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Review

# Phagocytosis Checkpoints in Glioblastoma: CD47 and Beyond

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**Abstract:** Glioblastoma multiforme (GBM) is one of the deadliest human cancers with very limited treatment options available. The malignant behavior of GBM is manifest in a tumor which is highly invasive, resistant to standard cytotoxic chemotherapy and is strongly immunosuppressive. Immune checkpoint inhibitors have recently been introduced in the clinic and have yielded promising results in certain cancers. GBM however is largely refractory to these treatments. The immune checkpoint CD47 has recently gained attention as potential target for intervention as it conveys a “don’t eat me” signal to tumor associated macrophages via the inhibitory SIRP alpha protein. In preclinical models, administration of anti-CD47 monoclonal antibodies have shown impressive results with GBM and other tumor models. Several well characterized oncogenic pathways have recently been shown to regulate CD47 expression in GBM cells and Glioma Stem cells (GSCs) include EGFR, beta catenin and LRIG2. Other macrophage pathways involved in regulating phagocytosis including TREM2 and glycan binding proteins are discussed as well. Finally, Chimeric Antigen Receptor Macrophages (CAR)-M could be leveraged for greatly enhancing phagocytosis of GBM and repolarization of the microenvironment in general. Here we comprehensively review the mechanisms that regulate about macrophage phagocytosis of GBM cells.

**Keywords:** Glioblastoma; glioma; macrophage; phagocytosis; CD47; CSF-1R; Siglec

## 1. Introduction

### 1.1. Glioblastoma and Immunotherapy

Glioblastoma multiforme (GBM) is an almost invariably fatal brain cancer with a median survival from time of prognosis of approximately 14 months [1]. Standard of care involves surgical resection and irradiation with temozolomide therapy. This treatment regimen however is largely ineffective and has considerable side effects. New therapies are urgently needed. Immunotherapy involves harnessing the immune system to mediate destruction of cancer cells. Immune Checkpoint Inhibitors (ICIs), such as monoclonal antibodies against cytotoxic T-lymphocyte antigen-4 (CTLA-4; Ipilimumab) and programmed cell death protein 1 /programmed cell death-ligand 1 (PD-1/PD-L1; nivolumab, Pembrolizumab) have been developed and are currently used in the clinic to treat a variety of cancers. These ICIs have demonstrated remarkable efficacy in a subset of patients however in others such as GBM there has been no measurable response. [2,3]. This is likely due to the fact that patients with immunologically “cold” tumors (such as GBM) are unlikely to mount a sufficient response to tumor antigens [2–4]. Recently, Immune checkpoints involved in tumor-macrophage interactions have gained attention. Macrophages are likely one of the first immune cell types that cancer cells encounter and these early interactions are likely to dictate the progression of the tumor.

### 1.2. Tumor Associated Macrophages

It is now widely appreciated that the microenvironment plays a central role in dictating the immune response to the tumor and their overall progression to malignancy [5,6]. The microenvironment consists of many immune cell types including lymphocytes and macrophages (TAMs), the latter being especially prevalent in GBM. Approximately 30-50% of the GBM tumor mass is comprised of macrophages, microglia and other cells of the myeloid lineage [7–11]. Labelling experiments have shown that most are derived from peripheral blood, although it is likely brain resident microglia also play an important and non-redundant role in tumor progression [12,13]. Extensive paracrine signaling occurs between glioma cells and TAMs [14–19]. In general, glioma cells secrete factors which recruit and induce TAMs to acquire a pro-tumoral phenotype (often referred to as M2). These reprogrammed TAMs in turn promote glioma cell invasion, chemoresistance and immunosuppression of the microenvironment. It is recognized that the standard “M1 vs M2” model of macrophage polarization is an oversimplification and macrophages display phenotypes along a continuum [20,21]. It is generally agreed however that M1 macrophages express cytokines such as IL-12 and cell surface markers CD80 and CD86, whereas M2 polarized macrophages express immunosuppressive cytokines such as IL-10 and TGF- $\beta$  and cell surface markers such as CD163 and CD206. An attractive strategy is to use therapy to “reprogram” TAMs away from an M2 toward an M1 anti-tumoral phenotype. This is likely to yield substantial benefits as the pro-tumorigenic effects mediated by M2 macrophages including glioma invasion and chemoresistance, and immunosuppression will be reversed and M1 polarized TAMs will have the ability to recruit and activate potent effector cells. These include cells such as NK cells and cytotoxic CD8<sup>+</sup> T lymphocytes to attack tumor antigen expressing glioma cells and the release of additional pro-M1 factors which would propagate a positive feedback loop.

There are subtleties in how the tumor interacts with the myeloid compartment of the microenvironment. For example, so called glioma stem cells (GSCs) are a subset of tumor cells which express a different profile of chemokines, growth factors and interleukins and other factors from bulk tumor population [22–26]. As a consequence of this differential cytokine expression GSCs are thought to interact in a more specialized way with TAMs. GSCs also express specific cell surface proteins such as CD44, CD133 and nestin which could mediate special interactions with TAMs within the microenvironment [27]. In addition to heterogeneity among the glioma cells, as mentioned previously there are various subpopulations of myeloid cells within the microenvironment including resident brain microglia, macrophages derived from monocytes in the blood, CD11c<sup>+</sup> dendritic cells, immature Gr1<sup>+</sup> monocytoïd cells and myeloid derived suppressor cells (MDSCs). Each of these cells in turn can have overlapping and distinct effects on tumor progression [9,11,28–33]. Further complicating the investigation of the relative contribution of these macrophage/myeloid subpopulations on GBM progression is that there are substantial differences in the cell specific markers between mice and humans employed to distinguish between macrophage subsets [34].

### 1.2. Macrophage Phagocytosis of Glioma Cells

Most of myeloid cell types associated with GBM tumors, including macrophages, microglia and dendritic cells, retain the capacity to carry out phagocytosis under certain conditions [35–43]. The current paradigm is that tumor cells experiencing oncogenic cellular stress express and presentation of “Eat Me” signals such as surface exposed calreticulin, High mobility group box 1 protein (HMGB1), phosphatidyl serine (PS) among others [44,45]. When these signals are detected by tissue macrophages, the result rapid and efficient phagocytosis of the tumor cell. However, tumor cells eventually upregulate surface “don’t eat me” receptors, most well characterized of which is CD47. CD47 is a transmembrane protein containing an extracellular immunoglobulin (Ig) domain which engages SIRP receptors on macrophages that strongly inhibits phagocytic signaling pathways [46]. There are three SIRP receptors in humans, the most studied being SIRP alpha [47]. The cytoplasmic domain of SIRP $\alpha$  contains an immunoreceptor tyrosine-based inhibition motif (ITIM) which recruit SHP1/2 phosphatases involved in downregulating immune signaling particularly pathways that are involved in phagocytosis [48]. The Weissman lab has pioneered the use of therapeutic anti-CD47

antibodies to treat solid tumors in a variety of mouse models [49–52]. Preclinical studies with anti-CD47 blocking antibodies have been promising in many cancer models and a humanized anti-CD47 monoclonal antibodies such as Hu5F9-G4 (Magrolimab) has been developed [53]. Unfortunately as is the case with most current immune checkpoint therapies, anti CD47 seems to be significantly less effective against solid tumors in clinical trials conducted thus far [54]. In addition, CD47 is expressed on high levels in red blood cells and other cell types which could make it less than ideal as a targeted monotherapy. Anti-SIRP approaches are currently in development to perhaps escape these limitations [55]. Other “Don’t Eat Me” surface immune checkpoint molecules include certain sialic acid containing glycoproteins and glycolipids which engage the Sialic acid-binding immunoglobulin type lectins (Siglec) proteins which inhibit the immune response.

Macrophages are also responsible for clearing apoptotic GBM cells [56–58]. Paradoxically, the pathways that regulate phagocytosis of apoptotic cells has been shown in many contexts to induce an anti-inflammatory response [59]. For example, bone marrow derived macrophage (BMDM) phagocytosis of GBM cells was shown *in-vitro* to result in lower secretion of IL-1b and TNF $\alpha$  and an increase in anti inflammatory IL-10 cytokine production [60]. Phagocytosis also resulted in an increase in macrophage expression of PD-L1 and PD-L2. These mechanisms almost certainly evolved to prevent an inappropriate inflammatory response during the clearance of apoptotic cells which occurs during normal physiological processes. It is unclear if inducing apoptosis of tumor cells will augment or inhibit *in-vivo* antigen presentation of tumor antigens. There has been some work showing alternative forms of cell death can be induced in cancer cells to overcome this immunosuppressive effect. For example downregulation of HSP70 resulted in a caspase-independent “apoptosis-like” effect in breast and colorectal tumor cells whereby phagocytic clearance was not accompanied by immunosuppressive cytokines [61]. Nonetheless, understanding the full spectrum of molecular pathways which govern TAM phagocytosis of GBM cells will likely result in great strides toward additional checkpoint inhibitor therapy. Here we review these pathways in a comprehensive fashion.

## 2. Pathways Regulating TAM Phagocytosis of GBM Cells

### 2.1. CD47/SIRP Pathway

As mentioned above, the “don’t eat me” signal protein CD47 has emerged as an authentic immune checkpoint target and humanized anti-CD47 monoclonal antibodies are currently in clinical trials [54]. Preliminary data from preclinical mouse models have shown anti-CD47 therapy to be very effective in treating breast, ovarian and GBM [49,53,62]. Anti-CD47 treatment of mice harboring orthotopically injected luciferase-expressing GBM xenografts resulted in almost complete inhibition of tumor growth as measured by bioluminescence photon flux [49]. An added benefit of anti-CD47 is that it only promotes phagocytosis but can promote M1 macrophage polarization which should promote a more immunologically “hot” tumor [63].

Preclinical studies have also focused on the ability of anti-CD47 to work in combination with other therapy. Anti-CD47 can synergize with IR or TMZ to prolong survival of human GBM xenograft implanted mice [64]. A recent study showed that TMZ was important for anti-CD47 induced phagocytosis of GBM and this was dependent on Stimulator of Interferon Genes (STING) [65]. Another study simultaneously blocked VEGF and CD47 using a novel bispecific fusion protein VEGFR1D2-SIRP $\alpha$ D1 [66]. This was effective at both enhancing phagocytosis as well as lowering blood vessel density and angiogenesis. This study also noted that preventing autophagy using chloroquine was able to further enhance these effects. Delivery of therapeutics has always been a challenge for GBM due in part to the blood brain barrier (BBB). Another laboratory employed an oncolytic virus which encodes an anti-CD47 antibody to improve survival in orthotopic human GBM models [67]. Several groups have been using implantation of hydrogel formulations into the cavity of freshly resected GBM in rodent brains [68,69]. Song et al injected hydrogels infused with TMZ and vectors encoding shRNA targeting CD47 [68]. In another study, use of temperature-sensitive hydrogel system hydroxypropyl chitin (HPCH) copolymer which encapsulates both anti-CD47 and

TMZ was able to provide a full curative effect in approximately 50% of the animals harboring GL261 murine glioma tumors [69].

As mentioned above, interfering with CD47 might have side effects as this protein is expressed on other cell types, most notably red blood cells [70]. Alternative approaches to interfere with CD47 function involve the use of a SIRPα-Fc fusion protein to bind to and prevent tumor CD47 from engaging SIRP receptors on TAMs [71–73]. Using SIRPα-Fc in an immunocompetent mouse model of GBM was effective in reducing tumor size, particularly when used in combination with autophagy inhibitors [74]. Interestingly, the SIRPα protein has also been detected in normal astrocytes and lower grade glioma however its expression decreases with increasing tumor grade [75,76]. Aggregation of the U373MG cell line resulted in an increase in tyrosine phosphorylation of SIRP which was attenuated with an anti-CD47 blocking antibody. It is unclear what role tumor-expressed SIRP proteins play in carcinogenesis or immune-evasion.

As alluded to above, therapeutic approaches which convert the GBM from an immunologically “cold” to a “hot” with the aim of rendering the tumor more amenable to immune checkpoint therapies [77,78]. Using TLR3 and TLR9 agonists, Huang et al were able to stimulate microglia phagocytosis and clearance of GBM cells in tissue culture, brain slices and in the GL261 mouse model [79]. Another study used “trojan horse” nanoparticles to deliver anti-CD47 along with a STING agonist into the brains of GBM bearing mice. It was observed in this study that polarization of TAMs within the tumor was strongly towards M1 phenotype [80].

Epigenetic regulation of the phagocytic immune checkpoint has gained attention recently. Tacedinaline (CI-994), a class I Histone Deacetylase (HDAC) inhibitor was identified in a screen as a apoptosis inducer in MYC-driven cancer cell lines including GBM lines [81]. CI-994 treatment significantly enhanced the expression of “eat me” signals calreticulin and HMGB1 on the surface of the medulloblastoma cell lines tested. Administration of CI-994 combined with anti-CD47 was effective in treating medulloblastoma in orthotopically injected mice. In macrophages, HDAC activity appears to inhibit phagocytosis [82]. Expression of miRNA22 in TAMs represses HDAC6 expression which in turn results in a higher level of phagocytosis of GBM cell lines. These studies suggest that HDAC inhibition could be an effective with checkpoint inhibitor therapy as it activates pro-phagocytosis pathways in both GBM and TAMs.

In addition to its ability to engage and activate SIRP receptors on TAMs, CD47 plays cell autonomous roles in GBM [83,84]. The matricellular protein Thrombospondin-1 (TSP-1) can also activate CD47 [85]. Activation of CD47 using a TSP-1 derived peptide agonist increased proliferation of U87 and U373 cells but not normal human astrocytes [83]. CD47 mediates invasion via the Phosphoinositol-3-Kinase (PI3K) pathway in U87 and T98G GBM lines [84]. It was also observed that ablation of CD47 in mouse and human GBM cells resulted in an increase in notch pathway signaling and concomitant upregulation of the extracellular matrix protein Tenascin-C [86]. This increase in Tenascin-C expression resulted in a higher level of TAM infiltration and phagocytosis. Work with glioma stem cells (GSC) has elucidated other mechanisms of CD47 regulation in this population of cells. It is known that irradiation of GBM is rarely effective as GSCs are radioresistant and have the ability to recreate the tumor within a short period of time [87]. It has been demonstrated that GSCs express higher levels of CD47 [88]. This increased CD47 expression seems to contribute to GSC proliferation and migration as treatment with anti-CD47 slows each of these processes. In a recent paper, it was shown that IR induces CD47 expression on GSCs via the 5' AMP-activated protein kinase (AMPK) pathway [89]. GSCs also typically display altered metabolic pathways relative to the bulk tumor. For example, GSCs utilize fatty acid oxidation (FAO) to a much greater extent than bulk GBM tumor cells [90]. In a study by Jiang et. al, the FAO pathway resulted in activation of NF-κB which in turn upregulates CD47 expression specifically in GSCs [91]. Blockade of FAO using etoximir, an inhibitor of a key enzymes in the FAO pathway, synergizes with anti-CD47 to strongly increase GBM phagocytosis and decrease tumor volume.

Some insight has been gained in understanding the molecular pathways which regulate CD47 expression and stability on GBM cells. The Leucine-Rich Repeats and Ig-Like Domain (LRIG) family of transmembrane receptors have been associated with neurological tumors [92,93]. There are three

LRIG genes in humans and they primarily regulate growth factor receptors by targeting them for ubiquitination. In glioma cells, LRIG1 and 3 act as tumor suppressors while LRIG2 has seemingly oncogenic function [92,94,95]. A recent study by Hu et al showed that LRIG2 can strongly prevent phagocytosis of GBM cells by upregulating components of the CD47 pathway [96]. In this report, soluble LRIG2 generated by A disintegrin and metalloprotease 17 (ADAM17)-mediated cleavage from GBM cells was shown to recruit TAMs and induce SIRPa expression on their surface. In addition to this, LRIG2 was shown to enhance the expression of CD47 on GBM cells via transcriptional activation of the CD47 gene. This study strongly implicates LRIG2 as a key regulator of the CD47 immune checkpoint via upregulation of both CD47 and SIRPa. The well-characterized beta-catenin oncogenic pathway can also stimulate CD47 expression in GBM cells [97]. Another study demonstrates how the EGFR pathway cooperates with CD47 to promote tumor progression. EGFR is commonly altered in GBM although single agent therapy with EGFR inhibitors have displayed modest efficacy at best [98]. In a recent study, EGF treatment or expression of the constitutively active truncation mutant EGFRvIII was able to increase the expression of CD47 in multiple established human GBM cell lines [99]. This effect was found to be mediated by SRC phosphorylation of CD47 at Y288 which prevents binding and polyubiquitination by Tripartite motif-containing protein 21 (TRIM21), an E3 ubiquitin ligase. GBM cells expressing a CD47 Y288F mutant are phagocytosed *in vivo* at much higher levels and animals orthotopically injected with these cells survive longer than wild type injected counterparts.

## 2.2. CSF-1/CSF-1R Pathway

The macrophage growth factor Colony Stimulating Factor-1 (CSF-1) is strongly pro-tumorigenic in most cancers as activation of Colony Stimulating Factor-1 Receptor (CSF-1R) promotes M2 polarization of TAMs [100–103]. It was originally observed that breast carcinoma invasion and metastasis is severely diminished in CSF-1 null (*op/op*) background mice [104]. Since that discovery, CSF-1 was shown to be associated with many malignant cancers and the establishment of a generally immunosuppressive microenvironment [105]. Our laboratory has shown that glioma cells express CSF-1 which results in TAM recruitment and invasion of tumor cells into normal brain parenchyma [14,106,107]. Blockade of CSF-1R signaling with PLX-3397, a CSF-1R pharmacological inhibitor that crosses the blood brain barrier, strongly attenuated invasion and was curative in some preclinical GBM models [14,108]. In the context of CSF-1R contribution to the phagocytic checkpoint, the balance of evidence points to an important role for CSF-1R signaling to rearrange actin during the various stages of phagocytosis [109]. Recently it was demonstrated that GW2580, another pharmacological inhibitor of CSF-1R, induced MHC-II expression, phagocytosis and T cell mediated killing of GBM tumor in patient derived 3D organoid models [110]. Interestingly, PLX3397 did not display these features. This discrepancy is likely because these inhibitors hit different off-target RTKs [111,112]. Under standard conditions, CSF-1 is released by cancer cells as soluble ligand which act on macrophages via the CSF-1R in a paracrine and possibly endocrine fashion [113]. However it was discovered that there is a splice variant of the CSF-1 gene which contains a transmembrane domain and results in a surface membrane bound form of CSF-1, referred to as mM-CSF [114]. Interestingly, glioma cells expressing mM-CSF are highly susceptible to phagocytosis and cytotoxic killing by TAMs [114–116]. The mechanism is unclear however the membrane bound mM-CSF is functional as it has the ability to stimulate macrophage colony formation [114]. Therefore, a potential therapeutic approach might be to promote alternative splicing of the CSF-1 gene in GBM tumors towards the membrane bound isoform.

## 2.3. BACE-1

A recent intriguing study identified the  $\beta$ -site amyloid precursor protein cleaving enzyme 1 (BACE1) as playing a role in preventing tumor phagocytosis. BACE1 is responsible for generating  $\beta$ -amyloid peptides which form plaques in the brains of Alzheimer Disease (AD) patients resulting in neuronal dysfunction associated with that disease [117]. Several groups have developed BACE-1 specific inhibitors for potential AD therapy. In a paper by Zhai et al, a screen for phagocytosis of

fluorescently labeled human patient derived GSCs was conducted using a library of compounds which have good blood brain barrier permeability and low toxicity [118]. The BACE-1 inhibitor MK-8931 was found to enhance phagocytosis. Furthermore, it was demonstrated that BACE-1 is expressed in tumor promoting macrophages and administration of MK-8931 along with IR was able to suppress malignant GBM growth in-vivo. Interestingly, oligomers of beta amyloid protein that are associated with AD can stimulate microglia phagocytotic activity against glioma cells [119]. As with many neurodegenerative disorders, microglia dysfunction seems to be a central feature of both gliomagenesis and AD [120].

#### 2.4. TREM2

Several very recent exciting, yet controversial studies have focused on the potential role of Triggering Receptor Expressed on Myeloid Cells 2 (TREM2) in regulating phagocytosis in GBM [121,122]. TREM2 is expressed primarily on microglial cells and can be activated by a variety of ligands including bacteria, polyanionic molecules, lipoproteins and nucleic acids [123] TREM2 signals through DNAX Activator Proteins 10 and 12 (DAP10 and DAP12). DAP10 and DAP 12 can activate several downstream pathways including PI3K/AKT and SYK, a tyrosine kinase which is involved in phagocytosis, particularly at the engulfment stage [124,125]. Peshoff et. al discovered that TREM2+ macrophages are increased in IDH wild type GBMs and its expression correlated with phagocytosis markers [121]. Unlike other cancer models where TREM2 knockout slows tumor growth, there was no effect of TREM2 ablation on GL261 or CT-2A glioma progression in-vivo syngeneic models. Similarly, Zheng et al showed a higher level of TREM2+ cells in GBM tumors and a strong association with phagocytosis however TREM2 deficiency did not have a beneficial effect on mouse survival using the GL261 model system. However Sun et.al demonstrated with different GBM cell lines (SB28 and NPA-C54B) that blockade of TREM2 increased IFN $\gamma$  expression, slowed tumor growth and enhanced animal survival [126]. Furthermore, this was accomplished using three different methods of TREM2 depletion including using TREM2 knockout mice, TREM2 antisense oligo (ASO) delivery and TREM2 blocking antibody administration. Whether or not this discrepancy is due to the different GBM cell lines used or some other subtle difference between model systems tested remains to be seen.

#### 2.5. SIGLECs

The pattern of glycosylated cell surface proteins and lipids is likely a strategy employed by vertebrates to distinguish self vs non-self [127,128]. The Sialic acid-binding immunoglobulin type lectins (Siglec) family of proteins are cell surface receptors expressed on most white blood cells that play a role in immune recognition and regulation [129] The extracellular region of siglec proteins contain a V-Set Ig domain which binds to sialic acid which is expressed on many glycoproteins and glycolipids. There are 14 human Siglecs and 9 murine siglecs they are thought to play an important role in immune checkpoints in several diseases. Siglecs often act as coreceptors and can activate or inhibit immune responses depending on their C-terminal domain structure. Siglecs can modulate several cellular functions including endocytosis, antigen presentation and phagocytosis. Most siglecs contain immunosuppressive ITIM and Immunoreceptor tyrosine-based switch motif (ITSM) motifs and are therefore immunosuppressive. However a subset of siglecs do not contain ITIMs and instead have a region which can associate with the adaptor DAP12 which as noted above is involved in immune activation and phagocytosis. Hyperglycosylation of tumor cells is associated with a poor outcome [130,131] Certain siglecs are expressed primarily on macrophages and microglia. These include Siglec-7,9,10 and 15 and they have been the subject of investigation for immune checkpoint therapy [132] For example, expression of Siglec-E in TAMs was found to inhibit tumor growth [133]. Furthermore Siglec-10 engagement of CD24 on breast carcinoma cells inhibited phagocytosis [134]. In the context of GBM, Siglec-H expression is increased in IFN $\gamma$  treated M1 polarized microglia [135]. Interestingly, Siglec-H only binds to murine GBM cells and not normal mouse cells highlighting the hyperglycosylated aspect of cancer cells. This interaction resulted in the phagocytosis of murine GBM cell lines SMA560 and GL261 and this was dependent on DAP12. Additional siglec family members

act as checkpoints on TAMs. Siglec-1 (also called CD169/Sialoadhesin) is expressed predominantly on macrophages and is the only member of the Siglec family seemingly which does not initiate either pro or anti immuno signaling [136,137]. The role of Siglec-1/CD169 was recently investigated in a GBM model [58]. Depletion of CD169 resulted in a decrease in CXCL10 expression and T cell infiltration. CD169 also played an important role in phagocytosis of GBM cells. Another Siglec that is mainly expressed on macrophages is Siglec-15. The role of Siglec-15 was investigated in a recent paper where it was discovered to be expressed primarily by peri-tumoral macrophages within GBM tumors [138]. The pattern of expression of Siglec-15 changes during the course of GBM progression as it reaches its highest expression in grade II astrocytoma. A negative correlation between Siglec-15 expression and CD3+ cell infiltration was noted. Knockout of Siglec-15 in a mouse macrophage cell line increased M1 marker expression, decreased M2 marker expression and enhanced phagocytosis of GL261 glioma cells.

#### 2.6. Phagocytosis Checkpoint Cooperation with Anti-CTLA4/PD-1/PD-L1 ICIs

There is some evidence that the immune checkpoint inhibitors currently approved for clinical use to reverse T cell inhibition may promote phagocytosis pathways. For example, IR and anti PD-L1 treatment resulted in an increase in T cell and TAM recruitment to the tumor in murine genetic models of GBM [139]. Anti PD-L1 was shown to strongly enhance macrophage phagocytosis of GBM cells and this was independent of T cells. Chen et al recently discovered that using anti CTLA4 antibodies resulted in an increase in IFN $\gamma$  release within GBM tumor which stimulated DC and microglia phagocytosis of tumor cells [140]. Phagocytic activity in this context was dependent on signaling from Axl and Mer RTKs.

#### 2.7. Chimeric Antigen Receptor-M

One of the approaches of modern immunotherapy involves *ex-vivo* manipulation of a patient's peripheral immune cells to be anti-tumorigenic followed by reintroduction into the patient [141,142]. Most work in this area has been with cytotoxic T cells. In particular, researchers have generated vectors which express chimeric antigen receptors whereby the ectodomain of the T cell receptor is replaced with a domain that specifically and directly interacts with target receptors on the surface of cancer cells [143]. In this way, the antigen presentation steps which involve multiple immune checkpoint coreceptors (discussed above) is completely bypassed. CAR-T has been quite effective for several cancers, especially leukemias [144,145]. Unfortunately, as with other immunotherapies, CAR-T has not delivered measurable clinical responses with GBM [146]. Other leukocytes are now being tested for CAR style therapy, including macrophages. CAR-Macrophage (CAR-M) are currently receiving a lot of attention from researchers and biopharmaceutical companies [147]. Unlike T cells, which often cannot penetrate solid tumors very well, macrophages are quite good at tumor infiltration [148]. One of the major strategies for CAR-M therapy is to prevent "don't eat me" signals, such as CD47, to be conveyed to the macrophage [149]. There is some evidence in animal models that M1 polarization can improve CAR-M therapy [150]. Macrophages transduced with a HER2-Fc-Receptor chimeric antigen receptor treated with M1 polarizing stimuli IFN $\gamma$  and LPS and were more effective than unstimulated controls in a breast carcinoma model. Finally, purposing CAR-M to specifically target GSCs might be an effective approach for eradicating these cells as a recent paper has indicated [151]. As this technology becomes more advanced and widespread, opportunities for targeting other checkpoint targets will be exploited.

### 3. Conclusions and Perspectives

We are in an exciting era of cancer therapy as gains are being made (albeit slowly) in treating metastatic cancers. Much work remains to be done but there are clear paths delineated to the discovery of multiple immune checkpoints. GBM treatment will likely require a multi-pronged approach utilizing chemotherapy to induce GBM cell death in combination with treatments that inhibit M2 and promote M1 macrophage polarity and block phagocytosis immune checkpoints. The



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