

Sialoadhesin in recognition of self and non-self

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Abstract The immune system is tightly regulated to maintain an appropriate balance between immune activation and tolerance. Macrophages play a key role in this process since they express many pathogen recognition molecules as well as receptors for ‘self’. Sialoadhesin is a major macrophage receptor that specifically recognizes sialic acid, an abundant component of host glycoconjugates but which can also be found on several human pathogens. In recent years, several studies have demonstrated that sialoadhesin can contribute to the uptake and processing of sialylated pathogens as well as playing an important role in regulating inflammatory and autoimmune responses via recognition of self.

Keywords Sialoadhesin · Sialic acid · Innate immunity · Pathogens

Introduction

A key role of the immune system is to discriminate between ‘self’ (the host) and ‘non-self’ (e.g. pathogens) and make appropriate responses to maintain tissue homeostasis. Macrophages (Mφs) express several proteins on their surface that distinguish ‘self’ from ‘non-self’, and therefore these cells are central to immune regulation via sensing and responding to pathogens [47]. Carbohydrates on the surfaces of both host cells and pathogens are critically involved in this discrimination

process. Here we focus on the role of the Mφ sialic acid receptor sialoadhesin (Sn) in the ‘self’ versus ‘non-self’ recognition and phagocytic functions of Mφs during immune responses.

Discovery and characterisation of Sn

Sn was first described in 1985 as a non-phagocytic sheep erythrocyte receptor (SER) on resident bone marrow Mφs (RBBMs) which naturally cluster with developing haemopoietic cells [12, 13]. SER activity was unaffected in the temperature range 0–37 °C, divalent cation independent and destroyed by trypsin. Interestingly, treatment of the erythrocytes with *Vibrio cholerae* sialidase abolished binding by up to 90%. The lectin-like properties of SER for binding sialic acid were further demonstrated by the ability of trisaccharide 3'-sialyllactose and ganglioside GD1a, but not lactose or GM1, to inhibit erythrocyte rosette formation [13].

SER activity was present on tissue ‘stromal’ Mφs isolated by collagenase digestion from the bone marrow, lymph nodes and spleen, but was absent from ‘free’ Mφs isolated from the peritoneal and pleural cavities. However, in vitro upregulation of SER on these Mφs could be mediated by a ~70 kDa species-restricted component in mouse plasma and serum [14]. This finding led to speculation that tissue Mφ expression of SER could be regulated by access to or local production of this component.

The isolation of a blocking monoclonal antibody called SER-4 from rats immunized with mouse serum-induced peritoneal Mφs was a key step in the characterisation [15], purification [17] and molecular cloning [18] of this receptor, which was subsequently renamed sialoadhesin (Sn). Sn is also sometimes referred to as CD169 and/or siglec-1. SER-4

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antibody was shown to immunoprecipitate a protein with a molecular weight of 185 kDa under non-reducing or 170 kDa under reducing conditions. By immunohistochemistry, SER-4 antigen was shown to be M ϕ -restricted, with high expression on F4/80+ M ϕ s in the bone marrow, subcapsular sinus and the medullary cords of the lymph nodes, marginal metallophils in the inner marginal zone of the spleen and weak expression on red pulp M ϕ s in the spleen and Kupffer cells in the liver [15]. In the nervous system, Sn is not expressed by the resident M ϕ s, microglia, but it is present on some M ϕ s that reside outside of the blood–brain barrier, such as in the choroid plexus and leptomeninges [56]. Sn was found to be induced on inflammatory M ϕ s in the central nervous system after sterile injury, expression correlating with leakiness of the blood–brain barrier and therefore providing additional evidence for a macromolecular factor in plasma that regulates Sn expression [56].

Definitive evidence that Sn is a lectin-like receptor came from studies of the purified protein following its isolation by antibody affinity chromatography from murine spleen [17]. Visualization of the isolated receptor following low angle shadowing and electron microscopy showed that it consisted of a globular head, measuring 9 ± 2 nm in diameter and tail, measuring 35 ± 4 nm in length. Sn binding properties were characterised using desialylated human erythrocytes reconstituted enzymatically with sialic acid in $\alpha 2 \rightarrow 3$ or $\alpha 2 \rightarrow 6$ linkages. This showed that Sn preferentially recognizes Neu5Ac $\alpha 2 \rightarrow 3$ Gal $\beta 1 \rightarrow 3$ GalNAc- over Neu5Ac $\alpha 2 \rightarrow 6$ Gal $\beta 1 \rightarrow 4$ GlcNAc-derivatized erythrocytes. The preference of Sn for $\alpha 2 \rightarrow 3$ over $\alpha 2 \rightarrow 6$ linked sialic acid in both O- and N-linked glycans was also demonstrated in inhibition experiments performed with sialylated derivatives of anti-freeze glycoprotein and glycophorin. Similar results were obtained when gangliosides were used. GD1a and GM3, which express terminal $\alpha 2 \rightarrow 3$ linked sialic acid, were recognized by Sn, whereas binding was absent or weak to the gangliosides GM1 and GM2 which only express an ‘internal’ sialic acid residue and to GD3 and GQIb which contain terminal $\alpha 2 \rightarrow 8$ linked sialic acid. This suggested that specific sialoglycoconjugates containing terminal $\alpha 2 \rightarrow 3$ linked sialic acid are preferred targets of Sn.

Sn protein primary structure

In 1994, the molecular cloning of murine Sn was reported based on screening a lambda phage cDNA library with degenerate probes derived from C-terminal peptide sequence of purified protein [18]. Unexpectedly, Sn was shown to be a member of the immunoglobulin (Ig) superfamily with 17 Ig-like domains (Fig. 1). Murine Sn was predicted to be a type I transmembrane glycoprotein consisting of 1,694 amino acids, with a short intracellular region

of 35 amino acids, a 21-amino acid transmembrane segment and a long extracellular region of 1,619 amino acids containing up to 15 N-linked glycans. The short cytoplasmic tail of Sn did not show any similarities with other proteins, but 5 potential phosphorylation sites were identified. The first domain of the extracellular N terminus of the molecule was shown to be a V-set domain containing an unusual arrangement of predicted disulphide bonds, including an intra-sheet disulphide bond between β -strands B and E (as opposed to the normal inter-sheet bond between β -strands B and F) and an interdomain disulphide linking the V-set domain to the adjacent Ig domain. The other 16 extracellular domains were shown to be C2-like, with similarities in length and sequence between domains 4, 6, 8, 10, 12, 14 and 16 and between domains 5, 7, 9, 11, 13, 15 and 17, whereas domain 3 was shown to be similar to even-numbered domains. Domains 1 and 2 at the N terminus were distinct. Therefore the ‘stem region’ of domains 4–17 within Sn appears to have evolved by repeated duplication of a two exon unit.

The first two Ig domains of Sn were seen to share both sequence similarity and structural features with the previously described Ig superfamily proteins CD22, myelin-associated glycoprotein and CD33. This raised the intriguing possibility that these proteins had all evolved to mediate sialic acid recognition, a prediction that was subsequently borne out using recombinant proteins and resialylated human red blood cells in rosetting assays [40]. Although initially described as the ‘sialoadhesin family’, these proteins were subsequently renamed the ‘sialic acid binding Ig-like lectins’, or ‘siglecs’ by consensus [19]. Following the discovery and characterisation of the species-variable CD33-related siglec subgroup, this family is now known to be made up of at least 14 members in humans, most of which are expressed in cells of the immune system (reviewed in [21]).

Molecular basis for Sn recognition of carbohydrates

The location of the sialic acid binding region of Sn was determined by generating a series of extracellular domain deletion constructs fused to the Fc portion of human IgG1 [51] which revealed that the N-terminal V-set domain is both necessary and sufficient. The molecular basis for carbohydrate binding by Sn was investigated by site-directed mutagenesis [70], X-ray crystallography [45] and nuclear magnetic resonance analysis [20]. The Sn V-set domain was crystallized as a complex with its ligand 3'-sialyllactose [45]. It was shown that arginine-97, which is conserved in Sn from all species (Table 1), forms a bidentate salt bridge with the carboxylate group of *N*-acetylneuraminic acid and two conserved tryptophans at positions 2 and 106 to make hydrophobic interactions with the *N*-acetyl and glycerol

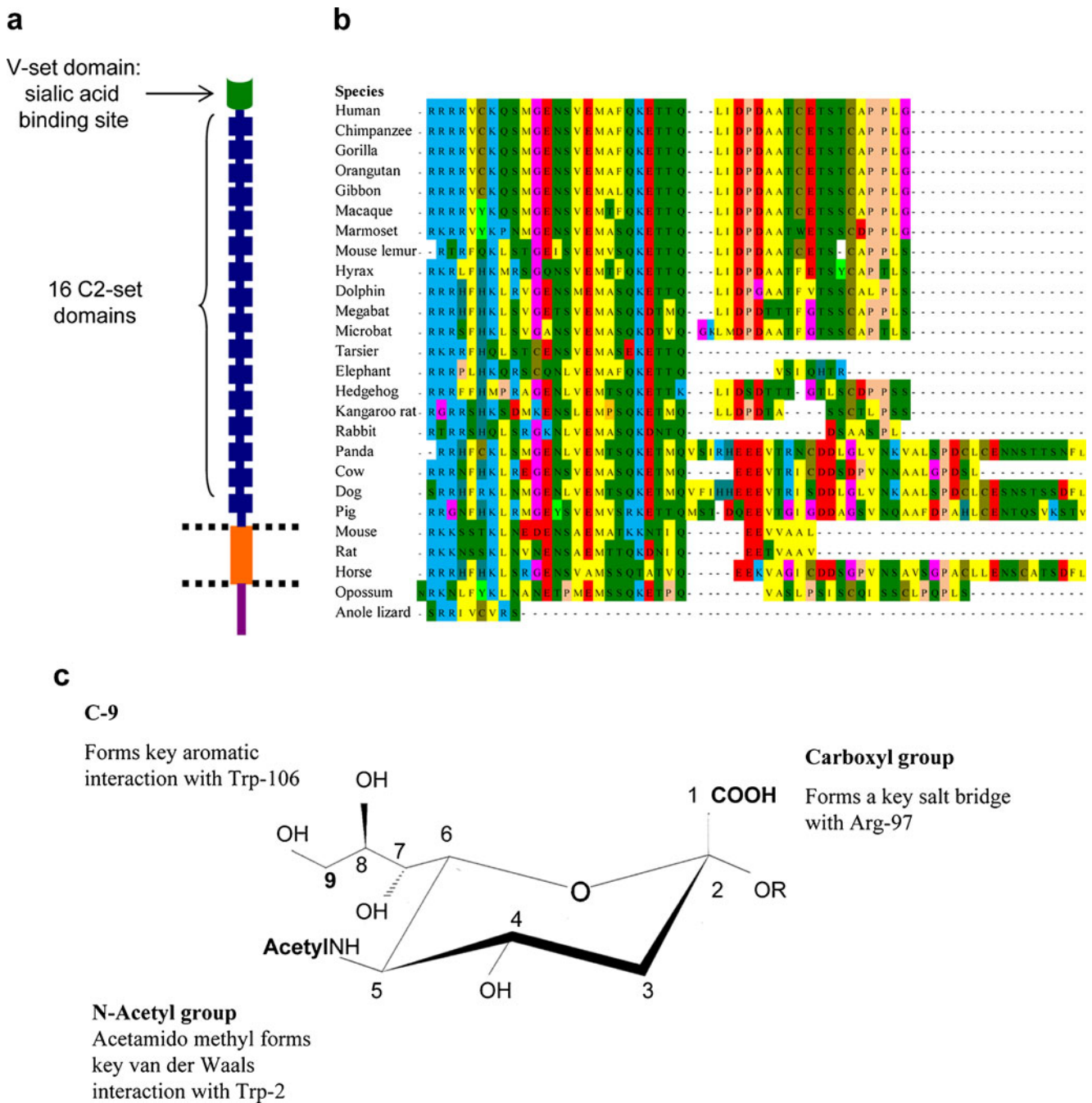


Fig. 1 The features of Sn. **a** Schematic diagram showing the domain organization of Sn protein. **b** Alignment of cytoplasmic tails of mammalian and reptilian Sn. **c** *N*-acetylneuraminic acid showing the

functional groups that make key contacts with the binding site of Sn. The Sn residues indicated are conserved in all Sn orthologues

moieties respectively (Fig. 1c, Table 1). Arginine-97 was shown to be crucially important for binding to sialic acid as it was demonstrated that even a conservative substitution of arginine with lysine results in about 10-fold loss in binding affinity of Sn [20]. The functional groups of sialic acids involved in binding to Sn were investigated using synthetic *N*-acetylneuraminic acid analogues either on resialylated human erythrocytes or as free α -glycosides in hapten

inhibition [41]. This study and others [39] have confirmed that Sn is specific for α Neu5Ac, the most abundant of the mammalian sialic acids, and does not recognize two other important sialic acids, Neu5Gc or Neu5Ac9Ac.

In common with many other lectins, the glycan binding site of Sn exhibits low millimolar binding affinities for naturally sialylated ligands [20]. Therefore, cell adhesion depends on clustering of both the receptor and the ligand

Table 1 Comparison of mammalian and a reptilian Sn orthologues

Species	Ig domains	Sia binding ^a	% Seq Id ^b	Cytoplasmic tail	
				Length	% Seq Id
Human	17	WRW	100	44	100
Chimpanzee	17	WRW	99	44	100
Gorilla	17	WRW	99	44	100
Orangutan	17	WRW	95	44	100
Macaque	17	WRW	95	44	93
Marmoset	17	WRW	89	44	81
Gibbon	17	WRW	89	44	95
Mouse Lemur	17	WRW	83	42	78
Dolphin	17	WRW	82	44	68
Cow	17	WRW	79	49	38
Horse	17	WRW	79	60	31
Microbat	17	W?W ^c	79	46	65
Megabat	17	WRW	79	44	65
Rabbit	17	WRW	78	33	43
Pig	17	WRW	77	64	34
Dog	17	WRW	77	65	34
Panda	17	WRW	77	64	38
Elephant	17	WRW	77	32	53
Mouse	17	WRW	73	32	34
Hedgehog	17	WRW	73	43	53
Rat ^d	17	WRW	72	32	32
Hyrax	17	WRW	71	44	70
Kangaroo Rat	17	WRW	67	40	50
Tarsier	17	WRW	57	25	64
Opossum	17	WRW	52	45	31
Anole Lizard	17	WRW	39	9	55

^a Designates the three amino acids in murine Sn required for interaction with sialic acid: W2 with the glycerol, R97 with the carboxylate and W106 with the *N*-acetyl moieties referred to in Fig. 1c and demonstrated in the crystal structure of Sn complexed with 3'-sialyllactose [45]

^b Sequence identity of full-length transcript compared to human Sn

^c The microbat sequence does not align over the 'R' residue

^d Domain 6 not fully sequenced in rat genome sequence GenBank: EDL80222.1

to mediate high avidity. Experimental evidence for the importance of ligand clustering was obtained using transfected CHO cells presented with up to 140 GT1b oligosaccharides attached to streptavidin and complexed with biotin-BSA [32]. In general, a linear increase in the number of ligands per molecule leads to a logarithmic increase in the binding affinity. Likewise, increasing the number of Sn molecules in the plasma membrane is important for achieving a critical density required for stable binding to appropriate targets. Following induction on Mφs with mouse serum, it was shown using ¹²⁵I labelled SER-4 Fab fragment that up to 10⁶ molecules of Sn can be expressed per cell, resulting in

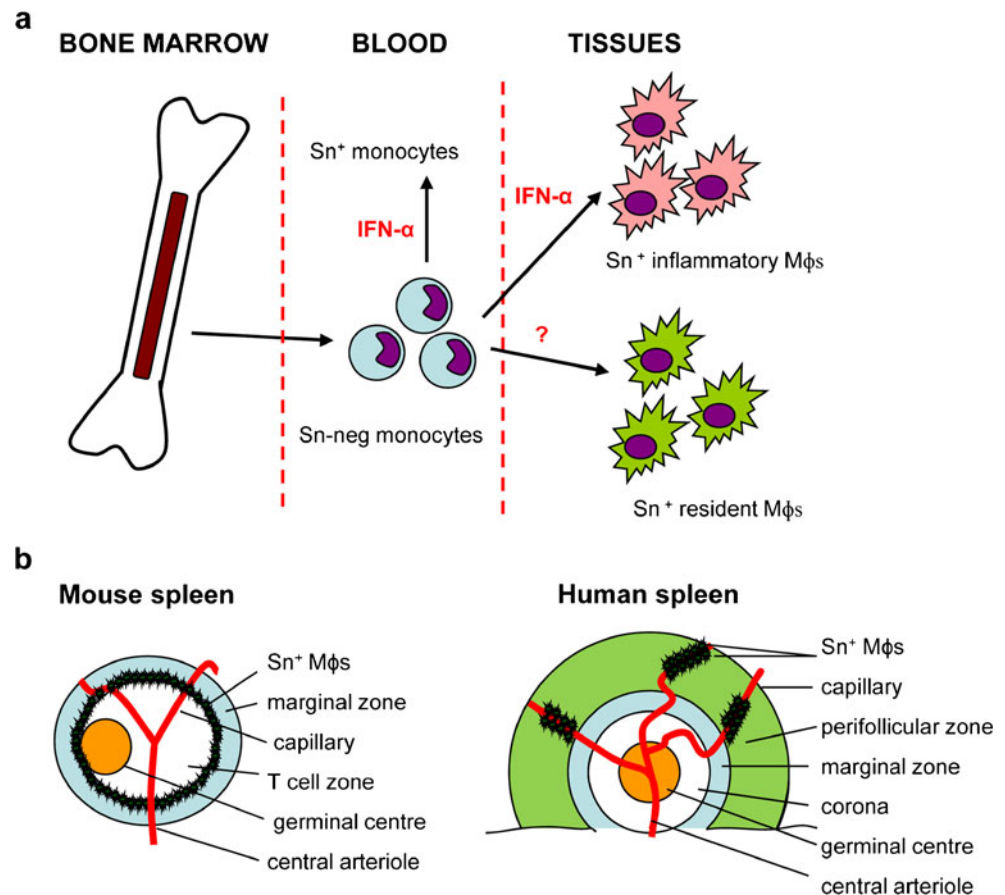
high avidity binding to red blood cells [15]. By altering the expression of Sn over a fairly narrow range, fine control over cellular interactions can be achieved via this avidity effect.

Expression of Sn on Mφ subsets and its induction by type I IFN

In all species examined so far, including human, pig, mouse and rat, Sn has been shown to be highly restricted in expression to cells of the mononuclear phagocyte system with highest expression on Mφ subsets in secondary lymphoid organs, such as lymph nodes and spleen (Fig. 2). In human samples, immunohistochemistry and FACS studies showed that Sn is not normally expressed on blood monocytes but is present on a wide variety of tissue Mφs in the spleen, lymph node, bone marrow, liver, colon and lungs [31]. Sn was also found to be highly expressed on inflammatory Mφs in rheumatoid synovial membrane in tissue samples from rheumatoid arthritis patients [31]. In humans, Sn+ Mφs are not found in the marginal zone of the spleen in contrast to rodents [63]. Human spleens contain an extra compartment, the perifollicular zone, which is located between the marginal zone and the red pulp (Fig. 2). It is a dynamic region which appears to be similar to the red pulp containing erythrocyte-filled spaces and strongly Sn+ Mφs that form sheaths around capillaries in the perifollicular zone. Weakly Sn-expressing Mφs could also be found in the perifollicular zone and the red pulp. In contrast to rodents, the marginal metallophilic cells are absent in humans and the human marginal zone does not contain any Sn+ Mφs.

A key factor that has been shown to upregulate Sn in all species examined is interferon-α (IFN-α). Molecules that trigger type I IFN responses can also upregulate Sn expression in Mφs, as demonstrated for LPS and poly I:C [72] that drive TRIF-dependent pathway of type I interferon induction via TLR-4 and TLR-3 respectively. Kirchberger and colleagues also demonstrated that Sn can be induced on monocyte-derived dendritic cell (DC) populations in vitro after treatment with inactivated human rhinovirus, probably via intracellular RNA sensors such as MDA-5 and RIG-I that drive type I IFN production [42]. Despite these in vitro effects on monocyte-derived DCs, no expression of Sn has been shown on bona fide DCs in vivo so the role of Sn in modulation of DC functions such as antigen presentation to naive T cells is unknown. In addition, Sn expression has been reported in monocytes after HIV-1 infection [58] and in patients suffering from systemic lupus erythematosus and systemic sclerosis [72]. These observations are consistent with the upregulation of type I interferon levels in the serum of patients with viral infections and autoimmune diseases [7, 55].

Fig. 2 The development and regulation of Sn expression on myelomonocytic cells. **a** Blood monocytes are derived from the haematopoietic precursor cells in the bone marrow where they move to tissues, either to become resident tissue Mφs that constitutively express Sn via unknown mechanisms or under the influence of IFN- α to become infiltrating Sn⁺ Mφs in inflammatory tissues. Virus-infected monocytes, e.g. in HIV-1 infection, can also upregulate Sn expression in the presence of IFN- α . **b** The anatomy and localization of Sn⁺ Mφs in mouse and human spleen



Conserved biological functions of Sn

A phylogenetic analysis of Sn using currently available genomic sequences shows that a Sn orthologue with 17 Ig domains and a highly conserved sialic acid binding site is present in all mammals (Table 1). Interestingly, a clear orthologue with 17 Ig domains and a sialic acid binding site is also present in the anolis lizard genome [1] showing that the Sn gene must have evolved prior to the split of the amniote lineage into the ancestral lineages of mammals and reptiles ~320 million years ago.

It has been proposed that Sn has evolved the unusually large number of 17 Ig domains to extend the sialic acid binding site above the dense glycocalyx to avoid *cis*-inhibition by the abundant sialic acids at the cell surface and thereby permit *trans* interaction with ligands on other cells [18, 50]. This feature of Sn is in striking contrast to other siglecs that usually contain between 2 and 7 Ig domains and are typically masked at the cell surface by *cis* interactions with sialic acids [21].

In comparison to the extracellular region, the cytoplasmic tail of Sn is very poorly conserved in both sequence and length varying from only 9 residues in the anolis lizard to 65 in the dog (Fig. 1b, Table 1). Taken together, these observations would indicate that the main conserved intrinsic role

of Sn is in mediating cellular interactions rather than cell signalling. However, via collaboration with other receptors, Sn may be important for triggering key signalling functions in Mφs that influence host responses to the extracellular environment (Fig. 3). In addition, the extended cytoplasmic tail seen in some species (Table 1) may provide novel species-specific signalling functions, as discussed below for porcine Sn.

Sn-deficient (Sn^{-/-}) mice were generated to study the biological functions of Sn in detail [53]. Sn^{-/-} mice are viable and fertile with no developmental abnormalities. Analysis of different tissues revealed that Sn^{-/-} mice show a small increase in CD8⁺ T cells and a small decrease in B220⁺ B cells in spleens and lymph nodes with slightly less follicular B cells and an increase in numbers of marginal zone B cells in spleen. The reduction of B cell number correlated with reduced immunoglobulin M (IgM) levels in Sn^{-/-} mice but similar titers of IgG subclasses were found. These observations suggested that the main role for Sn may be in regulating the immune system and not in directly regulating haematopoiesis as had previously been considered [16]. This contention is also consistent with the results of several studies investigating the role of Sn in autoimmune diseases. These include experimental autoimmune uveoretinitis, two models of inherited demyelinating neuropathies of the central and nervous systems [35, 43],

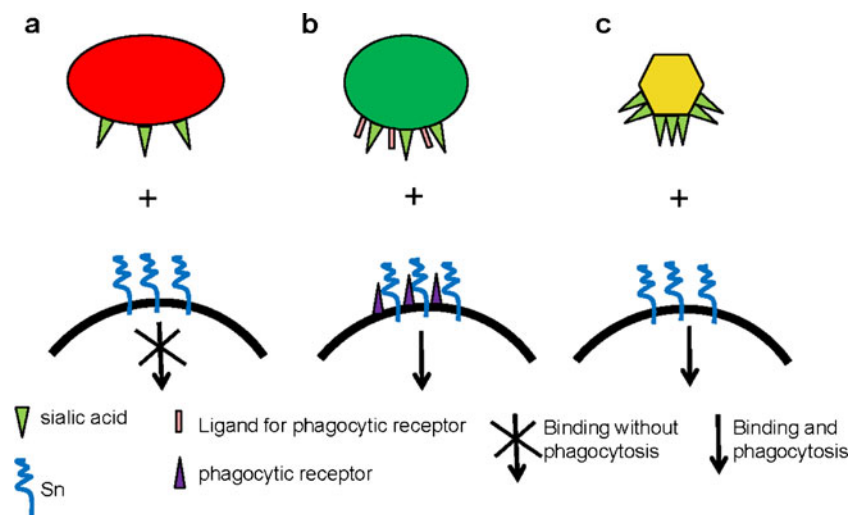


Fig. 3 Models of Sn-mediated uptake of sialylated particles. **a** In the case of cellular targets that have relatively low sialic acid density, such as erythrocytes, the particle binds to Sn+ M ϕ , but the avidity is not high enough to trigger phagocytosis. **b** If the sialylated particle displays additional ligands for a phagocytic receptor on Sn+ M ϕ , Sn and

the phagocytic receptor may synergize to mediate phagocytosis. **c** If the sialic acid density on the sialylated particle is high enough to create high avidity binding to Sn, as with certain pathogens, the particle may be directly phagocytosed by Sn+ M ϕ s

and experimental autoimmune encephalomyelitis (EAE) as a model for human multiple sclerosis [71]. In all cases, Sn^{-/-} mice developed less severe inflammatory responses, with reduced clinical signs of disease and lowered numbers of inflammatory M ϕ s and T effector cells. In the most recent study of EAE, it was shown that the proinflammatory role of Sn correlated with reduced numbers of anti-inflammatory CD4+ T regulatory cells (T-regs) which expressed high levels of Sn ligand [71]. It was demonstrated that co-culture of these T-regs with Sn+ M ϕ s led to reduced proliferation in vitro indicating that Sn-dependent M ϕ /T-reg interactions could lead to stronger adaptive immune responses. In the case of pathogens, this could be important in setting an appropriate balance of T-reg versus T effector populations during host adaptive immune responses. Thus, pathogen-driven upregulation of Sn expression on M ϕ s would be expected to suppress local T-reg expansion, resulting in stronger T effector activity, both for CD4+ and CD8+ T cell populations.

Sn as a putative endocytic and/or phagocytic receptor

Binding and uptake by either phagocytosis or endocytosis of self-constituents has to be highly regulated to lower the risk of autoimmune responses. Given that M ϕ s are the major phagocytic cells in the body with the potential to trigger autoimmune responses, regulation of uptake via receptors for self, such as Sn, is of considerable importance. The presence of Sn in endocytic vesicles of the subcapsular sinus M ϕ s (SSMs) in the lymph node [61] indicates that Sn is constitutively involved in endocytic functions of these cells.

Initial studies with Sn showed that it was a non-phagocytic receptor for red blood cells, but subsequent studies with *Neisseria meningitidis* challenged this view, as these bacteria were shown to be taken up by M ϕ s in a Sn-dependent manner [37]. Furthermore, and as discussed further below, Sn has been shown to mediate endocytosis of sialylated enveloped viruses and porcine Sn can endocytose the mouse anti-Sn monoclonal antibody 41D3 in a clathrin-dependent manner [27, 60, 68]. Endocytosis was claimed to require a porcine-specific motif F¹⁶⁷¹-YKL in the cytoplasmic tail of Sn that is recognized by the clathrin-associated endocytic adapter complex AP-2 as a first step in the formation of clathrin-coated vesicles [22].

A recent study showed that liposomes displaying a high affinity sialic acid-based ligand for Sn, but no other ligands, were rapidly cleared in mouse liver in a Sn-dependent manner [11]. Therefore, under certain circumstances such as when particles contain a high density of sialylated ligands, Sn may be capable of directly mediating uptake into M ϕ s. This could be of considerable importance in the host–pathogen interaction as discussed below as well as in some autoimmune diseases. However, under steady-state conditions, Sn-dependent uptake of material into M ϕ s is likely to involve synergy with additional ‘professional’ phagocytic receptors (Fig. 3).

Resident Sn+ M ϕ populations and antigen presentation

In the absence of infection, Sn is abundantly expressed on M ϕ s in the subcapsular sinus and medullary cords of the

lymph node, as well as on marginal metallophilic Mφs in rodent spleens or perifollicular zone Mφs in human spleen (Fig. 2b) [63]. Due to the strategic localization of splenic and lymph node Sn⁺ Mφs at portals of entry for blood and lymph respectively, it is likely that Sn plays a role in regulating the immune responses to pathogens and self-antigens that they encounter in blood or lymph.

Spleen marginal zone Mφs have been shown to collaborate with CD8⁺ DCs in generation of cytotoxic T cells [6]. Den Haan and colleagues showed that injection of ovalbumin-coupled anti-Sn monoclonal antibodies targeted to marginal metallophilic Mφs in the spleen results in strong activation of antigen-specific CD8⁺ T cell responses. These Sn⁺ Mφs were shown to transfer antigens exclusively to CD8⁺ splenic DCs, which led to efficient cross-presentation and activation of cytotoxic T lymphocytes. This leads to speculation whether sialylated pathogens could follow the same route of uptake by marginal metallophilic Mφs, transfer to CD8⁺ DCs and eventually activation of cytotoxic T cells and whether Sn has a role in the interactions between marginal metallophilic Mφs and DCs.

SSMs in the lymph node have been shown to act directly as antigen presenting cells as they capture antigens from the blood and translocate them across the sinus to the follicular space where they present the antigen to B cells [10, 38, 54, 57]. The B cells then transport antigens to germinal centers and initiate immune responses. The SSMs are highly positive for Sn but it is yet to be investigated whether Sn has a role in antigen presentation or phagocytosis/endocytosis of antigens that SSMs capture from the afferent lymph. In addition to being able to present antigens to B cells, recently it was shown that these cells can also capture and present lipid antigens to *i*NKT cells and therefore mediate early *i*NKT cell activation in lymph nodes [8].

In view of the role of SSMs as gatekeepers of adaptive immunity, the regulation of phagocytosis in this population of Mφs is likely to be very important in determining which antigens are available to B cells as opposed to those that are taken up by the SSMs and degraded and rendering them cryptic to the immune system. Dysregulation of phagocytosis, for example the failure to efficiently clear damaged or apoptotic host cells via SSMs, could therefore contribute to breakage of tolerance and development of autoimmune responses such as those seen in systemic lupus erythematosus. Conversely, exploitation of this tolerance pathway by pathogens might reduce their antigenicity and favor their survival in the host.

Sn⁺ Mφs have also been reported to have a crucial role in antitumour immunity by cross-presenting antigens from dead tumour cells to CD8⁺ T cells [4]. A recent publication showed that subcutaneously injected dead cells are transported to lymph nodes and SSMs phagocytose and directly cross-present dead cell-associated antigens to CD8⁺ T cells.

The depletion of Sn⁺ Mφs resulted in loss of tumour-specific CD8⁺ T cell activation and proliferation, indicating a critical role for these Mφs in antigen presentation. Subsequent tumour destruction was also shown to be controlled by Sn + SSMs because mice lacking Sn⁺ Mφs at the time of vaccination were shown to be unable to reject viable tumour cells. This Sn-mediated cross-presentation of tumour cell associated antigens was shown to be independent of migratory DCs and lymph node-resident conventional DCs.

Investigation of porcine Sn has revealed that Sn could directly participate in antigen uptake and/or presentation by antigen presenting cells (APCs) [60]. In order to investigate whether Sn can be targeted for delivery of antigens to APC for T cell stimulation, T lymphocytes from pigs immunized with mouse immunoglobulins were incubated with IFN- α treated monocytes or monocyte-derived DCs. Monoclonal antibody to Sn was shown to induce T cell proliferation in vitro at concentrations 100-fold lower than control antibody. These data indicate ligands that bind Sn gain access efficiently to the major histocompatibility complex processing and presentation pathways. However, a major caveat of experiments, such as these using intact IgG to target Mφ receptors like Sn, is that interactions with FcR cannot be ruled out. FcR are well-known signalling molecules that trigger multiple effects in Mφs including delivery of antigens to MHC class I and class II molecules for antigen presentation (reviewed in [52]). Nevertheless, the potential role of Sn in endocytosis and antigen presentation is an important area for future study as it could be exploited in vaccine or drug development by specifically targeting antigens, toxins or other compounds to immunomodulatory Sn⁺ Mφs.

While there is no clear evidence that DCs can express Sn in vivo, treatment of human monocyte-derived DCs with HRV14, a member of the major group of human rhinovirus family has been reported to induce Sn expression and inhibit the accessory function of DCs [42]. Despite the high levels of MHC and costimulatory molecules on infected DCs, the induction of Sn was shown to diminish DC-T cell stimulatory capacity and cause an anergic state in cocultured T cells. This inhibitory phenotype was shown to be reverted by a monoclonal antibody to Sn, suggesting that induction of Sn in infected DCs can lead to reduction in adaptive response during viral infection. A subsequent study showed that human DCs that are activated by rhinoviruses induce the production of IL-35 secreting T-regs, a pathway that can be blocked by antibodies to Sn and B7-H1 [62].

Sn and the regulation of tolerance for self-antigens

Sn⁺ Mφs in the marginal zone have been shown to have a critical role in regulating suppression of immune responses

to apoptotic cell associated antigens [48]. Miyake and colleagues showed that intravenously injected apoptotic cells that express a fragment of myelin oligodendrocyte glycoprotein (MOG) reduced MOG-specific T cell response and prevented the development of EAE. These apoptotic cells were shown to be selectively captured by CD8 α ⁺ DCs which are responsible for suppression of immune responses to cell-associated antigens. By using transgenic mice in which Sn⁺ M ϕ s could be deleted by injection of diphtheria toxin, the apoptotic cells were made available to CD8 α ⁻CD11b⁺ DCs which resulted in breach of tolerance, T cell activation and accelerated development of EAE.

The role of Sn⁺ marginal zone M ϕ s in regulation of immune tolerance was also supported by studies performed by McGaha and colleagues who also showed altered localization pattern and increased immune responses in mice after depletion of Sn⁺ marginal zone M ϕ s [46]. In the absence of Sn⁺ cells, apoptotic cells were found to be associated with T cell areas of the lymphoid follicles but also with red pulp M ϕ s which led to increased production of proinflammatory cytokines and enhanced lymphocyte responsiveness to apoptotic cell antigens. The breakage of tolerance to self-antigens in Sn⁺ cell depleted mice was also shown to promote SLE.

Although the mechanism of the phagocytosis of apoptotic cells is not completely understood, it has been proposed to be a two-step process. First, an interaction between putative ligands and receptors occurs and then the apoptotic cell is engulfed through recognition of PS exposed on the apoptotic cell surface [34]. Sn could fit into the proposed model by binding sialylated ligands on apoptotic cells and therefore increasing the contact area between the M ϕ and the sialylated target to promote uptake in synergy with phagocytic receptors such as the TIMs that recognize phosphatidylserine on apoptotic cells [29].

Sn as a potential receptor for sialylated pathogens

Although sialic acids are abundant in all higher organisms, they are less common amongst microorganisms and potential pathogens (reviewed in [3, 69]). It is therefore of great

interest that several medically important pathogens have evolved various mechanisms to synthesize or capture sialic acids and display them on their surfaces. Understanding the role of Sn in the immune response to these bacteria is particularly relevant because they include important human pathogens, such as *N. meningitidis*, *Haemophilus influenzae*, group B *Streptococcus*, *Campylobacter jejuni* and several pathogenic strains of *Escherichia coli*. In addition, enveloped viruses that use the host cell's glycosylation machinery to display glycans at the cell surface can present sialic acids recognized by Sn.

Due to strategic positioning in the spleen and lymph nodes of Sn⁺ M ϕ s on the border of lymphocyte rich regions and the entry of blood or lymph (Fig. 2), it has been speculated that Sn performs a role in the uptake and processing of sialylated pathogens. This view is also supported by observations that Sn can mediate recognition and promote uptake of various sialylated pathogens in vitro, such as PRRSV [2, 23–26, 64, 68], HIV-1 [58, 59, 65, 73], *N. meningitidis* [37], *C. jejuni* [33] and *Trypanosoma cruzi* [49] (Table 2). Each will be discussed in turn.

Porcine reproductive and respiratory syndrome virus

Porcine reproductive and respiratory syndrome virus (PRRSV) induces respiratory tract illness and reproductive failure in pigs which severely affects the swine industry worldwide. It belongs to the *Arteriviridae* family of single-stranded RNA viruses and infects cells of the monocyte/M ϕ lineage via receptor-mediated endocytosis. In 1998, it was reported that a monoclonal antibody named 41D3 could block the infection of PRRSV of porcine alveolar M ϕ s [28]. It was later demonstrated that this antibody recognises porcine Sn [68]. When porcine Sn was cloned and transfected into a cell line resistant to virus entry, the cells became permissive. Sialidase treatment of the virus was shown to prevent the attachment and infection of porcine alveolar M ϕ s with PRRSV, in addition, enzymatic removal of N-linked glycans reduced PRRSV infection. Another receptor that has been associated with PRRSV infection is heparin-like material which recognizes a viral matrix protein

Table 2 Human pathogens that can present sialic acid on the cell surface leading to recognition by Sn

Pathogen	Disease	Sialic acid ligand	References
PRRSV	Reproductive failure in breeding stock and respiratory tract illness in young pigs	M/GP5 glycoprotein complex in viral envelope	[64, 68]
HIV-1	AIDS	gp120 in viral envelope	[59, 73]
<i>Trypanosoma cruzi</i>	American trypanosomiasis (Chagas disease)	Neu5Ac α 2 \rightarrow 3Gal in mucins	[49]
<i>Neisseria meningitidis</i>	Meningitis	Neu5Ac α 2 \rightarrow 3Gal in LOS	[37]
<i>Campylobacter jejuni</i>	Gastroenteritis, Guillain-Barré syndrome	Neu5Ac α 2 \rightarrow 3Gal in LOS, GD1a, GM1b, GM3 mimic	[33]

[23]. Analysis of the kinetics of PRRSV entry revealed that heparin first mediates attachment of the virus but not the entry and it is gradually followed by Sn mediated internalization [25]. Using transfected CHO cells, it was shown that heparin enhances Sn mediated internalization but Sn-dependent binding and internalization of PRRSV occurs independently.

Using site-directed mutagenesis, it was shown that similar to mouse and human Sn, the V-set domain of porcine Sn functions as the sialic acid binding domain [26]. When R¹¹⁶ to E mutation was introduced in the V-set domain of porcine Sn, the PRRSV could no longer attach or enter the transfected CHO cells, suggesting that sialic acid binding capacity of Sn is required for the entry of the virus. This was confirmed by studies from a different research group, who showed using a series of truncated porcine Sn mutants that the first 150 amino acids that comprise the entire first N-terminal V-set domain is necessary and sufficient for PRRSV binding to cells [2].

To identify the sialic acid components of PRRSV, a soluble form of Sn was used [64]. The soluble Sn-Fc protein was shown to bind the virus in a sialic acid dependent manner and was able to block virus entry into porcine alveolar Mφs confirming the essential role for PRRSV infection. Sn was shown to recognize only the M/GP₅ glycoprotein complex of PRRSV in a sialic acid dependent manner, although in addition to GP₅, sialic acids are present on the GP₃ and GP₄ envelope glycoproteins of the virus as well. This insight into Sn-PRRSV interactions could be useful for vaccine development.

In addition to Sn, CD163, a group B scavenger receptor has also been described as a receptor for PRRSV [9]. Studies using transfected PK-15 cell line showed that when cells were transfected only with Sn, the virus was internalized but not uncoated; however, when Sn and CD163 were co-expressed, the virus was uncoated upon internalization and successfully replicated [66]. CD163 expression alone was shown not to be sufficient for virus entry, although cells became productively infected; but compared to Sn and CD163, the transfected cells expressing only CD163 produced less virus. These data indicate that Sn is required for the internalization of the virus and CD163 for virus uncoating. The same group also showed using dominant-negative Rab5 and Rab7 mutants, that PRRSV needs CD163+ early endosomes but does not continue through the endocytic pathway to late endosomes for productive infection [67]. The virus was shown to colocalize with Sn on the cell surface and beneath the plasma membrane, while CD163 colocalizes with the virus only in early endosomes in porcine alveolar Mφs.

HIV-1

The role of Sn in inflammatory and infectious diseases gained increased interest after the demonstration that Sn is

upregulated in monocytes from HIV-1 infected patients and that expression increases with disease progression [58, 59, 65]. Analysis of HIV patients has revealed that Sn mRNA is significantly elevated early after HIV-1 infection and a further increase is seen in AIDS patients [65]. This was confirmed by upregulation of Sn protein by FACS that showed that in infected patients up to 90% of CD14+ monocytes express Sn. This was followed by studies that showed that Sn expression directly correlates with viral load [59]. Monocytes were shown to bind to HIV-1 via Sn, as Sn + monocytes bound to approximately 3-fold more virus particles compared to normal control monocytes. Sn was shown to bind the virus through recognizing the sialic acid residues on the viral envelope glycoprotein gp120. Furthermore, Sn + monocytes enhanced HIV-1 infectivity by absorbing the cell-free virus from the culture and trans infecting permissive reporter cells [59].

A recent study showed that Sn and siglec-9 directly recognize viral gp120 proteins in HIV-1 envelope, which promotes the adhesion of viral particles to Mφs [73]. Compared to Sn and siglec-9, which showed affinities of recombinant dimeric proteins varying between 0.01–1 mM to different gp120 envelope proteins, siglecs-3, -5 and -7 displayed low affinity binding to gp120 using similar receptor densities. However, increasing the receptor immobilization density by 3- to 5-fold improved binding affinities for siglec-3, -5 and -7 between 100- to 1,000-fold. This indicates an important avidity contribution to the siglec-gp120 recognition by siglecs. In addition, the sialic acid on gp120 binding to Sn was shown to have a crucial role in infection of Mφs. This suggests that viruses can target Sn-mediated endocytosis to increase infectivity.

N. meningitidis

In parallel to the role of Sn in PRRSV infection, the role of mouse Sn in binding and uptake of sialylated *N. meningitidis* emerged [37]. Although Sn was not thought to function directly as a phagocytic receptor, the experimental data indicated that it could enhance Mφ phagocytosis of bacteria by binding to sialylated lipooligosaccharides (LOS) on the surface of *N. meningitidis* and therefore have an important role in the uptake of intact bacteria by Mφs [37]. Using sialylated and non-sialylated LPS derivatives of two serogroups of *N. meningitidis*, it was shown that the sialylated bacteria are specifically recognised by Sn in a sialic acid dependent manner. In addition to Sn, soluble recombinant siglec-5 was shown to bind sialylated *N. meningitidis* in vitro and Sn or siglec-5 transfected CHO cells showed increased binding to sialylated variants of *N. meningitidis*. The role of Sn in uptake of the sialylated bacteria was confirmed by analysis of phagocytosis by Mφs from wild-type and Sn^{-/-} mice which showed that Sn bound and phagocytosed sialylated bacteria in a sialic acid-dependent

manner. These results indicated that Sn can have a role in host defence against sialylated bacteria.

C. jejuni

C. jejuni is a common human pathogen that causes gastroenteritis and has been linked with an autoimmune disease called the Guillain–Barré syndrome [36]. Some clinical isolates have been shown to express sialylated LOS that display ganglioside-like terminal structures on the core oligosaccharides. Previous studies have demonstrated that sialylation of *C. jejuni* can enhance pathogenicity by increasing invasiveness in epithelial cells [44] and act as an immunosuppressor by blocking complement activation [30]. The initial report that siglecs might have a role in binding to sialylated *C. jejuni* showed that out of 10 siglecs screened, siglec-7 was found to bind purified LOS HS:19(GM1(+)) GT1a(+) from a sialylated isoform of *C. jejuni* in solid-phase binding assays and to intact bacteria [5]. A later study showed that Sn can also bind sialylated *C. jejuni* strains that carry LOS-ganglioside mimics with terminal $\alpha 2 \rightarrow 3$ -linked sialic acids, including GD1a, GM1b and GM3 [33]. Sn was shown to enhance the binding of sialylated *C. jejuni* to transfected CHO cells, which indicates that Sn can have an important role in immune responses to *C. jejuni*.

T. cruzi

In addition to sialylated viruses and bacteria, Sn has been shown to recognize a sialylated parasite, *T. cruzi* that naturally infects M ϕ s [49]. The proliferative forms of *T. cruzi*, epimastigotes, and the infective adhering forms of *T. cruzi*, trypomastigotes, were shown to associate with mouse peritoneal M ϕ s, in which Sn expression was induced with homologous mouse serum and this association could be blocked by monoclonal antibodies to mouse Sn. Desialylation of parasites was shown to decrease the M ϕ association, indicating a sialic acid dependent binding to Sn. Scanning electron microscopy confirmed the association of trypomastigotes to Sn-expressing M ϕ s and showed plasma membrane projections from the M ϕ s. Cytochalasin D, which blocks phagocytosis, abolished internalization of trypomastigotes. These data indicate that Sn may have an important role in the initial *T. cruzi* internalization and thus in the establishment of Chagas disease.

Conclusions

As a major M ϕ sialic acid receptor conserved in all mammals, Sn has evolved to mediate ‘self’ cell–cell interactions. Recent studies indicate that cross-talk between Sn and its ligands on lymphocytes play an important role in fine-tuning T and B cell

responses to antigens. A secondary consequence of this role is that Sn can also recognize a wide range of sialylated pathogens. Recent studies have shown that this Sn-dependent recognition can promote pathogen uptake in M ϕ s which could be important in antigen presentation and immune activation. A key unresolved question is whether this latter function is of benefit to the host in protective immunity or whether certain pathogens exploit this pathway to their advantage. In the case of porcine arterivirus, sialylated glycoproteins in the envelope provide Sn ligands that play an important role in binding to alveolar M ϕ s leading to infection of pigs. Whether a similar paradigm applies to other sialylated pathogens requires further study.

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