are connected to the collagen-like domain through the 'neck' region (24-28 amino acid residues) (Hoppe and Reid 1994). Furthermore, the neck region is involved in aligning the collagen chains.

### 4.2.1 Ligand Specificity of Collectins

A broad carbohydrate specificity is required by collectins in order to recognise and bind a large repertoire of (pathogen-associated molecular patterns) PAMPs. Such broad specificity is achieved by an open and flexible trough -like binding pocket found within the CRDs. The selection of ligands by this site depends on the positioning of vicinal hydroxyl groups of sugars, which form coordination bonds with a ligated calcium ion, hydrogen bonds and a polar Van der Waals contact (Ng et al. 1996). Ligand specificity of collectins is divided into two main sub-classes (mannosebinding or galactose-binding type), which is based on a three amino acid residue motif found in the Ca<sup>++</sup> ion binding site. The sequence 185-Glu-Pro-Asn is associated with binding of mannose-like sugars, while the sequence 185-Gln-Pro-Asp is associated with binding galactose-like sugars. The molecular differences based on which CRDs discriminate between mannose and galactose-type ligands depend on the orientation of C3 and C4 vicinal hydroxyl groups presented on monosaccharides. Mannose-specific CRDs bind ligands in which hydroxyl groups at the C3 and C4 positions are in an equatorial orientation (mannose, glucose, glucosamine), while in galactose these vicinal hydroxyls are in an axial orientation (Drickamer and Taylor 2015). Inhibition studies using monosaccharides have shown that most likely, all the

above described collectins, except CL-P1, prefer mannose ligands over galactose (Ohtani et al. 2001; Holmskov et al. 1994).

However, a wider range of binding specificity has been reported for MBL and lung surfactant proteins SP-A and SP-D, as these collectins are also capable of binding to nucleic acids (Nadesalingam et al. 2003), phospholipids (Sano et al. 1999), as well as non-glucosylated proteins.

Fucose, a hexose deoxy sugar is bound by mannose-specific CRDs in a different manner as it has equatorial hydroxyl groups placed on its C2 and C3 position of the sugar ring, not the C3 and C4 (Weis et al. 1991a, b; Ng et al. 1996; Jobst and Drickamer 1994). Computational docking studies have demonstrated that αD-glucose docks into the CRD of SP-D via vicinal equatorial hydroxyl groups on the 2- and 3- position of its sugar ring (Allen et al. 2001a, b). Although MBL affinity is reported to be very low for monosaccharide galactose, MBL crystallographic studies demonstrate that galactose is ligated in the MBL binding region via coordination bonds with hydroxyl groups placed at C1 and C2 position of the sugar ring (Ng et al. 1996). In addition to galactose and mannose, binding of collectins to a range of sugars has also been studied (Holmskov et al. 1994); they exhibit preferences for certain sugar residues over others. For instance, despite SP-D being structurally similar to conglutinin, it displays a greater affinity for maltose, a glucose disaccharide, which is a weak ligand for conglutinin. SP-D is suggested to have a lower affinity for GlcNAc, which is the best ligand for conglutinin. Moreover, binding of CL-43 to sugars is closely related to MBL, although the structure of CL-43 is closer to SP-D and conglutinin (Lu et al. 2002).

The sugar-binding specificity of CL-11/CL-K1 has been investigated (Venkatraman Girija et al. 2015). It has a larger recognition interface than MBL, and recognises predominantly mannose-rich structures, interacting with two sugar residues at a glycan terminal, rather than a single sugar.

### 4.3 Biosynthesis and Localisation of Collectins

Human MBL is synthesised by hepatocytes and secreted into the blood stream (Sastry et al. 1991; Ezekowitz et al. 1988; Hansen et al. 2000). Initially, MBL was isolated from the liver of the rabbit, rat and chicken, where expression levels were detected in the soluble cytosol, rather than on the cell surface. Two forms of MBL (MBL-A and MBL-C) were detected in rodents (Hansen et al. 2000; Drickamer et al. 1986), rabbits (Kawasaki et al. 1978; Kozutsumi et al. 1980) and rhesus monkeys (Mogues et al. 1996). However, only one form of MBL is present in humans and chimpanzees (Mogues et al. 1996). Although the liver is the main production site of MBL-A and MBL-C in mice, mRNA expression of MBL was also detected in various tissues (Table 4.1) (Shushimita et al. 2015). Substantial expression levels of MBL-A and MBL-C were reported in kidney and intestine (Table 4.1). Detection of MBL proteins in the small intestine suggests that MBL may have similar roles to secretory IgA (Reichhardt et al. 2012).

**Table 4.1** Origin of collectins and their tissue distribution

Collectins	Tissues of origin	Tissues of presentation	Remarks
MBL	Liver and small intestine	Serum	Two different variants of MBL (A and C) have been identified in animals, while only one variant is found in humans and chimpanzee.
Conglutinin, CL-43 and CL-46	Bovine liver	Serum	These bovine collectins plays an important role in the first line of defense against rumen microbes without eliciting general inflammatory response
SP-A and SP-D	Clara cells, intestinal mucosa, thymus, prostrate gland, Eustachian tube, paranasal sinuses, middle ear, synovium	Alveolar space, mucosal surfaces, semen	Extrapulmonary expression of SP-A is limited to a few organs, while SP-D expression has been detected in many non-pulmonary mucosal tissues
CL-P1	Placenta, and vascular endothelial cells	Endothelial cells	CL-P1 is the only membrane bound collectin with an intracellular domain. It is suggested to play many roles which differ from those of soluble collectins
CL-K1		Serum	Different from all other collectins, but seems to have functions phylogenetically similar to CL-L1

(continued)

The collectins SP-A and SP-D are primarily detected in the alveolar space of the lungs, and synthesised by alveolar type-II cells (Table 4.1) (Voorhout et al. 1992, Nayak et al. 2012), and nonciliated bronchial epithelial cells, also known as Clara cells (Voorhout et al. 1992; Crouch et al. 1992). Although the lung is the main

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Collectins	Tissues of origin	Tissues of presentation	Remarks
CL-L1	Liver and hepatocyte	Ubiquitous	Immunoblot analyses using human liver demonstrated that CL-L1 was distributed to the cytoplasm. It is also involved in embryonic development

site of SP-A and SP-D synthesis, presence of SP-D has also been reported at extrapulmonary sites. SP-D expression has been shown immunohistochemically in human trachea, brain, heart, kidneys, testis, salivary gland, placenta, prostate, small intestine, and pancreas (Table 4.1). A low expression level has been detected in spleen, uterus, adrenal gland and mammary glands (Fisher and Mason 1995; Madsen et al. 2000; Herías et al. 2007). Furthermore, immunoreactivity of SP-D has also been shown in the epithelial cells of both small and large ducts of the parotid gland, lacrimal and sweat glands, epithelial cells of intra-hepatic bile ducts and gall bladder, as well as esophagus, exocrine pancreatic ducts, and in the urinary tract (Madsen et al. 2000; Bräuer et al. 2007). In the case of SP-A, low levels are detected in small intestines from human and rat (Table 4.1) (Lin et al. 2001, van Iwaarden et al. 1990). In addition to its presence in the murine uterus, very low SP-A expression is found in human prostate, amniotic fluid, thymus and salivary gland (Madsen et al. 2003). SP-A and SP-D have also been localised in the fetal membranes, and choriodecidual layer of the late pregnancy uterus (Miyamura et al. 1994). As a result of pulmonary microbial infection, the protein levels of both SP-A and SP-D have been reported to increase in the alveolar compartment (Atochina et al. 2001). Thus, the level of SP-D increases in response to allergen-induced eosinophilia (Kasper et al. 2002), suggesting that both SP-A and SP-D may function as acute phase reactants within the lungs. Furthermore, hypoxia results in an increased concentration of both SP-A and SP-D in the alveolar compartment (White et al. 2001).

Conglutinin, CL-46 and CL-43 are serum collectins identified in bovidae and synthesised in the liver (Hansen et al. 2002). These collectins provide a first line of defense against microbial pathogens. CL-L1 mRNA was detected in the liver, and studies using Northern blot analysis have suggested that low levels occur in the placenta. Although most collectins are secreted, CL-L1 was found in the cytosol of hepatocytes, which may suggest its interaction with intracellular ligands (Ohtani et al. 1999). The presence of CL-P1 was reported in vascular endothelial cells (Table 4.1); CL-P1 is suggested to be membrane bound, and it contains an intracellular domain (Ohtani et al. 2001). Expression of MBL, SP-A and SP-D at the mucosal surfaces suggest the innate immune roles of these collectins against invading pathogens. During

*Helicobacter pylori* infection, an increased level of SP-D has been detected, suggesting the possible role of SP-D in the mucosal defense outside the lungs (Murray et al. 2002), eg. gastrointestinal tract.

#### 4.4 Role of Collectins in Microbial Infection

Collectins are important soluble pattern-recognition receptors (PRRs) of the humoral arm of the innate immune response. Collectins are able to recognise and bind to a wide variety of microbes and are involved in their clearance and forming a central link to adaptive immunity against microbial infections. In this section, we will discuss the well-known collectins: MBL, SP-A and SP-D, as well as newly discovered collectins: liver collectin (CL-L1), kidney collectin (CL-K1), and placenta collectin (CL-P1). We will also briefly discuss bovine collectins, conglutinin, CL-43 and CL-46. Microbes can be cleared by collectins via a number of mechanisms such as aggregation, opsonisation, phagocytosis, microbial growth inhibition, complement activation, as well as modulation of adaptive immunity.

#### 4.5 Interaction of Collectins with Bacteria

#### 4.5.1 SP-A and SP-D

Pulmonary surfactant is composed of 90% phospholipids and 10% proteins (made up of surfactant proteins, SP-A, SP-B, SP-C and SP-D. Whilst, SP-B and SP-C are hydrophobic and essential for the physiology of the alveolar surfaces, SP-A and SP-D are hydrophilic and contribute to lung immunity. An early study showed that pulmonary surfactant enhanced the killing of Staphylococcus aureus by alveolar macrophages (AM), in vitro (LaForce et al. 1973). Both Gram-negative and Grampositive bacteria are recognised by SP-A and SP-D, enhancing their phagocytosis by AMs (Fig. 4.3) (Pikaar et al. 1995). For Gram-negative bacteria, SP-A and SP-D both bind to lipopolysaccharide (LPS) but differ in preferential targets on the molecule. SP-A binds to the lipid A moiety of rough LPS (which lacks the O-antigen and shortened oligosaccharides) (Van Iwaarden et al. 1994), and enhances phagocytosis of bacteria by AM (Kalina et al. 1995), but not to smooth LPS (which contains the O-antigen) (Van Iwaarden et al. 1994). In contrast, SP-D binds strongly to smooth LPS from Escherichia coli and Salmonella species but does not recognise the lipid A moiety or oligosaccharide deficient LPS (Kuan et al. 1992). This indicates that SP-D preferentially targets the core terminal saccharides in the bacterial ligand, whilst SP-A prefers lipid A. SP-D has also able been shown to bind to rough LPS via its trimeric carbohydrate recognition domain (CRD), (targeting shortened oligosaccharides) and agglutinating E. coli (Kuan et al. 1992), and rough LPS from Klebsiella

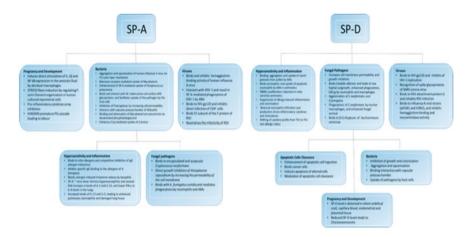


Fig. 4.3 Multiple functions of SP-A and SP-D in human health and disease

pneumoniae and Pseudomonas aeruginosa (Lim et al. 1994a, b; Kishore et al. 1996). In addition to LPS, SP-A is able to bind to capsular polysaccharides of *Klebsiella* species, enhancing their phagocytosis by AM (Kabha et al. 1997). However, bacterial peptidoglycan is not a ligand for SP-A (Murakami et al. 2002).

SP-A and SP-D directly inhibit the growth of several Gram-negative bacteria by increasing the membrane permeability of the bacterial cell wall (Fig. 4.3) (Wu et al. 2003). SP-A and SP-D also inhibit biosynthetic functions in strains of E. coli, K. pneumoniae and Enterobacter aerogenes (Wu et al. 2003), Similarly, SP-A inhibits the growth of *P. aeruginosa* by increasing membrane permeability (Van Iwaarden et al. 1994), but the bacterium can resist through quorum-sensing and the secretion of a flagellum-mediated exoprotease that degrades SP-A (Kuang et al. 2011a). Furthermore, SP-A downregulates TNF-α secretion via toll-like receptor 2/NF-κB mediated pathway, indicating its role in modulating inflammatory responses against bacterial ligands (Murakami et al. 2002). SP-A can bind to the outer membrane protein (OMP) of Haemophilus influenzae type A and to a lesser extent, type B (McNeely and Coonrod, 1994). SP-A can also aggregate and opsonise H. influenzae type A, facilitating killing by AM (McNeely and Coonrod 1994). Similarly, SP-A binds to the capsular polysaccharide of some strains of K. pneumoniae, agglutinating the bacteria and increase phagocytosis by macrophages (Kabha et al. 1997), and treatment with SP-A plus SP-B<sup>N</sup> (N-terminal saponin domain of SP-B) significantly reduced bacterial infection and enhanced neutrophil recruitment (Coya et al. 2015). SP-A has a bacteriostatic effect on Mycoplasma pneumoniae via binding to di-saturated phosphatidylglycerols on the bacterial membrane (Piboonpocanun et al. 2005). SP-A can interact with Mycobacterium tuberculosis putative adhesin Apa glycoprotein on its surface (Ragas et al. 2007). SP-D can also bind to Gram-positive bacterial ligands such as lipoteichoic acid and peptidoglycan via its CRD (van de Wetering et al. 2001) and to lipoarabinomannan (LAM) from M. tuberculosis and Mycobacterium

*avium* (Ferguson et al. 1999; Kudo et al. 2004). SP-D is also able to interact with cell membrane lipids of *M. pneumoniae* (Chiba et al. 2002).

It is intriguing that although both SP-A and SP-D bind and agglutinate *M. tuberculosis*, they have opposing effects on phagocytosis by macrophages. SP-A enhances phagocytosis via increased expression of mannose receptor on the host cell surface (Beharka et al. 2002), whilst SP-D inhibits phagocytosis by blocking the interaction of LAM with macrophage mannose receptor, and not as a result of bacterial agglutination by SP-D (Ferguson et al. 1999, 2002). In a mouse model of tuberculosis infection, SP-A<sup>-/-</sup>, SP-D<sup>-/-</sup>, and SP-A/D<sup>-/-</sup> knockout mice still had the ability to phagocytose and clear M. tuberculosis when given a low-dose aerosol challenge of the pathogen, suggesting that both SP-A and SP-D could be redundant in this animal model (Lemos et al. 2011). Similarly, both SP-A and SP-D can also bind to *Legionella pneumophila*, but seem to inhibit intracellular bacterial growth in the macrophage (Sawada et al. 2010).

SP-A and SP-D can also directly facilitate phagocytosis without the need for microbial binding, by up-regulating the expression of cell surface phagocytic receptors in macrophages, such as mannose receptor (Beharka et al. 2002; Kudo et al. 2004). In SP-A<sup>-/-</sup> knockout mice, expression of mannose receptor is down-regulated, showing that SP-A is important in regulating the expression of this receptor (Beharka et al. 2002). Similarly, SP-A is able to enhance phagocytosis of *Streptococcus pneumoniae* by AM, independent of its binding to the bacterium, via the increased expression of scavenger receptor A (SR-A) (Kuronuma et al. 2004). Interestingly, the vast majority of clinical strains of the opportunist *Pseudomonas aeruginosa* secrete an elastase that degrades SP-A and facilitates evasion of opsonisation by the collectin during phagocytosis (Kuang et al. 2011b).

SP-A and SP-D can play important roles in modulating the intracellular environment after phagocytosis by stimulating reactive oxygen and nitrogen intermediates facilitating the killing of intracellular pathogens. This is of particular note in mycobacteria, which are specialist intracellular bacteria. SP-A enhances the killing of intracellular  $Mycobacterium\ bovis\ BCG$  by increasing nitric oxide (NO) production, in addition to enhancing the release of inflammatory mediators such as TNF- $\alpha$  (Weikert et al. 2000). In contrast, in IFN- $\gamma$  primed AM, SP-A decreases NO production in response to intracellular infection with  $M.\ tuberculosis$  and  $M.\ avium$  by inhibiting TNF- $\alpha$  secretion and nuclear factor-kappa B (NF- $\kappa$ B) activation (Pasula et al. 1999; Hussain et al. 2003). SP-A can also enhance the intracellular killing of  $Mycoplasma\ pulmonis\ via\ a\ NO\ dependent\ mechanism (Hickman-Davis\ et\ al.\ 1998).$ 

Bacteria-derived cell-wall molecules such as LPS and peptidoglycan are potent stimulators of inflammation and can also interact with pattern-recognition receptors (PRRs) such as CD14 or toll-like receptors (TLR), via pathogen-associated molecular patterns (PAMPs), and activate downstream intracellular signalling. SP-A and SP-D can also directly bind to PRRs (e.g. TLR and CD14) and thus can modulate the inflammatory response. SP-A and SP-D can alter LPS interactions with CD14 via different mechanisms (SP-A via neck domain; SP-D via CRD) (Sano et al. 2000). Furthermore, via direct interaction with CD14, SP-A inhibits production of TNF-α induced by smooth LPS, but not rough LPS in U937 macrophages (Sano et al.

1999). In SP-A $^{-/-}$  knockout mice, TNF- $\alpha$  induced by smooth LPS, significantly increased, compared to wild-type mice (Borron et al. 2000), whilst SP-A has also been shown to inhibit TNF- $\alpha$  induction by peptidoglycan via direct binding to TLR-2 (Murakami et al. 2002). Thus, SP-A significantly decreases peptidoglycan or smooth LPS-induced pro-inflammatory responses (via NF- $\kappa$ B activation). SP-A has no effect or increases the inflammatory response induced by rough LPS. In tuberculosis, SP-A has pleiotropic effects being able to promote inflammation in the presence of infection and suppresses inflammation in uninfected macrophages, probably protecting uninfected lung areas from the deleterious effects of inflammation (Gold et al. 2004).

In humans, SP-A exists in two isoforms, SP-A1 and SP-A2, which are encoded by distinct genes. Fully assembled SP-A protein contains both gene products. A number of studies have described polymorphisms in these genes and the SP-D gene which may have a role in susceptibility to microbial infection, particularly tuberculosis. Polymorphisms within and flanking the SP-A1 and SP-A2 genes have been described which indicate protection or susceptibility toward pulmonary TB in the populations studied in Mexico, Ethiopia, India and China (Floros et al. 2000; Madan et al. 2002; Malik et al. 2006; Vaid et al. 2006; Yang et al. 2014). Two SP-A1 alleles (SFTPA1 307A, SFTPA1 776T) and two SP-A2 alleles (SFTPA2 355C and SFTPA2 751C) were associated with tuberculosis susceptibility in Ethiopia (Malik et al. 2006). The SFTPA2 751A/C polymorphism and the haplotype 1A<sup>3</sup> in SP-A2, which both affect the amino acids in CRD region of SP-A, may alter binding to M. tuberculosis and thus were found to be strongly linked with tuberculosis susceptibility (Malik et al. 2006). Another study also found two polymorphisms (SP-A2 G1649C and SP-A2 A1660G) in the introns of SP-A1 that were associated with tuberculosis in an Indian population, but none in the SP-A1 gene (Madan et al. 2002). In a Chinese population, the polymorphism 1649G in the SP-A2 gene was strongly associated with tuberculosis, mirroring the findings in the Ethiopian and Indian populations (Yang et al. 2014). The SP-A2 1649G leads to a transversion (proline to alanine), affecting the triple helical structure of SP-A (Yang et al. 2014). In SP-D, the polymorphism, G459A, is significantly associated with tuberculosis susceptibility in an Indian population, but the molecular basis for susceptibility is not understood (Vaid et al. 2006). These observations illustrate the complexities of host-pathogen interactions in bacterial infection mediated by these collectins.

#### 4.5.2 MBL

MBL is the recognition subcomponent of the lectin pathway of the complement system and is present mostly in the serum. The structure of MBL is similar to that of SP-A, and in the presence of Ca<sup>2+</sup>, it has been observed to target terminal sugars (e.g. D-mannose, L-fucose, and *N*-acetyl-D-glucosamine), on the surface of a number of Gram-positive and Gram-negative bacterial species (Ip et al. 2009; Lugo-Villarino et al. 2011). The binding of MBL to microbial surfaces can activate complement

through MBL-associated serine proteases (MASPs), resulting in enhanced microbial clearance via opsonisation (C3 and C4 deposition) and complement-mediated lysis. However, MBL also has complement-independent activity such as inhibition of bacterial adhesion (Jack et al. 2005) and opsonisation to enhance bacterial uptake (Kuhlman et al. 1989; Polotsky et al. 1997; Jack et al. 2005). Strong in vitro binding of MBL to S. aureus, Streptococcus pyogenes, Listeria monocytogenes and nonencapsulated Neisseria meningitidis has been described (Levitz et al. 1993; van Emmerik et al. 1994; Neth et al. 2000). Moderate levels of MBL binding were observed in E. coli, Haemophilus influenzae and Klebsiella species, whilst no binding has been observed for P. aeruginosa, Enterococcus species and Streptococcus pneumoniae (Levitz et al. 1993; van Emmerik et al. 1994; Neth et al. 2000). Bacterial pathogens have involved strategies to interfere with MBL binding and functions for survival, via the synthesis of a polysaccharide capsule and sialylation of LPS ligands on the bacterial surface which reduces the binding of MBL (Jack et al. 2005; Krarup et al. 2005). This effectively masks or alters the bacterial ligands for MBL interaction. A number of studies have characterised the bacterial ligands for MBL. MBL is able to bind to peptidoglycan and lipoteichoic acid from S. aureus (Polotsky et al. 1996; Nadesalingam et al. 2005a, b), LAM from M. avium (Polotsky et al. 1997), and mannosylated lipoarabinomannan (ManLAM) from a number of mycobacteria (M. tuberculosis, M. bovis, M. kansasii, M. gordonae and M. smegmatis) (Bartlomiejczyk et al. 2014). There is also a report of MBL binding to the antigen 85 (Ag85) complex of M. tuberculosis (Swierzko et al. 2016). Neisseria (M. meningitidis and M. gonorrhoeae) are Gram-negative diplococci that have shorter versions of LPS on their surface called lipooligosaccharides (LOS) that are commonly terminated in sialic (neuraminic) acid, instead of the O-antigen. Neisseria bacteria are able to decrease binding of MBL to their surface by the sialylation on LOS (Jack et al. 1998; Devyatyarova-Johnson et al. 2000; Jack et al. 2001; Gulati et al. 2002). M. meningitidis can also interfere with MBL binding through encapsulation (van Emmerik et al. 1994), whilst M. gonorrhoeae is not able to form capsules. Encapsulation seems to be less robust at decreasing MBL binding than sialyation of LOS (Jack et al. 1998). Bound MBL can activate complement and the ability of Neisseria species to cascade complement all the way to C9 (membrane attack complex (MAC)) is crucial for protection against infection, since they are otherwise poorly phagocytosed by neutrophils and macrophages when opsonised by C3 (Ross and Densen 1984). MBL bound to the surface of Neisseria is able to increase bacterial killing via increased complement activation (Jack et al. 1998, 2001; Gulati et al. 2002), and similar observations of bactericidal activity have been reported for E. coli and Salmonella species (Kawasaki et al. 1989; Ihara et al. 1991). For most other bacteria, complement activation to the C3 deposition stage is enough for protection via increased phagocytosis through opsonisation by complement products on the bacterial cell surface. MBL can increase C3b deposition on S. aureus (Neth et al. 2002), but this does not appear to result in increased complement activation (Cunnion et al. 2001). MBL targets wall teichoic acid in S. aureus and this interaction is particularly important in infants that have not developed adaptive immunity, leading to bacterial clearance via MBL-mediated complement activation (Kurokawa et al. 2016).

In addition to its complement-mediated activities, MBL is also has various intrinsic effects, being able to act as an opsonin independently and other direct effects. MBL enhances uptake and intracellular killing of Salmonella by neutrophils and monocytes (Kuhlman et al. 1989), but this may also involve interaction with fibronectin (Ghiran et al. 2000). Recently, MBL has also been shown to have a direct inhibitory effect on flagellar activity in pathogenic Salmonella bacteria, impairing their motility (Xu et al. 2016). MBL can also increase uptake of mycobacteria by macrophages (Polotsky et al. 1997) and *N. meningitidis* by neutrophils, monocytes and macrophages (Jack et al. 2001), but this uptake by neutrophils may not result in intracellular killing (Drogari-Apiranthitou et al. 1997). MBL also appears to improve the efficiency of internalisation of bacteria bound to the macrophage plasma membrane (Neth et al. 2002). MBL co-interacts with TLR2 in sensing *S. aureus* and thus influencing the subsequent inflammatory response (Nauta et al. 2003; Ip et al. 2008).

MBL deficiency increases susceptibility to microbial infection even though the majority of MBL-deficient individuals are usually healthy (Eisen and Minchinton 2003). The concentration of MBL in the plasma varies considerably in humans (0– 10, 000 ng/ml) due to polymorphisms in the MBL gene (Steffensen et al. 2000). MBL deficiency is commonly observed in around 25% of Caucasians (having low levels (<500 ng/ml)), which renders them susceptible to infection (Valdimarsson et al. 2004). MBL-deficient mice are susceptible to S. aureus infection (Shi et al. 2004), whilst MBL deficiency increases susceptibility to postburn infection with P. aeruginosa (Moller-Kristensen et al. 2006). A large cohort study has also found a strong association between MBL deficiency and meningococcal infection, and pneumococcal pneumonia, in patients undergoing chemotherapy (Gaynor et al. 1995; Kronborg et al. 2002; Roy et al. 2002). In contrast, normal or increased levels of MBL are linked to frequent infection with M. tuberculosis and M. leprae (Garred et al. 1994, 1997b), probably through complement-mediated phagocytosis of the pathogen. Up to 30% of healthy individuals have polymorphisms linked to MBL deficiency and these, together with serum levels, have been associated with susceptibility to tuberculosis and other inflammatory diseases in some ethnic populations (Takahashi and Ezekowitz 2005; Thiel et al. 2006; Goyal et al. 2016).

# 4.5.3 CL-L1, CL-K1, CL-P1 and the Bovine-Unique Collectins, Conglutinin, CL-43 and CL-46

Of the three more recently discovered collectins (CL-L1, CL-K1, CL-P1), CL-L1 and CL-P1 have been shown to have bacterial interactions. CL-K binds to *E. coli*, *K. pneumoniae*, *P. aeruginosa* and *M. tuberculosis* (Keshi et al. 2006; Hansen et al. 2010; Troegeler et al. 2015), whilst CL-P1 can bind to *E. coli* and *S. aureus* (Ohtani et al. 1999; Jang et al. 2009). Both CL-L1 and CL-K1 can activate the complement lectin pathway as can the heteromeric form CL-LK, which interacts with the MASPs (Henriksen et al. 2013). CL-P1 can activate the alternative and classical pathways

via its interaction with C-reactive protein (CRP) (Roy et al. 2016). There is limited data on the activity of CL-LK in vivo and in vitro, but due to average serum concentrations being below that of MBL (0.3 µg/ml vs. 1.5 µg/ml), pathogen recognition and clearance through complement activation is likely to have a minor role to play for these collectins. It is not clear whether these collectins can act directly as opsonins in a complement-independent manner. CL-L1 can bind D-mannose, Nacetylglucosamine, D-galactose, L-fucose and D-fructose in a Ca<sup>2+</sup> dependent manner (Ohtani et al. 1999; Axelgaard et al. 2013). Similarly, CL-K1 can also bind L-fucose, D-mannose and N-acetylmannosamine (Ohtani et al. 1999; Hansen et al. 2010). Furthermore, CL-LK was recently demonstrated to be a PRR for M. tuberculosis, being able to primarily target mannose-capped lipoarabinomannan (ManLAM), in a Ca<sup>2+</sup> dependent manner, on the surface of the mycobacterium, but not to M. smegmatis due to the lack of mannose caps on its LAM (Troegeler et al. 2015). Mice deficient in CL-K1 did not show altered susceptibility to M. tuberculosis infection and CL-LK opsonised M. tuberculosis did not result in altered phagocytosis or intracellular survival of the pathogen in human macrophages (Troegeler et al. 2015). Interestingly, the levels of CL-LK in serum of tuberculosis patients is reduced, compared to controls, correlating inversely to the immune response to M. tuberculosis and suggesting that it may be useful as a biomarker for the disease (Troegeler et al. 2015).

Conglutinin was the first mammalian collectin to be discovered and is found in Bovidae, together with other lesser known collectins (CL-43 and CL-46) (Hansen and Holmskov 2002). Conglutinin is similar in overall structure to SP-D and is able to bind to microbial surfaces in the presence of Ca<sup>2+</sup> (Hansen and Holmskov 2002). Conglutinin is secreted by the liver and found predominantly in bovine serum at an average concentration of 12 µg/ml (Holmskov et al. 1998). Conglutinin has been shown to have anti-microbial properties. Low serum levels of conglutinin have been associated with acute infections (e.g. pneumonia and metritis) and predisposition to respiratory infection (Ingram and Mitchell 1971; Holmskov et al. 1998). Conglutinin is able to bind many microbes, including Gram-negative bacteria such as E. coli and Salmonella typhimurium (Friis-Christiansen et al. 1990; Friis et al. 1991), LPS and peptidoglycan (Wang et al. 1995) and Gram-positive bacteria such as mycobacteria (Dec et al. 2012; Mehmood et al. 2019). Conglutinin is uniquely able to bind to iC3b, via the mannose sugars on the α-chain of iC3b (Laursen et al. 1994). Conglutinin is able to bind and agglutinate iC3b-coated erythrocytes (Lachmann and Muller-Eberhard 1968; Laursen et al. 1994), and as well as E. coli, increasing the respiratory burst of phagocytes (Friis et al. 1991). Conglutinin has also been shown to be protective against bacterial infection in vivo, being able to increase the survival of mice experimentally infected with highly virulent strains of S. typhimurium (Friis-Christiansen et al. 1990). A recombinant truncated form of conglutinin, composed of the  $\alpha$ -helical neck region and the CRD of conglutinin (Wang et al. 1995), was recently shown to bind to able to bind to the vaccine strain Mycobacterium bovis BCG (probably via LAM), and act as an anti-opsonin both in the presence and absence of complement deposition. Thus, Conglutinin can interfere with the uptake of the bacterium by THP-1 macrophages and alter their inflammatory response (Mehmood et al. 2019). This suggests that conglutinin interfers with uptake of mycobacteria by macrophages

via two important mechanisms: (1) blocking interaction of mycobacterial LAM with mannose receptor, and (2) blocking iC3b interaction with complement receptors CR3 and CR4 (Mehmood et al. 2019). These data potentially have important implications for bovine tuberculosis.

CL-43 and CL-46 are also bovine-unique collectins, but their role in the physiology and innate immunity against bacteria has not been fully studied. There is one report of CL-43 binding to *E. coli* strain K12, enhancing attachment to phagocytes (Hansen and Holmskov 2002).

#### 4.6 Interaction of Collectins with Viruses

#### 4.6.1 SP-A and SP-D

There are numerous studies that describe direct interaction of SP-A and SP-D with a range of viruses, enhancing their phagocytosis, as well as neutralising viral infection of host cells (Fig. 4.3). Experiments on SP-A<sup>-/-</sup> and SP-D<sup>-/-</sup> knockout mice infected with influenza A virus (IAV) suggest that both collectins are protective, but this is dependent on viral strain-specific factors, such as the nature of glycosylation in HA and NA (LeVine et al. 2001, 2002; Hawgood et al. 2004). Also, mice lacking both SP-A and SP-D, have an IAV infection phenotype almost identical to SP-D<sup>-/-</sup> mice (Hawgood et al. 2004). Moreover, SP-D, but not SP-A, enhanced the clearance of IAV infection in the mouse lung (LeVine et al. 2001). Thus, these studies suggest that SP-D plays a more significant role than SP-A in the host innate immune response to infection with IAV.

SP-A binds to IAV, neutralises the virus and inhibits the release of viral particles from infected cells, by targeting mannose residues of viral surface haemagglutinin (HA) or neuraminidase (NA) (Malhotra et al. 1994; Benne et al. 1995). SP-D strongly inhibits hemagglutination activity of IAV, resulting in viral aggregation and neutralisation (Hartshorn et al. 1994). SP-D is also able to inhibit NA activity, with inhibition being stopped in the presence of D-mannose (Reading et al. 1997). SP-D has a stronger inhibitory effect on NA compared to SP-A (Tecle et al. 2007). SP-D binds to mannosylated, N-linked sugars on viral HA and NA via its CRD, resulting in potent anti-IAV infectivity (Hartshorn et al. 1994, 2000). SP-D was able to inhibit virus-induced HA activity, block the enzymatic activity of viral NA, and neutralise the ability of seasonal H1N1 strains of IAV to infect human respiratory epithelial cells (Job et al. 2010). However, in the same study, some pandemic H1N1 were found to be resistant to SP-D inhibition that correlated with the degree of N-glycosylation in the globular head of HA (Job et al. 2010). It has been shown that porcine SP-D has an increased ability to inhibit, not just seasonal IAV strains, but also a number of pandemic and avian strains (van Eijk et al. 2003; Hillaire et al. 2012). This is important as pigs are a source of IAV pandemic strains (H1N1) that can be transmitted

to humans, so studying porcine SP-D could provide further insights into this host reservoir.

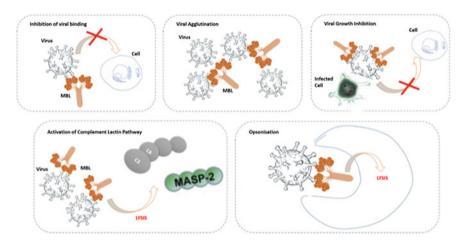
A recombinant truncated form of SP-A (rfhSP-A) made up of α-helical neck and CRD, promotes IAV infection, replication, upregulation of viral factors (M1) in lung epithelial A549 cells and enhances the pro-inflammatory response (Al-Qahtani et al. 2019). This contrasts with full-length SP-A which inhibits IAV infection and dampens the pro-inflammatory response, demonstrating that the full-length SP-A molecule is required for IAV protection (Al-Qahtani et al. 2019). However, in a similar study, a recombinant truncated form of SP-D (rfhSP-D) was shown to inhibit IAV entry, down-regulate viral factors (M1) and down-regulate the pro-inflammatory response (Al-Ahdal et al. 2018). These opposing effects of rfhSP-A and rfhSP-D provide further insight into IAV pathogenesis and the possible utility of rfhSP-D as a therapeutic molecule. In bronchoalveolar lavage (BAL), SP-D enhances IAV uptake and virus-induced respiratory burst by neutrophils (White et al. 2005), but other collectins (SP-A), mucins and gp-340 dampen SP-D's effect, and thus, significantly reduce the ability of SP-D to promote neutrophil oxidative response (White et al. 2005). Therefore, the net effect of BAL is to increase neutrophil uptake of IAV while reducing the respiratory burst response to virus (White et al. 2005).

SP-A is also able to bind to herpes simplex virus type 1 (HSV-1) via viral N-linked sugars and enhance phagocytosis of the virus by macrophages (van Iwaarden et al. 1991; Van Iwaarden et al. 1992a, b). The mechanism of binding of SP-A to HSV-1 is similar to binding to IAV, involving interaction with the sialylated carbohydrate on the collectin's CRD. SP-A also has an opsonin activity, increasing uptake of HSV-1 by AM (van Iwaarden et al. 1991). Similarly, SP-A binds to cytomegalovirus and enhances viral entry into rat lung cells (Weyer et al. 2000). It is unknown whether SP-D has any activity against other Herpesviridae. SP-A is able to bind to respiratory syncytial virus (RSV) targeting the F2 subunit of the viral F antigen and is able neutralise the virus (Ghildyal et al. 1999; Sano et al. 1999, 2000). Children with severe RSV infection have reduced levels of SP-A and SP-D in BAL samples compared to healthy controls (Kerr and Paton 1999). In SP-A<sup>-/-</sup> knockout mice, RSV infection was more severe than in SP-A+/+ mice and the addition of exogenous SP-A to SP-A<sup>-/-</sup> mice reduced viral load and inflammation, and enhanced RSV clearance (LeVine et al. 1999). SP-D can bind to RSV protein G and is able to neutralise RSV infectivity in vitro (Hickling et al. 1999). Interestingly, RSV itself can alter SP-A expression in human pulmonary epithelial cells, upon infection by interfering with protein translation (Bruce et al. 2009). SP-A binds to Human Immunodeficiency Virus 1 (HIV-1) via the viral envelope gp120 glycoprotein and inhibits direct infection of CD4<sup>+</sup> T cells (Gaiha et al. 2008). Yet, in dendritic cells (DC), SP-A increases HIV uptake, through enhanced binding to gp120 and facilitates transfer of HIV from DC to CD4<sup>+</sup> T cells (Gaiha et al. 2008). SP-D is also able to bind to HIV gp120 and inhibit viral infectivity (Meschi et al. 2005), whilst rfhSP-D was also able to bind to gp120 and prevent infection of Jurkat T cells, U937 monocytic cells and PBMC, and significantly suppress the HIV-1 induced cytokine storm in these cells (Pandit et al. 2014). Interestingly, a direct protein-protein interaction between rfhSP-D and DC-SIGN (dendritic cell-specific intercellular adhesion molecule-3-grabbing non-integrin) modulates the capture of HIV-1 and its transfer to CD4<sup>+</sup> T cells, revealing a novel and distinct anti-viral mechanism against HIV-1 by SP-D (Dodagatta-Marri et al. 2017). This same rfhSP-D has also been recently shown to restrict the transfer of HIV across the vaginal epithelial barrier, by altering the gene expression signature of the epithelium (Pandit et al. 2019). These recent studies demonstrate the therapeutic potential of rfhSP-D against HIV infection.

Elevated levels of serum SP-D have been reported in severe acute respiratory syndrome (SARS) coronavirus infected patients (Wu et al. 2009). SP-D is able to bind to the glycosylated spike protein (S-protein) on the SARS coronavirus (Leth-Larsen et al. 2007). Both SP-A and SP-D bind to coronavirus strain HCoV-229E, and inhibit viral infection of human bronchial epithelial (16HBE) cells. Whilst SP-A only modestly reduced infection in AM, whereas SP-D had no effect (Funk et al. 2012). Human and porcine SP-D can interact with Ebola virus glycoprotein and enhance viral infection in pulmonary cells, suggesting that SP-D may enhance viral spread (Favier et al. 2018). SP-A has been shown to enhance clearance of pulmonary adenovirus infection and inhibit lung inflammation (Harrod et al. 1999). Bovine SP-D is also able to bind to bovine rotaviruses via the VP7 glycoprotein and neutralise infectivity (Reading et al. 1998). SP-D binds to the A27 protein of vaccinia virus. SP-D<sup>-/-</sup> knockout mice challenged with vaccinia virus resulted in increased mortality, compared to SP-D<sup>+/+</sup> mice, suggesting that SP-D has a protective role against vaccinia infection (Perino et al. 2013).

#### 4.6.2 MBL

MBL is able to interact with a number of viral pathogens and its effect is generally protective, although there are examples of negative as well as positive outcomes for infection as a result of MBL-mediated binding (Fig. 4.4). Several studies have shown that MBL is a potent inhibitor of IAV infection (Hartley et al. 1992; Hartshorn et al. 1993b; Reading et al. 1995, 1997). Moreover, MBL also has the added ability to deposit complement on IAV-infected cells (Reading et al. 1995). There are also elevated levels of MBL in the lung during IAV infection, suggesting that it may be important for protection against IAV pathogenesis (Reading et al. 1997; Fidler et al. 2009). MBL can inhibit viral hemagglutination and directly neutralise IAV in either a complement-dependent or independent manner (Hartshorn et al. 1993b; Anders et al. 1994; Kase et al. 1999). MBL binds to IAV HA and NA, and without involving complement, neutralises the virus (Kase et al. 1999). However, some IAV strains are resistant to the effects of MBL which is dependent on the degree of glycosylation on the viral HA globular domain (Reading et al. 1997; Job et al. 2010; Tokunaga et al. 2011). Furthermore, MBL<sup>-/-</sup> mice were more susceptible to infection from highly glycosylated viral strains of IAV than wild-type mice (Chang et al. 2010). However, pandemic strain H1N1 and avian influenza A H9N2 produced more severe disease (enhanced production of pro-inflammatory response) in wild-type mice compared



**Fig. 4.4** Anti-viral activity of mannose-binding lectin (MBL). MBL binds to viruses, including influenza virus, acting as an opsonin (not through direct neutralisation), eliminating viral particles by phagocytosis. Binding of MBL to carbohydrate groups found on the surface of viral particles triggers the lectin activation pathway of complement leading to lysis

to  $MBL^{-/-}$  mice, suggesting that MBL may have a deleterious effect in some IAV infections (Ling et al. 2012).

MBL is able to neutralise HIV-1 in vitro by binding to the N-linked mannose glycans of viral gp120, and binding to HIV-1 infected CD4<sup>+</sup> T cells and monocytes and inhibiting reverse transcriptase activity (Ezekowitz et al. 1989; Teodorof et al. 2014). Another study has also shown MBL can also bind to viral gp41 as well as gp120 (Saifuddin et al. 2000), whilst MBL also activates complement on gp120 binding (Haurum et al. 1993). Studies have shown a tentative link between low levels of MBL and increased risk of HIV-1 transmission or progression to AIDS. but this remains contentious (Garred et al. 1997a; Takahashi and Ezekowitz 2005; Ballegaard et al. 2014). There has also been a report of a positive correlation between the rate of AIDS progression and MBL plasma concentration (Mangano et al. 2008). However, other studies have found no correlation between MBL levels and AIDS disease progression (Nielsen et al. 1995; McBride et al. 1998). In general, SP-D is better able to inhibit HIV-1 than MBL, but as is the case for MBL, SP-D's inhibitory activity against HIV-1 is lower than what has been observed for IAV (Meschi et al. 2005). MBL has also been shown to contribute to HIV-1 pathogenesis, where MBL mediates enhancement of HIV-1 dissemination to the brain by soluble gp120, which is taken up by the CXCR4 receptor on neurones, and then intracellularly trafficked by MBL, thus resulting in the apoptosis of neuronal cells (Bachis et al. 2006; Teodorof et al. 2014).

Epidemiological studies have revealed association of MBL with hepatitis B virus (HBV) and hepatitis C virus (HCV) infection and disease severity, based on genetic polymorphisms (Thomas et al. 1996; Matsushita et al. 1998; Yuen et al. 1999; Sasaki et al. 2000; Hakozaki et al. 2002). However, one study found no link between MBL

polymorphisms and HBV infection (Hohler et al. 1998). MBL is able to bind to HCV envelope glycoproteins, E1 and E2, and is able to activate complement (via MASP-2), resulting in the neutralisation of HCV particles (Brown et al. 2010). MBL probably binds to N-linked glycosylated forms or HBV surface antigen (HBsAg) (Brown et al. 2007), but it is unknown whether this interaction neutralises the infectivity of the virus.

MBL is also able to bind to Ebola virus via its envelope glycoprotein (GP), which contains high mannose glycan sites, and is able to inhibit the binding of Ebola (and Marburg) viruses to DC-SIGN, blocking attachment to host cells and also neutralise the virus through complement activation (Ji et al. 2005). Furthermore, soluble GP is a key component of Ebola viral pathogenesis and MBL was found to be able to negate GP activity and the virally induced cytokine storm (Escudero-Perez et al. 2014), and thus MBL could be involved in protection against increased vascular permeability which is a characteristic of Ebola haemorrhagic disease. Nevertheless, high dose MBL therapy in a mouse model, where mice we given recombinant human MBL at levels greater than seven times above average human levels, survived otherwise fatal Ebola viral infection and became resistant to reinfection (Michelow et al. 2011).

There is limited or circumstantial data on the interaction of MBL with a number of other viral pathogens. In mice, MBL appears to modulate the immune responses to HSV-2 (Gadjeva et al. 2004), MBL deficiency seems to be linked with recurrent infections (Gadjeva et al. 2004; Seppanen et al. 2009). MBL also binds to flaviviruses such as Dengue and West Nile virus and is able to neutralise infection through complement-dependent and independent mechanisms (Avirutnan et al. 2011; Fuchs et al. 2011). Genetic polymorphism affecting MBL serum levels may also contribute to the pathogenesis and disease severity of Dengue fever (Avirutnan et al. 2011).

# 4.6.3 CL-L1, CL-K1, CL-P1 and the Bovine-Unique Collectins, Conglutinin, CL-43 and CL-46

For collectins CL-L1, CL-K1, CL-P1, there is limited data on their interaction with viruses. Only CL-K1 has been shown to bind IAV and partially decrease the infectivity of the virus (Hansen et al. 2010; Selman and Hansen 2012). The binding of CL-L1 and CL-P1 to viruses has not been reported.

Like SP-D, conglutinin binds to IAV resulting in the inhibition of hemagglutination and infectivity of the virus (Hartshorn et al. 1993a). Conglutinin binds via its CRD to the high mannose sites on the viral HA. IAV treated with conglutinin also boosted neutrophil respiratory burst (Hartshorn et al. 1993a). Conglutinin, CL-43 and bovine SP-D have been reported to bind the bovine rotavirus Nebraska calf diarrhoea virus, targeting its VP7 glycoprotein (Reading et al. 1998). Binding resulted in hemagglutination and neuralisation of rotavirus, with CL-43 showing the highest activity against the virus; it is the first report of collectin activity against a non-enveloped virus (Reading et al. 1998). However, conglutinin has a higher inhibitory

activity against IAV (strain HKx31) than bovine SP-D or CL-43 (Reading et al. 1998). Conglutinin binds to HSV-2 and enhances infection in mice (Fischer et al. 1994). It is also able to bind to HIV-1 gp160 and inhibit interaction of the virus with the CD4 receptor (Andersen et al. 1991). Interestingly, a collectin-like protein analogous, to bovine conglutinin, was purified from human serum (called conglutinin-like protein) and this was demonstrated to bind to HIV-1 gp120 via its CRD and inhibit viral infectivity (Ushijima et al. 1992).

#### 4.7 Interaction of Collectins with Fungi

Collectins are able to recognise and bind to a number of fungi, both primary and opportunistic fungal pathogens, at various stages in their life cycle. Collectins can exhibit direct growth inhibition and enhance phagocytosis of fungi; in some cases, they can contribute to the fungal pathogenesis.

#### 4.7.1 SP-A and SP-D

Both SP-A and SP-D can bind to the conidia of *Aspergillus fumigatus*, via its  $\beta$ -(1-6)-glucan carbohydrate structures on the fungal cell surface in a Ca<sup>2+</sup> dependent manner (Fig. 4.3) (Madan et al. 1997a; Allen et al. 2001a, b). SP-A and SP-D can cause inhibition of conidia infectivity via agglutination, enhancement of phagocytosis and intracellular killing of *A. fumigatus* conidia by neutrophils and AM (Madan et al. 1997a). The fungal ligands of SP-A are 2 N-linked glycosylated glycoproteins (gp45 and gp55) isolated from culture filtrate and are also used for ELISA diagnosis of allergic aspergillosis (Madan et al. 1997b). Fungal melanin was recently determined to be the primary ligand for SP-D on the *A. fumigatus* conidia cell surface, and is able to facilitate fungal phagocytosis and modulate the anti-fungal immune response (Wong et al. 2018).

Utilising a mouse model of invasive pulmonary aspergillosis (IPA), SP-D, but not SP-A, was found to be protective against a normally fatal challenge of *A. fumigatus* conidia (Madan et al. 2001a, b). In this study, IPA mice-treated intranasally with purified human SP-D or rfhSP-D showed 60 and 80% survival respectively (Madan et al. 2001a, b). The basis of this therapeutic protection by SP-D and rfhSP-D was observed to be enhanced phagocytosis of conidia by macrophages and neutrophils, fungistatic effects on the growth of conidia and a dampening of pathogenic Th2 cytokines (IL-4 and IL-5), whilst enhancing protective Th1 cytokines (TNF- $\alpha$  and IFN- $\gamma$ ) (Singh et al. 2009). SP-D<sup>-/-</sup> knockout mice are more susceptible to IPA (Madan et al. 2010). However, SP-A<sup>-/-</sup> knockout mice demonstrate resistance to IPA, suggesting that SP-A may be involved in the pathogenesis of IPA (Madan et al. 2010). Both SP-A and SP-D also have a direct effect on *Histoplasma capsulatum*, inhibiting its growth by increasing the permeability of the fungal membrane (McCormack et al.

2003). However, no aggregation of *H. capsulatum* was observed by SP-A or SP-D, and neither collectin altered the phagocytosis of the fungus or inhibited the growth of macrophage-infected *H. capsulatum* (McCormack et al. 2003).

SP-A is also able to bind to *Cryptococcus neoformans*, both in its encapsulated and non- encapsulated yeast form, but this does not result in increased phagocytosis of the acapsular form (Walenkamp et al. 1999). SP-A binding was Ca<sup>2+</sup>-dependent and was inhibited by glucose and mannose, but not galactose (Walenkamp et al. 1999). Intranasal infection with C. neoformans gave the same survival outcome in SP-A<sup>-/-</sup> knockout mice and wild-type mice, suggesting that the fungus is resistant to SP-A mediated host defence mechanisms (Giles et al. 2007). A subsequent study found that SP-D increases the phagocytosis of hypocapsular C. neoformans by murine macrophages and that this facilitated fungal survival (Geunes-Boyer et al. 2009). Other studies have also shown that SP-D can agglutinate C. neoformans and A. fumigatus (Schelenz et al. 1995; Madan et al. 1997a). Furthermore, SP-D can bind to both encapsulated and acapsular C. neoformans and can aggregate acapsular C. neoformans in particular (van de Wetering et al. 2004a). The cryptococcal capsular components glucuronoxylomannan (GXM) and mannoprotein 1 (MP1) are the ligands for SP-D (van de Wetering et al. 2004a). SP-D is able to facilitate C. neoformans infection further by protecting the fungus against oxidative stress allowing for disease progression in the mouse model of infection (Geunes-Boyer et al. 2012).

SP-D is also able to bind *Blastomyces dermatitidis*, via β-glucan on its surface, and subsequently block interactions with β-glucan-receptors on AM (Lekkala et al. 2006). This study also showed a reduction in TNF- $\alpha$ , dampening the host inflammatory response and thus may facilitate disease progression (Lekkala et al. 2006). SP-D and SP-A can also bind to Coccidioides posadasii via its surface antigens. In a mouse model of infection, C. posadasii infection is able to suppress the expression of pulmonary SP-A and SP-D, possibly facilitating fungal disease progression and dissemination (Awasthi et al. 2004). SP-D can also bind to Candida albicans via its surface antigens and agglutinate the pathogen and directly inhibiting its growth without the requirement of macrophage dependent phagocytosis (van Rozendaal et al. 2000). Similarly, SP-A is able to bind to C. albicans and interfere with attachment to AM, inhibiting phagocytosis (Rosseau et al. 1997). SP-A is also able to dampen the pro-inflammatory response elicited by C. albicans by human AM and monocytes, which may be important in regulating excessive inflammation in the lung during Candida infection (Rosseau et al. 1999). In Saccharomyces cerevisiae, SP-D is observed to bind to its surface, but not SP-A, whilst the fungal ligand for SP-D is yeast  $\beta$ -(1-6)-glucan (Allen et al. 2001a, b).

The opportunistic fungus, Pneumocystis is able to infect a number of mammals with each species of the fungus displaying strict host specificity. For example, *P. carinii* and *P. wakefieldiae* infect rats, *P. murina* infects mice, *P. oryctolagi* infects rabbits, and *P. jirovecii* infects humans. SP-A and SP-D are able to recognise and bind Pneumocystis species via the major surface glycoprotein (MSG; also known as gpA) of the fungus (O'Riordan et al. 1995; McCormack et al. 1997a, b). MSG contains an N-linked carbohydrate chain made up of glucose, mannose, and *N*-acetylglucosamine and is involved in attachment of the fungus to alveolar epithelium

in Pneumocystis pneumonia (Zimmerman et al. 1992; Vuk-Pavlovic et al. 2001). Cruciform dodecamers and other large oligomers of SP-D have a higher affinity of binding to *P. carinii* than do smaller oligomeric versions of SP-D (Vuk-Pavlovic et al. 2001). SP-D is also able to recognise *Pneumocystis* cysts via surface β-glucans (Vuk-Pavlovic et al. 2001). However, SP-D binding does not appear to increase the phagocytosis of the fungus (McCormack et al. 1997a, b; Vuk-Pavlovic et al. 2001). Despite this, SP-D does aggregate *P. carinii* in large complexes that may restrict phagocytosis by macrophages and may allow for persistence of the fungus within the host lungs (Vuk-Pavlovic et al. 2001). Pneumocystis pneumonia does alter the expression of SP-A in the lungs (Atochina et al. 2001), with a threefold increase in the levels of SP-A and SP-D (Phelps et al. 1996; Aliouat et al. 1998; Qu et al. 2001), but decreases total phospholipid content (Atochina et al. 2001).

Human SP-A enhances attachment of *P. carinii* to rat AM in vitro (Williams et al. 1996). SP-A also reduces phagocytosis of *P. carinii* in human AM in vitro (Koziel et al. 1998). These data suggest that increased levels of SP-A during *Pneumocystis pneumonia* (Phelps et al. 1996) may contribute to the pathogenesis through binding to the fungus and interfering with its AM recognition (Koziel et al. 1998). Immunosuppressed SP-A<sup>-/-</sup> mice also have increased susceptibility to *P. carinii* infection (Linke et al. 2001), whilst removal of immunosuppression resulted in efficient clearance of the infection (Linke et al. 2006), showing that SP-A does not enhance *P. carinii* clearance, but does modulate the host immune response during the resolution of infection. SP-D modulates interaction of *P. carinii* with AM (Limper et al. 1995) and also aggregates *P. carinii*, impairing phagocytosis by AM (Yong et al. 2003). In SP-D<sup>-/-</sup> mice, there was delayed clearance of *P. carinii* infection, increased inflammation and altered nitric oxide response (Atochina et al. 2004). Similarly, in immunosuppressed mice, SP-D was found to enhance *P. carinii* infection (Vuk-Pavlovic et al. 2006).

#### 4.7.2 MBL

MBL has been reported to interact with various primary and opportunistic fungal pathogens. Low serum levels of MBL have been linked to increased likelihood of fungal disease (Mullighan et al. 2002; Granell et al. 2006). MBL is able to bind to *A. fumigatus* (Neth et al. 2000), *B. dermatitidis* (Koneti et al. 2008), *C. albicans* (Kitz et al. 1992; Neth et al. 2000; Ip and Lau et al. 2004; van Asbeck et al. 2008), *Candida parapsilosis* (van Asbeck et al. 2008), and *C. neoformans* (Chaka et al. 1997; van Asbeck et al. 2008). The ligands for MBL binding to *C. albicans* and *C. neoformans* are mannan and mannoprotein, respectively (Chaka et al. 1997; Ip and Lau, 2004), whilst 1,3-β-glucan and mannose are the MBL ligands on *B. dermatitidis* and *A. fumigatus*, respectively (Neth et al. 2000; Koneti et al. 2008).

MBL is able to bind *A. fumigatus* conidia showing aggregation, enhancing phagocytosis, and complement deposition (Kaur et al. 2007). However, MBL binding of conidia did not always result in the killing of *A. fumigatus* by phagocytes (Madan et al. 2005a, b; Kaur et al. 2007). Moreover, MBL may be less important in this

context, since it is mainly a serum protein and may not be in significant levels in the lung. Nevertheless, genetic polymorphisms in the MBL gene have been shown to be associated with severe aspergillosis (Crosdale et al. 2001; Vaid et al. 2007). Similarly, MBL deficiency is a risk factor for aspergillosis in immunocompromised patients, cancer patients and transplant recipients. In the mouse model of infection, MBL deficiency does not necessarily affect the survival of mice infected with *A. fumigatus* conidia, due to redundancy since mice having two copies of the MBL gene (Mbl1 and Mbl2), encoding MBL-A and MBL-C proteins in mouse serum (Hogaboam et al. 2004). However, treatment with recombinant MBL does enhance survival in IPA mice (Kaur et al. 2007). Thus, the role of MBL in *A. fumigatus* infection may also depend on the route of infection and the level of immunosuppression of the host.

MBL interaction with *B. dermatitidis* has only been studied in the mouse system. Both MBL mouse proteins (MBL-A and MBL-C) bind to *B. dermatitidis* yeast cells (Koneti et al. 2008). Inhibition of macrophage response to *B. dermatitidis* is also mediated by MBL, binding to 1,3-β-glucan ligand on *B. dermatitidis*, and thus inhibiting 1,3-β-glucan interaction with Dectin-1 receptor on macrophages and also decreasing TNF-α production (Brown et al. 2002; Kimberg and Brown 2008). Moreover, macrophage production of G-CSF, IFN-γ, MCP-1, and RANTES were significantly inhibited by MBL in response to *B. dermatitidis*, but not IL-6 (Brummer et al. 2007).

MBL can bind to C. albicans yeast and pseudohyphae and to C. parapsilosis yeast cells (Denton and Disalvo 1964; Sugar and Picard 1988; Brummer et al. 2005; van Asbeck et al. 2008). MBL is able to aggregate C. albicans resulting in its growth inhibition and complement deposition of C4b and C3b on its surface via MASPs (Ip and Lau 2004; van Asbeck et al. 2008). Similar levels of MBL-mediated complement deposition were also observed for C. parapsilosis (van Asbeck et al. 2008). However, the binding of MBL to C. albicans may inhibit its phagocytosis by macrophages or dendritic cells (Zimmerman et al. 1992; Schelenz et al. 1995; Chaka et al. 1997; Vuk-Pavlovic et al. 2001; Ip and Lau 2004; van de Wetering et al. 2004a). MBL seems to inhibit Candida-induced macrophage responses in THP-1 cells through TLR-2 and TLR-4, suggesting that C. albicans modifies TLR signalling pathways in the macrophage (Wang et al. 2013). However, in the case of neutrophils, MBL enhances the phagocytosis of both C. albicans and C. parapsilosis yeast cells (van Asbeck et al. 2008). MBL greatly facilitates complement-mediated uptake of C. albicans via CR1 receptor in neutrophils and this results in the stimulation of reactive oxygen species by intracellular Dectin-1, which recognises the phagocytosed fungal β-1,3 glucan (Li et al. 2012). The binding of MBL with C. albicans yeast also increases TNF-α production by monocytes in vitro (Ghezzi et al. 1998) and in vivo (Lillegard et al. 2006). Double knockout (MBL-A and MBL-C) mice were found to be more susceptible to systemic infection with C. albicans compared to wild-type mice (Held et al. 2008). Vaginal candidiasis is an important mycosis in women. MBL protein is present in vaginal secretions (Pellis et al. 2005); MBL levels seem to increase in vulvovaginal candidiasis. However, MBL levels were found to be lower in women

with recurrent vulvovaginal candidiasis, because of polymorphisms in their MBL gene (Babula et al. 2003; Liu et al. 2006; Giraldo et al. 2007; Donders et al. 2008; Milanese et al. 2008). The precise role of MBL in candidiasis remains to be fully explored.

MBL can bind to acapsular *C. neoformans* yeast cells (Chaka et al. 1997), but this does not cause aggregation (Eisen et al. 2008). However, MBL binding to acapsular *C. neoformans* did facilitate complement deposition and enhancement of fungal phagocytosis by neutrophils (van Asbeck et al. 2008). Furthermore, TNF- $\alpha$  production was induced in peripheral blood mononuclear cells by *C. neoformans* mannoprotein and this effect was enhanced by MBL (Chaka et al. 1997). It is unknown whether MBL binds to *H. capsulatum* or *P. carinii*. It is unlikely that MBL binds to *H. capsulatum*, since the cell wall contains 1,3- $\alpha$ -glucan (Rappleye et al. 2007); however, in *P. carinii*, the cell surface of cyst forms does contain  $\beta$ -1,3-glucan (Williams et al. 1996), which may bind MBL. In Coccidioides species, it is also unknown whether MBL interaction occurs, but patients with active coccidioidomycosis have been shown to have low serum MBL levels, compared to healthy individuals previously infected with Coccidioides, and that low levels of MBL were associated with polymorphisms in their MBL gene (Corredor et al. 1999).

# 4.7.3 CL-L1, CL-K1, CL-P1 and the Bovine-Unique Collectins, Conglutinin, CL-43 and CL-46

Very few studies have investigated the interaction of these minor collectins with fungal species. CL-K1 can bind *C. albicans* (Selman and Hansen 2012) and cellular extracts (mannan) of *S. cerevisiae* (Keshi et al. 2006; Selman and Hansen 2012). CL-P1 has also been reported to bind to *S. cerevisiae* and mediate phagocytosis of yeast-derived zymosan, suggesting that CL-P1 mediates phagocytosis for fungi in the vascular endothelium (Ohtani et al. 1999; Jang et al. 2009). Interestingly, CP-P1 also partially binds to *A. fumigatus*, via its CRD, and in association with properdin, can activate the complement alternative pathway, resulting in C3b deposition and formation of the membrane attack complex (Ma et al. 2015). This shows a novel mechanism of triggering the alternative pathway of complement (Ma et al. 2015). There are no reports of CL-L1 interaction with fungi.

There are also limited reports of the binding of bovine-unique collectins to fungi. CL-43 is able to bind to acapsular *C. neoformans* in vitro in a Ca<sup>2+</sup>-dependent manner (Schelenz et al. 1995), and immobilised yeast mannan (Holmskov et al. 1996). Conglutinin is able to bind to glycoproteins and polysaccharides derived from *S. cerevisiae* (*N*-acetylglucosamine, mannose, mannan) (Loveless et al. 1989; Lim and Holmskov 1996).

# **4.8** Interaction of Collectins with Protozoal and Helminth Pathogens

An area of collectin that is yet to be fully explored is the interaction of collectins with protozoal and helminth pathogens, which are responsible for some of the most important global infections. There are limited studies and these are mostly based on genetic polymorphisms in collectin genes that are associated with predisposition or severity of these diseases. There is a limited number of functional studies on the role of collectins in protozoal and helminth infections.

Increases in levels of SP-D were observed in serum, renal and cerebral tissues in mice experimentally infected with *Plasmodium berghei*, compared to control mice (Cahayani et al. 2016). Low MBL serum levels and genetic polymorphisms in the MBL gene have been associated with more severe malaria, particularly in children (Luty et al. 1998; Holmberg et al. 2008). MBL can bind to *P. falciparum* protein extracts, but it does not appear to inhibit the parasite directly (Klabunde et al. 2002). MBL does not opsonise *P. falciparum*, but it can bind to *P. falciparum*-infected erythrocytes, recognising the 78-kDa glucose-regulated stress glycoprotein of the parasite (Garred et al. 2003). MBL binding to *P. falciparum* merozoite adhesins have also been reported, having the ability to activate complement (Korir et al. 2014).

The complement lectin pathway can be activated by Trypanosoma and Leishmania (Cestari et al. 2013). MBL binds to glycosylated antigens on *Trypanosoma cruzi*, on the surface of metacyclic trypomastigotes, resulting in complement activation (Cestari Idos et al. 2009). In a mouse model of *T. cruzi* infection, MBL influences host resistance and pathology (Rothfuchs et al. 2012). In some strains of *T. cruzi*, MBL mediates resistance to complement lysis of the parasite and enhances invasion of host cells (Evans-Osses et al. 2014).

MBL also binds to major cell surface glycoconjugates (lipophosphoglycans) on Leishmania parasites, triggering lectin pathway activation and promastigote lysis (Green et al. 1994; Ambrosio and De Messias-Reason 2005). Certain genotypes of the MBL2 gene were also predictive for the risk for developing visceral leishmaniasis and other clinical complications in infections with *Leishmania chagasi* (Alonso et al. 2007). Similarly, there was a strong correlation found between serum levels of MBL and the probability of developing visceral leishmaniasis (Santos et al. 2001). Monocytes challenged with MBL-opsonised *L. chagasi* promastigotes secreted higher levels of TNF- $\alpha$  and IL-6 than controls, suggesting that MBL may play an important role in pathogenesis (Santos et al. 2001).

In helminth infections, MBL binds to the surface glycoproteins of *Schistosoma mansoni* cercariae and adult worms and is able activate the lectin pathway (Klabunde et al. 2000). Curiously, no differences in serum MBL levels were observed between patients infected with Schistosoma and in healthy controls (Klabunde et al. 2000). Another study has shown that high MBL serum levels are associated with protection in schistosomiasis (Antony et al. 2013). Interestingly, high levels of MBL and CL-K1 were inversely correlated with urogenital infections with *S. haematobium* (Antony

et al. 2015b). Although CL-K1 has not been shown to bind directly to the parasitic worm, it was observed to be a risk factor for urinary schistosomiasis (Antony et al. 2015a). Furthermore, concomitantly elevated IL-6 levels were also observed in urinary schistosomiasis cases compared to controls that correlated with MBL levels (Antony et al. 2015b). Similar findings linking IL-6 and MBL have also been described in patients with visceral leishmaniasis (Santos et al. 2001; Antony et al. 2015b).

SP-D has also been shown to bind to fucosylated glycoconjugates ( $\alpha$ -1–3 linked fucose) on the surface of *S. mansoni* larval stages, although the significance of this interaction remains unclear (van de Wetering et al. 2004b, c). However, a recent study has suggested that SP-D is essential for protection against helminth infection, using the experimental model nematode *Nippostrongylus brasiliensis* (Thawer et al. 2016). *N. brasiliensis* infection of SP-D<sup>-/-</sup> knockout mice resulted in severe susceptibility to parasitic disease, whilst treatment with rfhSP-D enhanced parasite clearance and anti-parasitic immune responses (Thawer et al. 2016). SP-D was determined to bind to *N. brasiliensis* larvae via its CRD, and to enhance their killing by AM (Thawer et al. 2016).

#### 4.9 Collectins and Allergy

A considerable number of in vitro and in vivo studies have focused on the immunomodulatory functions of collectins and their contribution to the host defense system. Through activation of complement, and production of pro-inflammatory cytokines, MBL makes a major impact on the generation and regulation of the immune-mediated inflammatory response. Allergen-mediated activation of the complement lectin pathway has been demonstrated (Varga et al. 2003). Allergen extracts (parietaria (PA) and house dust (HD) mite) were shown to bind purified MBL, and trigger the lectin complement pathway. Differences in plasma MBL levels may affect the degree of complement activation in different individuals, thus, susceptibility to allergic diseases. Significantly elevated serum MBL levels were observed in pediatric mild-asthma patients, suggesting the possible role of MBL in the pathogenesis of asthma by contributing to airway inflammation, or increasing the risk of asthma development (Uguz et al. 2005). Enhanced levels of serum MBL also correlate with an increased peripheral blood eosinophils in these individuals. It is also suggested that oxidative stress increases the MBL synthesis, and triggers complement activity. MBL can initiate complement activation following oxidative stress in asthma (Collard et al. 2000; Nadeem et al. 2003; Uguz et al. 2005), and aggravate inflammation. Significantly increased MBL levels and MBL pathway was also detected in patients with bronchial asthma, rhinitis and allergic bronchopulmonary aspergillosis (ABPA) (Kaur et al. 2005).

A higher level of plasma MBL is likely to contribute to activation of lectin pathway, and an increased severity, including enhanced blood eosinophil counts. In addition, production of MBL in the liver is suggested to increase by up to three fold in response

to environmental stimuli. Therefore, higher levels of plasma MBL in allergic patients, compared to the non-allergic patients, may result from elevated hepatic synthesis caused by allergen exposure. Furthermore, the circulating level of mouse MBL-A was also measured in *Aspergillus fumigatus* allergen-sensitised and non-sensitised mice. Increased level of mMBL-A was observed following allergic sensitisation, suggesting that challenging these mice with allergen may contribute to a higher level of MBL in sensitised mice as well as allergic patients (Kaur et al. 2005). Earlier in vivo studies using mouse MBLs have reported the likely role of MBL-A as a mediator of inflammation (Santos et al. 2001; Takahashi et al. 2002). Moreover, a substantial decline in the airway hyperresposiveness to *A. fumigatus conidia* was seen in MBL-A-deficient mice (MBL-A<sup>-/-</sup>) when compared to MBL-A<sup>+/+</sup> control mice, which suggest the possible role of MBL-A and its ability to trigger progression of airway hyper-responsiveness (Hogaboam et al. 2004).

Since levels of plasma MBL are genetically determined, it is of interest to study the genetic polymorphisms in MBL in relation to allergic susceptibility. In order to address the correlation between polymorphisms in the MBL gene and the progression of atopic diseases, Nagy et al. found a contribution of variant MBL alleles to the susceptibility to acute or chronic Chlamydia pneumoniae infection in asthmatic children (Nagy et al. 2003). Another study that focused on the genetic association of MBL related single nucleotide polymorphisms (SNPs) with allergic patients (Kaur et al. 2006), reported the identification of G1011A, an intronic SNP found in the MBL gene, and presence of 1011A allele of SNP G1011A to be associated with an enhanced level of plasma MBL., SNP G1011A has also been suggested to play a role in regulating MBL expression. Additional polymorphisms were found at positions 550 (H/L variants) and 221 (X/Y variants) in the promoter region of the MBL gene, which associated with high MBL levels in the plasma. 1011A allele was also associated with bronchial asthmatic patients with allergic rhinitis and ABPA, which positively correlated with allergic markers, including high peripheral blood eosinophil counts, and reduced levels of forced expiratory volume at timed interval of 1 s (FEV1) in these patients. However, no structural SNPs have been observed within the MBL gene in these allergic patients.

As carbohydrate recognition immune molecules, both SP-A and SP-D have been shown to interact with gp55 and gp45 of *A. fumigatus* in a calcium and carbohydrate specific dependent manner (Madan et al. 1997b). Both these collagenous molecules inhibit specific IgE binding to these glycoproteins, and block allergen triggered histamine release from human basophils isolated from Derp- and *A. fumigatus*-sensitised patients (Madan et al. 1997a, b). Dodecameric forms of human SP-D mediate binding, aggregation, and phagocytosis of starch granules, containing grass pollen allergens from *Dactylis glomerata* and *Phleum pratense* via alveolar macrophages (Erpenbeck et al. 2005). SP-D can suppress proliferation of PBMCs isolated from children with Derp–sensitive asthma (Wang et al. 1998), and suppress secretions of IL-2 by PBMCs (Borron et al. 1998). Suppressive effects of SP-A on the production and release of IL-8 by eosinophils were also reported, which is stimulated by ionomycin in a concentration-dependent manner (Cheng et al. 1998). Since IgE cross-linking, release of histamine and PMBCs proliferation are crucial immunological factors

contributing to the development of asthmatic symptoms, both SP-A and SP-D are crucial immune modulators in resisting allergenic challenge, as well as suppressing substantial hypersensitivity reactions in the lungs (Kishore et al. 2002).

Intranasal administration of SP-D or rfhSP-D caused reduced levels of peripheral and pulmonary eosinophilia, and the effect persisted up to 16 days in the ABPA mice. These observations therefore indicate the potential of SP-D as a therapeutic agent (Kishore et al. 2002; Madan et al.2001a; 2005a, b). In addition, protective role of rhfSP-D has also reported in murine model of Derp allergens-induced pulmonary hypersensitivity (Singh et al. 2003). Shifting of Th2 to a Th1 following SP-D treatments appeared to be crucial to the protective mechanism, since, IFN- $\gamma$  gamma is suggested to inhibit differentiation of Th2 in response to IL-4 (Elser et al. 2002). Additionally, production of nitric oxide was significantly inhibited when Derp mice derived alveolar macrophages are pre-incubated with rfhSP-D, and resulted in low levels of TNF- $\alpha$  in the rfhSP-D treated Derp mice (Liu et al. 2005). Culturing alveolar macrophages with allergen and SP-D has induced an increased production of IL-10, IL-12, and IFN- $\gamma$ , indicating a positive correlation between macrophages and SP-D triggered inhibition of airway inflammation and airway hyper-responsiveness (AHR) (Takeda et al. 2003).

A study by Madan et al. has focused on the susceptibility of SP-A $^{-/-}$  and SP-D $^{-/-}$  mice to challenge with *A. fumigatus* allergen compared to wild-type mice (Madan et al. 2005a, b).

Intrinsic hypereosinophilia and seven fold increase in IL-5 and IL-13 levels were seen in both SP-A $^{-/-}$  and SP-D $^{-/-}$  mice. However, lower levels of IFN-  $\gamma$  to IL-4 ratio in the lungs were observed, suggesting the possible Th2 basis of immune response. Treating these mice with exogenous intranasal SP-A and SP-D resulted in reversal of Th2 polarisation. SP-D $^{-/-}$  mice was reported to be more susceptible to *A. fumigatus* allergen-induced pulmonary hypersensitivity when compared to wild-type mice. However, resistant to sensitisation was seen with SP-A $^{-/-}$  mice. Intranasal administration of SP-D or rfhSP-D led to rescue of the sensitised SP-D $^{-/-}$  mice, while SP-A $^{-/-}$  mice demonstrated an enhanced levels of IL-5 and IL-13, causing greater pulmonary eosinophilia. Genetic polymorphisms in the collagen region of SP-A2 (SP-A2 G1649C and SP-A2 A1660G) may also increase susceptibility to allergic bronchopulmonary aspergillosis (ABPA) (Saxena et al. 2003).

### 4.10 Collectin (and C1q) Receptors

The collectins are structurally related to the complement protein C1q (having a collagenous region and similar overall tertiary structure. A common receptor for SP-A, MBL and C1q was described in 1990 (Malhotra et al. 1990) (Fig. 4.5), as collagen region binding cC1qR. This was subsequently identified as Calreticulin (~56kDa). Two other candidate receptors were subsequently proposed:

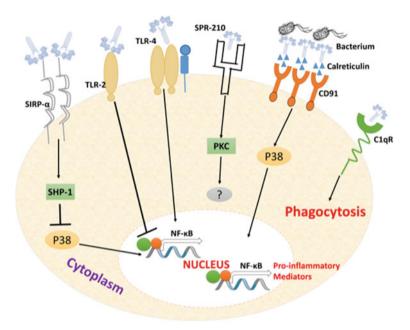


Fig. 4.5 Collectin receptors on immune cells. Collectins have been shown to bind a number of receptors and putative receptors, which lead to immunomodulatory responses. Binding of collectins to Toll-like receptor 2 (TLR-2), TLR-4, SP-A receptor 210 (SP-R210), CD91-calreticulin, and signal inhibitory regulatory protein-α (SIRP-α) alters production of pro-inflammatory mediators. For example, SP-A and SP-D binds to SIRP-α via their collagenous tails, and stimulates pro-inflammatory chemokine production via calreticulin/CD91 interaction. Furthermore, bacterium bound collectins induces the conformational changes of calreticulin/CD91 interaction, which then activates P38-mitogen-activated protein kinase (MAPK) signalling pathway, leading to transcriptional activation of NF-κB (nuclear factor kappa-light-chain-enhancer of activated B cells), and expression of pro-inflammatory cykines, including tumour necrosis factor alpha (TNF-α). SIRP- $\alpha$  is abundantly expressed in macrophages, and ligation of SIRP- $\alpha$  by lung collectins are crucial in preventing damage to the airways caused by the production of pro-inflammatory responses. Thereby, phosphorylated cytoplasmic region of SIRP-α recruits SHP-1 (Src homology region 2 domain-containing phosphatase-1), which in turn dephosphorylates protein substrates involved in mediating physiological effects. Thus, the interaction between SIRP- $\alpha$  and SHP-1 negatively regulates P38-MAP kinase signalling, and stimulates NF-kB activity, and cells become resistant to TNF-mediated effects, such as apoptosis

- C1qRp (CD93) (C1q receptor associated with phagocytosis stimulated by C1q, MBL or SP-A): but this has subsequently been shown not to bind any of these ligands. It may be an adhesion receptor (McGreal et al. 2002; Norsworthy et al. 2004).
- (2) CR1, the complement C3b receptor, does interact with C1q and MBL, but functional aspects are not yet widely explored (Jacquet et al. 2018).
- (3) Calreticulin remains the main candidate as a receptor/adapter involved in phagocytosis mediated by C1q and collectins (Ogden et al. 2001; Vandivier et al. 2002). Calreticulin bound to the cell surface CD91 mediates uptake of apoptotic cells

to which C1q, MBL, SP-A and SP-D are bound. It also mediates uptake of microorganisms targeted by the collectins.

SP-A and SP-D can interact with phagocytic receptors and are able to influence receptor-mediated uptake of bacteria (Lawson and Reid 2000). SP-A enhances the phagocytosis of S. aureus by monocytes but does not induce intracellular killing or the production of reactive oxygen intermediates (ROI) (Geertsma et al. 1994). SP-A is also able to enhance the uptake of M. tuberculosis and M. avium by macrophages via the increased expression of mannose receptor (Gaynor et al. 1995; Kudo et al. 2004), whilst SP-A enhances the scavenger receptor A (SR-A)-mediated uptake of Streptococcus pneumoniae by AM (Kuronuma et al. 2004). SP-A is also reported to bind to a 210-kDa SP-A receptor (SPR210) in U937 macrophages and rat AM and mediate uptake of Mycobacterium bovis bacillus Calmette-Guérin (BCG) via this receptor (Chroneos et al. 1996; Weikert et al. 1997); in rat macrophages, this led to enhanced mycobacterial killing and an increase in the production of inflammatory mediators, TNF-α and nitric oxide (Weikert et al. 2000). SP-A and SP-D can also bind to the major LPS receptor, CD14 that is present on alveolar macrophages. SP-A binds to the peptide portion of CD14, whilst SP-D interacts with the glycan of the receptor (Sano et al. 2000). SP-A modulates LPS-induced cellular responses by direct interaction with CD14 (Sano et al. 1999), serving as an important mechanism for the recognition and clearance of this endotoxin. As noted above, SP-A and SP-D can interact with the versatile protein calreticulin (Malhotra et al. 1990). When SP-A and SP-D bind to surface target ligands such as LPS or apoptotic cells, multiple collagen regions are presented on the surface, which interact with the Calreticulin -CD91 receptor complex (Gardai et al. 2003). This can then lead to the promotion of phagocytosis and initiation of cell signalling pathways leading to the production of pro-inflammatory cytokines and priming of adaptive immunity (Ogden et al. 2001; Vandivier et al. 2002; Gardai et al. 2003). In contrast, SP-A and SP-D can also suppress inflammatory responses by binding to signal regulating protein  $\alpha$  (SIRP- $\alpha$ ) on macrophages and epithelia via their CRD region, and this leads to a signalling pathway that blocks pro-inflammatory mediator production (Fig. 4.5) (Table 4.2) (Gardai et al. 2003). Therefore, the orientation of binding of SP-A and SP-D (collagen or lectin (CRD)) domains to host receptors Calreticulin-CD91 or SIRP-α, respectively, have opposing effects and illustrate a dual function of these collectins, which could be, (1) protection of the naïve lung via maintenance of immune homeostasis and (2) protection via the triggering of inflammation to clear pathogens, allergens, necrotic and apoptotic cells. Another receptor, gp-340 has also been found to bind to SP-D and SP-A (Holmskov et al. 1997a; Tino and Wright 1999), but any microbial interaction has been described for Influenza virus (Hartshorn et al. 2006a, b) and not bacteria, whilst binding of SP-A to gp-340 stimulates macrophage chemotaxis (Tino and Wright 1999).

Calreticulin (cC1qR) is a collectin binding protein of 56 kDa, and is known to bind C1q, MBL, SP-A, conglutinin and CL-43 (Fig. 4.5) (Table 4.2) (Malhotra et al. 1993). This interaction is independent of calcium ions, and ionic in nature. It is mediated by the collagen domain 'c' of the collectins (cC1qR). The C1q binding site has

**Table 4.2** Binding proteins and Receptors for lung collectins

Binding proteins/receptors	Cells expressing the receptors	Protein domain	Proposed functions
Calreticulin/CD91	Ubiquitous	Collagen region of SP-A and SP-D	Phagocytosis and production of pro-inflammatory cytokines
C1qRp/CD93	Monocytes, macrophages, neutrophils, platelets, endothelial cells and microglia	Reported as a receptor, but may not bind C1q or collectins	Initially proposed to have roles in phagocytosis
gp340	Soluble opsonin	CRD region of SP-A and SP-D	Stimulation and migration of alveolar macrophages
CD14	Alveolar macrophages	Neck region of SP-A which interacts with the peptide portion containing the leucine-rich repeats of CD14. CRDs of SP-D that binds and interact with carbohydrate moiety of CD14	CD14-LPS modulation and release of pro-inflammatory cytokines and chemokines
SIRP α/CD172	Antigen presenting cells, endothelial cells, myeloid cells, and neurons	CRD of SP-A and SP-D	Inhibition of pro-inflammatory cytokine and chemokine production
SPR210	Type II cells, alveolar macrophages, and bone marrow derived macrophages	SP-A- 36 residues collagen region composed of RGD motif	Regulation of phospholipid secretion and cytokine production, phagocytosis, and inhibition of T-cell proliferation

been mapped to the S-domain of calreticulin (Stuart et al. 1996). Conglutinin and CL-43 also bind C1qR and calreticulin (Dec and Wernicki 2006). SP-A receptor 210 (SP-R210) is a 210 kDa oligomeric molecule that earlier has been purified from the macrophage cell line U937 by affinity chromatography (Fig. 4.5 (Table 4.2) (Chroneos et al. 1996). SP-R210 is another candidate receptor for SP-A, and also found in type II cells and alveolar macrophages. The direct interaction between SP-R210 and SP-A occurs through the collagen region of SP-A. Antibodies raised against SP-R210 inhibit SP-A binding to alveolar type II cells and alveolar macrophages, thus, prevent SP-A-mediated uptake of *Mycobacterium bovis*, and block SP-A-bacillus Calmette-Guerin complexes to phagocytes. Furthermore, SP-R210 inhibited SP-A-mediated

phospholipid secretion by alveolar type II cells (Weikert et al. 1997). Additionally, a study by Yang et al. reported SP-R210 as a cell surface myosin 18A (Yang et al. 2005), and expressed in multiple isoforms. Gp340 is a 340 kDa SP-D binding glycoprotein purified from lung bronchoalvelar lavage of alveolar proteinosis patients (Holmskov et al. 1997), and belongs to the scavenger receptor superfamily, consisting of multiple scavenger receptor type B domains (Holmskov et al. 1999). Furthermore, gp340 has been shown to be identical to salivary agglutinin, and its binding interaction with Streptococcus mutans and Helicobacter pylori has been reported (Ligtenberg et al. 2001). The direct binding of SP-D to gp340 occurs in a calcium dependent manner, and is inhibited by EDTA. The interaction is not affected by the presence of maltose, suggesting that the binding is a protein-protein interaction via the CRD region of SP-D rather than a lectin-carbohydrate interaction. Similar binding pattern was observed between gp340 and rfhSP-D, composed of trimeric neck region and CRD (Holmskov et al. 1997). Gp340 exists in a soluble form, and acts as an adaptor for SP-A and SP-D, but how gp340 is anchored in the membrane and the mechanism of binding to cell surface has not been elucidated fully yet (Table 4.2). SP-D can bind to human neutrophil defensins (HNPs) via its neck and CRD region (Hartshorn et al. 2006a, b). The interaction between SP-D and HNPs can trigger anti-viral activity in the BAL fluid. HD6, human β-defensins, and human neutrophil peptide (HNP)-4 bind SP-D with weaker affinity, while HNP-1-3 bind SP-D with high affinity and trigger inhibition of SP-D mediated anti-viral activity (Doss et al. 2009). Additionally, SP-D binds human decorin from amniotic fluid in a calcium dependent manner via sulphated N-acetyl galactosamine moiety of decorin (Nadesalingam et al. 2003). rfhSP-D interacts with dermatan sulphate moiety of decorin, and core protein of decorin interacts with SP-D via the collagen-like region.

The interaction between lung collectins (SP-A and SP-D) and native as well as recombinant CD14 has been reported (Table 4.2) (Sano et al. 1999). CD14 is a soluble receptor for LPS, and the neck domain of SP-D has been shown to bind the leucine-rich peptide portion of CD14, whilst the carbohydrate moiety of CD14 interacts with the lectin domain of SP-D (Sano et al. 1999). Thus, both these surfactant proteins appear to modulate the cellular response to smooth and rough LPS by interaction with CD14. (Sano et al. 1999). Furthermore, the association of SP-A and SP-D with toll-like receptors (TLR), and or the TLR-associated molecule, could be one of the mechanisms by which they function as modulators of inflammation an inflammatory mediators (Sano et al. 1999). Studies have reported direct involvement of SP-A in TLR2 signalling, and inhibition of downstream gene activation (Murakami et al. 2002). SP-A interacts directly with TLR4 and myeloid differentiation factor 2 (MD-2), which are known critical signalling receptors for LPS (Billod et al. 2016). Thus, binding of SP-A with extracellular domain of TLR4 and MD-2 was revealed in a calcium-dependent manner, involving the CRD region. Additionally, SP-A has attenuated cell surface binding of smooth LPS, and induced NF-kB activation in cells expressing TLR4 and MD-2 (Murakami et al. 2002). SP-D does not have significant effect on TLR4 expression, but it down-regulates the TLR4-mediated signalling against LPS (Henning et al. 2008). Thus, SP-A's ability to dampen TLR2 and TLR4 signalling is associated with decrease in the phosphorylation of IkappaBalpha, a key regulator of NF- $\kappa$ B activity, and nuclear translocation of p65, resulting in reduced TNF- $\alpha$  secretion in response to TLR ligands. Furthermore, the same study also reported diminished phosphorylation of Akt, an essential regulator of NF- $\kappa$ B and potentially MAPKs. Therefore, there is a critical role for SP-A in modulating lung inflammatory reactions by regulating macrophage-mediated TLR4 activity.

As noted above, calreticulin was identified as a common receptor for C1q, MBL and SP-A (Malhotra et al. 1990). Calreticulin is mainly an intracellular protein but it is present on cell surfaces bound to CD91 and, thus, acts as an adaptor or co-receptor while binding to collagenous region of these collectins (Fig. 4.5) (Table 4.2) (Ogden et al. 2001; Vandivier et al. 2002). Uptake of apoptotic cells by phagocytes mediated by C1q or MBL binding to calreticulin-CD91 complex was revealed (Vandivier et al. 2002). HLA class I heavy chain (Arosa et al. 1999), or CD59 have been shown to act as a calreticulin-binding proteins on cells which do not express CD91, allowing C1q or MBL coated particles to adhere to the cells. Although a number of collectin receptors have been identified, there is still a need to fully elucidate how collectins stimulate phagocytes, and mediate phagocytosis, as well as other signalling transduction pathways. More studies on the structural aspects of receptors are needed, especially how these receptors are anchored in the membrane of immune and non-immune cells and, which co-receptors and signalling pathways are involved.

In conclusion, collectins appear to play important roles in controlling lung allergy, inflammation and hypersensitivity, in addition to dealing with a wide variety of pathogens at pulmonary and extra-pulmonary sites. They act against pulmonary allergens through their ability to resist allergen challenge by interfering with allergen triggered IgE interaction, degranulation of mast/basophils, cellular infiltration, and polarisation of helper Th response. Their roles have been also implicated in altering profiles of pro-inflammatory cytokines and chemokines as a result of infection, and allergen challenge. Further research is needed to characterise specific collectin receptors that are crucial for collectin functions other than phagocytosis.

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