

Review

Inhibiting the Unconventionals: Importance of Immune Checkpoint Receptors in $\gamma\delta$ T, MAIT, and NKT Cells

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Simple Summary: All conventional major histocompatibility complex (MHC)-restricted T cells transiently express immune checkpoint/inhibitory receptors (ICRs) following activation as a means to counter-regulate overactivation. However, tumors promote chronic ICR expression rendering T cells chronically unresponsive or “exhausted”. Checkpoint inhibitor (CPI) therapy targets and blocks ICRs, restoring T cell activation and anti-tumor immunity. However, CPI therapy often fails, partly because of the tumor’s many abilities to inhibit MHC-driven T cell responses. In this regard, our immune system contains an arsenal of unconventional non-MHC-restricted T cells, whose importance in anti-tumor immunity is rapidly gaining momentum. There is currently little knowledge as to whether unconventional T cells can get exhausted and how CPI therapy affects them. In this article we review the current understanding of the role of ICRs in unconventional T cell biology and discuss the importance of targeting these unique immune cell populations for CPI therapy.



Citation: Catafal-Tardos, E.; Baglioni, M.V.; Bekiaris, V. Inhibiting the Unconventionals: Importance of Immune Checkpoint Receptors in $\gamma\delta$ T, MAIT, and NKT Cells. *Cancers* **2021**, *13*, 4647. <https://doi.org/10.3390/cancers13184647>

Academic Editor: Cristina Bottino

Received: 30 July 2021

Accepted: 13 September 2021

Published: 16 September 2021

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Abstract: In recent years, checkpoint inhibitor (CPI) therapy has shown promising clinical responses across a broad range of cancers. However, many patients remain unresponsive and there is need for improvement. CPI therapy relies on antibody-mediated neutralization of immune inhibitory or checkpoint receptors (ICRs) that constitutively suppress leukocytes. In this regard, the clinical outcome of CPI therapy has primarily been attributed to modulating classical MHC-restricted $\alpha\beta$ T cell responses, yet, it will inevitably target most lymphoid (and many myeloid) populations. As such, unconventional non-MHC-restricted gamma delta ($\gamma\delta$) T, mucosal associated invariant T (MAIT) and natural killer T (NKT) cells express ICRs at steady-state and after activation and may thus be affected by CPI therapies. To which extent, however, remains unclear. These unconventional T cells are polyfunctional innate-like lymphocytes that play a key role in tumor immune surveillance and have a plethora of protective and pathogenic immune responses. The robust anti-tumor potential of $\gamma\delta$ T, MAIT, and NKT cells has been established in a variety of preclinical cancer models and in clinical reports. In contrast, recent studies have documented a pro-tumor effect of innate-like T cell subsets that secrete pro-inflammatory cytokines. Consequently, understanding the mechanisms that regulate such T cells and their response to CPI is critical in designing effective cancer immunotherapies that favor anti-tumor immunity. In this Review, we will discuss the current understanding regarding the role of immune checkpoint regulation in $\gamma\delta$ T, MAIT, and NKT cells and its importance in anti-cancer immunity.

Keywords: immune checkpoint receptors; cancer; immunotherapy; $\gamma\delta$ T cells; MAIT cells; NKT cells

1. Introduction

Although the term “T lymphocyte” is synonymous with adaptive immune responses generated by B and CD4⁺ or CD8⁺ alpha beta ($\alpha\beta$) T cells, over the last 20 years or so, an increasing number of T cell populations have been proven to have innate-like properties. The unconventional innate-like T cells can be $\alpha\beta$ or gamma delta ($\gamma\delta$) in origin with either

invariant or diverse T cell receptors (TCR), which often are not major histocompatibility complex (MHC)-restricted and recognize non-peptide antigens either via direct interactions or in the context of non-polymorphic antigen-presenting molecules, such as CD1 and MR1 [1]. Innate TCRs thus have been shown to interact with lipids, glycolipids, vitamin derivatives, phosphoantigens, butyrophilins, and stress ligands to name a few, inducing an immediate immune response [1–5]. Such TCR-antigen interactions are reminiscent of how innate immune cells recognize pathogen and danger associated molecular patterns (PAMPs and DAMPs). In addition to their unique TCRs, all innate-like T cell subsets can respond directly to cytokines independent of antigen or TCR engagement, exemplifying their non-adaptive immune role [5–7]. The most well-studied unconventional T cell subsets include $\gamma\delta$ T cells, mucosal associated invariant $\alpha\beta$ T cells (MAIT) and natural killer $\alpha\beta$ T cells (NKT). Innate-like T cells and their TCRs are conserved in evolution, appearing in bony and cartilaginous fish and amphibians [8]. Jawless fish, such as lamprey, have T-like cells that resemble both $\alpha\beta$ and $\gamma\delta$ T cells [9], indicating that diversification of innate-like T cells occurred before the emergence of recombinase activating genes and adaptive immunity. Thus, we have at our disposal a unique army of T cells, whose function evolved over millions of years to be rapid and targeted at the same time.

However, unchecked cellular activation and proliferation come at a price, often in the form of tissue damage, which may perpetuate as a chronic inflammatory disease. One of the mechanisms that immune cells have evolved in order to counteract their own efficiency is the expression of inhibitory, or immune checkpoint receptors (ICRs) as most commonly referred to. Most of what we know about the immunological importance of ICRs stems from work done in conventional $CD4^+$ and $CD8^+$ T cells, while detailed biological insight regarding innate leukocytes or unconventional T cells is not as extensive. However, recent data suggest a critical role of the ICR PD-1 (programmed death-1) in myeloid cells [10,11], while evidence from mouse and human studies supports a potential important role for different ICRs in innate-like T cell subsets.

After a brief overview on basic ICR biology and exhaustion, we will discuss why we think studying ICR biology in unconventional innate-like lymphocytes would be clinically beneficial. We will later summarize the current state-of-the-art regarding the role of ICRs in innate-like T cell biology. We would like to emphasize that upon researching the literature for this review article we discovered that there are surprisingly few studies investigating the importance of ICRs in unconventional T cells. We have therefore selected to discuss ICRs for which there was substantial information on their potential role MAIT, NKT, or $\gamma\delta$ T cells.

2. Immune Checkpoint Receptors and the Path to Exhaustion

Most of the well-studied ICRs, such as PD-1 (programmed cell death-1), CTLA-4 (cytotoxic T lymphocyte antigen-4) or BTLA (B and T lymphocyte attenuator) are members of the immunoglobulin superfamily (IgSF); however, some can be C-type lectin-like receptors [12]. They are expressed on the surface of cells either constitutively (e.g., BTLA) or are induced soon after activation (e.g., PD-1) and in T cells often prevent overt proliferation and cytokine production [12–14]. At the molecular level, the majority of ICRs contain intracellular immunoreceptor tyrosine inhibitory or switch motifs (ITIM or ITSM), which can recruit the Src-homology-2 phosphatases 1 and 2 (SHP-1 and SHP-2) [12,15]. Upon ligand binding, the ITIM/ITSM motif will be phosphorylated, resulting in the recruitment and activation of SHP-1 and SHP-2, which in turn will initiate a cascade of de-phosphorylation events, counteracting therefore ongoing molecular events that promote cellular activation [12,14]. In addition to direct signaling, ICRs can inhibit cell activation by competing for ligands that otherwise bind activating receptors [12]. This is the main pathway by which CTLA-4 inhibits T cell activation. Hence, CTLA-4 binds with high affinity the B7 ligands CD80 and CD86 on the surface of antigen presenting cells and can thus outcompete CD28 [16]. The CD28-CD80/86 interaction is critical for T cell co-stimulation and its disruption by CTLA-4 shuts down T cell mediated responses. A more intricate inhibitory function has

been shown for BTLA, whose only ligand is the tumor necrosis factor (TNF) superfamily receptor HVEM (herpes virus entry mediator) [17]. *Trans* binding of HVEM induces SHP1/2-mediated signaling downstream of BTLA [17]. However, BTLA and HVEM are co-expressed on T cells and can exist in a *cis*-complex, which restricts HVEM from binding its other ligands CD160 and LIGHT, suppressing thus HVEM-driven activation of the canonical nuclear factor kappa-B (NF- κ B) pathway [18–20].

Since expression of ICRs and their ligands is driven by stimulation, inhibitory signals will persist for as long as the antigen is around and there is ongoing immune activation. This creates an equilibrium between T cell activation and T cell inhibition, allowing a regulated response and avoiding potential autoimmune reactions (Figure 1A). However, during chronic antigen persistence, the balance between activation and inhibition may break depending on the nature of the antigenic stimulus and the microenvironment where the T cell is recruited to. Hence, in autoimmune diseases, chronic antigenic stimulation and a microenvironment overwhelmed by pro-inflammatory cytokines favors chronic activation, leading to T cell mediated tissue destruction (Figure 1B). In contrast, in chronic viral infections and in many solid cancers, the persistent antigen is accompanied by immunosuppressive factors such as type I interferons (IFN), interleukin(IL)-10 and transforming growth factor- β 1 (TGF- β 1), shifting the balance towards inhibition [22] (Figure 1C). Consequently, the T cell is overcome by ICR-mediated negative signals, leading to its functional exhaustion and inability to fight transformed or infected cells.

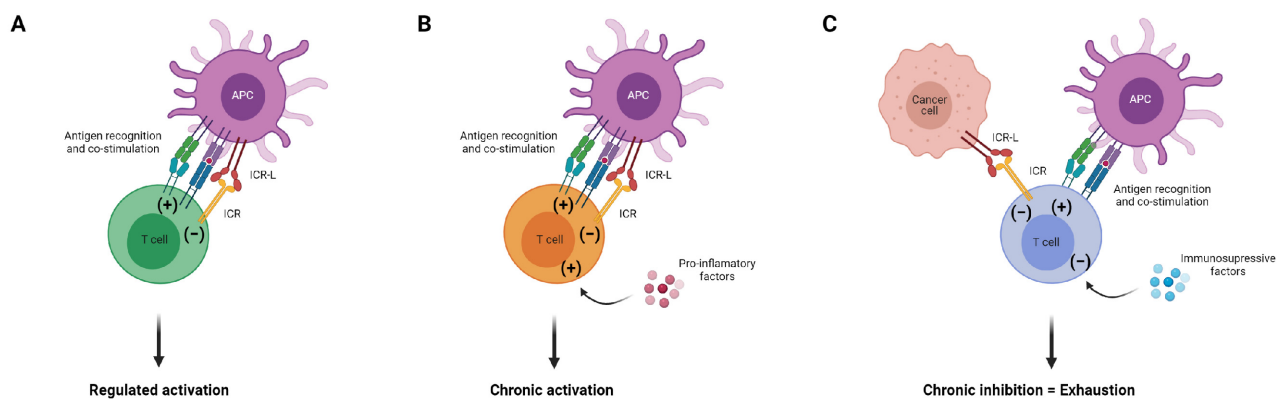


Figure 1. Balance between T cell activation and T cell inhibition. (A) Under normal conditions, the inhibitory signals mediated by ICR ligation down-regulate T cell responses to prevent immunopathology and autoimmunity. (B) During chronic inflammation, T cells are overwhelmed by several activation signals, overcoming ICR inhibition and tipping the balance towards constitutive T cell activation. (C) Despite the presence of antigen, in chronic viral infection and cancer, the immunosuppressive factors in the microenvironment break the equilibrium towards chronic T cell inhibition or exhaustion. APC: antigen-presenting cell; ICR: immune checkpoint receptor; ICR-L: immune checkpoint receptor ligand.

3. Checkpoint Inhibitor Therapy: From Conventional to Unconventional

Reversing T cell exhaustion in cancer is the goal of checkpoint inhibitor (CPI) therapy. CPIs are monoclonal antibodies, which are designed to block ICRs on the surface of exhausted CD8⁺ T cells, releasing them thus from chronic inhibition, and restoring anti-tumor functionality [23] (Figure 2A). This therapeutic strategy has become a gold standard for many immunotherapies and for some cancers, such as melanoma, and may result in prolonged survival (2–3 years) for approximately 20–30% of patients [24]. Thus far only CPIs that target the PD-1 and CTLA-4 pathways have been approved for clinical use and include the anti-CTLA4 antibody ipilimumab, the anti-PD-1 antibodies nivolumab, pembrolizumab, cemiplimab, and the anti-PDL-1 antibodies atezolizumab, avelumab, and durvalumab [25].

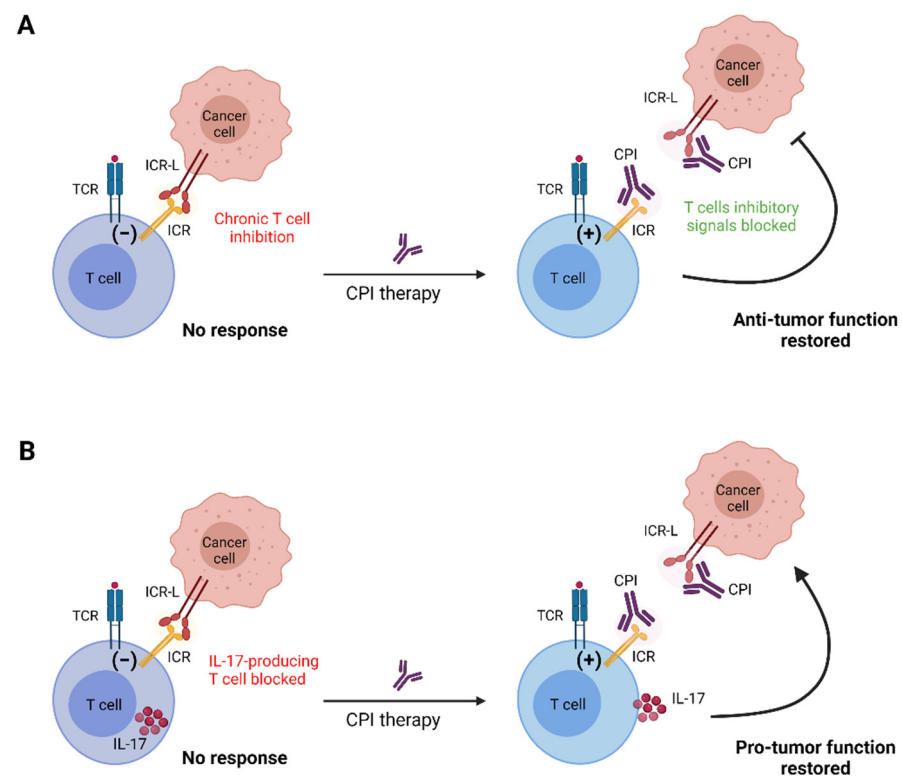


Figure 2. Checkpoint inhibition therapy. (A) ICR signaling in the tumor microenvironment inhibits T cell responses, thus contributing to tumor immune escape; CPI administration blocks ICR/ICR–L interactions, restoring T cell antitumor responses. (B) ICR-mediated inhibition of IL–17-producing T cells blocks their pro-tumor activity; CPI therapy targeting these cells will promote tumor growth. CPI: checkpoint inhibitor; ICR: immune checkpoint receptor; ICR–L: immune checkpoint receptor ligand; IL–17: interleukin 17; TCR: T cell receptor.

Despite the frequently positive clinical results, many patients do not respond to CPI therapy [26], illustrating the need to better understand the underlying cellular and molecular mechanisms that lead to T cell exhaustion in order to improve efficacy. In this regard, resistance to CPI therapy is most often associated with impaired generation of tumor-specific primary and memory CD8⁺ T cells [27]. This is owing to the numerous ways by which the tumor microenvironment (TME) can suppress MHC-restricted antigen-driven immunity, and substantial efforts are underway in order to overcome this [27,28]. Most of these efforts are directed towards improving antigen recognition by CD8⁺ T cells [27,28]. However, in order to win the race against cancer, it is our view that efforts to overcome resistance to immunotherapy should expand in immune cell populations other than conventional T cells, especially given the fact that ICRs are expressed by most leukocytes. Excellent work for example demonstrated that the targeting of monocytes and macrophages could restore successful anti-tumor immunity [10,11,29]. We reason that it will be beneficial for CPI therapies to begin targeting non-MHC restricted anti-tumor T cells, such as $\gamma\delta$ T, NKT, or MAIT cells. In this regard, it is critical to consider that innate-like T cell subsets have potent IL-17-producing capacities, which support tumor growth (see review by Paget and colleagues and Neubauer and colleagues in this issue). We and others have shown before that lack of ICR signaling can promote IL-17-driven $\gamma\delta$ T cell immunity [30,31] and that pro-inflammatory cytokines can induce the expression of various ICRs on the surface of $\gamma\delta$ T cells [32]. Furthermore, CPI therapy is frequently associated with adverse effects resembling various autoimmune disorders [33]. Given the potential rapid innate activation of unconventional T cells by ICR blockade, it is plausible that these cell subsets are actively involved in mediating such adverse effects. It will therefore be important to avoid that CPI therapy unleashes IL-17-producing T cells, which

will favor tumor growth (Figure 2B) or induce side effects (Figure 3). To achieve this, it is important that we study and understand the biology of different ICRs in unconventional innate-like T cells.

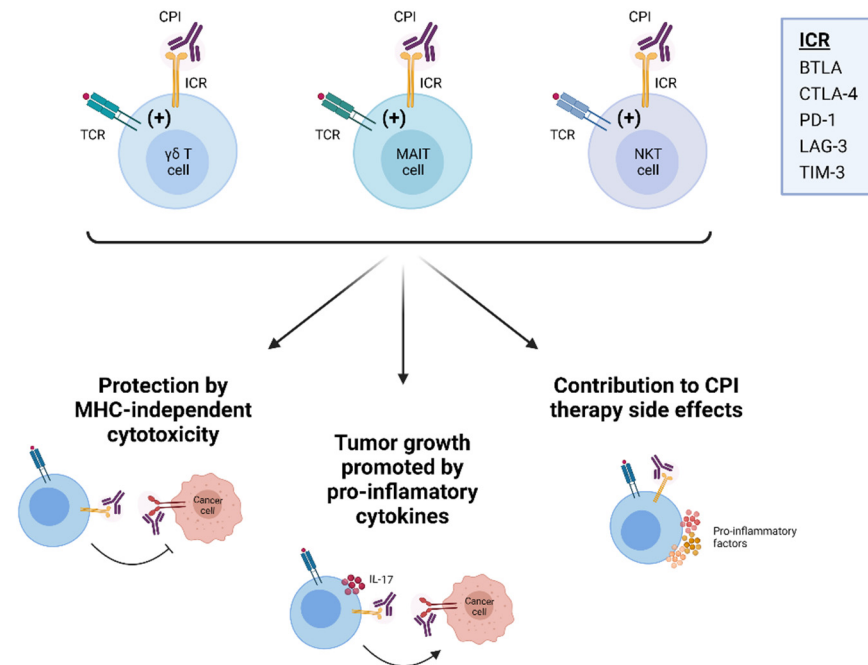


Figure 3. Potential importance of unconventional T cells during CPI therapy. Targeting $\gamma\delta$ T cells, MAIT cells and NKT cells with CPI therapy may lead to strong MHC-independent anti-tumor responses. However, this treatment could also trigger the production of pro-inflammatory cytokines that promote tumor growth. In addition, unconventional T cell responses might contribute to the side effects often seen during CPI therapy. Abbreviations as in text.

4. The Three “Unconventionals”: $\gamma\delta$ T, NKT and MAIT Cells

Of the unconventional trio, $\gamma\delta$ T cells were the first ones discovered, and being the first T cell subset expressing non- α and non- β TCR variable genes, automatically made them the original member of the “unconventionals”. There is strong evidence from mouse and human that $\gamma\delta$ T cell subsets with innate and innate-like function are pre-programmed in the thymus [34–37]. Interestingly, at least in the mouse, such innate subsets appear to have hyporesponsive TCR [38], despite the requirement for TCR signaling during their development [39,40]. Instead of recognizing antigen (Ag), cell activation is achieved through responses to cytokines, similar to innate lymphoid cells [41]. However, human $\gamma\delta$ TCRs have been shown to recognize diverse non-peptide ligands, such as the B7-like molecules butyrophilins [2,4,42,43], MR1 [3], or annexin A2 [44]. $\gamma\delta$ T cells can play key roles in many cancers [45–47], while their therapeutic potential in adoptive cell transfer immunotherapies has been recently demonstrated in pre-clinical models and clinical trials with varying success [47–51]. Furthermore, there is evidence for $\gamma\delta$ T cell memory [52,53], indicating their importance in conferring both short- and long-term protection against cancer or infection.

Natural killer T (NKT) cells are $\alpha\beta$ T cells that recognize lipid molecules in the context of CD1d presentation and can have invariant or diverse TCRs. Invariant or type I NKT cells were first described to react to the marine sponge derived α -galactosylceramide (α -GalCer) and since, a number of bacterial derived glycolipids have been identified as type I NKT antigens, demonstrating their unequivocal role in protective immunity and cancer [54]. Although antigen recognition leads to rapid activation and cytokine production, the type of response varies depending on the NKT cell subset and can be of type 1 (IFN- γ -secreting), type 2 (IL-4/13-secreting), or type 3 (IL-17-secreting) [5]. NKT cells with a more diverse TCR

that do not react to α -GalCer are known as type II, and similar to their type I counterparts they too display functional diversity [54]. As expected, NKT cells have been found to promote immunity against pathogens and cancer, but to also be pathogenic in various inflammatory settings. In this regard, a number of clinical trials have investigated the potential of NKT cells in cancer immunotherapy (reviewed by Godfrey et al. [54]).

Similar to NKT, MAIT cells rearrange invariant α and biased β TCRs, however, they display reactivity to the non-polymorphic, MHC-like molecule MR1, which presents vitamin B metabolites [1]. Their exact role in both humans and animals is still not fully determined, however, they are believed to be critical for anti-bacterial responses. As the name suggests, MAIT cells are located in the mucosae, however, they can be found in blood and secondary lymphoid organs [1,54]. As is the case with their other unconventional partners, MAIT cells have recently been shown to have a strong association with anti-tumor responses, and in this regard, we would like to refer you to two excellent reviews by O’Neill et al. and Cogswell et al. in this issue [55,56].

5. Immune Checkpoint Receptor Inhibition in Unconventional T Cells

In the remaining sections we will discuss the importance of the ICRs BTLA, CTLA-4, PD-1, LAG-3, and TIM-3 (Table 1) in regulating unconventional T cell responses.

Table 1. ICRs with potentially important regulatory role in unconventional T cells. For each ICR, intracellular signaling domains, ligands, drugs in ongoing clinical trials, and drugs approved for use in cancer immunotherapy are shown. BsAb: bispecific antibody; all other abbreviations as in text.

Receptor	Signaling Domains	Ligands	Drugs in Clinical Trials	Approved Drugs
BTLA	ITIM/ITSM	HVEM	TAB004 JS004	
CTLA-4	Tyr-Val-Lys-Met	B7.1 B7.2	AGEN1884 AGEN1181 BMS-986218 IBI310 CS1002 KN044 MGD019 (BsAb PD-1/CTLA-4) SI-B003 (BsAb PD-1/CTLA-4) AK104 (BsAb PD-1/CTLA-4)	Ipilimumab
PD-1	ITIM/ITSM	PD-L1 PD-L2	Toripalimab BAT1306 SHR1210 Sym021 AGEN2034 JS001 CS1003	anti-PD-1: Nivolumab Pembrolizumab Cemiplimab anti-PD-L1: Avelumab Atezolizumab Durvalumab
LAG-3	FSAL motif KIEELE motif EX/EP repeats	MHC class II FGL-1 Gal-3 LSEctin	Relatlimab MGD013 (BsAb PD-1/LAG-3) LAG-525 REGN3767 IMP321 EMB-02 (BsAb PD-1/LAG-3) Sym022 BMS-986016 RO7247669 (BsAb PD-1/LAG-3) FS118 (BsAb LAG-3/PD-1) INCAGN02385 TSR-033 BMS-986213	
TIM-3	Tyr256 (Tyr265 in human) Tyr263	Gal-9 PtdSer Ceacam-1 HMGB-1	TSR-022 RO7121661 (BsAb PD-1/TIM-3) BGB-A425 Sym023 INCAGN02390 MGB453 LY3321367	

6. BTLA

BTLA is constitutively expressed by most lymphocytes and is the only ICR with a TNF receptor superfamily ligand, HVEM [19]. As mentioned above it can inhibit both by direct SHP-mediated signaling but also by preventing HVEM induction of NF- κ B. It can inhibit B, T and dendritic cells (DCs) and seems to play an intricate role in regulating anti-tumor responses [57] with a very prominent role in follicular lymphomas [58]. In mouse $\gamma\delta$ T cells, BTLA is expressed by both IL-17- and IFN- γ -producing subsets. Its expression is repressed by the transcription factor ROR γ t and as a result IL-17-producing $\gamma\delta$ T cells ($\gamma\delta$ T17) as well as other ROR γ t-expressing lymphocytes have very low levels of surface BTLA [30]. Its expression however can be induced by cytokine activation, including IL-7, IL-23, and IL-1 β [32]. Despite its low levels, mice deficient in BTLA have increased numbers of $\gamma\delta$ T17 cells that are hyperactive and more pathogenic in the context of skin inflammation [30]. In humans, BTLA has been studied in V γ 9V δ 2 cells. It was shown that through interactions with HVEM, BTLA could suppress V γ 9V δ 2 cell proliferation, most likely by attenuating TCR signaling [59]. Importantly, BTLA was highly expressed by V δ 2⁺ cells in the lymph nodes of patients with lymphoma, and could suppress their proliferation upon ligation by HVEM on primary tumors [59]. The importance of BTLA in suppressing human $\gamma\delta$ T cell proliferation was recently confirmed [60]. The role of BTLA in MAIT cells or human NKT cells has not been investigated. Mice deficient in BTLA, however, are more susceptible to Con-A induced hepatitis due to hyperactive type I NKT cells [61,62]. In these mice, NKT cells produced higher amounts of cytokine in response to α -GalCer stimulation [61,62], suggesting that BTLA may be regulating the strength of signaling downstream of the TCR. In a mammary tumor mouse model, Weigert and colleagues showed that intratumoral type I NKT cells express high levels of BTLA, which is required to suppress their anti-cancer activity [63].

7. CTLA-4

CTLA-4 was one of the first ICRs to be cloned and early studies into its function established that it tightly regulates B7-CD28 mediated T cell co-stimulation [64,65]. The lymphoproliferative disorders and multi-tissue damage in CTLA-4 deficient mice affirmed the idea that T cell inhibition is a critical immunological function [66–68]. It was later shown that blockade of CTLA-4 with monoclonal antibodies could restore anti-tumor responses in mice [69], establishing the foundations for CPI therapy. Similar to BTLA, CTLA-4 can transmit inhibitory signals either through SHP1/2 or by antagonizing by binding with activating receptors, in this case CD28. Despite the overwhelming insight on the biology of CTLA-4 in conventional CD4⁺ and CD8⁺ T cells, and its successful targeting in cancer, we know remarkably little about how CTLA-4 may be regulating innate-like T cell responses in either mouse or human (e.g., we could not find any substantial study correlating CTLA-4 and NKT function).

In the context of infection, *Plasmodium vivax* infected individuals have exhausted $\gamma\delta$ T cells with characteristically high levels of CTLA-4 among other ICRs [70], however, its contribution is undefined. A study that collected patient samples during the 2014–2015 Ebola virus outbreak, showed that infection led to very low numbers of blood V δ 2⁺ cells, and that patients who survived had lower levels of surface CTLA-4 on their V δ 2⁺ cells [71]. In melanoma, patients with decreased frequencies of V δ 2⁺ cells, had reduced overall survival upon treatment with ipilimumab, the CTLA-4 antagonist [72]. Although only correlative, these studies pinpoint towards a suppressive role of CTLA-4 in $\gamma\delta$ T cells. Interestingly, CD86-expressing V δ 2⁺ cells could suppress $\alpha\beta$ T cells by engaging CTLA-4 [73]. In a transplantation mouse model, CTLA-4 synergized with NKG2D to suppress $\gamma\delta$ T17 cells and prolong cardiac allografts [74].

CTLA-4 was found to be highly expressed in liver resident and blood MAIT cells from patients with autoimmune liver disease [75]. Besides CTLA-4, these patients' MAIT cells expressed classic markers of exhaustion and displayed reduced capacity for IFN- γ production, paradoxically, however, secretion of MAIT-associated IL-17 was enhanced [75]. Similarly,

MAIT cells from individuals with chronic hepatitis B infection expressed high levels of CTLA-4, together with PD-1, and were impaired in producing IFN- γ and granzyme B [76]. In line with this data, intratumoral MAIT cells of a cohort of hepatocellular carcinoma patients, co-expressed high levels of both CTLA-4 and PD-1, which correlated with mild exhaustion. However, whether MAIT-expressed CTLA-4 is directly or indirectly implicated in any of these diseases is currently not known. Recent transcriptional analyses showed that by comparison to blood, oral mucosa resident MAIT cells expressed very high levels of *CTLA4* [77]. In vitro stimulation experiments additionally suggested that cytokines alone, without the need for TCR engagement, are sufficient to induce robust surface CTLA-4 in MAIT cells [77].

8. PD-1

PD-1 is an IgSF ICR, first identified as a T cell receptor in 1992 [78], which interacts with two IgSF ligands, PDL-1, and PDL-2. While PDL-1 shows ubiquitous expression [79], PDL-2 is mainly expressed by innate immune cells [80]. Upon ligand binding, PD-1 initiates its inhibitory function via ITIM/ITSM-dependent recruitment of SHP1/2 [81,82]. The importance of PD-1 and its ligands in the immune system are exemplified by the six, thus far, FDA approved anti-PD-1/PDL blocking antibodies that are used for cancer therapy [25]. Although PD-1 is expressed by unconventional T cells, its role and relevance in these populations is underexplored.

In vitro studies with $\gamma\delta$ T cells showed that similarly to conventional $\alpha\beta$ T cells, V δ 2 cells upregulate PD-1 shortly after antigenic stimulation [83]. In adult V δ 2 cells, the expression of PD-1 peaks between 2 to 4 days after TCR activation, and subsequently declines gradually to moderate levels [83,84]. Neonatal V δ 2 cells, on the other hand, maintain high expression of PD-1 on their surface for longer periods of time following TCR stimulation [85]. Both cytotoxicity and IFN- γ production of in vitro activated PD-1⁺ V δ 2 cells could be inhibited following PDL-1 ligation [83]. In the context of cancer, high PD-1 expression has been reported on $\gamma\delta$ T cells isolated from a variety of tumors, including metastatic neuroblastoma [86], colorectal cancer [87], and multiple myeloma [88]. In this regard, V γ 9V δ 2 cells isolated from the bone marrow of multiple myeloma patients showed higher levels of PD-1 expression compared to V γ 9V δ 2 cells derived either from blood or control bone marrow [88]. Furthermore, these PD-1⁺ $\gamma\delta$ T cells showed impaired proliferative capacity upon antigen stimulation, which was partially restored by blocking PD-1 signaling [88]. Interestingly, a recent study revealed that PD-1 blockade enhances antibody-dependent cellular cytotoxicity (ADCC) of follicular lymphoma cells by CD16⁺ V γ 9 lymphocytes in an in vitro culture system [89]. In contrast to the previous studies, a recent report found no effect of PD-1 blockade in the cytotoxic activity of human $\gamma\delta$ T cells towards leukemia cell lines [84]. PD-1 inhibition did increase IFN- γ production by $\gamma\delta$ T cells after zoledronate (Zol) stimulation and after challenge with Zol-treated THP-1 cells as well as Zol-sensitized acute myeloid leukemia blasts, but there was no significant difference in the proliferation of these cells, or the expression of CD107a on their surface [84]. A meta-analysis comparing single-cell RNA-sequencing (scRNAseq) datasets from melanoma patients that responded or not to anti-PD-1 therapy, showed that there was a population of $\gamma\delta$ T cells that its presence in the tumor correlated with non-responders [90]. However, further investigation into this $\gamma\delta$ T cell subset (e.g., cytokine profiling) is missing.

Despite evidence that PD-1 can inhibit $\gamma\delta$ T cell function and thus may alter protective anti-tumor responses, mouse studies have shown that PD-1 can also modulate $\gamma\delta$ T17 cells, which, as mentioned above, can promote tumor growth. As such, PD-1-deficient mice showed elevated numbers of $\gamma\delta$ T17 cells and were more susceptible to $\gamma\delta$ T17-driven skin inflammation [31], while activation of PD-1 signaling by PDL-1-Fc suppressed the production of IL-17A by $\gamma\delta$ T cells and reduced psoriatic inflammation [91]. The possibility of adverse effects following anti-PD-1 therapy through $\gamma\delta$ T17 over-activation was recently shown in a mouse model of combination therapy. Acute radiation-induced lung injury was worsened in mice that received anti-PD-1 monoclonal antibodies, due to the increased

production of IL-17A by $\gamma\delta$ T cells [92]. Therefore, deepening our understanding of ICR regulation on not only bulk but also functionally distinct subsets of $\gamma\delta$ T cells will be critical for designing efficacious PD-1-related combination therapies with minimal side effects.

PD-1 expression is also upregulated on invariant NKT cells following antigenic stimulation [93,94]. Early reports showed that PD-1⁺ NKT cells had an impaired capacity to produce IFN- γ , IL-4, and IL-12 after α -GalCer stimulation [93,95,96]. PD-1 blockade was able to restore NKT cell proliferation and cytokine production, leading to effective anti-tumor responses in a model of melanoma [93,97]. In contrast, a different study observed little impact of anti-PD1 treatment in rescuing anergic NKT cells [98]. In line with this, PD-1 blockade could prevent the development of dysfunctional NKT cells when administered at the same time as primary α -GalCer stimulation, but the treatment was not able to restore cytokine production once anergy had been established [95]. Thus, the beneficial effects of PD-1/PDL-1 blocking agents on type I NKT cells seem to be most pronounced when given at the time of antigen stimulation [99]. The therapeutic potential of α -GalCer/anti-PD-1 combination therapy was recently evaluated in a pre-clinical model of colorectal cancer. In this setting, the individual administration of α -GalCer or anti-PD-1 had very limited effect on cancer progression [100]. The combination of both therapies, however, resulted in increased activation and proliferation of NKT cells in the tissues, and strongly suppressed the development of polyps in both small intestine and colon [100]. In addition, α -GalCer/anti-PD-1 significantly increased PLZF⁺Tbet⁺ NKT cells in the polyps over other invariant NKT cell subtypes [100], suggesting that PD-1 regulation of NKT cells could be subset-dependent. The regulatory role of PD-1 on NKT cells is not limited to murine models [94,101]. NKT cells obtained from non-small cell lung cancer patients show increased expression of PD-1 and reduced proliferation capacity compared with healthy controls [94]. α -GalCer stimulation induced PD-1 expression on human NKT cells, which inhibited cytokine production [94]. In addition, PDL-1 blockade increased the cytotoxicity of NKT cells against several tumor cells lines [94]. Thus, PD-1 inhibition seems to influence NKT cell responses in human cancers.

PD-1 expression during chronic inflammation has also been associated with functional impairment of MAIT cells [76,102,103]. Moreover, PD-1 blockade was able to restore cytokine production in dysfunctional MAIT cells derived from active tuberculosis patients [102]. In the context of cancer, elevated levels of PD-1 have been reported on MAIT cells derived from hepatocellular carcinoma, esophageal adenocarcinoma, and colorectal cancer patients [104–106]. In the latter study, PD-1⁺ MAIT cells that co-expressed TIM-3 showed increased proliferative capacity and diminished polyfunctionality compared to their PD-1⁻ TIM-3⁻ counterparts [106]. In addition, a recent report compared MAIT gene expression profiles in paired samples from cancer patients before and after anti-PD-1 therapy. PD-1 blockade increased the expression of activation genes in MAIT cells derived from basal and squamous cell carcinoma patients, suggesting a functional role of PD-1 in the regulation of this cell type [107]. Moreover, scRNAseq profiling of intratumoral lymphocytes of metastatic melanoma patients revealed that highly active MAIT cells can correlate with better prognosis to PD-1 blockade [108].

9. LAG-3

Lymphocyte activation gene-3 (LAG-3), also known as CD223, is expressed on multiple cell types including conventional T cells, NK cells, B cells [109], and unconventional T cells [109–111]. LAG-3 is an IgSF transmembrane protein with four extracellular domains that have similar folding patterns with CD4 in both humans and mice, indicating that LAG-3 can also bind to MHC-II, although at a different site than CD4 [112]. However, the intracellular regions of LAG-3 and CD4 do not have similarities [109,112]. Other LAG-3 ligands include FGL-1 (Fibrinogen-like Protein 1), Gal-3 (Galectin-3), and LSECtin (Lymph Node Sinusoidal Endothelial Cell C-type Lectin) and each has been shown to induce LAG-3-mediated inhibition of T cell activation [113–115], supporting the idea that LAG-3 could exert its inhibitory action independently of CD4. Unlike other ICRs,

the intracellular region of LAG-3 lacks a typical cytoplasmic inhibitory ITIM or ITSM motif to inhibit T cell activation. Instead, the cytoplasmic domain of LAG-3 has three conserved regions in mice and humans that are not found in other ICRs [112,116]. Such regions include: an FSAL motif, a KIEELE motif, and an EX/EP repeat motif in the C-terminal region [109,116]. A study to identify the role of each motif in the inhibitory function of LAG-3, highlighted the importance of FSAL and dismissed the significance of KIEELE [117]. In particular, it was demonstrated that LAG-3 can transduce its inhibitory signals through the FSAL motif and EX/EP repeats by inhibition of IL-2 production [117]. Other in vitro and in vivo studies have demonstrated the importance of a lysine residue in KIEELE motif for the negative regulatory function of LAG-3 [118,119]. Furthermore, a LAG-3 associated protein (LAP) capable of interacting with the EX/EP motif has been identified [120]. Although it was proposed that LAP would be important in clustering LAG-3 into lipid rafts to promote signal transduction [120], there is not enough evidence in support of this hypothesis. Besides, it has been demonstrated that mutants lacking the EP motif are able to maintain LAG-3 activity [118], indicating that LAP may not be important for LAG-3 function. Although the available evidence suggests a discrepancy in the importance of the intracellular motifs of LAG-3, it is clear that LAG-3 inhibits immune cell activation through non-canonical inhibitory mechanisms compared to other ICRs. This suggests that the use of LAG-3 in immunotherapy combined with other ICRs would yield synergistic effects.

It has been reported that the inhibitory function of LAG-3 is correlated with its expression levels on the cell surface [117]. In a recent study, melanoma patients showed higher proportions of both circulating and tumor-infiltrating $\gamma\delta$ T cells expressing LAG-3 compared to control groups, suggesting that LAG-3 may be crucial for immune escape and tumor progression by inhibition of $\gamma\delta$ T cells [121]. Furthermore, the expression of LAG-3 in tumor-infiltrating $\gamma\delta$ T cells was associated with earlier relapse and shorter overall survival [121]. More detailed studies on the putative role of LAG-3 in $\gamma\delta$ T cells in the context of cancer are lacking. LAG-3 together with an assortment of exhaustion markers are highly expressed in $\gamma\delta$ T cells derived from patients infected with *Plasmodium vivax* compared to uninfected controls [70]. In mice infected with *P. berghei* XAT, IFN- γ production by $V\gamma 1^+$ $\gamma\delta$ T cells was significantly reduced in the late phases of infection, which coincided with increased expression of LAG-3, as well as other ICRs [122].

Mass cytometry by time-of-flight (CyTOF) analysis from non-small cell lung cancer (NSCLC) patient samples showed that LAG-3 and PD-1 were mainly expressed in type I NKT and CD8⁺ T cells [123]. Consistent with this, the co-expression of these ICRs was associated with higher levels of activation markers, such as CD69, granzyme-B, and Ki-67, among others [123]. Besides, the authors suggested that LAG-3 expression could be considered for the selection of patients for immunotherapy since LAG-3 overexpression was negatively correlated with survival in patients with NSCLC that had been treated with PD-1 inhibitors, indicating that tumors in which immune evasion is mediated by LAG-3 are less sensitive to PD-1 blockade [123]. In this regard, early results in a clinical trial with LAG-3 inhibitors showed promising results in patients with advanced melanoma with resistance to PD-1 blockers [123,124]. Whether LAG-3-mediated regulation of NKT cells is of critical importance in cancer immunity remains to be elucidated. Similar to other cell types, chronic infection, such as HIV, results in elevated surface LAG-3 on type I NKT cells and reduced inhibition cytokine production [125]. Besides evidence that the exhausted phenotype of MAIT cells following exposure to bacterial antigens can be reversed by LAG-3 blockade [126], the role of LAG-3 in these cells in the context of cancer or inflammation is unknown.

10. TIM-3

T cell immunoglobulin and mucin-domain containing-3 (TIM-3) is an IgSF member expressed on the surface of T cells, B cells, NK cells, DCs, macrophages, and other immune cells [127–130]. TIM-3 can bind several ligands commonly found in the tumor microen-

environment, including galectin-9 (Gal-9), HMGB-1, phosphatidylserine (PtdSer), and cell adhesion molecule 1 (Ceacam-1) [131–134]. The downstream signaling triggered by TIM-3 ligation is complex and is still being studied. In contrast to most inhibitory receptors, TIM-3 does not contain classical ITIM or ITSM motifs [135]. In the absence of ligand, HLA-B-associated transcript 3 (Bat3) binds to the cytoplasmic tail of TIM-3, which results in the recruitment of the active form of Lck, known to promote TCR signaling [136,137]. The activation of TIM-3 by Gal-9 or Ceacam-1, on the other hand, triggers the phosphorylation of conserved tyrosine residues on the cytoplasmic tail of this receptor [136]. As a result, Bat3 is released and SH2-domain containing kinases such as Fyn can be recruited in its place [138]. The interaction of Fyn with TIM-3 leads to the activation of PAG and CSK, which in turn phosphorylates an inhibitory residue on Lck, resulting in the inhibition of TCR signaling [136]. TIM-3 ligation has been shown to downregulate antitumor $\alpha\beta$ T cell responses [131,135]. Thus, TIM-3-blocking agents are currently being tested in the clinic [131,135,139].

Recent studies suggest that TIM-3 also plays a role in the regulation of $\gamma\delta$ T cell responses. This was first described in the infection field, where children exposed to *Plasmodium falciparum* exhibited higher TIM-3 expression in V δ 2 cells [140]. These TIM-3⁺ V δ 2 cells showed reduced proliferation and cytokine production following stimulation, which was associated with asymptomatic malaria infection [141]. More recently, V δ 2 cells isolated from acute myeloid leukemia (AML) and colorectal cancer patients displayed increased TIM-3 expression and a dysfunctional phenotype when compared to healthy controls [142–144]. Activation of TIM-3 with Gal-9 lowered V δ 2 cell cytotoxicity towards colon cancer cell lines by reducing production of perforin and granzyme B through the ERK1/2 pathway [144]. In addition, V δ 2 cells from AML patients showed impaired proliferative capacity upon IL-21 stimulation, which was restored by blocking TIM-3 signaling [142]. When both TIM-3 and PD-1 expression were investigated, V δ 2 cells that co-expressed TIM-3 and PD-1 exhibited the lowest production of IFN- γ and TNF- α compared to all other V δ 2 populations [143]. Interestingly, anti-TIM-3 or anti-TIM-3 plus anti-PD-1 blocking antibodies, but not anti-PD-1 alone, increased cytokine production [143], highlighting the importance of TIM-3 inhibition for functional restoration of $\gamma\delta$ T cells.

In line with the above, blockade of TIM-3 signaling increased cytokine production by V δ 2 cells, but did not affect their proliferation [145]. The authors found that V δ 2 cells upregulated TIM-3 following TCR or TNF stimulation, and that TIM-3 ligation induced apoptosis through caspase-3, which was reversed by TIM-3 blockade [145]. Furthermore, in a murine model of breast cancer, combining adoptive transfer of $\gamma\delta$ T cells and anti-TIM-3 antibodies enhanced anti-tumor responses compared to $\gamma\delta$ T cell transfer alone [145]. The beneficial effects of $\gamma\delta$ T cell transfer/anti-TIM-3 could be further improved by the addition of a bispecific anti-CD3/anti-EpCAM antibody, again showing the potential benefits of combination therapies involving TIM-3 inhibition [145]. Since several stimuli including not only TNF and TCR activation, but also IL-21 and anti-PD-1 administration have been reported to upregulate TIM-3 on V δ 2 cells [16,17], the previous study poses an interesting strategy in combining TIM-3 blockade with $\gamma\delta$ T cell adoptive transfer protocols to prevent functional impairment of the transferred cells.

The role of TIM-3 on MAIT and NKT cells remains largely unknown. Elevated levels of TIM-3 have been reported on these cells during infection and in cancer patients, often in combination with other inhibitory receptors [76,104,106,126,146–148]. In addition, some studies show TIM-3 upregulation following MAIT or NKT cell activation [106,149–151]. There is, however, very limited evidence regarding the functionality of TIM-3 on these unconventional T cells. A study showed that following α -GalCer stimulation, murine hepatic NKT cells that express TIM-3 increase proliferation and produce higher levels of IFN- γ and IL-4 compared to their TIM-3⁻ counterpart [149]. In contrast, TIM-3⁺ NKT cells obtained from chronic hepatitis B patients, showed an impaired capacity to produce IFN- γ and IL-4 upon stimulation, which was partially reverted by TIM-3 or PD-1 blocking

agents [150]. The ability of TIM-3/Gal-9 to induce apoptosis on NKT cells is currently unclear [149,152].

11. Concluding Remarks

It is evident from the above that our understanding of how ICRs regulate innate-like T cell responses is at its infancy. There are many fundamental questions that remain unanswered. Given their unconventional TCR interactions, how do ICRs inhibit $\gamma\delta$ T, MAIT and NKT cells? Is innate activation by cytokines regulated by ICRs? Importantly, can we target innate-like T cells with CPI therapy in order to restore anti-cancer immunity, while at the same time subverting the tumor's ability to evade MHC-restricted T cells? What are the chances that CPI therapy will over activate tumor-promoting IL-17-producing innate-like T cells? Are adverse effects associated with CPI therapy driven by unconventional T cells? We would like to propose (as shown in Figure 3) that elucidating the biological implications of ICR-mediated inhibition of unconventional T cells has the potential to unravel novel and important therapeutic avenues, particularly in the context of cancer immunotherapy.

Author Contributions: Writing—review and editing, E.C.-T., M.V.B. and V.B.; funding acquisition, V.B. All authors have read and agreed to the published version of the manuscript.

Funding: This work was supported by funding to V.B. from the Danish Cancer Society (Kræftens Bekæmpelse, grant number R269-A15747), the Leo Foundation (Leo Fondet, grant number LF-OC-20-000550) and the Novo Nordisk Foundation (Novo Nordisk Fondet, grant number NNF20OC0065160).

Acknowledgments: Figures and illustrations were prepared using [BioRender.com](https://www.biorender.com) (accessed on 12 September 2021).

Conflicts of Interest: The authors declare no conflict of interest.

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