



Putting the brakes on phagocytosis: “don’t-eat-me” signaling in physiology and disease

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Abstract

Timely removal of dying or pathogenic cells by phagocytes is essential to maintaining host homeostasis. Phagocytes execute the clearance process with high fidelity while sparing healthy neighboring cells, and this process is at least partially regulated by the balance of “eat-me” and “don’t-eat-me” signals expressed on the surface of host cells. Upon contact, eat-me signals activate “pro-phagocytic” receptors expressed on the phagocyte membrane and signal to promote phagocytosis. Conversely, don’t-eat-me signals engage “anti-phagocytic” receptors to suppress phagocytosis. We review the current knowledge of don’t-eat-me signaling in normal physiology and disease contexts where aberrant don’t-eat-me signaling contributes to pathology.

Keywords ‘don’t-eat-me’; anti-phagocytic receptor; efferocytosis; ITIM; phagocytosis

Subject Categories Immunology; Membranes & Trafficking; Molecular Biology of Disease

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See the Glossary for abbreviations used in this article.

Introduction

Removal of unwanted or noxious cells is important for proper development, tissue integrity, and protection against pathogenic and immunogenic damage to the host (Arandjelovic & Ravichandran, 2015). Phagocytosis is a highly efficient process, and dying cells are rarely observed *in vivo* during homeostasis despite routine cellular turnover in several tissues (Elliott & Ravichandran, 2016). The “clearance crew” mediating phagocytosis can be divided into two broad categories: “professional phagocytes” and “non-professional phagocytes” (Arandjelovic & Ravichandran, 2015). Innate immune cells (e.g., immature dendritic cells, monocyte-derived macrophages, tissue-resident macrophages, and microglia) are considered professional phagocytes as they can sense and migrate toward target cells, as well as rapidly and successively internalize multiple targets

(Elliott *et al.*, 2009; Ariel & Ravichandran, 2016; Medina *et al.*, 2020). Other tissue-resident cells (e.g., epithelial cells, fibroblasts, and endothelial cells) also play important roles in phagocytosis, albeit less efficiently, and are considered non-professional phagocytes (Wood *et al.*, 2000; Monks *et al.*, 2005; Juncadella *et al.*, 2013; Arandjelovic & Ravichandran, 2015; Lee *et al.*, 2016; Davies *et al.*, 2018). The phagocytic response can be described in four phases: “smell”, “taste”, “ingestion”, and “digestion/response”; and the molecular details promoting the clearance of dying cells have been excellently reviewed (Arandjelovic & Ravichandran, 2015; Morioka *et al.*, 2019).

The phagocytic process must be tightly controlled, however, to prevent unwarranted removal of healthy cells. Regulation during the taste phase involves “integrated” recognition of eat-me signals and don’t-eat-me signals expressed on the target cell. Eat-me signals include antibody and complement opsonins, exposed phosphatidylserine (PS), calreticulin, oxidized low-density lipoprotein, cell-bound thrombospondin (TSP), modified intracellular adhesion molecule ICAM-3, annexin I, and other modifications to surface proteins (Arandjelovic & Ravichandran, 2015). While living cells generally do not express eat-me signals, there are specific physiologic contexts when some living cells transiently express markers that partially mimic a dying cell such as during lymphocyte activation, skeletal muscle formation, and sperm–egg fusion (Elliott *et al.*, 2005; Gardai *et al.*, 2005; Hochreiter-Hufford *et al.*, 2013; Hochreiter-Hufford *et al.*, 2015; Rival *et al.*, 2019). Thus, the expression of don’t-eat-me signals provides an additional regulatory mechanism to prevent unwarranted clearance of “healthy” cells.

In this review, we discuss the current knowledge of don’t-eat-me signaling in phagocytosis with an emphasis on anti-phagocytic receptors that mediate the recognition of don’t-eat-me signals. Most known anti-phagocytic receptors are single-pass, type I transmembrane proteins belonging to the immunoglobulin (Ig) superfamily that contain one or more immunoreceptor tyrosine-based inhibitory motifs (ITIM) in their cytoplasmic tail (Daeron *et al.*, 2008). The canonical ITIM consensus sequence is (I/V/L)xYxx(L/V), where x can be any amino acid. Many anti-phagocytic receptors also have non-canonical “ITIM-like” motifs with a more divergent sequence (I/V/L/SxYxxL/V/I), as well as immunoreceptor tyrosine-based switch motifs (ITSM) and other protein-binding domains (Ravetch & Lanier, 2000; Daeron *et al.*, 2008). In this review, we refer to all inhibitory motifs as ITIMs in an effort to reduce complexity. Anti-phagocytic

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Glossary

18F-FDG	fluorodeoxyglucose ¹⁸ F	NOD	non-obese diabetic
Aβ	amyloid beta	NSG	NOD scid gamma
AD	Alzheimer's disease	PD-1	programmed cell death protein 1
ADCP	antibody-dependent cellular phagocytosis	PD-L1	programmed death ligand 1
AIHA	autoimmune hemolytic anemia	PD-L2	programmed death ligand 2
B2M	beta-2 microglobulin	PECAM-1	platelet endothelial cell adhesion molecule-1
C3	complement component 3	PET/CT	positron emission tomography/computed tomography
cDC₂	classical dendritic cell 2	PI3K	phosphoinositide 3-kinase
dLGN	dorsal lateral geniculate nucleus	PLCγ	phospholipase C gamma
F4/80	EGF-like module-containing mucin-like hormone receptor-like 1 (EMR1)	PS	phosphatidylserine
FAK	focal adhesion kinase	Pyk2	proline-rich tyrosine kinase 2
Fc	fragment crystallizable	RGC	retinal ganglion cells
Gas6	growth arrest-specific protein 6	RhoA	Ras homolog family member A
Grb2	growth factor receptor-bound protein 2	RIG-I	retinoic acid-inducible gene 1
ICAM-3	intracellular adhesion molecule-3	SFK	Src family kinase
IFNγ	interferon gamma	SH2	Src homology 2
Ig	immunoglobulin	SH3	Src homology 3
IL-10	interleukin 10	SHIP	Src homology 2 domain-containing inositol polyphosphate 5-phosphatase
IL-6	interleukin 6	SHP-1	Src homology region 2 domain-containing phosphatase-1
ITIM	immunoreceptor tyrosine-based inhibitory motif	SHP-2	Src homology region 2 domain-containing phosphatase-2
ITSM	immunoreceptor tyrosine-based switch motif	Siglec	sialic acid-binding immunoglobulin-type lectin
LILRB1	leukocyte immunoglobulin-like receptor B1	SIRPα	signal regulatory protein α
LRP1	low-density lipoprotein receptor-related protein 1	SMCs	smooth muscle cells
mAb	monoclonal antibody	SP-A	surfactant protein-A
MerTK	mer proto-oncogene tyrosine kinase	SP-D	surfactant protein-D
me^v	viable motheaten	Syk	spleen tyrosine kinase
MFG-E8	milk fat globule EGF factor VIII	TAM	tumor-associated macrophage
MHC class I	major histocompatibility complex class I	TGFβ	transforming growth factor β
MI	myocardial infarction	TIDC	tumor-infiltrating dendritic cell
MIAT	myocardial infarction-associated transcript	TLR	Toll-like receptor
MyD88	myeloid differentiation primary response 88	TNFα	tumor necrosis factor α
NF-κB	nuclear factor-kappa B	TSP	thrombospondin
NK	natural Killer		

receptor activation induces tyrosine phosphorylation of the cytoplasmic ITIMs and binding of cytosolic SH2 domain-containing phosphatases, such as the SHP tyrosine phosphatases and the SHIP1/2 inositol phosphatases (Neel *et al*, 2003; Daeron *et al*, 2008). These phosphatases act as downstream effectors to mediate the inhibitory function of anti-phagocytic receptors, although their downstream substrates have been challenging to identify. In antibody-dependent cellular phagocytosis (ADCP) of opsonized targets, the Fc γ RIIb inhibitory receptor plays an important regulatory role via activation of SHIP1/2 (Aman *et al*, 2000; Getahun & Cambier, 2015). Most other anti-phagocytic receptors dependent on SHP-1 and/or SHP-2 tyrosine phosphatases for their inhibitory function, and we will focus our discussion on anti-phagocytic receptor signaling mediated by these tyrosine phosphatases (Getahun & Cambier, 2015). Structurally, SHP-1 and SHP-2 contain two N-terminal SH2 domains, a catalytic phosphatase domain and a C-terminal tail (Lorenz, 2009). Phosphorylation of two tandem ITIMs is thought to be required for SHP binding and activation downstream of anti-phagocytic receptors, but the exact molecular details are not entirely clear (Lorenz, 2009; Getahun & Cambier, 2015).

We will first discuss the CD47-SIRP α axis, as it represents one of the better characterized don't-eat-me checkpoints. Next, we will highlight what is known about other don't-eat-me checkpoints, and discuss several diseases with potential links to dysregulated phagocytosis as a result of aberrant anti-phagocytic signaling.

SIRP α as a prototypic anti-phagocytic receptor

Molecular characterization of SIRP α

SIRP α (also known as SIRP α 1, PTPNS1, SHPS-1, BIT, p84, MFR, MyD-1, and CD172a) is a 115–120 kDa glycoprotein of the SIRP paired receptor family (Fujioka *et al*, 1996; Comu *et al*, 1997; Kharitonov *et al*, 1997; Yamao *et al*, 1997; Matozaki *et al*, 2009). It is expressed in most tissues and enriched on monocytes, macrophages, CD8 α classical type II dendritic cells (cDC2), neutrophils, and osteoclasts, as well as microglia and neurons. It is also moderately expressed on fibroblasts, endothelial cells, and some epithelial cells (Adams *et al*, 1998; Veillette *et al*, 1998; Johansen & Brown, 2007). The extracellular region of SIRP α contains an N-terminal IgV domain followed by two IgC domains (Fig 1) (Fujioka *et al*, 1996; Kharitonov *et al*, 1997; Yamao *et al*, 1997). Species and tissue-specific differences in the molecular weight and ligand affinity of SIRP α are attributed to the highly polymorphic IgV domain and the varying number of N-linked glycosylation sites in the extracellular region (Yamao *et al*, 1997; Takenaka *et al*, 2007). Conversely, the cytoplasmic tail of SIRP α is highly conserved with four ITIMs and a proline-rich region predicted to bind SH3 domain-containing proteins (Fig 1) (Fujioka *et al*, 1996; Kharitonov *et al*, 1997; Yamao *et al*, 1997; Veillette *et al*, 1998). Although originally identified in 1990 as an adhesion protein on neurons, SIRP α was independently characterized as an ITIM-containing receptor and a substrate of activated

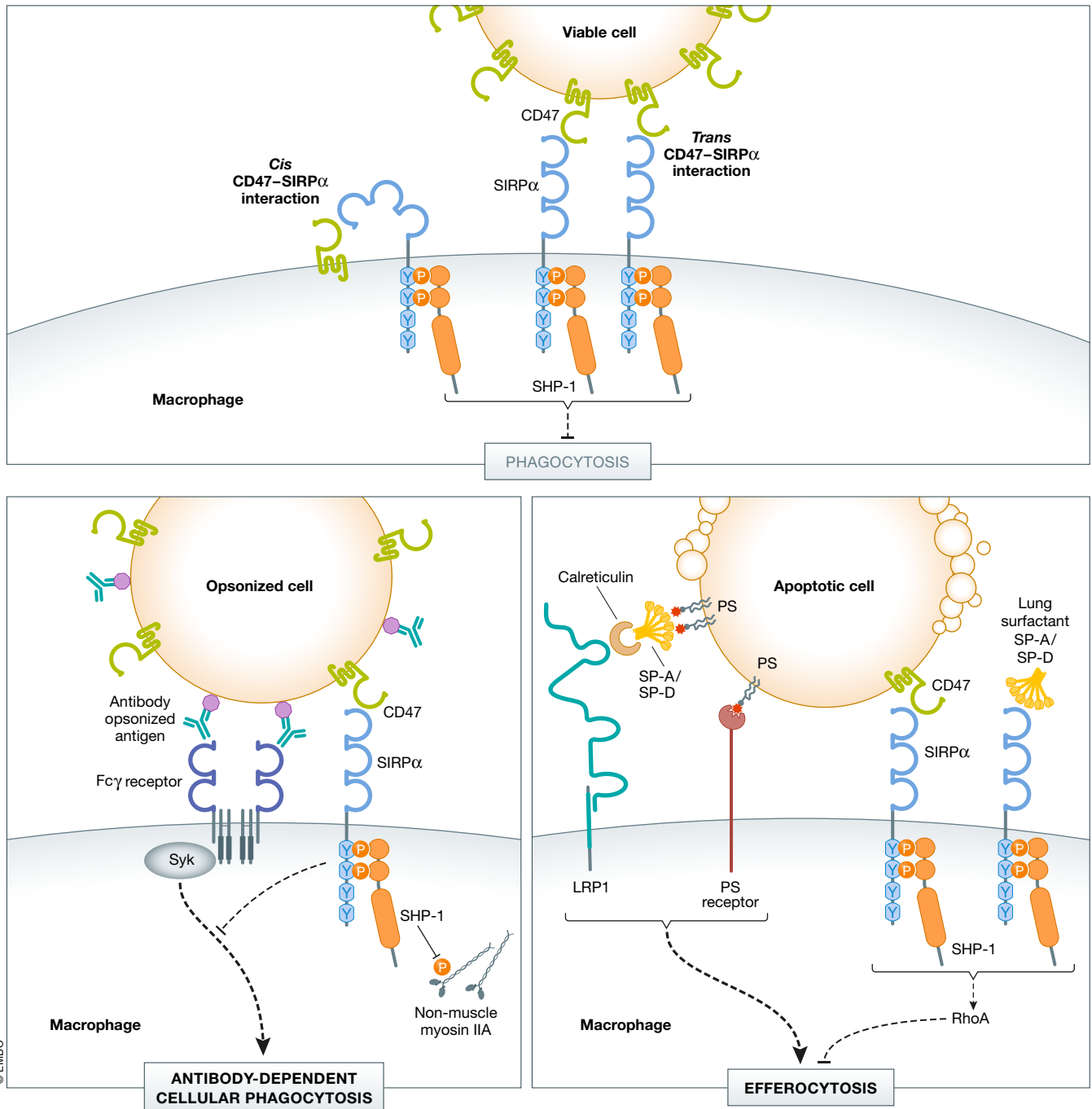


Figure 1. Inhibition of phagocytosis by SIRP α .

Engagement of the CD47-SIRP α axis occurs in *cis* and in *trans*, which induces tyrosine phosphorylation of the ITIMs in the cytoplasmic tail of SIRP α . Phosphorylation at Y429 and Y453 of human SIRP α mediate binding of tyrosine phosphatase SHP-1 (Myers *et al*, 2020). Dephosphorylation of non-muscle myosin IIA is one proposed substrate of SHP-1, resulting in disassembly of the actomyosin cytoskeleton. (top) Viable cells express don't-eat-me signals such as CD47 and lack expression of eat-me signals, thus limiting phagocytic clearance. (bottom-left) Antibody-dependent cellular phagocytosis (ADCP) is also negatively regulated by the CD47-SIRP α axis (Zent & Elliott, 2017). (bottom-right) Efferocytosis by alveolar macrophages in the lung can be negatively regulated by SIRP α activation in response to binding CD47 and surfactant proteins, SP-A and SP-D. The mechanism of this suppression is thought to involve activation of the GTPase RhoA (Janssen *et al*, 2008).

receptor tyrosine kinases in response to various growth factors and mitogens (Chuang & Lagenaur, 1990; Fujioka *et al*, 1996; Noguchi *et al*, 1996; Comu *et al*, 1997; Kharitonov *et al*, 1997; Yamao

et al, 1997; Veillette *et al*, 1998). Additionally, SIRP α is tyrosine phosphorylated in response to integrin-mediated adhesion to specific extracellular matrix components (Tsuda *et al*, 1998; Oh *et al*, 1999).

The tyrosine kinases responsible for direct phosphorylation of SIRP α have remained unclear and may be context-specific; however, Src family kinases (SFK), as well as focal adhesion kinase (FAK) and proline-rich tyrosine kinase 2 (Pyk2), have been implicated in SIRP α signaling (Takeda *et al*, 1998; Timms *et al*, 1999). Nonetheless, tyrosine phosphorylation of SIRP α at specific ITIMs permits the binding of SHP-1 or SHP-2 via their SH2 domains, which relieves repression on the catalytic phosphatase domain and allows for dephosphorylation of their respective substrates (Neel *et al*, 2003; Lorenz, 2009). It remains unclear whether these phosphatases compete for the same binding site(s), or bind distinct sites on SIRP α ; however, current evidence supports the latter model (Takada *et al*, 1998; Myers *et al*, 2020). In addition to being a binding partner, SIRP α is also a substrate of these phosphatases (Timms *et al*, 1998). In professional phagocytes such as macrophages, SHP-1 predominantly mediates inhibitory signaling downstream of SIRP α , consistent with the abundant expression of SHP-1 in hematopoietic cells (Veillette *et al*, 1998; Lorenz, 2009; Abram & Lowell, 2017). Conversely, SHP-2 is ubiquitously expressed and predominately binds SIRP α in non-hematopoietic cells in response to stimulation with growth factors, mitogens, and cellular adhesion (Kharitonov *et al*, 1997; Tsuda *et al*, 1998; Barclay & Van den Berg, 2014). While SHP-2 can modulate cytokine receptor signaling and macrophage activation states, whether it has a direct role in regulating phagocytosis is unclear (Neel *et al*, 2003; Tao *et al*, 2014; Niogret *et al*, 2019).

The best-known ligand of SIRP α is CD47 (also known as integrin-associated protein, OV-3, and Rh-related protein), which is a conserved, ubiquitously expressed 45–55-kDa transmembrane glycoprotein belonging to the Ig superfamily (Brown *et al*, 1990; Lindberg *et al*, 1993; Lindberg *et al*, 1994; Reinhold *et al*, 1995; Jiang *et al*, 1999). CD47 has a single N-terminal extracellular IgV domain followed by five hydrophobic membrane-spanning segments and a short C-terminal cytoplasmic tail that is alternately spliced to form four isoforms (Fig 1) (Brown *et al*, 1990; Lindberg *et al*, 1993; Reinhold *et al*, 1995). CD47-SIRP α binding via their IgV domains regulates many cellular processes, including leukocyte transmigration, lymphocyte homeostasis, dendritic cell maturation and activation, and bone resorption (Latour *et al*, 2001; de Vries *et al*, 2002; Liu *et al*, 2002; Hagnerud *et al*, 2006; Van *et al*, 2006; Lundberg *et al*, 2007; Saito *et al*, 2010; Legrand *et al*, 2011; Maile *et al*, 2011; Sato-Hashimoto *et al*, 2011). As we will discuss in the following sections, it is also one of the most studied don't-eat-me checkpoints in suppressing phagocytosis.

CD47 is a marker of “self” for phagocytosis

Seminal work by Oldenborg *et al* (2000) established CD47 as a marker of “self” on erythrocytes to prevent their premature clearance from circulation. The average circulating lifespan of wild-type murine erythrocytes is between 40 and 60 days (Goodman & Smith, 1961; Ishikawa-Sekigami *et al*, 2006; Oldenborg, 2013). In stark contrast, CD47-negative erythrocytes were shown to be rapidly cleared from circulation within 24 h of transfusion into syngeneic wild-type recipient mice in a manner independent of complement and adaptive immunity. Rather, splenic red pulp macrophages were found to facilitate the clearance of CD47-negative erythrocytes, as splenectomy and depletion of macrophages using liposomal clodronate permitted their circulation in wild-type mice. Moreover, blockade of SIRP α on wild-type splenic macrophages enhanced the

clearance of wild-type erythrocytes *ex vivo*. Since this work, several studies over the past two decades have shown that other cell types use CD47 to avoid phagocytosis, including platelets, lymphocytes, and hematopoietic stem cells (Blazar *et al*, 2001; Yamao *et al*, 2002; Olsson *et al*, 2005; Ahrens *et al*, 2006; Ishikawa-Sekigami *et al*, 2006; Jaiswal *et al*, 2009; Catani *et al*, 2011; Kuriyama *et al*, 2012). These data are consistent with the mild thrombocytopenia and lymphopenia observed in mice globally deficient in either CD47 or SIRP α expression (Lindberg *et al*, 1996; Yamao *et al*, 2002; Ishikawa-Sekigami *et al*, 2006; Li *et al*, 2012). Recent evidence suggests that the CD47-SIRP α axis also regulates neuronal pruning by microglia during postnatal development (Lehrman *et al*, 2018). Retinal ganglion cells (RGCs) extend axons in the dorsal lateral geniculate nucleus (dLGN) of the thalamus to synapse with relay neurons (Guido, 2008). RGC inputs need to be refined for proper development of eye-specific territories, and this process involves phagocytosis of RGC inputs by microglia in the dLGN (Guido, 2008; Schafer *et al*, 2012). CD47 was found enriched on active RGC inputs and its expression protected against microglial phagocytosis in a manner dependent on SIRP α (Lehrman *et al*, 2018). An observed reduction in CD47 on less active RGC inputs suggests that microglia use this marker, at least in part, to decide which inputs to remove (Lehrman *et al*, 2018). Together, these data support a role for the CD47-SIRP α axis as a brake on the phagocytosis of “self”.

Given the importance of the CD47-SIRP α axis in protecting host cells from phagocytosis, it is confounding that mice deficient in either CD47 or SIRP α expression do not have severe developmental or homeostatic abnormalities (Lindberg *et al*, 1996; Li *et al*, 2012). Moreover, CD47-deficient mice are tolerant to transfused syngeneic CD47-negative bone marrow cells, suggesting a more complex role for this signaling axis than previously thought (Blazar *et al*, 2001). A phagocytic “licensing” role for CD47 has been hypothesized, analogous to licensing of natural killer (NK) cells for functional cytotoxicity. Inhibitory receptors expressed on the surface of NK cells must interact with MHC class I molecules on host cells in order for NK cells to acquire proper cytotoxic function (Jonsson & Yokoyama, 2009). Elegant bone marrow reconstitution studies suggest that CD47 expression on non-hematopoietic cells is important for regulating CD47-dependent phagocytosis (Wang *et al*, 2007). Endogenous and donor CD47-negative leukocytes were tolerated in CD47-deficient mice that were either partially or fully reconstituted with wild-type bone marrow (Wang *et al*, 2007). Conversely, wild-type recipient mice reconstituted with bone marrow lacking CD47 expression rapidly eliminated donor CD47-negative cells.

Senescent erythrocytes are known to be cleared by F4/80^{high} splenic red pulp macrophages of yolk-sac and fetal liver origin; however, bone marrow-derived monocytes can contribute to the F4/80^{high} splenic macrophage population to a certain degree (Schulz *et al*, 2012; Williams & van de Laar, 2015; Gonzalez & Castrillo, 2018). Interestingly, both wild-type mice and CD47-deficient mice reconstituted with wild-type bone marrow rapidly eliminated donor CD47-negative erythrocytes 24 weeks post-bone marrow transplantation (Wang *et al*, 2007). Perhaps, in this situation the donor monocyte-derived splenic macrophages contributed to the clearance of CD47-deficient erythrocytes. Alternatively, erythrocytes may lack expression of other don't-eat-me signals expressed on nucleated cells, thus making CD47-deficient erythrocytes more vulnerable to clearance. Mechanism notwithstanding, these findings suggest an

important role for CD47 in phagocyte development and/or effector function, with relevance for CD47-based immunotherapies currently attempted.

CD47-SIRP α axis in antibody-dependent cellular phagocytosis

After identifying CD47 as a marker of “self” on erythrocytes, Oldenburg *et al* (2001) showed that the CD47-SIRP α axis suppresses pro-phagocytic signaling downstream of activated Fc γ receptors and complement receptors. In this study, IgG-opsonized CD47-negative erythrocytes were completely absent from circulation within 8 h post-transfusion into wild-type syngeneic recipient mice, whereas unopsonized CD47-negative erythrocytes and IgG-opsonized wild-type erythrocytes remained for > 24 h. These data are consistent with the earlier onset and more severe autoimmune hemolytic anemia (AIHA) observed in CD47-deficient non-obese diabetic (NOD) mice, which are prone to autoimmune diseases (Oldenburg *et al*, 2002; Wong *et al*, 2014). Moreover, IgG-opsonized wild-type and CD47-negative erythrocytes were also eliminated from circulation within 8 h post-transfusion into viable motheaten (*me^v/me^v*) recipient mice, which have markedly reduced SHP-1 phosphatase activity (Shultz *et al*, 1984; Kozłowski *et al*, 1993; Shultz *et al*, 1993; Oldenburg *et al*, 2001). While target cell binding and Fc γ receptor activation appear mostly unaffected by CD47-induced inhibitory signaling, the mechanism of suppression at least partially involves regulation of cytoskeletal elements important for target cell internalization (Lowry *et al*, 1998; May & Machesky, 2001; Diakonova *et al*, 2002; Kant *et al*, 2002; Tsai & Discher, 2008; Gomez & Descoteaux, 2018). Global tyrosine phosphorylation is reduced in phagocytes following activation of CD47-SIRP α signaling, including reduced tyrosine phosphorylation of the non-muscle myosin IIA motor protein, which was previously shown to be a direct substrate of SHP-1 following B-cell activation (Fig 1) (Baba *et al*, 2003; Tsai & Discher, 2008). CD47-SIRP α -mediated inhibition of inside-out integrin activation may also reduce macrophage spreading around the bound target cell (Tsai & Discher, 2008; Morrissey *et al*, 2020). Phagocytic receptors are suggested to be restricted in lateral movement on the plasma membrane due to interactions with the underlying cytoskeleton (Freeman *et al*, 2018). SIRP α has been shown to form clusters near Fc γ RI receptors in resting macrophages, and engagement of the CD47-SIRP α axis promotes receptor clustering, whereas unligated SIRP α is suggested to be excluded from the phagocytic cup following Fc γ RI stimulation with IgG or disruption of filamentous actin (Lopes *et al*, 2017). Thus, co-ligation of pro-phagocytic receptors (e.g., IgG activation of Fc γ receptors) and anti-phagocytic receptors (e.g., CD47-SIRP α axis) may function to fine-tune phagocytosis in some contexts, perhaps to allow for proper antigen digestion and presentation. In the absence of anti-phagocytic receptor co-ligation, such as during the clearance of apoptotic cells as we will discuss in the next section, these phagocytic “brakes” are mostly excluded from the phagocytic synapse.

Studies investigating the role of the CD47-SIRP α axis in phagocytosis have largely focused on *trans* engagement of CD47 expressed on the target cell with SIRP α expressed on the phagocyte (Fig 1). It is important to note that many professional and non-professional phagocytes express both CD47 and SIRP α on their surface. Recent work investigating the potential for *cis* engagement of the CD47-SIRP α axis showed that loss of CD47 on macrophages also enhanced phagocytosis of unopsonized and IgG-opsonized erythrocytes *in vitro*

(Hayes *et al*, 2020). Additionally, compared to wild-type macrophages, CD47-deficient macrophages bound more soluble CD47, presumably due to the lack of *cis* CD47-SIRP α interactions. Basal tyrosine phosphorylation of macrophage SIRP α was also reduced following deletion of macrophage CD47, and the loss of phosphorylation signal correlated with the loss of CD47 expression (Johansen & Brown, 2007; Hayes *et al*, 2020). Together, these data support a model whereby the SIRP α extracellular domains bend over to interact with the CD47 IgV domain *in cis* to influence the dynamics of cell clearance (Fig 1). Interestingly, other immune receptor-ligand pairs have been shown to engage *in cis*, suggesting that this may be a more general regulatory mechanism for immune cell function such as phagocytosis (Doucey *et al*, 2004). Whether the signaling strength downstream of SIRP α differs by binding CD47 *in cis* versus *in trans* remains unclear (Hayes *et al*, 2020). Localization and clustering of CD47-SIRP α signaling complexes near the phagocytic cup is clearly an important determining factor as to the potency of inhibitory signaling and the overall impact on phagocytosis. The conformational state of these molecules may also influence differences between *cis* and *trans* signaling downstream of SIRP α (Hayes *et al*, 2020).

Together, these data support an inhibitory role for the CD47-SIRP α axis in ADCP via activation of SHP-1 and subsequent inhibition of contractile forces necessary for internalization of the target cell.

CD47-SIRP α axis in apoptotic cell clearance

Over 200–300 billion cells die in the human body every day as a part of routine cellular turnover, and most of these cells are thought to die by apoptosis (Arandjelovic & Ravichandran, 2015). The clearance of apoptotic cells, also referred to as efferocytosis, is not only immunologically silent, but also actively immunosuppressive via the secretion of anti-inflammatory mediators such as lactate, IL-10, and TGF β (Gardai *et al*, 2003; Morioka *et al*, 2018; Perry *et al*, 2019). An early event following induction of apoptosis is loss of phospholipid asymmetry and exposure of phosphatidylserine (PS), a potent eat-me signal for efferocytosis, as well as membrane blebbing (Fig 1) (Fadok *et al*, 2001). Given the importance of the CD47-SIRP α axis in suppressing other forms of phagocytosis, its potential role in regulating efferocytosis has been explored, albeit to a lesser extent. Reduced CD47 expression is observed on some cell types (e.g., neutrophils, fibroblasts) following induction of apoptosis *in vitro*, as well as on senescent erythrocytes (Gardai *et al*, 2005; Khandelwal *et al*, 2007; Lv *et al*, 2015). However, CD47 expression changes are not evident on other cell types such as Jurkat T cells and thymocytes during early stages of apoptotic cell death. Changes in the localization of CD47 on the plasma membrane of dying cells have also been observed such that fewer molecules of CD47 engage SIRP α within the phagocytic synapse, thus reducing the binding avidity and inhibitory signaling strength downstream of SIRP α (Gardai *et al*, 2005; Lv *et al*, 2015). Further, tyrosine phosphorylation of SIRP α has been shown to be reduced in macrophages co-cultured with apoptotic cells, suggesting less involvement of the CD47-SIRP α axis in regulating efferocytosis. Interestingly, the activation of SIRP α signaling by cross-linking or recombinant CD47 has been shown to reduce efferocytosis *in vitro* (Gardai *et al*, 2005; Janssen *et al*, 2008; Lv *et al*, 2015). Thus, the CD47-SIRP α axis is capable of inhibiting efferocytosis, at least in some conditions. “Brakes” for phagocytosis such as the CD47-SIRP α axis may largely be excluded from the phagocytic synapse during efferocytosis to prevent delayed

clearance of apoptotic cells, which can result in secondary necrosis and chronic inflammatory pathologies (Morioka *et al*, 2019).

Paradoxically, a pro-phagocytic role for CD47 has also been suggested in efferocytosis. In the presence of serum, CD47-deficient apoptotic cells were shown to be engulfed less efficiently than their wild-type counterparts *in vitro* (Tada *et al*, 2003; Nilsson & Oldenborg, 2009). CD47 is known to bind the C-terminal RFYVVM domain of thrombospondins (TSP), which are platelet-derived soluble coagulation factors, and TSP-1 promotes efferocytosis by acting as a molecular bridge between apoptotic cells and specific pro-phagocytic receptors (e.g., CD36 and $\alpha\text{v}\beta\text{3}$ integrin) (Savill *et al*, 1992; Arandjelovic & Ravichandran, 2015). Moreover, erythrocyte aging studies suggest that oxidative stress induces a conformational change in CD47 that permits TSP-1 binding via its C-terminal domain, suggesting that under specific conditions CD47 may be converted to an eat-me signal (Gao *et al*, 1996a; Gao *et al*, 1996b; Burger *et al*, 2012). In some contexts, ligation of CD47 has also been reported to induce a form of cell death that is phenotypically similar to apoptosis, including PS exposure, but often lacks nuclear changes and is caspase-independent (Oldenborg, 2013). It is not clear to what extent, if any, CD47-induced cell death contributes to cellular turnover or the clearance process.

Other don't-eat-me ligands for SIRP α : lung surfactant proteins

Surfactant proteins A and D (SP-A and SP-D, respectively) are oligomeric structures of the collectin family that are present in lung surfactant and participate in innate host defense (LeVine & Whitsett, 2001; Wright, 2005). In addition to modulating inflammation, SP-A and SP-D can facilitate phagocytosis of microorganisms and apoptotic cells by alveolar macrophages (Schagat *et al*, 2001; Vandivier *et al*, 2002; Reidy & Wright, 2003). The globular lectin domain of SP-A and SP-D binds the target cell, and the collagenous domain binds to pro-phagocytic calreticulin/low-density lipoprotein receptor 1 (LRP1) complexes on the phagocyte membrane. Paradoxically, the globular lectin domain of SP-A and SP-D has also been shown to interact with SIRP α on alveolar macrophages to suppress efferocytosis and pro-inflammatory cytokine production via tyrosine phosphorylation of SHP-1 and activation of the GTPase, RhoA (Fig 1) (Gardai *et al*, 2003; Tosello-Tramont *et al*, 2003; Janssen *et al*, 2008). Alveolar macrophages deficient in SHP-1 demonstrated enhanced efferocytosis *in vitro*, presumably due to loss of inhibitory signaling downstream of the SP-A/SP-D:SIRP α axis (Janssen *et al*, 2008). However, peritoneal macrophages lacking SHP-1 were not significantly affected in efferocytosis, suggesting tissue context differences (Janssen *et al*, 2008). In response to lung infection and trauma, SIRP α was recently shown to suppress alveolar macrophage phagocytosis and promote an immunosuppressive microenvironment conducive to secondary infection (Roquilly *et al*, 2020). Collectively, these observations support a role for SIRP α in suppressing alveolar macrophage function. The mechanisms regulating the dichotomous functions of SP-A and SP-D are not clear and may depend on other factors present in the lung environment.

Additional anti-phagocytic receptors

In addition to SIRP α , several other ITIM-containing receptors have also been suggested to inhibit phagocytosis via activation of SHP-1

and/or SHP-2 tyrosine phosphatases. Many of these receptors have been studied in the context of disease, and further studies are needed to assess the roles of these inhibitory receptors in modulating phagocytosis in normal physiology. Of note, CD31 (also known as PECAM-1) is an ITIM-containing receptor that has been shown to promote de-attachment of viable cells from phagocytes; however, its proposed mechanism differs from the anti-phagocytic receptors discussed in this review (Brown *et al*, 2002).

CD300a and CD300f

Inhibitory receptors of the CD300 family include CD300a and CD300f, and both contain a single extracellular IgV domain (Borrego, 2013). In humans and mice, these inhibitory receptors are primarily expressed on myeloid cells, and to varying levels on some lymphoid subsets (Borrego, 2013). Phosphatidylserine (PS) is thought to be a ligand for CD300a and CD300f as both receptors have been shown to bind apoptotic cells and PS-containing liposomes in a calcium-dependent manner (Choi *et al*, 2011; Nakahashi-Oda *et al*, 2012a; Nakahashi-Oda *et al*, 2012b; Simhadri *et al*, 2012). Additionally, the PS-binding proteins annexin V and milk-fat globule EGF factor VIII (MFG-E8) can block apoptotic cell binding to CD300a and CD300f. Other lipids have been suggested as ligands for these receptors, but further studies are warranted to clarify conflicting studies (Borrego, 2013).

CD300a

The cytoplasmic tail of human CD300a contains four ITIMs, whereas mouse CD300a contains two ITIMs and a third tyrosine associated with a tyrosine-based sorting motif (Fig 2) (Borrego, 2013). Activation of CD300a by PS induces SHP-1 binding and inhibits efferocytosis (Nakahashi-Oda *et al*, 2012a; Nakahashi-Oda *et al*, 2012b; Simhadri *et al*, 2012). The PS-dependent inhibitory function of this receptor is confounding since PS is a potent eat-me signal for efferocytosis. A potential explanation is that CD300a may be important to inhibit inflammatory responses to apoptotic cell uptake, albeit potentially at the expense of reduced efferocytosis (Simhadri *et al*, 2012). In support of this hypothesis, CD300a expression is induced on several types of immune cells in response to inflammatory stimuli and has been shown to inhibit MyD88 inflammatory cytokine production (Kim *et al*, 2012; Borrego, 2013). Additionally, activation of CD300a on human neutrophils was shown to suppress production of reactive oxygen species in response to Fc γ RIIa stimulation (Alvarez *et al*, 2008). Thus, CD300a expression is modulated on several immune cell types in response to infection and downregulates inflammatory responses to prevent excessive tissue damage. Whether CD300a plays a role in regulating efferocytosis in the absence of inflammatory stimuli such as during homeostatic cell clearance warrants further investigation.

CD300f

Both human and mouse CD300f have three cytoplasmic ITIMs, as well as binding motifs for PI3K and Grb2 signaling molecules (Fig 2) (Borrego, 2013). The role of CD300f in regulating phagocytosis is more complex. Studies suggest both anti-phagocytic and pro-phagocytic functions, depending on the cell type and activation context, perhaps due to its ability to bind SHP-1 and SHP-2 (Borrego, 2013). Activation of CD300f was shown to promote apoptotic

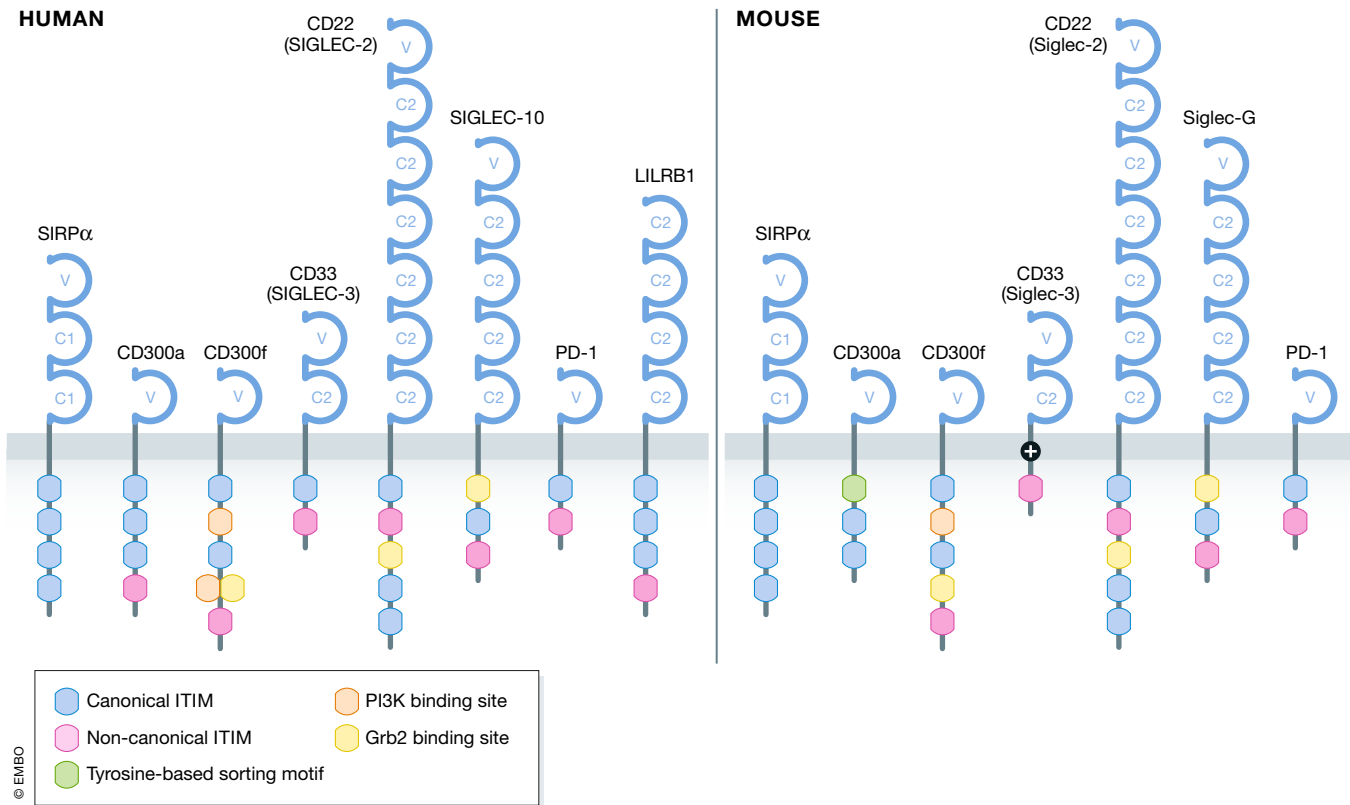


Figure 2. The structure of human and mouse anti-phagocytic receptors.

Several anti-phagocytic receptors have been identified in humans and mice. These are single-pass type I transmembrane receptors belonging to the immunoglobulin (Ig) superfamily and contain one or more immunoreceptor tyrosine-based inhibitory motifs (ITIM) in their cytoplasmic tails. Many of these receptors also have additional binding sites for signaling molecules that can endow these receptors with activation functions.

cell binding and internalization in a manner dependent on Y276 phosphorylation and p85 α -PI3K signaling for phagocytic cup formation (Choi *et al*, 2011; Tian *et al*, 2014; Tian *et al*, 2016). Conversely, the other four tyrosines and expression of SHP-1 had an inhibitory effect on efferocytosis *in vitro*, and loss of CD300f enhanced efferocytosis and T-cell priming by dendritic cells, suggesting that it also functions as an anti-phagocytic receptor (Tian *et al*, 2014; Tian *et al*, 2016). Thus, the role of CD300f in modulating efferocytosis is complex and likely depends on interactions with other receptors, as well as available signaling molecules within different types of phagocytes.

Siglecs

Siglecs, or sialic acid-binding Ig-like lectins, are a large family of receptors primarily expressed on immune cells and have important roles in attenuating inflammatory responses to pathogen and damage-associated molecular patterns, mediating adhesion and phagocytosis, and regulating immune cell activation (Pillai *et al*, 2012). Many of these lectins bind specific sialic acid-containing glycoconjugates *in cis*, as well as *in trans*, to fine-tune responses following immune cell activation (Pillai *et al*, 2012). Below, we will focus our discussion on three Siglecs suggested to function as anti-phagocytic receptors.

CD33/Siglec-3

Human CD33 (also called Siglec-3) has an extracellular region consisting of one IgV domain and one IgC domain, and a cytoplasmic tail containing two ITIMs (Fig 2) (Ulyanova *et al*, 1999; Pillai *et al*, 2012). It is expressed on cells of the myeloid lineage and microglia (Pillai *et al*, 2012; Griuciu *et al*, 2013). Human CD33 binds α 2,3- and α 2,6-linked sialic acid-containing glycans (Brinkman-Vand der Linden *et al*, 2003). Activation of CD33 induces SHP-1 binding, and the membrane proximal ITIM is necessary and sufficient for SHP-1 activation (Ulyanova *et al*, 1999). Genome-wide association studies of genetic variants associated with Alzheimer's disease (AD) suggested a potential link to the CD33 loci (Hollingsworth *et al*, 2011; Naj *et al*, 2011). Further analysis revealed a positive correlation in CD33 expression on microglia and the presence of insoluble A β 42 levels and amyloid plaque burden in AD patients (Griuciu *et al*, 2013). Moreover, loss of CD33 in mouse models of AD was sufficient to reduce insoluble A β 42 levels and amyloid plaque burden via enhanced uptake by microglia (Griuciu *et al*, 2013; Griuciu *et al*, 2019). These studies suggest CD33 as an anti-phagocytic receptor on microglia and its potential involvement in AD pathogenesis.

Unlike human CD33, the mouse ortholog has one ITIM and a positively charged lysine residue in the transmembrane region that

forms a putative binding site for signaling molecules associated with immune cell activation (Fig 2) (Brinkman-Vand der Linden *et al*, 2003; Pillai *et al*, 2012). Given these structural differences, divergent functions between human and mouse CD33 orthologs may exist and one study suggests that mouse CD33 may not regulate A β 42 phagocytosis (Bhattacharjee *et al*, 2019). The reasons for these conflicting data are not clear.

CD22/Siglec-2

CD22 (also called Siglec-2) has an extracellular region that contains an N-terminal IgV domain followed by six IgC domains, and the cytoplasmic tail contains four ITIMs and a Grb2 binding motif (Fig 2) (Pillai *et al*, 2012). It is highly expressed in B cells, as well as some myeloid-derived cells and microglia (Pillai *et al*, 2012). Mouse CD22 binds Neu5Gc glycans, and human CD22 binds both Neu5Ac and Neu5Gc glycans, although the specific glycoconjugates are not fully clear (Pillai *et al*, 2012). Activation of CD22 has been shown to bind and activate SHP-1, as well as a variety of other signaling molecules (Doody *et al*, 1995; Law *et al*, 1996; Blasioli *et al*, 1999; Poe *et al*, 2000; Otipoby *et al*, 2001). A recent study investigating age-related genes involved in microglial phagocytosis found CD22 enriched on microglia from aged mice and its expression negatively correlated with cognitive function (Pluvinage *et al*, 2019). CD22 was shown to inhibit microglial phagocytosis, presumably via activation of SHP-1, and loss of CD22 enhanced the clearance of several neurodegenerative factors, including myelin debris, A β oligomers, and α -synuclein fibrils *in vitro* and *in vivo* (Pluvinage *et al*, 2019). Thus, in addition to CD33, this study suggests that microglia also utilize CD22 as an anti-phagocytic receptor to restrict phagocytosis in the central nervous system, perhaps in early development as well as pathological contexts when there is an overabundance of cellular debris. Additional studies are needed to assess whether blockade of CD22 is of benefit in treating age-related cognitive decline and neurodegenerative diseases.

Siglec-10

Human Siglec-10, or mouse Siglec-G, has an extracellular region consisting of an N-terminal IgV domain followed by four IgC domains, and a cytoplasmic tail containing two ITIMs as well as a Grb2-binding motif (Fig 2) (Munday *et al*, 2001; Pillai *et al*, 2012). It is expressed on myeloid cells and some lymphocytes, and binds both SHP-1 and SHP-2 (Munday *et al*, 2001; Whitney *et al*, 2001; Pillai *et al*, 2012). CD24 is a sialylated glycosyl phosphoinositol-anchored protein and a cognate ligand of human Siglec-10, and mouse Siglec-G (Chen *et al*, 2009). Signaling through this axis suppresses NF- κ B-mediated inflammation in response to damage-associated molecular patterns via SHP-1 activation (Chen *et al*, 2009; Chen *et al*, 2011). Additionally, NF- κ B activation has been shown to increase Siglec-G expression in innate immune cells in response to viral infection, leading to retinoic acid-inducible gene I (RIG-I) degradation and attenuation of anti-viral responses in a manner involving SHP-2 (Chen *et al*, 2013). Mouse Siglec-G has also been shown to negatively regulate MHC class I-peptide cross-presentation by CD8 α^+ dendritic cells (Ding *et al*, 2016). Mechanistically, the activation of SHP-1 downstream of Siglec-G led to an increase in phagolysosomal pH such that MHC class I-peptide complex formation was impaired (Ding *et al*, 2016). Recently, CD24 was also identified as a don't-eat-me signal that is highly expressed on several cancers (Barkal *et al*,

2019). This study showed that tumor-associated macrophages (TAMs) from ovarian and breast tumors also expressed Siglec-10 (Barkal *et al*, 2019). Blockade or genetic depletion of either CD24 on tumor cells, or Siglec-10 on macrophages, enhanced tumor cell clearance *in vitro* and *in vivo*, presumably by disrupting *trans* engagement of this inhibitory axis (Barkal *et al*, 2019). Thus, in addition to dampening inflammatory responses, the CD24-Siglec-10 axis also regulates phagocytosis processes in professional phagocytes. Additional studies are needed to investigate the mechanism(s) driving increased expression of CD24 on tumor cells, and Siglec-10 expression on TAMs, and if blockade of this signaling axis would provide enhanced anti-tumor immunity in cancers resistant to clinically available therapies. Future studies should also evaluate dysregulation of this don't-eat-me signaling axis in other contexts where impaired phagocytosis is evident such as in cardiovascular diseases.

PD-1

PD-1 (also known as programmed cell death protein 1 and CD279) is a well-known immune inhibitory receptor of the B7/CD28 family and has been extensively studied in suppressing T-cell activation, at least in part via SHP-2 (Okazaki *et al*, 2013; Rota *et al*, 2018; Marasco *et al*, 2020; Patsoukis *et al*, 2020). Structurally, it has one extracellular IgV domain and two cytoplasmic ITIMs (Fig 2) (Patsoukis *et al*, 2020). Its two cognate ligands are PD-L1 (also known as CD274 and B7-H1) expressed on non-lymphoid cells, and PD-L2 (also known as CD273 and B7-DC) expressed on antigen-presenting cells (Okazaki *et al*, 2013). In addition to being expressed on lymphocytes, PD-1 expression is induced in macrophages in response to infection, which is negatively associated with an inflammatory macrophage phenotype and pathogen clearance (Huang *et al*, 2009; Shen *et al*, 2016; Gordon *et al*, 2017). Upon microbial infection, Toll-like receptor/NF- κ B activation induces PD-1 expression in macrophages, and PD-1 activation in turn suppresses NF- κ B/p65-mediated inflammatory responses (Bally *et al*, 2015; Chen *et al*, 2016). In several cancers, a subset of TAMs and tumor-infiltrating dendritic cells (TIDCs) highly express PD-1, which negatively correlates with anti-tumor immune responses (Karyampudi *et al*, 2016; Gordon *et al*, 2017). Specifically, PD-1 expression on TAMs correlated with reduced phagocytosis of tumor cells, and inhibition of the PD-L1:PD-1 axis in lymphocyte-deficient tumor-bearing mice reduced tumor burden and extended survival, suggesting its potential role in don't-eat-me signaling (Gordon *et al*, 2017). Together, these studies establish a model whereby PD-1 is induced in innate immune cells to modulate their inflammatory state and act as a rheostat to prevent excessive inflammation and tissue damage, which can indirectly influence phagocytic activity to specific targets (Yurdagul *et al*, 2020). Additional studies are needed to assess whether PD-1 plays a more direct role in modulating phagocytic processes such as target cell internalization.

LILRB1

Human LILRB1 (leukocyte immunoglobulin-like receptor B1; also known as CD85J, ILT2, LIR-1) is an inhibitory receptor expressed on myeloid cells and subsets of lymphoid cells (Borges *et al*, 1997; Colonna *et al*, 1997; Fanger *et al*, 1998). Structurally, it has an extracellular region consisting of four IgC domains and a cytoplasmic tail containing four ITIMs (Fig 2) (Borges *et al*, 1997; Samaridis & Colonna, 1997). Tyrosine phosphorylation of the two membrane-distal

ITIMs permits SHP-1 binding and activation (Fanger *et al*, 1998; Bellon *et al*, 2002). LILRB1 binds MHC class I molecules expressed on all nucleated cells, and the invariant β_2 -microglobulin subunit of MHC class I has been shown to be important for this interaction (Borges *et al*, 1997; Colonna *et al*, 1997; Fanger *et al*, 1998; Barkal *et al*, 2018). In a recent study, MHC class I expression was shown to protect some cancer cells from phagocytosis via engagement of LILRB1 (Barkal *et al*, 2018). Loss of either MHC class I or LILRB1 was shown to enhance tumor cell phagocytosis *in vitro* when combined with antibody opsonization to provide eat-me signaling through Fc receptor activation (Barkal *et al*, 2018). Additionally, loss of both MHC class I and CD47 don't-eat-me signals on tumor cells provided better anti-tumor immune responses in a manner dependent on macrophages, as well as contribution from adaptive immune cells *in vivo* (Barkal *et al*, 2018). This study highlights MHC class I as an additional don't-eat-me signal utilized by some cancers to avoid clearance. Activation of LILRB1-SHP1 inhibitory signaling has previously been shown to suppress early tyrosine phosphorylation events downstream of Fc γ RI signaling (Fanger *et al*, 1998). Thus, it is likely that engagement of the MHC class I-LILRB1 axis suppresses ADCP, and loss of this inhibitory axis allows for better uptake of opsonized cells.

Regulation gone awry: don't-eat-me signaling in disease

The expression of don't-eat-me signals by host cells is thought to prevent their unwarranted removal by neighboring phagocytes, and dysregulation of this innate immune checkpoint has pathological consequences. In addition to the studies discussed in the previous sections, below we highlight two disease categories where enhanced CD47 expression contributes to pathology.

Cancer

CD47 expression is upregulated in many cancers, including both hematologic and solid tumor malignancies, and its expression correlates with poor prognosis (Campbell *et al*, 1992; Jaiswal *et al*, 2009; Majeti *et al*, 2009; Willingham *et al*, 2012; Weiskopf *et al*, 2016; Michaels *et al*, 2018). The mechanisms contributing to enhanced CD47 expression differ among cancer subtypes, but aberrant transcriptional regulation is a commonality (Zhang *et al*, 2015; Case *et al*, 2016; Betancur *et al*, 2017; Liu *et al*, 2017). Blocking the CD47-SIRP α axis was shown to promote phagocytosis of tumor cells *in vitro*, and tumor regression in animal models, when an eat-me signal was available to activate pro-phagocytic signaling (Fig 3). A first-in-human phase I trial evaluated the efficacy of a humanized anti-CD47 monoclonal antibody (called magrolimab or Hu5F9-G4) as monotherapy for advanced solid tumors and lymphomas, but limited anti-tumor responses were observed (Sikic *et al*, 2019; Veillette & Tang, 2019). Conversely, Advanti *et al* reported partial or complete responses in 50% of patients with relapsed/refractory non-Hodgkin's lymphoma enrolled in a small phase 1b trial where patients received co-administration of magrolimab and rituximab (an anti-CD20 monoclonal antibody). Additionally, 95% of responding patients were previously refractory to single agent rituximab treatment (Advani *et al*, 2018; Veillette & Tang, 2019). These studies provided the first clinical evidence that loss of CD47 don't-eat-me signaling promotes anti-tumor immunity at least partially via ADCP. Mild anemia and

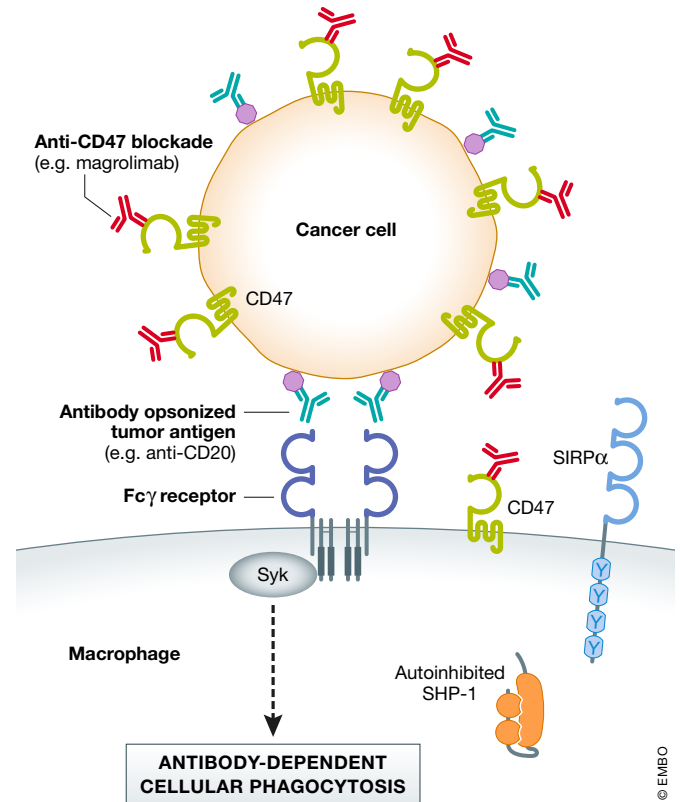


Figure 3. Therapeutically blocking the CD47-SIRP α axis to enhance cancer cell phagocytosis.

Many cancer cells have increased expression of CD47. Preclinical and clinical studies have shown promise in enhancing anti-tumor immunity when anti-CD47 blockade is used in combination with other immunotherapies such as the anti-CD20 monoclonal antibody Rituximab. This strategy provides an eat-me signal via activation of antibody-dependent cellular phagocytosis (ADCP) while concurrently blocking the CD47-SIRP α don't-eat-me signaling axis.

lymphopenia were the only low-grade adverse events observed with magrolimab treatment, suggesting promising tolerability to CD47 blockade, albeit larger trials with longer follow-ups are needed to fully assess treatment-related toxicities, including potential cognitive-related issues (Advani *et al*, 2018; Sikic *et al*, 2019; Veillette & Tang, 2019). Additional clinical trials investigating the efficacy and safety of immunotherapies targeting the CD47-SIRP α axis are currently underway for both hematologic and solid tumors, including their use as single agents and in combination with other checkpoint blockade therapies, as well as azacitidine—a hypomethylating agent (Feng *et al*, 2019). Blocking strategies include the use of several different anti-CD47 monoclonal antibodies, as well as a recombinant SIRP α Fc fusion protein (TTI-621) consisting of the Fc region of human IgG1 and the extracellular IgV domain of human SIRP α (Feng *et al*, 2019). Altogether, these initial observations suggest that immunotherapies targeting the CD47-SIRP α axis to enhanced tumor cell ADCP are well-tolerated and demonstrate promising anti-tumor effects. Future studies investigating the efficacy of targeting other don't-eat-me signaling molecules are needed for cancers showing resistance to CD47 blockade (Barkal *et al*, 2018).

Cardiovascular disease**Atherosclerosis**

Atherosclerosis is a major contributing factor to cardiovascular and cerebrovascular diseases, and mortality worldwide (Benjamin *et al*, 2019). In the early stages of atherosclerosis, modified circulating lipoproteins become trapped in the subendothelial space of arteries and stimulate inflammatory leukocyte recruitment into the vessel wall (Doran *et al*, 2019). A portion of macrophages that phagocytose entrapped lipoproteins become cholesterol-laden and undergo apoptosis (Yurdagul *et al*, 2018; Morioka *et al*, 2019). These dying cells are removed by other plaque-associated macrophages, but over time efferocytosis becomes impaired in diseased vessels and advanced

plaques form. The accumulation of uncleared dying cells forms the “necrotic core” of advanced plaques, which are prone to rupture.

A combination of aberrations contributes to impaired efferocytosis in atherosclerotic lesions. These include reduced surface expression of pro-phagocytic receptors such as LRP1 and the Mer proto-oncogene tyrosine kinase (MerTK) via proteolytic cleavage and receptor degradation (Fig 4) (Doran *et al*, 2019). Additionally, enhanced CD47 expression was observed in human lesions, and blockade of CD47 in murine atherosclerotic models showed fewer plaque-associated dead cells and smaller necrotic cores (Kojima *et al*, 2016; Gerlach *et al*, 2020). One mechanism contributing to enhanced CD47 expression on plaque cells involved NF- κ B

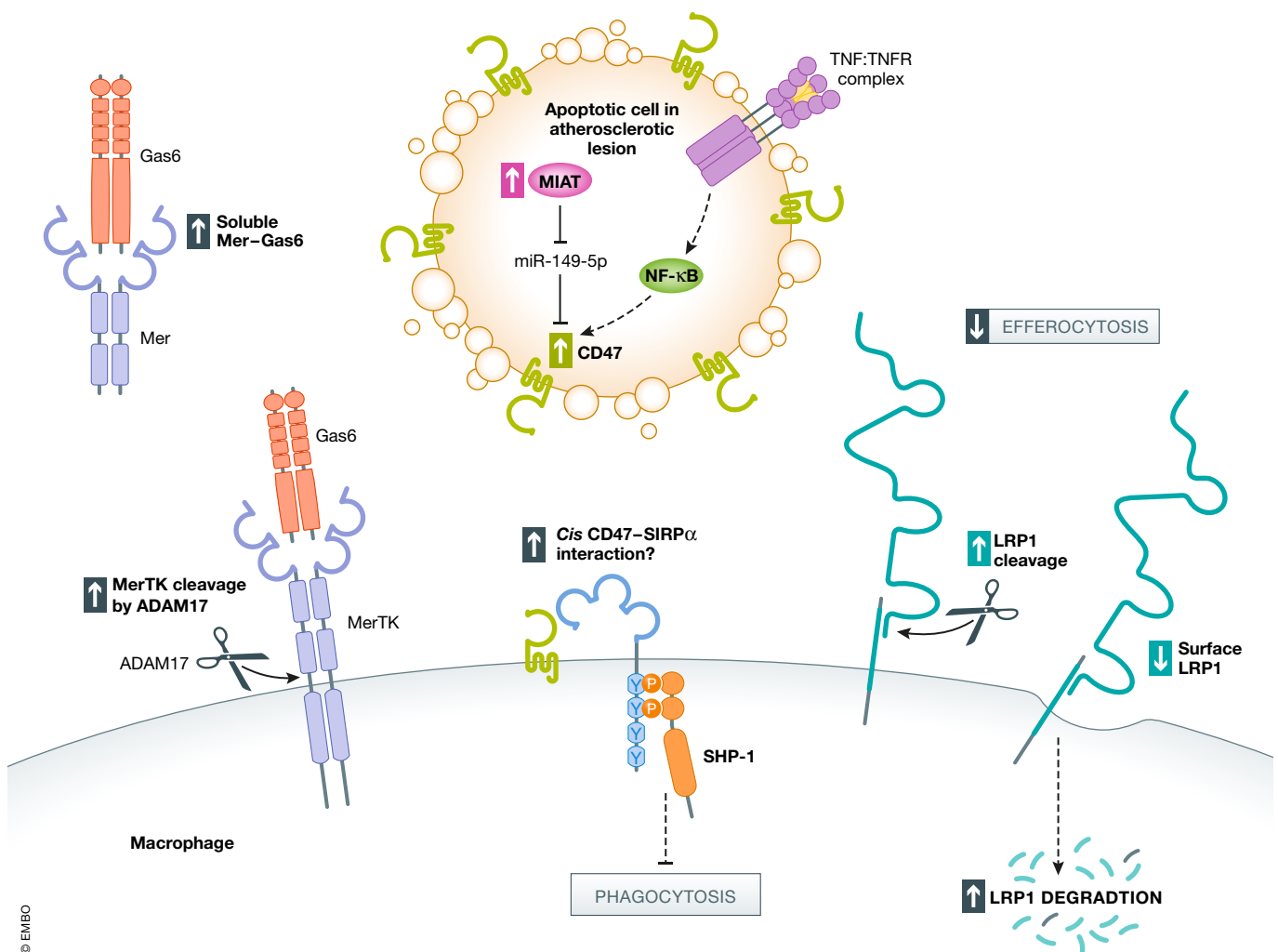


Figure 4. Impaired efferocytosis in cardiovascular disease.

Several mechanisms contribute to impaired efferocytosis in cardiovascular diseases, such as atherosclerosis (Doran *et al*, 2019). Tumor necrosis factor (TNF) signaling through the TNF receptor activates the nuclear factor- κ B pathway leading to enhanced CD47 expression on apoptotic cells in atherosclerotic lesions. Enhanced expression of the “myocardial infarct-associated transcript” (MIAT) long non-coding RNA inhibits processing of the microRNA, miR-149-5p, and in turn, results in increased CD47 expression. CD47 can bind SIRP α *in cis* on the phagocyte surface to inhibit phagocytosis. Loss of pro-phagocytic receptors on the phagocyte surface including LRP1 and MerTK contributes to impaired efferocytosis. Metalloproteinase ADAM17 cleaves MerTK, resulting in soluble Mer that may act to sequester growth arrest-specific protein 6 (Gas6) needed for recognition of phosphatidylserine (PS) on the surface of apoptotic cells. Parts of this figure were adapted from Doran *et al* (2019).

activation downstream of tumor necrosis factor (TNF) signaling (Kojima *et al.*, 2016). In agreement with this finding, other reports in a variety of disease contexts have also linked pro-inflammatory signaling to increased CD47 expression, suggesting that CD47 is induced in response to some inflammatory conditions to fine-tune inflammatory responses (Betancur *et al.*, 2017; Cui *et al.*, 2020; Tal *et al.*, 2020; Wang *et al.*, 2020). It is possible that increased CD47 expression on plaque-associated phagocytes may also contribute to impaired efferocytosis via *cis* engagement of the CD47-SIRP α axis (Fig 4) (Hayes *et al.*, 2020; Wang *et al.*, 2020). Increased expression of the long non-coding RNA called “myocardial infarction-associated transcript” (MIAT) was also observed in advanced lesions (Ye *et al.*, 2019). MIAT was shown to negatively regulate the microRNA miR-149-5p, thereby relieving repression of CD47 expression (Fig 4) (Ye *et al.*, 2019). Knockdown of MIAT *in vitro* and in murine atherosclerosis promoted efferocytosis, reduced plaque necrosis, and improved plaque stability, presumably via reduced CD47 expression (Ye *et al.*, 2019).

Potential therapeutic benefit in blocking CD47 for atherosclerosis was suggested based on a retrospective analysis of 9 patients enrolled on the Advanti trial (Jarr *et al.*, 2021). Reduced inflammation in the carotid arteries was observed by 18F-FDG PET/CT scans following combination treatment with magrolimab and rituximab. Future trials directly evaluating the efficacy of blocking CD47 for treating atherosclerosis are needed. It should also be noted that one study using CD47-deficient mice with hypercholesterolemia showed larger atherosclerotic plaques compared with wild-type mice, and this phenotype was associated with enhanced lymphocyte activation, particularly INF γ -producing CD90⁺ NK cells (Engelbertsen *et al.*, 2019). Thus, CD47 appears to play a more general role in controlling both innate and adaptive immune responses, and detailed studies are needed to evaluate both on-target and off-target effects of CD47 blockade.

Myocardial infarction

Heart failure after myocardial infarction (MI) is another major source of cardiac-related mortality (Frangogiannis, 2012). Efficient clearance of dying cardiomyocytes and timely resolution of acute inflammation following myocardial infarction is critical to cardiac repair (Frangogiannis, 2012; Doran *et al.*, 2019). Cleavage of the MerTK receptor is one mechanism of impaired cardiomyocyte efferocytosis (Wan *et al.*, 2013; DeBerge *et al.*, 2017). Cardiomyocytes associated with infarcted tissue also express more CD47, and acute blockade of CD47 or SIRP α during reperfusion injury could enhance cardiomyocyte clearance and reduce infarct size and collagen content (Zhang *et al.*, 2017). The mechanisms underlying enhanced CD47 expression on cardiomyocytes in infarcted tissue remain unclear, and additional studies are needed to assess the benefit of blocking the CD47-SIRP α axis following ischemic injury.

While professional phagocytes are important for reparative responses post-myocardial infarct, non-professional phagocytes such as cardiac myofibroblasts can assist in the clearance process (Nakaya *et al.*, 2017). The physiological response to myofibroblast efferocytosis in the damaged myocardium remains unclear. It is also not known if efferocytosis by non-professional phagocytes such as cardiac myofibroblasts is regulated by don't-eat-me signaling, and future studies are needed to explore this area of phagocytosis research in more depth.

Conclusions

Efficient clearance of dying and pathogenic cells is critical to preventing unnecessary inflammation and maintaining immune quiescence. However, this process must be tightly controlled to avoid aberrant removal of healthy cells. Regulation during the late phase of phagocytosis involves phagocyte recognition of eat-me and don't-eat-me signals expressed on host cells. In general, it is thought that don't-eat-me signaling raises the activation threshold needed for phagocytosis to occur.

In ADCP, evidence supports a role for the CD47-SIRP α axis, and other don't-eat-me checkpoints, in fine-tuning the clearance response. Many anti-phagocytic receptors play important roles in controlling inflammatory responses by suppressing cytokine and TLR signaling, and in some cases, antigen presentation for the activation of adaptive immune responses. Additional studies are needed to decipher how don't-eat-me signaling directly regulates phagocytosis, and this includes identifying the cellular substrates of SHP-1 and SHP-2 following anti-phagocytic receptor activation. Specifically, whether regulation beyond suppression of integrin activation and the actomyosin cytoskeleton occurs needs to be defined (see also Box 1).

Box 1: In need of answers

- What is (are) the mechanism(s) by which anti-phagocytic receptors regulate phagocytosis? Specifically, what are the substrates of SHP-1 and SHP-2 regulating phagocytosis?
- Is there specificity in which phagocytes are regulated by particular anti-phagocytic receptors?
- Do anti-phagocytic receptors cooperate or compensate, and in which tissue contexts?
- Which types of anti-phagocytic receptors are important for regulating ADCP versus efferocytosis?
- Does dysregulation of phagocytosis via aberrant don't-eat-me signaling contribute to fibrosis?
- What are the long-term consequences of therapeutically blocking anti-phagocytic receptors?

During efferocytosis, exclusion of some anti-phagocytic receptors from the phagocytic synapse may reduce the activation threshold to allow for efficient removal of dying cells. Additionally, efferocytosis is immunologically silent and can actively promote anti-inflammatory responses. Engagement of anti-phagocytic receptors may contribute to suppressing inflammation in response to the uptake of apoptotic cells. The degree of regulation on efferocytosis by anti-phagocytic receptors is less understood and requires further investigation.

Several new don't-eat-me checkpoints have been identified in recent years, specifically in cancers. Similarly, several pro-phagocytic receptors have been identified for efferocytosis, and while initially thought to be a matter of redundancy, evidence suggests that pro-phagocytic receptor expression is likely tissue and phagocyte-specific (Penberthy *et al.*, 2017). Is there similar specificity for anti-phagocytic receptors? Do anti-phagocytic receptors regulate phagocytosis by non-professional phagocytes? Studies aimed at genetically deleting individual anti-phagocytic receptors in specific phagocyte populations will be useful to address these questions (see also Box 1).

Lastly, we and others have reviewed several examples of how impaired phagocytosis contributes to pathology (Doran *et al*, 2019; Feng *et al*, 2019; Morioka *et al*, 2019). Currently available studies evaluating the efficacy and safety of blocking the CD47-SIRP α axis have shown promising results. Additional studies are needed to evaluate the long-term safety and efficacy of these therapies, as well as therapeutically targeting other don't-eat-me checkpoints (see also Box 1). Finally, are there other diseases where aberrant don't-eat-me signaling contributes to pathology? Recent studies suggest that CD47 and PD-L1 are upregulated in pulmonary fibrosis, but it is unclear from these studies if dysregulated phagocytosis contributes to fibrotic pathologies (Wernig *et al*, 2017; Cui *et al*, 2020).

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Conflict of interest

The authors declare that they have no conflict of interest.

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