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DIALing-up the preclinical characterization of gene-modified adoptive cellular immunotherapies

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The preclinical characterization of gene modified adoptive cellular immunotherapy candidates for clinical development often requires the use of mouse models. Gene-modified lymphocytes (GML) incorporating chimeric antigen receptors (CAR) and T-cell receptors (TCR) into immune effector cells require *in vivo* characterization of biological activity, mechanism of action, and preclinical safety. Typically, this characterization involves the assessment of dose-dependent, on-target, on-tumor activity in severely immunocompromised mice. While suitable for the purpose of evaluating T cell-expressed transgene function in a living host, this approach falls short in translating cellular therapy efficacy, safety, and persistence from preclinical models to humans. To comprehensively characterize cell therapy products in mice, we have developed a framework called “DIAL”. This framework aims to enable an end-to-end understanding of genetically engineered cellular immunotherapies *in vivo*, from infusion to tumor clearance and long-term immunosurveillance. The acronym DIAL stands for Distribution, Infiltration, Accumulation, and Longevity, compartmentalizing the systemic attributes of gene-modified cellular therapy and providing a platform for optimization with the ultimate goal of improving therapeutic efficacy. This review will discuss both existent and emerging examples of DIAL characterization in mouse models, as well as opportunities for future development and optimization.

KEYWORDS

CAR-T cells, immunotherapy, adoptive cell therapy, tumor microenvironment, animal models

1 Introduction

Mouse models are routinely used in the preclinical characterization of gene-modified adoptive cellular immunotherapy candidates for clinical development. Adoptive transfer studies in mice, initially in the context of allograft transfer, underpin our understanding of T cell function, trafficking, and therapeutic potential (1–3). The first human studies of gene-modified T cells occurred in the 1980s (4), where a neomycin resistance cassette was retrovirally transduced into tumor-infiltrating lymphocytes (TIL) from patients with

melanoma before infusion into patients. These pioneering studies demonstrated the ability of autologous lymphocytes transferred into patients, along with interleukin-2 (IL-2) treatment, to persist for months. The persistence of the transgene was determined through a PCR-based detection assay, which enabled detection of the adoptively transferred cells. Prior to this landmark human clinical study, a similar approach employing TIL therapy was successfully implemented in mice, resulting in complete regression of syngeneic murine tumors (5). Thus, the mouse study served as a valuable early model for investigating the distribution and function of adoptively transferred tumor-infiltrating lymphocytes.

The development of gene-modified chimeric T-cell receptors that enhance T cell function toward tumor cells in an MHC-independent manner was first described by Eshhar and colleagues in 1989 (6). These chimeric receptors, termed immunoglobulin T-cell receptor (TCR) chimeras, combined an extracellular antibody-like antigen binding molecule with a TCR and an intracellular CD3 zeta (CD3 ζ) signaling domain. While effective *in vitro*, these initial designs lacked the co-stimulatory framework that enabled enhanced T-cell function and persistence *in vivo*.

In 2002, the “second generation” chimeric antigen receptor (CAR) was introduced, addressing the limitations of the previous design (7). This evolved design enabled transduced T cells to produce high levels of endogenous IL-2, supporting the maintenance of cytotoxic function and persistence. Over the years, multiple second-generation CAR-T were developed, incorporating co-stimulatory domains such as CD28 or 4-1BB (8). These designs differed from the first-generation constructs by their ability to drive T cell expansion in the presence of continual antigen exposure (9). The functional improvement was further demonstrated by the requirement of co-stimulation for tumor regression in mouse models of ALL (10, 11).

A few years later, the second-generation CAR-T design was reduced to practice with the first evidence of CAR-T-mediated tumor responses in human clinical trials in advanced follicular lymphoma (12). Subsequent clinical trials led to the development of second generation CAR-T therapy targeting CD19, resulting in the approval of tisagenlecleucel and axicabtagene ciloleucel for the treatment of refractory lymphoma and pediatric leukemia. Thus, the preclinical validation of second-generation CAR-T in mice informed the subsequent clinical development and approval of gene-modified lymphocyte (GML) therapy.

In parallel with second-generation CAR-T, transgenic T-cell receptor (TCR-T) therapy gained momentum as another genetically modified approach for redirecting potent T-cell responses in solid tumors. Building upon the initial success of TIL therapy, Rosenberg et al. engineered autologous gene-modified TCR-T against the melanosome antigen MART-1 (13). These modified TCR-T cells demonstrated persistence and induced tumor regressions in a limited number of patients. The development of the PMEL-1 mouse model, targeting another prevalent melanosome antigen in mice, provided strong preclinical evidence. In this model, transgenic PMEL-1 (gp100) directed T cells were transferred into mice bearing melanotic, poorly immunogenic B16 tumors (14). In both preclinical and clinical settings, tumor regression and persistence of the TCR-T were observed, accompanied by autoimmune responses such as vitiligo, which were observed in both mice and humans (15, 16).

The future development of therapies against HLA-restricted cancer-testis (CT) antigens including NY-ESO-1, PRAME, MAGE-A3 and MAGE-A4, among others, showcased additional opportunities for the efficacy of TCR-T against solid tumors. However, the development of a fully analogous mouse model posed challenges due to the lack of homology, expression and/or cross-reactivity of TCRs with mouse peptide-MHC (pMHC). In most cases, representative antigens with known high-affinity CD8 TCRs such as PMEL-1, tyrosinase-related protein 1 (TRP1) or ovalbumin (OVA/OT-I) were used as proxies for human TCR-T.

The process of preclinical validation for GML is constantly evolving, and new guidance is emerging (17). However, the primary objective of preclinical testing remains consistent: to confirm the biological activity, mechanism of action, and preclinical safety of the therapy before its use in patients.

While animal models, particularly severely immunocompromised mice, are commonly employed for CAR-T validation, the current approach often focuses on assessing fundamental attributes such as dose-dependence, on-target on-tumor activity, and the absence of uncontrolled proliferation and toxicity. While these attributes validate the functionality of the transgene and the manufacturing process, they overlook several critical aspects that should be considered when designing GML as therapeutics for oncology.

These aspects include modeling on-target, off-tumor toxicity and exhaustion, understanding the impact of lymphodepleting chemotherapy (LDC) on toxicity or cell expansion, evaluating tumor heterogeneity and antigen escape, evaluating the tumor microenvironment (TME) with its soluble factors and immune suppressor cells, overcoming barriers to infiltration, exploring the consequences (both positive and negative) of long-term expansion and persistence, and evaluating toxicities such as cytokine-release syndrome (CRS) and immune effector-cell-associated neurotoxicity syndrome (ICANS).

To characterize the cell therapy product and its design attributes more comprehensively, we have developed a framework called “DIAL”. This framework provides a holistic understanding of genetically engineered cellular immunotherapies *in vivo*, encompassing their journey from infusion to tumor regression and continued immunosurveillance. The acronym DIAL represents Distribution, Infiltration, Accumulation, and Longevity, which serve to compartmentalize the systemic attributes of gene modified cellular therapy (Figure 1). Additionally, DIAL serves as a platform for optimizing these attributes, with the ultimate goal of enhancing overall therapeutic efficacy. This review will discuss both existing and emerging examples of DIAL optimization, their characterization in mouse models, and potential avenues for future development. Given the rapidly evolving nature of this field, it is not feasible to cover each topic exhaustively with examples of each emerging technology. Instead, each section will focus on key examples, emphasizing areas for improvement and future advances.

2 Distribution

Optimal drug distribution refers to the efficient and rapid delivery of drug material to the desired site of action from the site

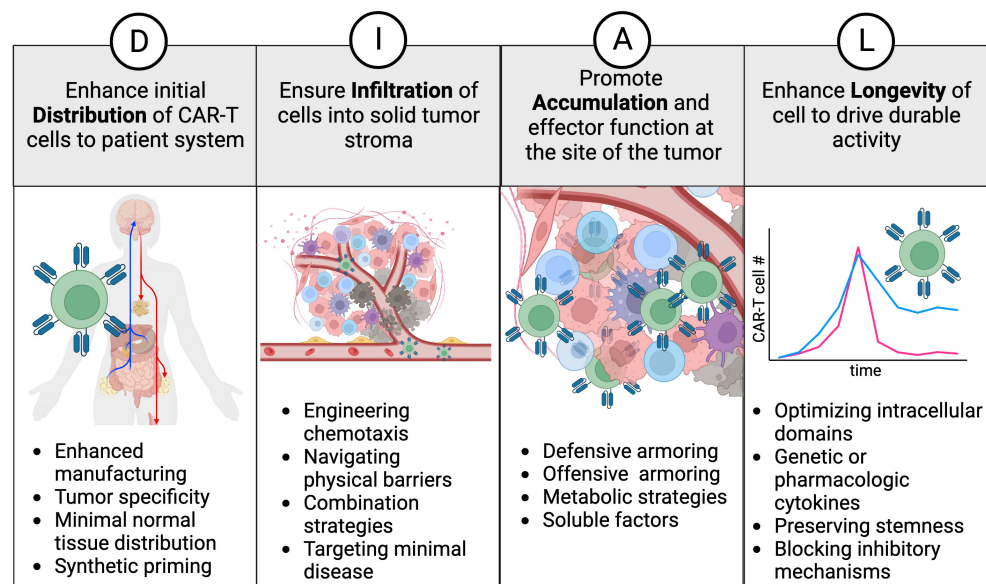


FIGURE 1

The DIAL framework. Distribution, infiltration, accumulation, and longevity are classified as key attributes and areas to focus on for enhancing cell therapy products. Examples of interventions are provided for each attribute and discussed in the text.

of administration. The distribution of adoptively transferred lymphocytes for cellular therapy is analogous to pharmacologic distribution of biologics and small molecules, with certain key distinctions.

As donor-derived “living drugs”, infused GML exhibit a distribution pattern similar to endogenous lymphocytes (18–20). Following intravenous infusion, T-lymphocytes follow the vascular circulation, extravasate into tissues, diffuse into target sites, and recirculate through uptake in lymphatic tissue via high endothelial venules, ultimately returning to the vasculature through either the thoracic duct or vascular circuits (21). While the initial use of CAR-T focused on treating of B cell malignancies in the periphery it is important to note that GML also can distribute in compacted tissues and encounter their cognate antigens. This interaction allows them to receive survival and proliferation signals, promoting their expansion.

The expansion phase of GML products induced by antigen encounter sets adoptive cell therapy (ACT) apart from other therapeutic approaches. During this phase, the levels of the therapeutic cells (measured by the presence of CAR or TCR-positive cell by flow cytometry or gene copy number by PCR) increase relative to the infusion levels. The peak and duration of this elevation depends on the antigenic burden and the microenvironmental context of antigen encounter, both of which influence the extent of proliferation and expansion. Over time, the infused cells undergo apoptosis in various tissues. The initial phase of decay occurs rapidly after the initial expansion, while the second phase of decay proceeds gradually over weeks to months. This gradual decline may be attributed to factors such as loss of stimulation, activation-induced cell death, and exhaustion (22).

The composition of cell therapy infusion products plays a pivotal role in determining their distribution. When accounting for effector, memory and naïve subsets, both rodents and human

exhibit a similar distribution pattern for ACT (21, 23–25). Factors such as cell size and the presence of receptors that govern lymphatic tropism (such as L-selectin and CCR7) can influence the survival and recirculation of cells post-infusion. Further, the relative composition of these subsets can impact the proliferative and metabolic potential of the transferred lymphocytes.

In the case of commonly used laboratory mice (*Mus musculus*), variations in CAR-T and TCR-T distribution may be attributed to factors like strain differences, extent of immune competence, and discrepancies in housing and sourcing facilities. Nonetheless, working with laboratory mice generally offers the advantage of predictability and consistency in experimental outcomes.

2.1 Distribution – cellular manufacturing

The ex vivo manipulation and expansion of GML, often referred to as cellular manufacturing, represents the initial stage where subsequent distribution patterns can be influenced. The manufacturing process involves complex interplay of factors that dictate the cellular kinetics (CK) of the grafted cells, including post-infusion cell survival, tissue infiltration, antigen-induced expansion, recirculation through the lymphatics into the bloodstream, terminal differentiation, and elimination.

Early T cell manufacturing processes focused on scaling up large numbers of cells for infusion into patients who would subsequently receive supportive doses of IL-2 (26, 27). In comparison, CAR-T therapy had key distinctions, requiring fewer cells for infusion and demonstrating the ability to persist without patient-administered IL-2. However, many of the principles established with TIL therapy, such as T cell activation through their TCR using anti-CD3 antibodies or antigen-presenting cells, and expansion in the

presence of moderately high (>100 IU/mL) levels of IL-2 for 1-2 weeks, were initially maintained in GML protocols.

However, it was observed that sustained expansion in IL-2 could lead to cell exhaustion and limited persistence *in vivo* (28). Consequently, various protocol modifications were adopted in cellular manufacturing to preserve the fitness and persistence of the transferred cells post-infusion (29, 30).

In the years following the development of the initial CD19 CAR-T therapy, numerous modifications to manufacturing protocols were explored. These included the use of CD3/CD28 beads and alternative cytokines such as IL-7, IL-15, and IL-21, which promoted a stem cell memory phenotype (31–33). Additional enhancements involved incorporating small molecules into expansion media to further boost memory characteristics, promote persistence, and increase anti-tumor activity (34–39). The results demonstrated that process modifications preserving a memory cell phenotype enabled enhanced persistence, as determined by factors such as proliferative potential, resistance to stress (e.g., serial antigen stimulation or low cell dosing), and improved distribution to lymphatics and secondary lymphoid organs, facilitating recirculation (40).

Administration of high doses of CAR-T cells after prolonged manufacturing times and in conjunction with supportive IL-2 can lead to severe toxicities and lack of long-term durability, even when the target antigen is not present in normal tissues (41). Because of these potential issues, many of the recent advancements in autologous cellular manufacturing focus on preserving GML stemness as a means of improving potency and reducing toxicity, with a heightened focus on the T memory stem-cell (T_{SCM}). This subset of memory T cells with self-renewal capacity was first identified in mice (34) and subsequently in human (28) and non-human primate (42). T_{SCM} have similar cell surface markers and metabolic potential compared to naïve T cells, and have an enhanced proliferative potential compared to other memory and effector subsets. For CAR-T, it is important to consider that recently activated naïve T cells are often not distinguished from native T_{SCM} cells and thus may differ in functional capacity and fate. There are a variety of ways to enhance the CAR- T_{SCM} fraction: mechanical enrichment of naïve/memory subsets (29, 43), addition of factors or cytokines to induce stemness (31, 37, 44), and shortening the manipulation of peripheral cells and reducing manufacturing time (45, 46). Although much of the modeling for CAR- T_{SCM} is performed using human cells in immunocompromised mice, the underlying principles can be applied to immunocompetent strains as well.

Murine T cell manufacturing processes are not optimal for translation to human CAR-T cell manufacturing. Mouse T cells exhibit many dissimilarities compared to their human counterparts. Additionally, available protocols for murine T cell transduction and expansion, as well as lymphodepletion, create disparities in comparison to humans.

To begin with, murine T cells do not expand *ex vivo* to the same extent as human T cells. They require different media and conditions for activation and do not consistently expand for greater than approximately 10-14 days. Furthermore, the source of cells differs between murine and human protocols. Murine

protocols primarily utilize splenic T cells, whereas human protocols rely on peripheral blood T cells (47, 48).

Lastly, lymphodepletion in mouse typically involves low-dose (<5 Gy) whole-body irradiation, whereas lymphodepleting chemotherapy (LDC) is almost exclusively used in humans. These differing protocols can lead to variations in the dynamics of lymphopenic immune cell recovery and cytokine production, which are crucial for supporting the expansion of transferred cells and promoting memory phenotypes.

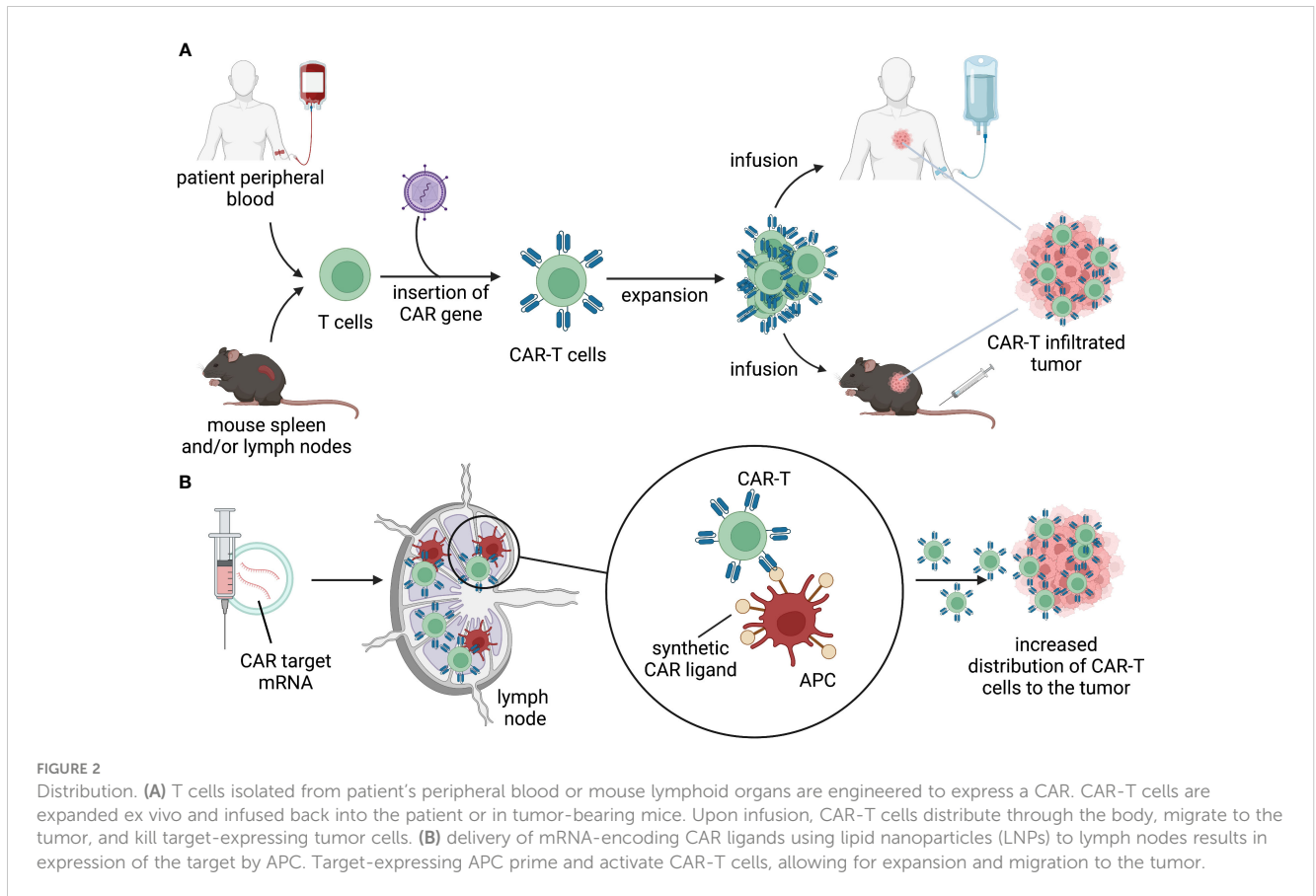
Despite these differences, genetically engineered fully murine model systems can still be utilized to highlight many of the advantages of generating stem-like T cells for ACT (49–55). In the future, the development and engineering of GML could benefit from a combination of both immunocompetent syngeneic murine and immunocompromised human xenograft model systems. This approach would provide a more comprehensive understanding of the various factors required to achieve optimal cell distribution.

2.2 Distribution – choice of antigen

The choice of antigen and context of antigen encounter will influence the initial distribution of the gene-modified cells. After intravenous infusion, cell therapy products follows a pattern of distribution that involves vascular circulation, extravasation, diffusion into tissue, and recirculation primarily through lymphatics and vascular circuits. GML can distribute in tissues and encounter their cognate antigens in the tumor, triggering survival and proliferation signals that allow for expansion and continued distribution (Figure 2A). Different types of lymphocytes may have varying tendencies to distribute to tissues and lymphatics.

In cases where antigen is readily accessible in blood-based tumors, the process of expansion and distribution is facilitated. However, when the antigen is confined to poorly vascularized or compacted tissues, both the accessibility and the context of antigen encounter are compromised. Non-genetically modified lymphocytes, particularly T cells, have the capability to produce cytokines and transcription factors that promote proliferation and antigen-induced expansion. GML, with their expressed receptors, further enhance antigen-induced expansion to exaggerated levels, which can be augmented by preceding lymphodepletion. It is important to note that the differences between mouse and human lymphodepletion, as discussed earlier, can also lead to discrepancies in interpreting preclinical models when evaluating antigen-specific expansion in humans.

Antigens that exhibit a tumor-specific expression profile facilitate confined and intended cell expansion. On the other hand, more promiscuous antigens increase the risk of “off-tumor” toxicities and promote effector differentiation, which can lead to eventual dysfunction. When target-directed activity induces both direct cytotoxicity and paracrine effects through cytokine production, widespread antigen expression outside the tumor can exacerbate systemic inflammation. This, in turn, hampers the cells’ ability to infiltrate the tumor efficiently. This phenomenon is commonly referred to as on-target, off-tumor toxicity. However,



promiscuous antigen expression can also impede cell expansion and distribution by diverting cells into non-tumor tissues, effectively excluding a portion of the transferred GML from their intended target.

The ideal antigen for tumor targeting would be uniquely expressed in the tumor and absent in normal tissues. However, for CAR-T therapy, such antigens are rare, with only a few examples like EGFRvIII and aberrantly glycosylated protein glycoforms such as Muc1 falling into this category (56, 57). Most CAR targets show a preference for tumor expression but are also detected in normal tissues. The most successful CAR targets have been observed in B cell malignancies, where normal expression occurs in cells that are apparently dispensable. Another wave of CAR targets is emerging, with lower levels of normal tissue expression but not complete absence. These targets aim to strike a balance between effective tumor targeting and minimizing off-target toxicities. It is challenging to achieve complete avoidance of target engagement in normal tissues, so efforts are focused on selecting targets with reduced normal tissue expression to mitigate potential toxicity while still enabling successful tumor targeting.

This expanded repertoire of CAR targets opens up new possibilities for successful immunotherapy beyond B cell malignancies, where targets expressed in dispensable tissues have shown promising outcomes. Preclinical mouse models provide certain examples where on-target, off-tumor toxicity can be monitored. However, it's important to note that these models often involve immunocompromised mice using mouse cross-

reactive single-chain variable fragments (scFvs) or transgenic approaches to introduce the human antigen.

For instance, one study showed that a low-affinity Her2 CAR-T specifically targeted Her2-expressing tumors while avoiding accumulation in the mouse liver, where Her2 was artificially expressed using adenovirus (58). In another example, an affinity-tuned, mouse cross-reactive GPC3 CAR-T was able to avoid lethal toxicity against GPC3 expressed in the mouse lung and induce regression of human hepatocellular carcinoma tumors (59). However, caution must be exercised when interpreting off-tumor toxicities in mice, as some results may not align with human studies. For instance, a high-affinity GD2 CAR-T demonstrated lethal CNS toxicity in a mouse model of neuroblastoma (60), whereas human clinical trials using a similar GD2-targeted CAR-T via intravenous and intracerebroventricular therapy showed good tolerability without signs of off-tumor CNS toxicities (61).

In contrast to CAR therapy, GML TCR therapy offers access to certain tumor-specific targets, particularly due to its ability to recognize intracellular proteins presented as peptides in the context of the major histocompatibility complex (pMHC). These targets primarily fall into the categories of cancer-testis antigens, tumor-viral antigens, and mutant neoantigens. The presence of these unique tumor-specific targets presents opportunities for precise and personalized immunotherapy approaches.

GML TCR therapy allows for the targeting of antigens that are specifically expressed by tumor cells, offering potential advantages in terms of enhanced tumor specificity and reduced toxicity

compared to CAR therapy. This approach broadens the range of tumor-specific antigens that can be targeted, expanding the possibilities for developing effective treatments against various types of cancer. However, achieving broad targeting will necessitate the rapid development of personalized TCR-T therapies (62), which cannot be practically modeled in mice.

For the majority of the aforementioned targets, fully mouse surrogate CAR/TCR systems, transgenic mice, or cross-reactive mouse antibodies are not typically used in preclinical studies. While on-tumor activity can be measured, there remains a significant gap in the investigation of off-tumor inflammation and toxicity. Consequently, examples of off-tumor engagement by GML are predominantly observed in human clinical trials, and the overall implications for cell survival, distribution, and toxicity in these scenarios remain poorly understood.

Furthermore, it's worth noting that many GML TCR therapy approaches are often combined with interleukin-2 (IL-2) to enhance cellular expansion and persistence. However, the use of IL-2 in these therapies brings its own considerations and potential dose-limiting toxicities. These toxicities may include vascular leak syndrome, hypotension, and renal dysfunction. Modeling IL-2 toxicity in mice is challenging, primarily because mice can tolerate high levels of IL-2 without experiencing the dose-limiting toxicities observed in humans.

A recent advancement in GML engineering is the application of combinatorial antigen targeting technology. This approach aims to more precisely target tumor tissues while avoiding off-tumor inflammation and promoting optimal GML distribution. However, it is important to note that most logic-gated CAR-T systems have only been demonstrated at the preclinical level in mouse models.

Logic gating approaches typically involve two distinct binding events and can fall into different categories:

1. OR gating: Both antigen-binding fragments can simultaneously engage with the target and trigger signaling. This can occur through tandem engagement, where both antigen-binding molecules are joined and signal through a shared intracellular domain (ICD), or through the expression of separate CARs in a bicistronic format.
2. AND gating: Both antigen-binding fragments are required to engage the target in order to initiate signaling.
3. ON gating: The CAR is not expressed or fully functional until the addition of a second pharmacologic agent, which can be a small molecule, protein, or antibody-like drug. "Universal CARs" also fall in this category.
4. NOT gating: The second antigen-binding fragment can disable or "turn off" the signaling initiated by the first antigen binder, typically expressed in normal tissues.
5. IF ... THEN gating: The first antigen binder drives signaling through a secondary transcription factor, leading to the expression of the second protein, which can be a fully competent CAR molecule.

While "OR" gated CAR-T, used in multiple dual and tandem formats, is being evaluated in clinical trials for hematologic

malignancies, most logic-gating approaches have only been described and validated in preclinical studies in mice (63–66). Since most logic-gating strategies require two separate events to initiate signaling, they may have limitations such as leakiness or a loss of precise temporal control. For a more detailed discussion on the benefits and challenges associated with various logic-gating approaches to mitigate on-tumor, off-target toxicity, a recent review provides in-depth coverage (67).

An innovative approach aims to address some of the challenges faced by other technologies by combining distinct antigen binding domains with mutually dependent signaling domains downstream of the TCR complex. Researchers proposed coupling the intracellular domains (ICDs) of SLP76 and LAT to single-chain variable fragment (scFv) domains that recognize different antigens. By engineering mutations that prevent simultaneous binding of the Grb2 family member GADS, this approach creates a tightly regulated logic gate that has the potential to enable tumor-specific expansion of dual CAR-T cells (68).

The SLP76/LAT logic gate was validated using a commonly used xenograft model of acute lymphoblastic leukemia (NALM6) in NSG mice, where the tumor cells expressed ROR1 and CD19 antigens as dual targets. Encouragingly, this approach demonstrated an improved balance between efficacy and off-tumor toxicity compared to traditional "split CAR" and "Syn-NOTCH" logic-gating strategies. The development of technologies that provide more precise control over dual antigen targeting in the future may not only help in managing off-tumor toxicity but also enhance the distribution properties of CAR targeting molecules.

This advancement opens up possibilities for the exploration of dual-antigen-defined tumor types. It offers the potential for improved efficacy by combining the favorable attributes of TCR GML (tumor specificity) and CAR GML (targeting broader indications).

2.3 Distribution – cell priming strategies

To enhance GML expansion, strategies have been explored to mimic peripheral priming mechanisms in secondary lymphoid organs (SLO) by targeting oxygen, nutrient, and co-stimulatory ligand-accessible regions of the body. Initially, the concept of enhancing adoptive T cell therapy involved using viral-specific T cells as a platform for tumor-directed CAR or TCR transgenes. These priming responses can be engaged passively, through endogenous viral antigen presentation, or actively, via vaccination against the viral antigen (69, 70). In recent approaches, *in vitro* priming of CAR-T cells with oncolytic viruses through their native TCR has been combined with *in vivo* boosting, leading to impressive responses in preclinical models of melanoma and glioma (71).

Despite the early enthusiasm and adoption of viral-specific T cells as a CAR platform, and the development of innovative approaches to prime peripheral expansion of CAR-T, only a limited number of human clinical trials have been initiated using these approaches. It's important to note that most viral-specific T cells are being explored as an allogeneic platform due to their reduced potential for alloreactivity (NCT04288726, NCT03740256,

NCT01475058, NCT01430390). In addition to viral-specific T cells, other lymphocyte lineages such as NK cells, iNKT cells, $\gamma\delta$ T cells, and MR1 T cells that can recognize non-MHC antigens in tumors may also be considered as GML platforms (72–75). While these alternative ACT platforms have the ability to naturally expand in the presence of their cognate ligands, similar to viral-specific T cell priming, and show potent responses in mouse models, it remains to be seen if they exhibit similar expansion and distribution potential to $\alpha\beta$ CAR-T cells in human patients.

Recent synthetic approaches to enhance CAR-T expansion include “CAR vaccine” strategies, which involve the delivery of mRNA-encoded CAR ligands using lipid nanoparticles (LNPs) to lymph nodes (Figure 2B). This allows CAR-T cells to undergo *in vivo* expansion and stimulation in lymphatic regions. The CARVac strategy demonstrated that LNP-mediated delivery of the CLDN6 antigen to antigen-presenting cells (APCs) in the lymphoid compartments of mice could promote robust expansion of CLDN6 CAR-T cells and improved anti-tumor efficacy (76). Another approach involved *in vivo* expression of “amphiphile ligands” that could be delivered by LNPs and inserted into the membrane of APCs to present cognate ligands, facilitating GML proliferation (77, 78). Interestingly, neither of these approaches resulted in substantial elimination of the CAR-antigen expressing APCs. Clinical testing of CARVac is underway to enhance CAR-T expansion against CLDN6-positive solid tumors (NCT04503278). Although data generated in mouse models demonstrated a significant increase in expansion and improved anti-tumor efficacy, data from human trials are still in the early stages and inconclusive regarding the priming benefits of the “CAR vaccine” approach. Nonetheless, these and future strategies to safely enhance peripheral CAR-T expansion can be effectively modeled in mice and have the potential to drive GML activity using lower infused doses or lymphodepletion-free regimens.

3 Infiltration

Following successful systemic distribution, transferred immune cells may encounter various physical and chemical barriers as they navigate towards tumor-associated antigens and exert their cytotoxic function. In the case of hematologic malignancies, GML may not require extensive infiltration to encounter antigens. However, this is not the case for the majority of carcinomas. Fortunately, immune cells, such as T cells, possess receptors that facilitate extravasation from the vasculature into inflamed tissues and further penetration into the extracellular matrix (ECM) based on chemokine receptor expression, cytokines, and chemical gradients (79). While most CXC and CC chemokine receptors are already expressed on peripheral T cells at various activation stages (80), there are instances where enforced overexpression of these receptors enhances GML’s ability to access tumors by leveraging native chemical gradients.

3.1 Infiltration – engineering chemotaxis

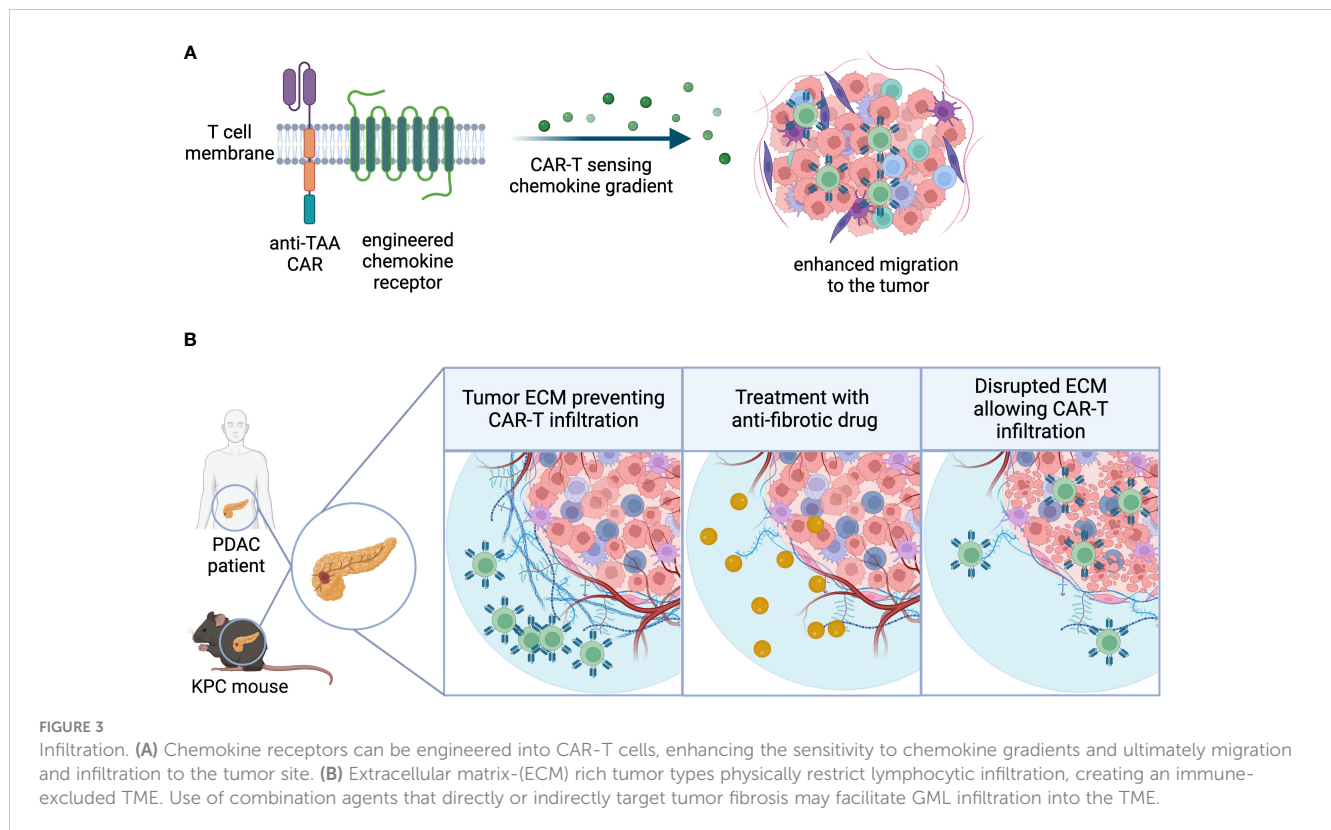
One important aspect of successful infiltration is the ability of T lymphocytes to undergo extravasation and chemotaxis towards sites

of inflammation. Naturally circulating T cells acquire this capacity as a result of effector differentiation following antigen recognition and priming in secondary lymphoid organs (SLO). As described earlier, there are various methods to enhance GML priming using synthetic and natural mechanisms. Additionally, receptor overexpression in GML has been shown to augment their infiltration capacity. Some approaches focus on tumor-specific cues to modify chemotactic receptor expression, while others aim to increase lymphoid-homing capacity, recirculation, and survival in a more general manner, thereby enhancing anti-tumor function (81). Proof-of-mechanism for tumor-specific strategies primarily comes from engineered preclinical mouse models and xenograft model systems, where overexpression of the chemokine receptor can influence the infiltration and accumulation of CAR-T cells compared to their unmodified counterparts. Chemokine receptor overexpression in GML has been utilized to address potential trafficking deficiencies in solid tumors (Figure 3A). The strategic rationale behind these approaches is often similar:

1. Tumors are found to express sufficient levels of chemokine ligands, creating chemotactic gradients.
2. Peripheral T cells or endogenous tumor-infiltrating lymphocytes (TIL) show low levels or downregulation of the cognate or paired chemokine receptor(s).
3. Re-expression of the lost or downregulated receptor is shown to synthetically augment and/or restore infiltration in preclinical mouse models.

Examples of receptors engineered into GML include CCR2, CCR4, CXCR2, CXCR3, CXCR4, and CX3CR1 (82–88). Recent examples showed overexpression of CXCR2 enhanced infiltration of CAR-T hepatocellular carcinoma xenografts where the tumors were shown to express high levels of CXCR2 ligands including CCL2, CXCL1, CXCL2, and CXCL5 (89); CXCR1 overexpression enhanced T and NK CAR cells to migrate into ovarian or pancreatic tumors (90, 91) and CCR2 transduction into MSLN CAR-T cells enhanced migration into CCL2 positive malignant pleural mesotheliomas (86, 92). Although some of these examples exploit chemotactic gradients that may be generally expressed in inflamed tissues rather than specifically in tumors, a recent study used a tumor-specific strategy by forcing overexpression of the chemokine receptor CXCR6 on mesothelin-targeted CAR-T cells. This approach led to enhanced regression of pancreatic tumor xenografts. CXCR6, which is normally lowly expressed on peripheral blood T cells, is naturally attracted to its counterpart ligand CXCL16. In this case, CXCL16 was found to be highly expressed by malignant pancreatic epithelial cells, making it an attractive tumor-specific strategy (93).

Other strategies have been explored to improve infiltration and survival of transferred ACT without directly targeting the tumor. Some of these strategies involve factors such as IL-7/CCL19 or L-selectin overexpression to increase tumor penetration of ACT (81, 94). Notably, L-selectin overexpression in mice allowed for equivalent tumor infiltration and improved anti-tumor function of CAR-T cells by decreasing the activation threshold of the transferred cells, contrary to the presumed improvement in



lymphoid organ homing. While these strategies have shown therapeutic merit in preclinical models, few have been validated in human clinical trials. It remains to be seen whether these strategies can enhance the success of GML-based solid tumor therapy.

A recent report suggested that ex vivo expansion of CAR-T cells in the presence of TGF- β could significantly enhance tumor infiltration and efficacy in xenograft tumor models (95). This approach aimed to epigenetically rewire peripheral blood T cells toward a resident memory T cell phenotype (T_{RM}), which would enhance accumulation and promote stemness of the transferred CAR-T cells targeting MSLN. In CAR- T_{RM} treated, regressing xenograft tumors, there was a marked increase in CAR-T cell infiltration, and depletion of CD103+ cells diminished the benefits of the so-called CAR- T_{RM} cells. Interestingly, overexpression of the T_{RM} transcription factor RUNX3, which had been used previously to enhance TRM expansion in murine tumor models, did not phenocopy the CAR- T_{RM} cells (96). This expansion strategy represented the first attempt to enhance CAR-T infiltration in murine models using ex vivo process engineering. Intriguingly, a similar protocol was used in human clinical trials to enhance neoantigen-directed TCR-T cells targeting mutant KRAS G12D pMHC (97). In this clinical trial, a TGF- β -based ex vivo expansion protocol was employed to enhance TCR-T cell infiltration in pancreatic ductal adenocarcinoma, leading to a dramatic reduction of lung lesions and a durable clinical response in one patient.

Another strategy to improve GML infiltration involves introducing chemotactic factors or cytokines into tumor-targeted therapeutics, such as engineered oncolytic viruses (OVs). Studies

using mouse models demonstrated that intra-tumoral injection of adenovirus engineered to produce IL-15 and RANTES could promote GD2 CAR-T cell infiltration into solid tumors in immunocompromised mice (98), and this approach is also being explored in human clinical trials (NCT03740256). Subsequent efforts showed that intra-tumoral injection of OV, such as vaccinia, could promote T cell infiltration by producing high systemic levels of CXCL11 (99). Other combinations propose introducing cytokine or immune checkpoint blockade (ICB) payloads into OVs, which, together with the oncolytic activity of the virus, can enhance CAR-T cell infiltration and survival in preclinical models of solid tumors (100–102). Unexpectedly, OV-mediated introduction of intra-tumoral Type 1 interferon (IFN β) was shown to drive CAR-T cell apoptosis, which was prevented by deleting IFNAR1 in the engineered cells (103). Given that many OVs naturally induce the production of Type I interferon, a deeper understanding of the potential benefits, pitfalls, timing, and sequencing of combination OV and CAR-T therapy is warranted (104). The combination of OV and CAR-T therapy for solid tumors is a subject of ongoing research and a separate review (105).

3.2 Infiltration – navigating physical barriers

In addition to challenges posed by suboptimal chemotactic gradients, solid tumors often create physical barriers that promote immune exclusion. Immune exclusion can be caused by immune or non-immune stroma in the TME, which may impede immune cell

infiltration. The next section of this review will delve into the discussion of soluble and metabolic factors that contribute to immune exclusion. This section will primarily focus on tumors characterized by fibrogenic stromal cells, also known as cancer-associated fibroblasts (CAFs), which produce collagen-containing matrices that physically restrict lymphocytic infiltration. However, it is important to note that certain human tumors, such as pancreatic ductal adenocarcinoma, possess extensive stroma that cannot be accurately modeled in preclinical species. Despite this limitation, preclinical strategies have been developed to counteract non-immune stromal cells using CAR-T cells, either by directly eliminating CAFs or indirectly targeting stromal-derived barriers. In addition, use of combination agents that directly or indirectly target tumor fibrosis may represent an alternative strategy to improve GML infiltration into extracellular matrix-(ECM) rich tumor types (Figure 3B).

Developing strategies to target the extracellular matrix (ECM) presents multiple challenges. One of the key challenges is the development and validation of preclinical models that accurately replicate CAF-containing fibrogenic stroma observed in pancreatic, colon, hepatocellular, gastric, esophageal, head and neck, cervical, and breast cancers. While mouse models can partially capture certain aspects of fibrotic tumors, such as modeling the increased interstitial fluid pressure induced by fibrosis (106), they are likely to fall short in simulating the complexity of combining fibrosis-targeting agents with GML. Additionally, CAFs, like other components of the immune stroma, are heterogeneous and play diverse roles in cancer, some of which may not be adequately modeled in mice. Furthermore, fibrogenic stroma in humans often develops in the pre-metastatic niche, resulting from the recruitment of factors from the bone marrow and facilitating vascular access before tumor establishment. Most of the strategies mentioned above have been described using cell line-derived xenograft (CDX) or genetically engineered mouse models (GEMM), which rarely fully replicate the extent of stiff, fibrotic ECM seen in cancer patients.

Strategies encoded in GML to target fibrosis include directly eliminating fibrogenic cells in the tumor. One of the prominent targets on CAFs is the fibroblast-associated protein (FAP) (107–109). Murine reactive FAP CAR-T cells have shown effectiveness in multiple preclinical models, but potential toxicity concerns arise due to the depletion of FAP-expressing bone marrow stromal cells (110, 111). There have been limited opportunities to test this concept in human clinical trials, but FAP CAR-T cells appear to be tolerated at subtherapeutic doses (NCT01722149). Another genetic strategy to enhance access to ECM-rich tumors involves engineering CAR-T cells to secrete ECM-degrading enzymes, such as hyaluronidase or heparinase (112, 113). In both preclinical examples, the encoded and secreted enzymes did not interfere with CAR-T cell function and effectively degraded the matrix in mouse xenograft tumor models. Although these efforts have shown benefits in various murine models, there is limited proof-of-concept evidence from human clinical trials regarding ECM degradation and/or fibroblast targeting.

Myeloid cells can also impede GML infiltration into tumors. Targeting tumor-associated macrophages (TAMs) and myeloid-derived suppressor cells (MDSCs) broadly for depletion can be

challenging due to potential toxicities. However, recent studies suggest that certain receptors may serve as tumor-specific targets, allowing for safer targeting of these suppressive cell types. For TAMs, targeting the folate receptor β (FR β) with a CAR in syngeneic mouse models was shown to be safe and promoted increased infiltration of MSLN CAR-T cells in multiple tumor models (114). MDSC targeting was facilitated by a DR5 agonist costimulatory CAR expressed on the cell surface of Mucin 1 (MUC1) CAR-T cells (115). This approach demonstrated improved anti-tumor activity in an MDSC-admixed tumor model, presumably through increased infiltration, although direct evidence was not provided. Interestingly, the concept of targeting MDSCs with DR5 agonist antibodies has been previously tested in mice and humans, showing promising results and offering a novel approach to enhance GML infiltration (116, 117).

3.3 Infiltration – combination strategies

An indirect approach to disrupt factors that suppress lymphocytic infiltration involves tumor debulking through surgery, chemotherapy, or radiation. However, these therapies can have a dual effect as radiation and chemotherapy-resistant tumors often develop fibrosis as a consequence of treatment (118). This fibrotic response can vary depending on the therapeutic regimen but is a common outcome due to oxidative stress in the TME. To address therapy-induced fibrosis, targeted therapies have been explored to inhibit cancer-associated fibroblasts (CAFs), the extracellular matrix (ECM), or overall tumor architecture.

In terms of targeting the ECM, small molecule inhibitors of lysyl oxidase (LOX) and LOX-blocking antibodies have shown impressive activity in a GEMM of breast cancer. However, these approaches have not yet demonstrated success in human clinical trials (119, 120). Other small molecule inhibitors such as fasudil (ROCK inhibitor) and defacitinib (FAK inhibitor) have been used to attenuate focal adhesion signaling in tumor cells, influencing ECM remodeling by reducing matrix metalloproteinase (MMP) deposition and the desmoplastic response, respectively (121). Both fasudil and defacitinib have shown improved survival in mouse models of pancreatic cancer (LSL-KrasG12D/+; LSL-Trp53R172H/+;Pdx-1-Cre), and early-stage clinical trials combining defacitinib with immune checkpoint inhibitors (ICI) have demonstrated stable disease with increased T cell infiltration in post-treatment biopsies. Although there are currently no planned clinical studies with fasudil, its potential remains to be explored. Recombinant hyaluronidase or pegylated recombinant hyaluronidase 20 (PEGPH20) have been tested in combination with chemotherapy for pancreatic ductal adenocarcinoma (PDAC) based on strong combination activity observed in KPC mouse models (106). PEGPH20 was able to reduce interstitial fluid pressure (IFP) in these models and improve the response to chemotherapy (gemcitabine + nab-paclitaxel). However, a randomized controlled Phase III trial of this combination did not demonstrate a significant benefit. The reasons why the KPC mouse model was not predictive of an improved combination response remain unclear. Another preclinical strategy involves targeting discoidin

domain receptor 1 (DDR1) with neutralizing antibodies to disrupt collagen-containing stromal fibers (122). Targeting DDR1 to reduce collagen disposition enhanced the effects of chemotherapy and GML in orthotopic tumor models and mouse models of pancreatic cancer (KPC mice). To date, GML combinations with targeted inhibitors of ECM deposition have shown strong effects in multiple mouse models but have not translated successfully in clinical trials. This highlights the need to develop more predictive preclinical models of desmoplasia and matrix deposition to improve the infiltration of GML into tumors.

Administration of GML directly following chemotherapy may improve infiltration by exerting anti-fibrotic effects and shifting suppressive myeloid cells to a pro-inflammatory phenotype. Murad et al. demonstrated improved infiltration following chemotherapy in murine preclinical studies using cyclophosphamide prior to PSCA CAR-T administration in metastatic prostate and pancreatic cancer models (123). Interestingly, cyclophosphamide has been used to treat pulmonary fibrosis due to its lymphodepleting mechanism of action, which can suppress fibrotic inflammation (124). Alternative preconditioning therapies, such as fludarabine/cyclophosphamide (Flu/Cy) plus nab-paclitaxel (FNC), have been used in human clinical trials of CLDN18.2 CAR-T (125). These regimens, incorporating taxanes in addition to standard Flu/Cy, may improve GML efficacy by reducing tumor burden, conditioning the TME, and enhancing infiltration. However, there is a lack of preclinical mouse studies supporting the use of FNC preconditioning. The differences in metabolism of conventional chemotherapies between mice and humans make it challenging to model these combinations accurately, but exploring indication-specific regimens to improve responses should be considered.

Another potential approach to enhance GML infiltration involves intra-tumoral injection of surgically resected or debulked tumors to facilitate T cell-mediated clearance of minimal disease. Mouse models utilizing gel-embedded CAR-T have been described, demonstrating clearance of partially resected MSLN+ xenograft tumors (126). The fibrin gel-embedded MSLN CAR-T enabled clearance of tumor cells at the margin of surgical resection, minimizing on-target, off-tumor toxicity and complications associated with wound healing. The fibrin glue appeared to support CAR-T survival and infiltration into the tumor margin, clearing minimal residual tumor cells and preventing additional treatment-induced inflammation and fibrosis. A study to explore this approach in locally advanced breast cancer is planned.

4 Accumulation

In comparison to hematological malignancies, solid tumors present numerous challenges within the TME that hinder the activation and functionality of T cells, thereby limiting the efficacy of cell therapies (Figure 4A). Various factors within the TME can impede the successful accumulation and subsequent expansion of T cells, including metabolic properties (such as hypoxia, nutrient limitation, and ionic imbalance), the presence of suppressive cell types (such as TAMs, MDSCs, and Tregs), and the presence of suppressive cytokines or soluble factors (such as

TGF- β and IL-10) (114, 127). Genetic engineering strategies for CAR-T cells aimed at counteracting the suppressive TME are commonly referred to as “armoring” approaches (128).

While there are diverse strategies to enhance the performance of CAR-T cells, a primary objective is to improve their accumulation within the TME. This can be achieved by enhancing their survival or promoting increased cell division rates. In this review, we classify accumulation strategies as either “defensive” or “offensive.” Defensive strategies aim to protect GML from factors that suppress their proliferation or survival, while offensive strategies involve the elimination of suppressive cells or factors to facilitate GML accumulation (Figure 4B). To provide preclinical validation, we will also assess the feasibility of modeling these strategies in mice.

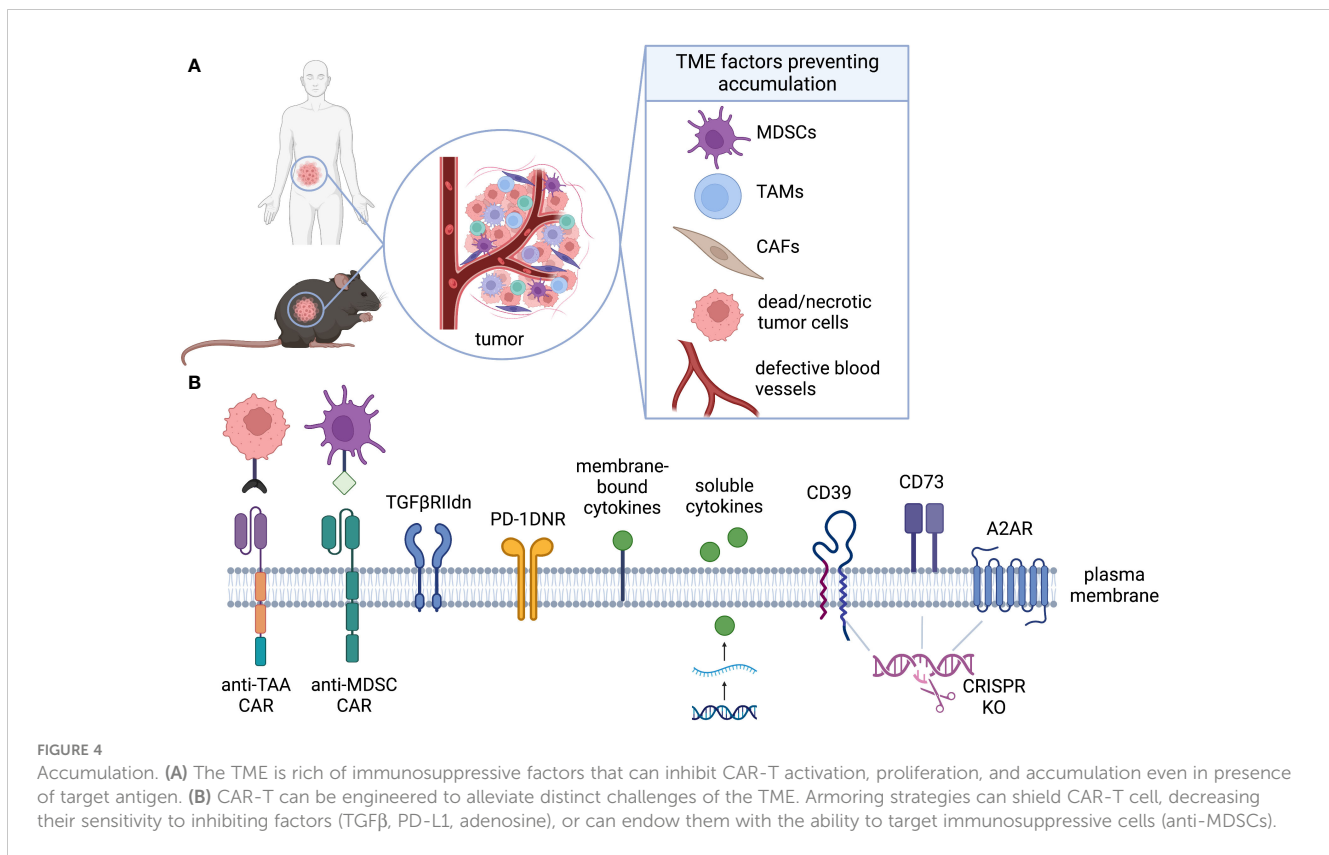
4.1 Accumulation - defensive strategies

4.1.1 Metabolism

T-cell metabolism plays a crucial role in determining both cell survival and the effectiveness of antitumor immune responses. However, understanding the intricate metabolic crosstalk between CAR-T cells and TME poses challenges for *in vitro* modeling. Therefore, the utilization of *in vivo* models becomes highly significant in dissecting the complex metabolic pathways involved in this interaction. Syngeneic models have emerged as valuable tools for investigating T-cell metabolism due to their flexibility in engineering specific immune subsets and accurately representing immune components within the TME.

Chang et al. utilized a sarcoma model expressing or lacking the spectrin- β 2 antigen, which determines tumor rejection, to investigate T-cell fitness in different TMEs. Expanding upon these findings, the researchers further investigated T-cell metabolism using OT-I mice. Their groundbreaking work revealed a fundamental concept: the competition for glucose between CAR-T cells and the TME leads to reduced cytokine production and facilitates tumor growth (129). Additional insights into aerobic glycolysis-induced T-cell differentiation came from studies employing CD4^{Cre}Ldha^{fl/fl} mice lacking LDHA in T cells. These studies demonstrated that aerobic glycolysis promotes effector T-cell differentiation, highlighting LDHA as a critical therapeutic target (130). Subsequently, transgenic PMEL-1 mice were used to explore the modulation of LDHA in cell therapy. This study demonstrated that the metabolic characteristics of antigen-specific T cells, along with their persistence, accumulation, and antitumor immunity, could be effectively modulated through the administration of exogenous cytokines (131).

The adjustment of T cells to hypoxic and nutrient-deprived tumors triggers a metabolic switch to glycolytic metabolism, primarily mediated by the transcription factor HIF-1 α (132, 133). The critical role of HIF-1 α in inducing T cell effector status has been demonstrated using HIF-1 or HIF-2 α ^{fl/fl} dlck^{CRE} mice (134). However, under chronic hypoxia, this metabolic switch might lead to terminal differentiation, anergy, and exhaustion. This is particularly relevant for transferred lymphocytes, which lack access to native priming mechanisms that can maintain memory cell



persistence for extended periods. Therefore, rewiring the hypoxia response could potentially tailor T-cell differentiation, sustain persistence, and enhance antitumor responses in CAR-T cells.

Syngeneic mice have also played a critical role in exploring the importance of amino acids (such as arginine, tryptophan, and glutamine) in the biology of tumor-infiltrating lymphocytes (TILs). The scarcity of these amino acids in the TME can drive dysfunction of CAR-T cells and TILs. The essential role of arginine in T-cell activation, proliferation, and cytokine production has been demonstrated in TCR transgenic mouse models of CD4⁺ T cells specific for the influenza HA110–119 peptide (135). Sustained Arg1 activity require transport of arginine into the cell through cationic amino acid transporters. CAT2B is thought to be the most efficient in the transport of arginine into cells. Indeed, M-MDSCs or PMN-MDSCs derived from *Cat2^{-/-}* mice adoptively transferred in tumor-bearing mice displayed a significantly reduced ability to inhibit T cell proliferation in *in vitro* assays (136). This was confirmed *in vivo* in a thymoma tumor model, where the anti-tumor activity of adoptively transferred antigen-specific CD8⁺ T cells was significantly enhanced in *Cat2^{-/-}* vs. wild-type mice as a result of decreased ability of *Cat2^{-/-}* MDSCs to suppress T cell function and proliferation (136, 137).

4.1.2 Soluble factors

In addition to its role in forcing metabolic reprogramming, hypoxia induces the accumulation of extracellular adenosine. The ectonucleotidases CD39 and CD73 lead to the sequential dephosphorylation of extracellular ATP and their expression on tumour cells, immune cells, fibroblasts, endothelial cells, and

stromal cells is upregulated by hypoxia and TGFβ in the TME (138). Activated T effector cells can sense extracellular adenosine through the adenosine A2A receptor (A2AR), which triggers accumulation of intracellular cyclic adenosine monophosphate (cAMP) and limits TCR-mediated activation and expansion of effector T cells (139).

Numerous preclinical studies have demonstrated the potential advantages of inhibiting the adenosine pathway to augment the *in vivo* function of CAR-T cells (140–142). However, it is worth noting that the regulation of the adenosine pathway differs significantly between mice versus human. In mice, Tregs express CD39 and exhibit high levels of CD73 on their cell surface. This allows them to degrade ATP and generate adenosine, which has a dual impact: inhibiting effector T cells while enhancing the suppressive capabilities of Tregs (143, 144). Conversely, in the human T cell compartment, CD73 expression is primarily observed on the surface of naïve CD8 T cells and is only present in a small fraction of mature CD4 and CD8 memory T cells (145). Importantly, CD73 expression on Tregs is nearly absent, making the co-expression of CD73 with CD39 on Tregs a rare occurrence (146).

Transforming growth factor-β (TGFβ) is produced by multiple cells in the TME, and its expression is further enhanced by hypoxia (147). Due to its potent immunosuppressive effect and widespread presence in solid tumors, TGFβ has emerged as a popular target for cell therapy. Two commonly used strategies to modulate TGFβ activity involve the expression of dominant negative TGFβRII or targeted knockout (KO) of TGFβRII (148–155). The complex nature of TGFβ poses challenges for systemic therapies, as they

often result in a wide range of side effects. In contrast, intrinsic T cell approaches offer a more targeted solution that avoids these issues. However, it's important to note that testing the impact of TGF β inhibition in cell therapy often relies on xenograft mouse models. While these models provide valuable insights, they do not fully replicate certain aspects such as lymphopenic proliferation following LDC or the interaction with endogenous adaptive immune cells, which are known to be influenced by TGF β (156, 157). Therefore, the use of syngeneic or humanized murine models may be crucial to fully elucidate the effects of TGF β -based armoring strategies on cell therapies.

4.1.3 Inhibitory molecules

Engineering inhibitory molecules to bypass negative signaling is a promising approach to enhance CAR-T cell accumulation. Inhibition of the programmed death-1 (PD-1) checkpoint pathway through the expression of a dominant negative PD-1 receptor (PD-1 DNR) has shown efficacy in enhancing the antitumor function of mesothelin-targeted CAR-T cells in xenograft models of pleural mesothelioma with high PD-1 expression (158). PD-1 DNR expression demonstrated superior efficacy compared to systemic PD-1 blockade, which required multiple doses to achieve effectiveness. Additionally, fusion receptors combining the PD-1 ectodomain and CD28 endodomain, known as switch receptors, have also been shown to enhance the antitumor function of CAR-T cells in xenograft models (158–160).

In addition to PD-1, CAR-T cells have been equipped with a dominant negative receptor for tumor necrosis factor receptor superfamily member 6 (TNFRSF6), also known as FAS. In syngeneic tumor models, expression of FAS DNR in CAR- or TCR-engineered T cells protected the cells from FAS ligand (FASL)-induced apoptosis, leading to improved *in vivo* persistence and tumor eradication (161). Lymphocyte activation gene-3 (LAG-3) knockout CAR-T cells have also been tested in xenograft models (162). However, when exploring inhibitory molecules like CTLA-4, which requires interaction with its ligands CD80 and CD86 expressed on myeloid cells, the use of syngeneic or humanized models becomes crucial (163).

4.2 Accumulation - offensive strategies

4.2.1 Cytokines

Improving the effectiveness of CAR T-cell therapy hinges on strategies that can shape the immune regulatory milieu within tumor tissue. In this context, offensive armoring strategies play a significant role. One approach is to engineer CAR-T cells with a transgenic cytokine that can overcome the insufficient production of pro-inflammatory factors in the TME. The transgenic cytokine can provide autocrine stimulation to sustain the survival and amplification of CAR-T cells, as well as paracrine modulation of the endogenous immune cell environment, thereby reducing systemic toxicity and remodeling the TME.

IL-12 has been studied as a cytokine for armoring CAR T cells, and its antitumor efficacy has been demonstrated in xenograft and

immunocompetent syngeneic mouse models of ovarian cancer or hepatocellular carcinoma (164, 165). To further enhance the therapeutic potential of IL-12-secreting CAR T cells, Zhang et al. developed an NFAT-inducible membrane-bound IL-12, combining tumor-specific and inducible T-cell-mediated delivery with membrane-restricted localization (166). However, establishing a direct correlation between preclinical data and clinical toxicity remains challenging, as toxicity associated with IL-12 utilization is a primary concern. Variability in immune responses and toxicities, which occur in a dose-dependent manner, must be carefully considered in ongoing and future clinical trials (167).

IL-18 is another proinflammatory cytokine being explored in preclinical models and early clinical trials for cell therapy. Similar to IL-12, the efficacy of CAR T cells engineered to secrete IL-18 has been studied in xenograft and syngeneic mouse models (168, 169). Murine T cells expressing 19m28mz-P2A-mIL18 CAR were infused in C57BL/6 hCD19+/- mCD19+/- mouse model (169). This immune-competent, conditioning-dependent, tumor model uses systemic hCD19 modified EL4 (EL4[hCD19]) thymoma tumors infused into C57BL6 mice with a knockout murine CD19 (mCD19-/-), knock-in human CD19 (hCD19+/-) phenotype (C57BL6 [mCD19-/- hCD19+/-]) (170). These mice have restricted expression of one functional copy of the hCD19 gene in normal B cells, resulting in a retained immune-competent phenotype (170, 171). This model showed that IL-18 secreting CAR-T cells are efficacious in the absence of lymphodepleting chemotherapy. IL-18 secreting CD19 CAR-T demonstrated encouraging efficacy in an early clinical trials or the treatment of patients with relapsed/refractory B-cell non-Hodgkin lymphomas (NHL) or chronic lymphocytic leukemia (CLL) (NCT04684563) (172).

IL-15 is a pleiotropic cytokine that plays a role in innate and adaptive immune cell homeostasis and peripheral immune function. CD19 CAR T cells, IL-13R α 2 CAR T cells, and GD2 CAR T cells engineered to secrete IL-15 have shown increased expansion and *in vivo* anti-tumor activity in xenograft mouse models of Burkitt lymphoma, glioma, and metastatic neuroblastoma, respectively (173–175). However, there are concerns about prolonged exposure to IL-15, as IL-15 transgenic mice developed leukemia with a T-cell or NK-cell phenotype (176). The use of IL-15 to enhance the performance of CAR T cells will be further discussed in the section on longevity.

4.2.2 Direct targeting of immunosuppressive populations

Enhancing the accumulation of GML in the TME can be achieved by directly targeting and eliminating immunosuppressive cell populations, as discussed earlier for CAFs and MDSCs. Tumor-associated macrophages (TAMs) are another important target in cancer treatment due to their abundance in tumors and association with poor prognosis (177). One example of targeting TAMs is the use of CAR-T cells directed against CD123, which is expressed on both Hodgkin lymphoma (HL) cells and TAMs within the TME. These CAR-T cells recognize and eliminate both HL cells and TAMs, overcoming immunosuppression and exhibiting sustained clearance in xenograft models of progressive Hodgkin lymphoma. In mouse

models, rechallenging with the same tumor cell line resulted in controlled tumor growth, suggesting a protective memory response (178). However, caution should be exercised when interpreting long-term survival and persistence of T cells in immunocompromised mice, considering the role of homeostatic cytokines, potential compensatory mechanisms, and the broader context of human immunology.

Another approach involves equipping CAR-T cells with an additional CAR targeting FR β , which is specifically expressed on immunosuppressive TAMs (114). Specific targeting and elimination of TAMs was addressed in the previous section as a means of improving infiltration into solid tumors, however, this strategy can have benefits in repolarizing the suppressive TME. In syngeneic murine tumour models of C57BL/6 mice bearing ID8 RFP-*fluc* tumors (which lack mFR β expression), transfer of CAR-T cells following cyclophosphamide preconditioning selectively eliminated FR β + TAMs, recruited pro-inflammatory monocytes and tumor-specific CD8+ T cells, and reduced tumor growth. This targeting approach shows promise in modulating TAMs and enhancing the antitumor immune response.

Regulatory T cells (Tregs) can also be targeted by cellular immunotherapies. However, systemic blockade of Tregs has led to life-threatening autoimmune side effects in patients due to depletion of CD25+ effector T cells. While there is early *in vitro* proof-of-concept showing that NK-92 cells expressing an anti-CD25 CAR can target Tregs, *in vivo* data are lacking, and concerns about on-target, off-tumor toxicity remain (179). *In vivo* studies in syngeneic models have shown that an immunotoxin targeting CD25 can selectively kill intratumoral Tregs while boosting endogenous immunity (180). Although incorporating such an approach into GML-based therapy is tempting, further studies are required to better understand the risk of on-target, off-tumor toxicities.

5 Longevity

One of the unique characteristics of GML which sets it apart from traditional therapeutics, is its ability to persist in the host for months or even years. This prolonged persistence enables GML to potentially drive long-term disease remission and provide ongoing immunosurveillance against residual tumor cells (Figure 5A). The potential for long-term persistence is becoming increasingly evident over time, as seen in patients with leukemia who have experienced 10 or more years of clinical remission with ongoing evidence of CD19 CAR-T cell function (181). While studies have demonstrated long-term engraftment of memory CD8 cells in mice through serial transfer (182), there is currently no known research on the persistent functional exposure of GML in mice.

Long-term engraftment of human T cells in NOD-scid IL2R γ null (NSG) mice is complicated by xenograft-versus-host (xGvHD) immune-reactivity. This immune reactivity arises from both the MHC mismatch between human and mouse and the compromised immune system of the NSG mice, which is unable to reject the human T cell graft. Consequently, long-term engraftment studies in NSG mice may be confounded by toxicity that is specific

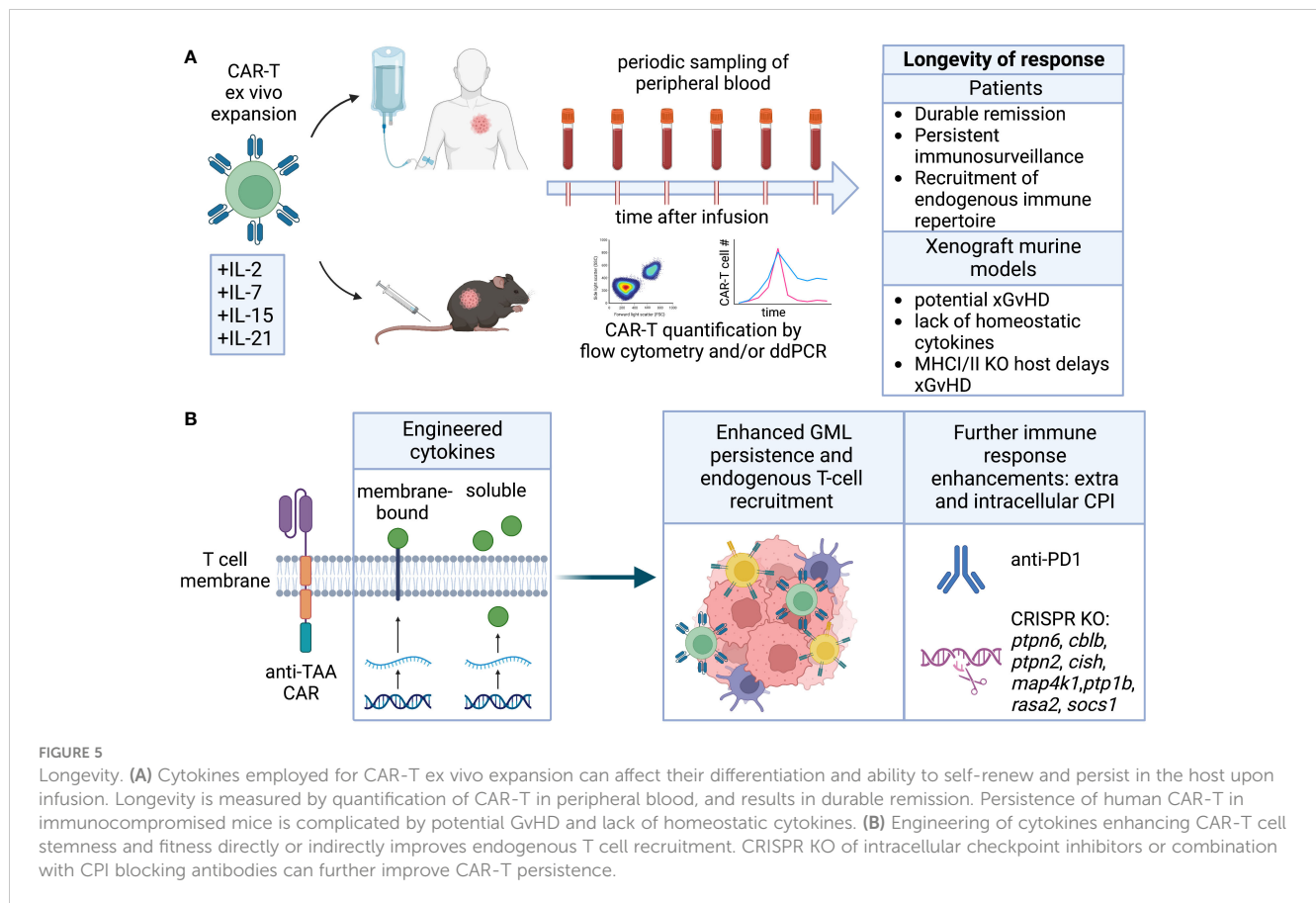
to the model and may not accurately represent autologous GML therapy in humans. While NSG mice with Class I and Class II MHC knock-out can attenuate this toxicity (183, 184), they remain severely immunocompromised and may still generate xGvHD responses through the interaction of non-classical MHC molecules (e.g., CD1) or stress molecules (MICA/B) (185). Therefore, conducting short-term studies (~30 days) or using mouse models that can predict the consequences of long-term engraftment and endogenous immune conditioning and repertoire spreading may be more feasible and informative. Immunocompetent or syngeneic models, on the other hand, are not often used to study persistence due to challenges with T cell engineering, expansion, and the lack of models with slow tumor growth and endogenous antigen expression. Nonetheless, there are examples suggesting that transduced and expanded murine GML can be effective and persistent, and further development of these models is warranted (186).

Modifications aimed at enhancing GML longevity encompass various approaches, including alterations to intracellular domains, introduction of cytokines through genetic or pharmacological means, and deletion of intracellular inhibitory proteins that limit lymphocyte function, cytotoxicity, and persistence. These strategies not only promote the longevity of GML but can also be utilized to recruit endogenous lymphocytes, thereby extending the durability of the therapeutic response (Figure 5B).

5.1 Longevity – co-stimulatory domains

Early clinical trials with CD19 CAR T cells demonstrated that incorporating the 4-1BB co-stimulatory domain in the intracellular domain (ICD) of second-generation CARs, referred to as BB ζ , resulted in enhanced persistence compared to CARs containing the CD28 co-stimulatory domain (CD28 ζ). The enhanced persistence of BB ζ CAR-T cells was attributed to 4-1BB's ability to activate TRAF/NF- κ B signaling, promoting fatty acid oxidation and mitochondrial biogenesis, which contrasted with the predominantly glycolytic signaling downstream of CD28 (187). Clinical data showed that CD28 ζ CAR-T persistence rarely exceeded 42 days (188, 189), while BB ζ CAR-T persistence often exceeded 1 year in patients achieving complete responses (190).

Subsequent investigations consistently revealed distinct metabolic responses between CD28 ζ and BB ζ CAR-T cells, with CD28 ζ CAR-T cells exhibiting a “fast burn” metabolic response driven by PI3K-induced aerobic glycolysis, and BB ζ CAR-T cells displaying a “slow burn” oxidative metabolism primarily fueled by fatty acid breakdown, aligning with 4-1BB's role in T memory development and longevity (191). These findings indicated that the design of the CAR ICD can directly influence its persistence. Researchers have since developed various versions of second-generation CARs containing additional costimulatory domains such as ICOS and OX40 (192, 193), as well as third-generation CARs, aiming to enhance the balance between anti-tumor cytotoxicity and persistence (194, 195). While these versions have demonstrated strong activity in mouse xenograft tumor models using NSG mice, clinical evidence of persistence superior to second-generation BB ζ CAR-T cells in humans is yet to be established (196).



Although preclinical mouse models cannot fully replicate the persistence of engrafted T cells observed in humans, studies comparing BB ζ and CD28 ζ CAR-T cell performance in standard xenograft models have shown similar tumor-clearing effects between the two at high doses. However, at lower doses, BB ζ CAR-T cells demonstrated functional superiority, indicating better memory conversion and resistance to the stress of low cell dosing (197). While mouse models can indirectly predict the longevity and persistence of GML based on the design of the CAR's intracellular domain (ICD), it is essential to acknowledge the limitations of these models in fully replicating the long-term engraftment and endogenous immune-conditioning observed in humans.

5.2 Longevity – role of cytokines

In clinical trials for TIL and TCR-T therapy, IL-2 is commonly used to support the function and persistence of the adoptively transferred cells. However, in the case of CAR-T therapy, IL-2 is rarely used to enhance CAR-T persistence. This may be attributed, in part, to the CAR-T cells' ability to produce paracrine IL-2 through the engagement of co-stimulatory CAR intracellular domains (ICD). Additionally, IL-2 is avoided in GML therapy due to the toxicities associated with higher doses needed to maintain the anti-tumor function of transferred T cells (198).

Recent advancements have led to the development of orthogonal versions of IL-2 that can be genetically engineered into CAR-T cells, promoting expansion and longevity with limited systemic toxicities (199, 200). By engineering CD19 CAR-T cells to express mutated IL-2R β receptors, which can only be activated by cell-encoded, mutated orthogonal IL-2 (ortho-IL-2), selectivity can be achieved without encountering the negative effects of IL-2 binding on wild-type T or NK cells. Two separate groups have described this mutant IL-2 "orthokine" pair and demonstrated its effectiveness in combination with suboptimal doses of CAR-T cells, leading to CAR-T expansion, tumor reduction, and persistence without the need for repeated CAR-T infusions. Interestingly, in preclinical xenograft models using NSG mice, higher doses of ortho-IL-2 were found to induce weight loss, although this toxicity was determined to be unrelated to xGvHD based on studies with TCR knockout mice. The authors speculated that the observed toxicity, which occurred at doses much higher than those required for tumor regression, was target-dependent, as weight loss and toxicity were observed in mice bearing NALM6 tumors but not in tumor-deficient mice (201). A human clinical trial testing the IL-2 orthokine and CAR-T pairing (STK-009) is currently enrolling patients with relapsed or refractory CD19 positive hematologic malignancies to evaluate the combination of autologous CD19 CAR-T cells with orthogonal IL-2 (201). This trial aims to assess the safety and efficacy of this approach in a clinical setting.

The differentiation status of T cells directly influences their longevity and antitumor activity. T cells with a stem-like phenotype, characterized by enhanced self-renewal and proliferation capacity, are associated with better clinical responses (202–207). Manipulating the differentiation status of T cells is a commonly explored strategy to improve the quality and efficacy of GML. Common-gamma chain cytokines such as IL-7 and IL-15 are frequently used in cell therapy to either promote a less differentiated product during the expansion stage or engineered into GML as an armoring strategy for *in vivo* enhancement (207).

IL-15 plays a crucial role in the homeostasis and development of CD8+ T cells by inhibiting activation-induced cell death (AICD) and upregulating antiapoptotic mediators like Mcl1 and Bcl-2 (208). IL-15-secreting CAR-T cells exhibited a less differentiated phenotype compared to unarmored CAR-T cells in a syngeneic model of subcutaneous B16 melanoma. They also showed reduced expression of PD1, prolonged persistence, and superior cellular activity (48). In another study, IL-15-armored CAR-T cells completely prevented tumor relapse in a xenograft model but were associated with severe liver toxicity and a GvHD score (209). Clinical studies have also reported IL-15 administration-related toxicity in cancer patients (210).

To mitigate IL-15 toxicity, researchers generated CD19 CAR-T cells that overexpressed both IL-15 and IL-15 receptor alpha. This strategy successfully blocked toxicity while maintaining the persistence and anti-tumor activity of CAR-T cells induced by IL-15 (209). However, the observed toxicity in mice is a subject of debate, as another study found that CD19 CAR-T cells expressing membrane-bound chimeric IL-15 delayed leukemia development, exhibited sustained resistance after tumor clearance, and generated long-lived TSCM cells without any associated toxicity (211).

Interleukin-7 (IL-7) plays a crucial role in enhancing the homeostasis and survival of memory and naïve T cells by upregulating Bcl-2 and repressing proapoptotic markers (212). Several studies have demonstrated that *in vitro* expansion of CAR-T cells with IL-7 leads to a higher frequency of cells exhibiting a memory stem cell phenotype (33). These cells retained a less differentiated phenotype and exhibited increased resistance to dysfunction upon repetitive encounters with antigens.

Early reports showed that constitutive expression of IL-7 enhanced the *in vivo* efficacy of CD19 CAR-T cells in a xenograft model of leukemia. However, it did not improve long-term persistence compared to CAR-T cells expressing IL-2 or IL-15 (213). IL-7-expressing CLDN18.2 CAR-T cells demonstrated increased proliferation, decreased apoptosis, and lower expression of exhaustion markers compared to unarmored CAR-T cells (214). However, IL-7 signaling specifically suppresses IL7R α transcription as a homeostatic regulatory mechanism, promoting the survival of the maximum possible number of T cells given the available IL-7 (215).

To overcome the potential loss of IL-7 responsiveness, IL-7R α was engineered into EBV-CTLs, resulting in an efficient response to IL-7 and *in vivo* activity in a xenograft model (216). Similarly, the introduction of a constitutively active IL-7 receptor (C7R) improved the *in vivo* antitumor activity of GD2-CAR-T cells in a

xenograft model of metastatic neuroblastoma and EphA2-CAR-T cells in an orthotopic xenograft model of glioblastoma (217). It is important to note that GD2-CAR-T cells expressing C7R are currently being tested against relapsed or refractory neuroblastoma and other GD2-positive cancers (NCT03635632). Although autonomous or antigen-independent proliferation was not reported in this study, activating mutations of IL7R are present in 10% of pre-T-cell acute leukemias, raising concerns about unwanted proliferation associated with this approach.

Interleukin-21 (IL-21) is a crucial cytokine involved in regulating the function of CD8+ T cells and has emerged as a potential target for cancer immunotherapy. IL-21 enhances CD8+ T cell activity by promoting their proliferation, differentiation, and increasing the expression of cytotoxic molecules like perforin and granzyme B (218). Additionally, IL-21 indirectly enhances anti-tumor activity by promoting antibody production by B cells, aiding in targeting and killing tumor cells (219).

Recent studies have demonstrated the effectiveness of IL-21 in improving the anti-tumor effect of CAR-T cells. GPC3 CAR-T cells expressing IL-15 and IL-21 exhibited significantly greater anti-tumor efficacy in mice compared to CAR-T cells without IL-21 expression (220). These IL-21 expressing CAR-T cells are currently being evaluated in clinical trials for the treatment of hepatocellular carcinoma (HCC) (NCT02932956 and NCT02905188). Another study utilized NFAT-inducible secreted IL-21, which demonstrated increased anti-tumor efficacy in NSG mice and resistance to immune suppression induced by chronic lymphocytic leukemia cells (221). Engineered switch receptors have also been explored to provide IL-21 signaling. Wang et al. tested a receptor composed of the IL-4 ectodomain and the IL-21 endodomain and compared it to a receptor with the IL-7 endodomain (222). The IL-4/IL-21 inverted receptor conferred enhanced *in vivo* efficacy to GPC3 CAR-T cells against a xenograft model expressing varying levels of GPC3, compared to unarmored CAR-T cells or those with the IL-4/IL-7 inverted receptor. The study also observed a higher number of CD3+ T cells in the peripheral blood of mice receiving cells expressing the IL-4/IL-21 inverted receptor, indicating improved *in vivo* persistence (222). However, as previously mentioned, conclusions about *in vivo* persistence in xenograft models should be interpreted with caution.

Another interesting approach is the incorporation of a motif for STAT3 recruitment at the C-terminus of CD3 ζ , enabling IL-21 signaling upon CAR engagement (223). CD19 CAR-T cells expressing this chimeric receptor demonstrated enhanced proliferation and cytokine polyfunctionality compared to control CAR-T cells in xenograft models of NALM6 human leukemia cells and subcutaneous CD19+ tumors, suggesting a key role for STAT3 in suppressing terminal differentiation of T cells (223–225).

5.3 Longevity – blocking inhibitory mechanisms

GML therapy can benefit from strategies that overcome co-inhibitory mechanisms, which naturally restrict long-term

proliferation of T cells. One approach is to induce intra-tumoral production of checkpoint inhibitor (CPI) antibodies, antibody-like fragments, or soluble PD1. Several studies have reported the use of CAR-T cells engineered to secrete constitutive or inducible CPI in mouse models (226–228). While these preclinical studies in xenograft mouse models have shown improved CAR-T function, such as enhanced expansion, cytolytic activity, or effector function, similar enhancements have not yet been observed in human clinical trials (229, 230). It is worth noting that the human trials utilized CPI in combination with CD19 CAR-T for CPI-insensitive indications, leaving open the possibility of using CPI-secreting CAR-T for CPI-sensitive tumors. However, since multiple versions of CPI antibodies are available as co-therapy, it remains unclear whether there are advantages or disadvantages to driving their expression from the GML itself. Further research is needed to elucidate the potential benefits and drawbacks of this approach.

Additional T cell checkpoints can hinder the expansion of GML, although their impact on longevity remains uncertain. Knocking down CTLA-4 expression using shRNA did not enhance the function or persistence of CD19 CAR-T cells based on 28 ζ , but co-expression of CD80 alongside a first-generation CAR containing CD3 ζ significantly increased expansion when CTLA-4 was knocked down (231). Currently, there are no known human clinical trials combining the CTLA-4 antibodies ipilimumab or tremelimumab with CAR-T or TCR-T. Trials testing CAR-T cells that produce CTLA-4 and PD1 antibodies against MUC1, EGFR, and MSLN are enrolling, but no preclinical or clinical data have been reported (NCT03179007, NCT03182816, NCT03182803). Blockade of LAG3 using CRISPR/Cas-mediated knockout did not show benefit in *in vitro* preclinical models but was not tested in mice (162). On the other hand, blockade of PD1 and Tim3, either alone or in combination, improved the activity of CD123-directed CAR-T cells in xenograft models of AML (232). Other T cell checkpoints include soluble molecules such as TGF β and adenosine, which, as discussed in the previous section, can regulate both GML accumulation and longevity. Moreover, intracellular T cell checkpoints have been validated through gene deletion or expression of dominant-negative receptors (DNR), revealing additional mechanisms that can limit GML expansion. Several molecules, including SHP-1, CBLB, PTPN2, CISH, HPK1, PTP1B, RASA2, and SOCS1, have been identified as intrinsic checkpoints that can constrain T cell effector function, accumulation, and expansion (233–240). While targeting these intrinsic checkpoints individually is an active area of research, combinations of checkpoint deletions have also emerged (241). For instance, double knockout (DKO) of both regnase-1 and roquin-1 greatly increased T cell effector function, accumulation, and expansion in xenograft models compared to single knockout alone. However, the DKO also resulted in uncontrolled lymphoproliferation and toxicity in some mice. This finding emphasizes the need to understand the interaction of intracellular checkpoints in GML and develop mechanisms to prevent their uncontrolled expansion in patients, as unregulated persistence can have undesirable consequences.

6 Discussion

“All models are wrong, but some are useful” – George E.P. Box.

GML have transformed the therapeutic landscape for multiple B cell malignancies and are making steady progress into additional tumor types and even autoimmune diseases. As with any evolving therapeutic class, GML are undergoing continual modifications to improve their activity and safety profiles in order to broaden their applicability. As the diseases that can be targeted with GML are theoretically unlimited, the solution set for therapeutic design will inevitably diverge from those used for the treatment of B cell malignancies. In order for these designs to be validated and implemented, preclinical models are required.

Until robust three-dimensional or organotypic models that can recapitulate human tumor and normal tissue biology are readily available, GML development will continue to be dependent on the mouse as the default preclinical model to understand safety and efficacy profiles before human clinical trials. Mouse models for GML are simultaneously useful and distracting. They can be very useful to understand on-target activity and efficacy, acute GML expansion and pharmacodynamics, and proximal effector functions such as cytokine release. However, they are distracting in that they miss key aspects of GML challenges such as off-tumor toxicities, representative secondary cytokine secretion from myeloid, epithelial, or stromal cells, and control of metastatic and heterogenous disease similar to human tumors. Additional artifacts include xenograft-versus-host reactivity of human T cells engrafted in NSG mice, lack of validation of fully murinized GML designs and protocols, differences in lymphodepletion regimens, and studies in pathogen-free facilities that do not account for the influence of natural indigenous gut microbiota.

Due to the varied and unpredictable behavior of GML between mice and humans, a framework called “DIAL” has been developed to compartmentalize and study individual GML behaviors. The framework allows for understanding of aspects of the cell journey that can be studied and optimized in isolation. For example, distribution studies which require vaccine-like cell priming can be studied using immunocompetent syngeneic mouse models while human GML manufacturing optimization may be best studied in NSG mice. Infiltration can be explored using genetically engineered mouse models that mimic tumor fibrosis (242), and early passage patient-derived xenograft (PDX) models in NOG or NSG mice might retain sufficient stroma to prevent immune-infiltration and exclude unmodified GML (243). PDX models can likewise be used to study accumulation, where native human tumor architecture, soluble factors, and hypoxia can affect GML survival. Likewise, syngeneic models can be deployed to complement the PDX model to capture immunosuppressive facets of TME that prevent accumulation. Strategies to enhance GML longevity can be limited due to technical factors such as development of xGvHD (NSG mice) and the challenges of optimizing murine GML manufacturing or treating rapidly growing tumors in most syngeneic models. Still, certain cytokines and intracellular designs have the potential to improve GML activity in NSG mice at

suboptimal doses, which can serve as surrogates for extended longevity. Longevity of GML response can also be demonstrated using tumor rechallenge studies in immunocompetent mice, demonstrating that GML-induced long-term immunity can be acquired via the expansion of endogenous anti-tumor T cells (244). These studies provide rationale for modification of GML with membrane bound cytokines or checkpoint inhibitors to bring about long-lasting remissions against heterogeneous tumors.

Following the success of CAR and TCR-T therapies in multiple tumor types, next-generation approaches will incorporate increasing complexity through genetic editing and engineering to augment GML functions. As each of these functions require validation through mechanistic and safety data, extensive preclinical testing in animals will be highly warranted if not required. While mice remain the most popular animal model for preclinical GML testing, canine and non-human primate (NHP) studies have also been conducted. Studies in non-murine species facilitate the study of unique GML attributes against tumors; canines present with spontaneous and heterogeneous tumors and are pathogen-exposed, as are several NHP species that provide the most genetically similar model to human, and present the most relevant model to recapitulate the consequences of LDC as well as allowing longitudinal sampling (245). Until non-murine models are more consistently used and understood, however, a mixture of murine models to deconstruct multiple GML functions will still be preferred. Future development of complex GML may benefit from co-evolution of efficient and specific murine and human gene-editing tools and vectors to more accurately predict these functions preclinically in order to decrease drug development cycle times, and improve efficacy and safety of the next wave of cell-based therapeutics.

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Conflict of interest

All authors are employees of AstraZeneca, PLC and have financial interest in the company.

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