

Deciphering human $\gamma\delta$ T cell response in cancer: lessons from tumor-infiltrating $\gamma\delta$ T cells

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ABSTRACT

The finding that $\gamma\delta$ T cells are present amongst tumor-infiltrating lymphocytes in humans suggest they participate in tumor immune surveillance, but their relevance is unclear because the relative frequencies of tumor-infiltrating $\gamma\delta$ T cells correlate with tumor remission or progression, or do not correlate at all with prognosis. This is suggestive of the fact that tumor-infiltrating $\gamma\delta$ T cells may play substantially different effector or regulatory functions, and correlation with patient's prognosis relies on distinct $\gamma\delta$ T cell subsets in the context of the tumor. There is interest to exploit $\gamma\delta$ T cells in tumor immunotherapy, but to make this approach successful there is urgent need to fully understand the biological functions of $\gamma\delta$ T cells and of how they can be manipulated *in vivo* and *ex vivo* to safely provide benefit to the host.

This review focuses on our previous and ongoing studies of tumor-infiltrating $\gamma\delta$ T lymphocytes in different types of human cancer. Moreover, we discuss the interaction of tumor-infiltrating $\gamma\delta$ T cells with other cells and molecules present in the tumor microenvironment, and their clinical relevance on the ground, that better knowledge in this field can be used further for better immunotherapeutic intervention in cancer.

Running title: Tumor-infiltrating $\gamma\delta$ T lymphocytes.

Key words: $\gamma\delta$ T lymphocytes, colon cancer, tumor-infiltrating lymphocytes; tumor microenvironment; clinical correlation.

1. GENERAL INTRODUCTION ON ANTIGEN RECOGNITION BY $\gamma\delta$ T CELLS.

Human $\gamma\delta$ T lymphocytes are typically classified based on the $V\delta$ chain used to make their T cell receptor (TCR). The prevalent (>70%) $\gamma\delta$ T lymphocytes in human blood and secondary lymphoid organs of adult individuals express a TCR heterodimer composed of the $V\gamma 9$ and $V\delta 2$ chains [1]. These cells are commonly named as $V\gamma 9V\delta 2$ T lymphocytes, and recognize non proteic pyrophosphate metabolites called phosphoantigens (PAgs), which derive either from the mevalonic acid (MVA) pathway [2] or the microbial non-mevalonate Rohmer cycle ((E)-4-Hydroxy-3-methylbut-2-enyl pyrophosphate, HMB-PP) [3].

Butyrophilin-3A1 (CD277) is necessary but not sufficient for PAg recognition by $V\gamma 9V\delta 2$ T cells [4-6]. Another BTN molecule, BTN2A1, has been recently identified as a key ligand that associates on the cell surface with BTN3A1 independent of PAg and binds to the $V\gamma 9V\delta 2$ TCR. In particular, the surface of the BTN2A1 IgV domain directly binds to germline-encoded $V\gamma 9$ regions of the $V\gamma 9V\delta 2$ TCR, while somatically recombined CDR3 regions implicated in PAg recognition are uninvolved. It is then likely that binding of a second ligand, possibly BTN3A1, to a separate TCR $V\delta 2$ domain is also required [7,8].

In agreement with the very restricted antigen recognition pattern, the $V\gamma 9V\delta 2$ TCR repertoire is invariant or semi-invariant, suggestive of an innate-like modality of PAg recognition [9,10]. However, there is evidence [11] that in addition to the PAg-reactive $V\gamma 9^+$ T lymphocytes, the $V\delta 2$ population also includes another subset of $V\gamma 9^-$ T lymphocytes with a diverse repertoire and with adaptive-like characteristics, as indicated by the finding that this population selectively clonally expands during acute cytomegalovirus (CMV) infection.

$\gamma\delta$ T lymphocytes expressing the $V\delta 1$ or $V\delta 3$ TCRs, are less represented than $V\gamma 9V\delta 2$ cells in adult blood but predominate in tissues [1], and have quite different antigen reactivity. $V\delta 1$ T lymphocytes physiologically reside in the skin, lung, intestine and colon epithelia

where they represent the major $\gamma\delta$ T cell subset and recognize stress antigens overexpressed upon CMV-infection and tumor transformation [12-15]. V δ 3 cells are even rarer than V δ 1 T cells in blood but abundant in the liver and gut and are expanded in patients with CMV infection or B cell leukemia. Few studies have provided evidence for MHC class I and CD1d restricted V δ 1 T cells [16] and a V γ 8V δ 3 T lymphocyte population recognize Annexin A2 overexpressed by stressed and tumor cells [17].

Differently than $\alpha\beta$ T cells, and with the exception of very rare V δ 3 T cells, $\gamma\delta$ T cells lack genetical (i.e. HLA, CD1 or MR1) restriction, and are independent on co-stimulatory signals (i.e. CD28) [1]. However, $\gamma\delta$ T cells share several features with $\alpha\beta$ T cells: in fact, similar to T CD8 $\alpha\beta$ subset, they can be distinguished into “naive”, “central memory”, “effector memory” and “terminally differentiated” subsets with different recirculation pattern and effector functions [18]. Moreover, $\gamma\delta$ T cells may acquire highly diverse effector functions in the presence of certain cytokine combinations and polarize to Th1, Th2, Th17, follicular T helper, Th9 and T regulatory (Treg) cells [19-29] and this wide flexibility highlights the capacity of $\gamma\delta$ T cells to rapidly respond to different antigenic challenges.

2. $\gamma\delta$ T CELL FUNCTIONS IN TUMOR IMMUNOLOGY.

The evolutionary divergence between human and mice has been the major obstacle in the scientific research in the field of $\gamma\delta$ T lymphocyte. In fact, cells with repertoire and reactivity of human $\gamma\delta$ T lymphocytes, particularly V γ 9V δ 2 T lymphocytes, are only found in humans and higher primates, but absent from rodents [1], in which pre-clinical studies are performed. Thus, the lack of a suitable animal model has greatly limited our knowledge of the role of $\gamma\delta$ T lymphocytes in immune responses to pathogens.

Nevertheless, robust evidence that $\gamma\delta$ T cells have anti-tumor activity has been firmly established by studies of Hayday and coworkers showing that $\gamma\delta$ T lymphocytes control cutaneous carcinogenesis in mice [30], and by the finding that human $\gamma\delta$ T lymphocytes are able to exert potent HLA-unrestricted cytotoxicity *in vitro* against a variety of tumor cells (reviewed in 31). Moreover, human $\gamma\delta$ T lymphocytes expanded *ex vivo* and then adoptively transferred into immunodeficient mice xenografted with tumor cells have demonstrated efficient anti-tumor activity [30].

The most important effector function of $\gamma\delta$ T cells which is relevant to tumor immunology is their cytotoxic activity. $\gamma\delta$ T cells recognize antigens (stress molecules, PAg/BTN3A1 complexes, other unknown molecules) broadly expressed on many different tumor cells and in the absence of genetic-restriction. Thus, the capacity to recognize antigens which are common to many different tumors and in the absence genetic restriction, may allow a broader clinical utilization of $\gamma\delta$ T cells in the global heterogeneous population and across many different tumor types. Upon tumor antigen recognition by the $\gamma\delta$ TCR or NKG2D and NCRs receptors [32-35], $\gamma\delta$ T lymphocytes establish immunological synapses with target tumor cells and kill them using the same mechanisms as NK and CD8⁺ cytotoxic T cells, namely granule exocytosis with release of perforin, granzymes and granulysin and activation of death receptors by the respective ligands [36-40]. Moreover, human $\gamma\delta$ (both V δ 1 and V δ 2) T lymphocytes express CD16 (the low affinity Fc γ RIII) and perform antibody-dependent cell-mediated cytotoxicity (ADCC) [41].

In addition to their prominent cytolytic activity, upon antigen stimulation in the presence of polarizing cytokines, human $\gamma\delta$ T lymphocytes polarize towards different phenotypic and functional subsets [18-29] and acquire different cytokine secretion patterns [see above], thereby modulating tumor growth by orchestrating downstream immune responses.

Thus, human $\gamma\delta$ T lymphocytes help B lymphocytes to produce different antibody classes [26-28], promote 4-1BB-mediated NK cell cytotoxicity [42], induce dendritic cells maturation [43,44] and reprogram their functions to become professional antigen-presenting cells to induce proliferation and expansion of conventional CD8 cytotoxic T lymphocytes [45-47].

3. TUMOR-INFILTRATING $\gamma\delta$ T CELLS: HOW CAN WE DETECT THEM?

The identification of tumor-infiltrating $\gamma\delta$ T lymphocytes in humans is a major issue for establishing their prognostic value and for cancer immunotherapy, as these pleiomorphic cells which are located in most healthy organs are often misidentified when not unidentified at all [48,49]. Typically, detection and characterization of $\gamma\delta$ T lymphocytes in healthy or tumor tissues relies on a combination of cell surface markers labeled by immunostaining and visualized by immunohistochemistry. This technique requires access to fresh tumor samples and furthermore, immunohistochemical spotting of $\gamma\delta$ T cells remains largely hampered by the paucity of anti-TCR reagents compatible with staining of formalin-fixed paraffin embedded samples. There is only one anti-pan $\gamma\delta$ TCR mAb on the market which works well on paraffin embedded tissues and which has been made commercially available only very recently [50], but this mAb does not distinguish between V δ 1, V δ 2 and V δ 3 subsets of $\gamma\delta$ T cells. Alternatively, or in addition, $\gamma\delta$ T lymphocytes in tissues may be visualized by flow cytometry [48,49]. However, this is a quite demanding process which requires digestion of tissue samples large enough to obtain a sufficient number of viable cells for subsequent phenotypic and functional analysis. Nevertheless, both these techniques have been used to identify the frequency, phenotypes and functions by $\gamma\delta$ T lymphocytes obtained from different types of human cancer tissues.

However, given the recent developments in $\gamma\delta$ T cell-based therapies of cancer, it is important to know not only the rate of tumor-infiltrating $\gamma\delta$ lymphocytes from any tumor biopsy, but also their subset distribution, maturation/activation/exhaustion states and functional profiles likewise, but this has remained unclear so far. The large number of transcriptomic datasets obtained using microarrays or mRNA sequencing (RNAseq) of bulk tumor biopsies, and currently available from public databases (GEO database, The Cancer Genome Atlas, etc.) represented an invaluable resource and unique opportunity to address these issues by datamining approaches. One such method, called deconvolution, consists in algorithmic learning transcriptomic profiles of several specific cell types taken individually, followed by algorithmic deduction of their respective rates from the bulk transcriptome of a complex cell mixture. Hence theoretically, deconvolution can determine the cell composition from any bulk tumor biopsy, provided the cell type components have previously been learned [51]. Accordingly Gentles et al. deconvoluted 19,000 tumors using their algorithm CIBERSORT to decipher the composition of TILs and found that $\gamma\delta$ TILs were the most significant favorable cancer-wide prognostic populations [52]. In a subsequent deconvolution of 15,000 biopsies from 50 solid and hematologic malignancies however, we showed that due to insufficiently learnt $\gamma\delta$ T cell transcriptomes ($n=2$ low resolution microarrays), CIBERSORT massively misidentifies both $\gamma\delta$, CD8, and NK cell types [53]. These three closely related cell types have highly multicollinear transcriptomes [54], which require much larger learnings from many more $\gamma\delta$ T cell transcriptomes to return reliable results. In addition, determining their TCRV subsets and further intrinsic hallmarks such as stage of maturation or exhaustion are out of reach for the same reasons. Hence current published deconvolution studies might provide us with misleading conclusions about $\gamma\delta$ T cell infiltrating human cancers.

The recent developments in single cell RNA sequencing are complementing and updating immunochemistry and flow cytometry methodologies, and now provide us with the finest level of resolution for the gene expression patterns of large sets of cells, unveiling much finer aspects of cells and allowing their classifications from human tissues.

Nevertheless, for the same above reasons, plus impossibility to determine TCRV γ and δ gene usage from short reads of 3' mRNA ends, the identification of $\gamma\delta$ T lymphocytes in scRNA-seq data remained elusive, so $\gamma\delta$ T remain barely identified in most scRNAseq studies of PBMC or tissues. By providing the first scRNA-seq dataset of cell-sorted TCRV δ 1 and TCRV δ 2 $\gamma\delta$ T lymphocytes purified from PBMC of healthy individuals with known CMV serology, we defined a gene signature identifying human $\gamma\delta$ T cells in scRNAseq datasets [55] (Figure 1). By this approach, scarce $\gamma\delta$ TILs of either TCRV δ 1 and TCRV δ 2 subtypes could be detected in a small series of published cancer scRNASeq datasets, with cell counts suggesting a decorrelation of $\alpha\beta$ TILs and $\gamma\delta$ TILs across human cancers. These advances paved the way to further metaanalyses of $\gamma\delta$ TILs aiming at reliably determining their presence, TCR usage, maturation/differentiation, and activation/exhaustion status in the tumor microenvironment of a large spectrum of human cancers.

4. $\gamma\delta$ T LYMPHOCYTES IN CHRONIC INFLAMMATORY BOWEL DISEASE AND COLO-RECTAL CANCER

Patients with inflammatory bowel disease (IBD) have an elevated risk to develop colorectal cancer (CRC), that is associated with the duration and extent of chronic inflammation [56,57]. The role of $\gamma\delta$ T cells in the pathogenesis of IBD is still poorly known, because of the conflicting findings of studies showing either increased or decreased frequencies of $\gamma\delta$ T cells in IBD patients, as compared to control subjects. Moreover, most studies have

looked at circulating $\gamma\delta$ T cells, which do not necessarily mirror the situation in gut tissue [58,59].

In a murine model of IBD, $\gamma\delta$ T cells that participate to chronic inflammation express the gut-homing molecules CD103 and $\alpha 4\beta 7$ and produce IL-17 [60] which is known to sustain chronic inflammation in the intestine and contribute to cancer development [53, 61].

Moreover, a population of gut-tropic $\gamma\delta$ T cells that express β integrin and produce TNF- α has been detected in the blood and in mucosa samples of IBD patients [62].

As $\gamma\delta$ T cells may play a role in the regulation of the integrity of the mucosa barrier [63], it is important to understand whether $\gamma\delta$ T cells participate to the pathogenesis of IBD and contribute to the transition from IBD to CRC.

In recent years we have been interested in studying $\gamma\delta$ T cells and their V δ 1 and V δ 2 subsets in long-standing IBD patients (as a model of chronic gut inflammation) and in CRC patients [64,65], with the aim to establish their role in the pathogenesis of chronic IBD and CRC.

Results from a large number of tissue specimens have confirmed that V δ 1 T cells are the dominant $\gamma\delta$ subset in normal colon tissue, while V δ 2 T cells are poorly represented. Patients with long standing (chronic) IBD have low frequencies of gut V δ 1 T cells but an increased frequency of V δ 2 T cells which correlates with the duration and severity of the inflammatory response [65].

From a functional point of view, gut V δ 1 T cells from healthy subjects and chronic IBD patients express relatively low percentages of IFN- γ and TNF- α . Gut V δ 2 T cells from healthy donors similarly produce low levels IFN- γ and TNF- α , but V δ 2 T cells from the gut of long lasting IBD patients produce more TNF- α and IL-17 [65]. These results indicate that V δ 2 T cells are recruited to the gut during chronic IBD and contribute to the whole TNF- α production. Moreover, our study identified a yet unappreciated role of V δ 2 T cells

in contributing to IL-17 production in the gut of chronic IBD patients, and account for approximately one-third of all IL-17-producing cells. These results, together with the finding that the frequency of gut V δ 2 T cells significantly correlates with the severity of IBD, strongly support the view that V δ 2 T cells contribute to chronic inflammation in IBD patients (Figure 2).

These findings were confirmed by the analysis of a cohort of IBD transcriptomes showing that expression of the *TRDV2* or *CD3D* genes was significantly correlated with expression of *IFNG*, indicating that T cells in general and V δ 2 T cells in particular contribute to IFN- γ production in IBD samples [66]. Transcriptome analysis also revealed a significant correlation between *TRDV2* and *IL17A* gene expression but surprisingly, there was no significant correlation between *TRDV2* and *CD3D* gene expression, suggesting the existence of two diverse V δ 2 T cell populations, one CD3^{high} and one CD3^{low} (our unpublished results and [67]). Moreover, expression of the *TRDV2* gene did not correlate with expression of the *TRGV9* gene [63], suggesting the presence of two different V δ 2 T cell populations, one V γ 9⁺ and one V γ 9⁻, that adopt divergent features, as above discussed [11].

Finally, we could not find any significant correlation between *TRDV2*, *TRGV9*, *CD3D* and *TNF* gene, indicating that *TNF* production arises from more heterogeneous cell sources than *IFNG* and *IL17*.

Chronic inflammation is the third highest risk condition for CRC [68]. Therefore, we analysed $\gamma\delta$ T cells in CRC specimens with the expectation to find out similarities between chronic IBD and CRC [64]. Instead, by using both flow cytometry and transcriptomic we detected comprised a similar rate of $\gamma\delta$ T cells (4% on average) in CRC tissue and normal adjacent tissue, with the majority expressing V δ 1. The majority of V δ 1 and V δ 2 T cells had

an effector memory phenotype but had a very low, if any, production of IFN- γ and TNF- α and did not produce at all IL-17.

In an independent cohort of CRC transcriptomes, expression of *TRGV9*, *TRDV2* and *CD3D* genes was correlated with expression of the *IFNG* gene, suggesting that T cells in general and V δ 2 T cells in particular contribute to IFN- γ production in CRC patients. In contrast, we did not find any significant correlation between *TRGV9* and *TRDV2* and *IL17A* gene expression, suggesting that IL-17 production arises from more diverse cell sources than IFN- γ [64]. This finding was unexpected, because another study in Chinese patients reported that $\gamma\delta$ T cells are the main source of IL-17 in CRC [61]. Potential explanations to such apparently conflicting findings might be clinical scenarios, differences in the clinical cohorts focussed on, or alterations in microbiome.

5. IDENTIFICATION OF A HUMAN INTESTINAL INTRAEPITHELIAL V δ 1 T CELL SUBSET EXPRESSING NKP46 AND EQUIPPED WITH CYTOLYTIC AND ANTI-TUMOR ACTIVITY.

NKp46 is a member of the NCRs family of NK activating receptors that are involved in the recognition and killing of target cells, including tumor cells [69-72]. Although NCRs are not expressed by circulating T cells [35], expression of both NKp46 and NKp44 was detected on $\alpha\beta$ intestinal intraepithelial lymphocytes (IELs) in patients affected by celiac disease [73]. In this context, NCR expression was induced by IL-15 and overexpressed in celiac patients [74]. These NCR⁺ $\alpha\beta$ IELs had potent cytotoxic activity and an highly restricted TCR repertoire, likely suggesting that they had undergone to TCR-mediated clonal expansion [73].

While studying $\gamma\delta$ T cells infiltrating CRC, we have identified a subset of V δ 1 T cells constitutively expressing NKp46, equipped with high cytolytic potential, and representing the

most abundant $\gamma\delta$ T cell subset in healthy human intestine [75]. Expression of NKp46 significantly contributes to the cytotoxic activity of NKp46⁺ V δ 1 IELs freshly purified from the gut, since cytotoxicity is blocked by addition of a Mab to NKp46.

Additionally, we found that NKp46⁺ V δ 1 IELs are not phylogenetically conserved across species, and are neither present in other human tissues nor in the blood. Therefore, they represent a unique population of gut-resident IELs.

The origin and development of IELs is still unclear, but by analogy with model of $\gamma\delta$ T cell development, it is likely that NKp46⁺ $\gamma\delta$ T cells develop in the thymus and migrate to the gut where IL-15, secreted by multiple cellular sources including intestinal epithelial cells [76] supports their growth [77,78]. In our *in vitro* studies, stimulation of thymocyte precursors with IL-2 or IL-15 promotes the development NKp46⁺ V δ 1 IELs with the same phenotype and functions as those of their intestinal counterpart, and also induces the expression of CCR9 which, in turn, allows recruitment of NKp46⁺ V δ 1 T cells to the gut [79]. However, and differently than IL-2 and/or IL-15-activated $\gamma\delta$ thymocyte precursors, gut-resident NKp46⁺ V δ 1 IELs lack the expression of NKG2A, an inhibitory receptor expressed by NK cells and specifically binding the nonclassical MHC Class I molecule HLA-E. One explanation for this apparent discrepancy is that NKp46⁺ V δ 1 T cells generated *in vitro* from thymic precursors do not interact with intestinal epithelial cells that constitutively express high levels of HLA-E [80]. Conversely, binding of HLA-E to NKG2A on NKp46⁺ V δ 1 intestinal IELs might cause NKG2A downregulation and thus explain its low expression.

Altogether, our results indicate that the biological properties of the NKp46⁺ V δ 1 IELs are dictated both by distinctive features of human V δ 1 thymocytes and by the gut microenvironment.

6. CLINICAL RELEVANCE OF TUMOR-INFILTRATING $\gamma\delta$ T CELLS.

The clinical relevance of tumor-infiltrating $\gamma\delta$ T lymphocytes is still unclear because of contrasting results. In fact, in different studies that have utilized either immunohistochemistry or flow cytometry, the frequency of tumor-infiltrating $\gamma\delta$ T cells, has been reported to correlate with tumor remission, or with tumor progression, or even failed to correlate with prognosis [49,50]. These findings are strongly suggestive of the fact that $\gamma\delta$ T cells at the tumor site may play opposite (anti- or pro-tumor) functions, and thus might show positive or negative correlation with prognosis depending on the $\gamma\delta$ T cell subset infiltrating the tumor site (Figure 3).

Recent studies suggest that the differential expression of IFN- γ and IL-17 by tumor infiltrating $\gamma\delta$ T cells observed in several tumor mouse models, may also extend to cancer patients [81]. Thus, the percentage of IL-17-producing $\gamma\delta$ T cells amongst tumor-infiltrating lymphocytes was significantly higher in patients with squamous cell carcinoma at advanced stage, while the percentage of IFN- γ -producing $\gamma\delta$ T cells in the tumor tissue was higher in patients at early stage. Along these lines, other studies have demonstrated that the frequency of either total $\gamma\delta$ T cells or $\gamma\delta$ T cells expressing IFN- γ correlate with better survival [48,49,81], while $\gamma\delta$ T cells expressing IL-17 are associated with bad prognosis in patients with gallbladder [82] and colon [61] cancers.

In the colon cancer study by Wu et al. [61], $\gamma\delta$ T cells constitute the major source of IL-17 in tumor biopsies, and the frequency of $\gamma\delta$ T cells expressing IL-17 at the tumor site positively correlates with overall tumor progression. This is in sharp contrast with a subsequent study by our group [64] showing that in colon cancer patients an high frequency of tumor-infiltrating $\gamma\delta$ T cells significantly correlated with higher 5-year disease-free survival rate. Unlike murine $\gamma\delta$ T cells, human $\gamma\delta$ T cells have a Th1-type signature (they produce IFN- γ and TNF) and the presence of $\gamma\delta$ T cell subsets making IL-17 in humans has been more

controversial and is less generally accepted. This suggests that accumulation of $\gamma\delta$ T cells making IL-17 at the tumor site may be the consequence of tumor-associated inflammation. This is consistent with our findings in children with bacterial meningitis, where $\gamma\delta$ T cells expressing IL-17 were detected in the cerebrospinal fluid but were absent from the circulation [23]. It is likely that as with mouse $\gamma\delta$ T cells, IL-1 β , IL-6, IL-23, and TGF- β account for $\gamma\delta$ T cell polarization to IL-17-production also in humans [23].

In our study in human CRC, we initially investigated whether intratumoral $\gamma\delta$ T cells had any clinical relevance, by data mining transcriptomes and clinical files from a large cohort of CRC samples [64]. The leucocyte deconvolution of this dataset demonstrated a link between genetic and molecular markers of CRC and their abundance of TILs, whether of the $\alpha\beta$ or $\gamma\delta$ T cell subtype. For instance, the KRAS mutation status made no difference for these criteria, but the abundance of both subsets of $\alpha\beta$ or $\gamma\delta$ TILs was significantly higher in mismatch repair-deficient (MMR-D) than -proficient (MMR-P) tumors, in BRAFmutated versus BRAFwt, and in TP53wt versus TP53 mutated tumors. A higher content of $\alpha\beta$ or $\gamma\delta$ TILs was also apparent in tumors positive for the CPG island methylator phenotype (CIMP) as compared to their negative counterparts, and in tumors negative for the chromosomal instability phenotype (CIN) as compared to their positive counterparts. Importantly, each of these prognostic factors influenced in the same direction the abundance of both $\alpha\beta$ and $\gamma\delta$ TILs [64].

We then correlated the relative abundance of $\gamma\delta$ T cells with clinical features by analyzing the independent dataset of those CRC patients which follow-up was available. Across the whole cohort, those patients with more abundant $\gamma\delta$ TILs had a better disease-free survival (DFS), as confirmed by stratifying patients according to expression of the *TCRGV9* gene.

Patients with higher expression of the *IFNG* gene also had a higher DFS, whereas those with higher expression of the *IL17A* gene had a significantly lower DFS [64]. This $\gamma\delta$ - and IFN- γ -associated favorable pattern was still maintained when reducing the whole cohort to those patients without lymph node invasion. By contrast, the IL17-dependent unfavorable pattern was rather observed in patients with lymph node metastasis. Stratifying the entire cohort according to both $\gamma\delta$ TIL abundance and *IFNG* gene expression produced groups with strikingly different DFS, and demonstrated most notably that $\gamma\delta$ TIL abundance overweighted *IFNG* gene expression in contributing to better patient's outcome [64]. This suggests the antitumor activity of $\gamma\delta$ T cells amongst TILs might be attributable mostly to their cytotoxic activity, rather than to IFN- γ production. The role of V δ 1 T cells could not be investigated likewise using the microarray data set which lacks the *TRDV1* gene and in which the correlated levels of *TRGV9* and *TRDV2* genes indicated presence of TCR V γ 9V δ 2 T lymphocytes.

In another study, the frequencies of $\gamma\delta$ T cells among TILs of squamous cell cancer (SCC) patients did not substantially change with disease stage but the frequencies of IFN- γ -producing V δ 1 and V δ 2 T cells were higher in SCC patients at stages I and II and with favorable outcome (absence of lymph node metastasis, cancer relapse and overall survival), but significantly decreased in patients with advanced disease (stages III and IV) [81]. The percentages of $\gamma\delta$ T cells among TILs of melanoma patients did not change similarly, but the frequencies of V δ 2 T cells that expressed IFN- γ decreased in parallel with disease progression [83].

Therefore, a common feature of the three cancer types studied so far (CRC, SCC and melanoma) is that frequencies of IFN- γ -producing V δ 2 T cells amongst TIL are significantly correlated with favourable prognosis.

Moreover, it also emerged from our studies, that a reduced frequency of V δ 1 T cells among TILs was positively associated (although not always significantly), with the severity of melanoma, SSC, and CRC [81,64]. This include also the NKp46⁺ V δ 1 IELs subset which was substantially scarce in the intestinal tissues surrounding the tumor mass in patients with CRC and the low frequency of NKp46⁺ V δ 1 IELs correlated with rapid tumor progression toward metastatic disease [75]. Interestingly, a recent report showed that NKp46-mediated production of IFN- γ by NK cells is able to control tumor progression and decreases metastasis *in vivo* [84].

$\gamma\delta$ T cells may play a pro-tumor role not only by producing IL-17, but also by the adoption of suppressive functions that impair dendritic cell maturation and functions. For instance, an immunochemistry study on breast cancer specimens [85] has revealed massive infiltration by $\gamma\delta$ T cells that correlates positively with advanced tumor stages and the presence of lymph node metastasis, and negatively with patient survival.

Moreover, in a murine model of pancreatic ductal cancer, $\gamma\delta$ T cells in the tumor tissue express the programmed death ligand 1 (PD-L1) and suppress CD4⁺ and CD8⁺ T cell recruitment and function [86]. It remains to be established whether PD-L1 expression by $\gamma\delta$ T cells is exclusive to the pancreatic microenvironment or extended to other tumor types. PD-1 is upregulated by *in vitro* activated V δ 2 T cells and modulates IFN- production [87], but it is unclear how long is PD1 expression maintained [88,89].

Therefore, there is a urgent need to in deep characterize human $\gamma\delta$ T lymphocytes at the site of tumor and in adjacent healthy tissue in order to understand their impact on cancer progression.

7. TUMOR MICROENVIRONMENT IMPARTS DISTINCT FUNCTIONAL FEATURES ON $\gamma\delta$ T CELLS.

The mechanism responsible for the massive reduction of V δ 1 TILs in CRC patients remains unknown. Possible hypothesis includes terminal differentiation and exhaustion of the V δ 1 T cell subset due to repeated stimulation by the V δ 1 TCR ligands, MICA/MICB, which are overexpressed in colon cancer cells. Other possibilities include, activation-induced V δ 1 T cell anergy and death by neglect drive by inadequate signals delivered during activation, or V δ 1 T cell intrinsic features. Finally, alterations in the normal microbiota as occurs in CRC [61], influenced by many factors, and/or increases in immunosuppressive cytokines in the CRC microenvironment, can result in loss of V δ 1 T cells at mucosal level (reviewed in [90]).

To investigate the reciprocal interactions between the tumor environment and $\gamma\delta$ T cells present in TILs, we purified colon cancer stem cells (CSC) and colon cancer-associated fibroblasts (CAF) from tissue samples of CRC patients, cultured them in medium and tested the effect of the 48-hrs culture supernatants on polyclonal $\gamma\delta$ T cell lines (containing both V δ 1 and V δ 2 T cells) obtained from the peripheral blood of healthy donors [64]. We found that supernatants from colon CSCs caused significant inhibition of $\gamma\delta$ T cell proliferation and IFN- γ production, whereas supernatants from CAF had very limited suppressive ability. The colon CSC supernatants also inhibited IFN- γ production by CD4 and CD8 $\alpha\beta$ T cells, clearly indicating that inhibitory molecules produced by colon CSC have a profound immunosuppressive effect on both adaptive $\alpha\beta$ and $\gamma\delta$ T cell subset.

We do not have evidence on the nature of the responsible molecule(s) and our attempts to its/their identification have been inconclusive so far. By comparing molecules which were

differentially overexpressed in the inhibitory supernatants from CSC and in the non inhibitory supernatants from CAF, we found out only 3 such differentially expressed cytokines IL-8, IL-12 and VEGF. By definition, IL-12 does not inhibit T cell proliferation and IFN- γ production, which eventually leaves IL-8 and VEGF as potential candidates of the immunosuppressive activities of the colon CSC secretome [64]. However, neither IL-8 and VEGF alone, or in combination, were capable to inhibit proliferation and IFN- γ production by $\gamma\delta$ T cell (our unpublished results), which leaves open the question of the nature of the suppressive molecule(s) in the CRC microenvironment. Moreover, it may also be possible that in the *in vivo* setting, suppressive molecules in the CRC microenvironment may target other cell types like dendritic cells, myeloid-derived suppressor cells, M2 macrophages and Treg cells [91,92] and thus indirectly inhibit immune responses. Finally, it is also possible that molecules/elements like prostaglandins [93], kynurenins [94] or potassium [95] may be responsible for the immunosuppressive activity.

The immunosuppressive tumor microenvironment may also explain the loss of NKp46⁺ V $\gamma\delta$ 1 T cells around the tumor mass in CRC [75]. In fact, incubation of NKp46⁺ V $\gamma\delta$ 1 T cells with the colon cancer cell line Caco2 or TGF- β (overproduced in CRC) [96] significantly inhibited their expansions.

8. WHAT HAVE $\gamma\delta$ T CELL-BASED CLINICAL TRIALS IN CANCER IMMUNOTHERAPY TAUGHT US ?

The participation of $\gamma\delta$ T cells to stress surveillance immune responses [96] and their capacity to exert numerous effector functions relevant to tumor immunology, has led to a great interest in exploring their potential use in novel immunotherapies in cancer.

A remarkable boost to the utilization of $\gamma\delta$ T cells in cancer immunotherapy came from the discovery that aminobisphosphonates (N-BP), like Zoledronate, which inhibit FPPS the downstream enzyme of the MVA pathway, cause accumulation of endogenous PAg and together with IL-2 promote activation and differentiation of human $\gamma\delta$ T cells. Assessing that N-BPs were already widely used in the clinic, in the early 2000s the Wilhelm group in Wuerzburg [98] and our group [99] conducted for the first time phase I clinical studies in hematologic and solid malignancies, respectively, using N-BPs and IL-2 *in vivo* to intentionally activate $\gamma\delta$ T cells.

Several small scale clinical trials have been conducted in patients with different types of cancer, which have used either PAg or n-BPs and IL-2 to activate V γ 9V δ 2T cells *in vivo* or adoptive T cell therapy with V γ 9V δ 2 T cell taken from patients and expanded *ex vivo*[31].

Despite a systematic assessment of safety and efficacy which includes the most recent clinical studies is missing, a meta-analysis we performed on data available up to 2014 showed that in both settings $\gamma\delta$ T cell therapy was safe and gave some clinical benefit in the short term [100].

However, more recent results rather suggest very low objective response rates which implies the need to carry out larger and double-blinded clinical studies.

Nevertheless, the results of these clinical trials, although generally disappointing, have proven useful because they have provided us several possible explanations for the long-term limited efficacy of the $\gamma\delta$ T cell therapy and how to overcome them.

First, there are clinical reasons related to the heterogeneity of the studies (low number of patients enrolled, advanced disease, previous chemotherapy, different tumor types, different protocols used to expand $\gamma\delta$ T cells *in vivo* or *ex vivo*, different treatment schedules). [31].

Second, it is known that *in vivo* administration of PAgS or N-BPs and IL-2 causes a progressive loss of $\gamma\delta$ T cell number and response and this is a critical factor in cancer patients, especially the older ones, which have significantly reduced $\gamma\delta$ T cell numbers and responses [101]. The loss of the $\gamma\delta$ T cell response is likely to be due to activation-induced exhaustion and cell death, and this in turn poses the question of whether IL-2, which has pro-apoptotic effects, is the right cytokine to achieve $\gamma\delta$ T cells *in vivo*. Accordingly, IL-15 in contrast to IL-2, promotes $\gamma\delta$ T cell activation in the absence of apoptosis [102]. In addition, IL-15 sustains those $\gamma\delta$ T cells with cytotoxic activity [78] and induces the differentiation of antigen-presenting capacity $\gamma\delta$ T cells [102] that activate classical CD8 cytotoxic T lymphocytes. Therefore, it would be desirable in future trials of $\gamma\delta$ T cell therapy to compare the effects of IL-2 and IL-15.

Third, peripheral blood neutrophils internalize N-BPs and produce hydrogen peroxide that inhibits $\gamma\delta$ T cell activation [103].

Fourth, and concerning the adoptive transfer therapy, a major issue is how to sustain *ex vivo*-expanded $\gamma\delta$ T cells, because results of few studies have been inconsistent so far [104-107].

Fifth, despite effective in activating $\gamma\delta$ T cells in the peripheral blood *in vivo*, we have no evidence until now that the administration of PAgS or N-BPs and IL-2 also promotes activation of $\gamma\delta$ T cells in the tumor microenvironment. Similarly, we lack robust evidence that adoptively-transferred $\gamma\delta$ T cells (that are usually injected intravenously) are capable to localize to the tumor site.

To be successful, $\gamma\delta$ T cell-based cancer immunotherapies certainly will require updated protocols and strategies. Thus $\gamma\delta$ T cells can be redirected to the cancer cell using bispecific antibodies or other immunoligands, in which one site binds to a tumor-specific antigen and the other binds to CD3 or the $\gamma\delta$ TCR; such bispecific antibodies have shown efficacy in preclinical mouse models[108]. Another approach is a chimeric molecule in which the variable regions of a $\gamma\delta$ TCR is linked to the Fc fragment of human IgG1[109]. This chimeric construct binds to several ovarian cancer cells and promotes the killing of the cells *via* ADCC mediated by binding of the Fc region of the chimeric construct to CD16. Moreover, it is also possible to engage $\gamma\delta$ T cells independently on the $\gamma\delta$ TCR: for instance chimeric immunoligands composed by a tumor antigen-specific single-chain variable fragment (scFv) joined to MICA or ULBP2[110] bind to NKG2D constitutively expressed by $\gamma\delta$ T cells (and other cells expressing NKG2D). Similarly, a bispecific antibody recognizing HER2, a tumor antigen, and CD16 redirects $\gamma\delta$ T cells (and other cells) which express CD16, to the tumor cell and enhance their cytotoxic activity[111].

An alternative strategy consists of the utilization of $\gamma\delta$ -based CARs such as $\gamma\delta$ T cells transduced with a CD19-specific CAR which confers to the $\gamma\delta$ T cells the capability to kill CD19 leukemia cells[112]. Other approaches consist in transducing peripheral CD3 lymphocytes (including both $\gamma\delta$ and $\alpha\beta$) with a high-affinity $\gamma\delta$ TCR[113-115] or introduce a tumor-specific $\alpha\beta$ TCR into $\gamma\delta$ T cells[116-118].

Some of the above approaches have already entered clinical trials typically in patients with hematologic malignancies and may represent attractive strategies to promote tumor cytotoxicity of $\gamma\delta$ T cells.

9. CONCLUSION

Despite some recent study has documented elevated percentages of $\gamma\delta$ T lymphocytes infiltrating different types of cancer, more recent evidence indicate that $\gamma\delta$ are detected in most human cancer types but at an average of $\sim 4\%$ of TILs.

Moreover, the nature of this association and the underlying mechanisms remain unknown to date, and whether or not the presence of tumor-infiltrating $\gamma\delta$ T lymphocytes is a definite prognostic factor similarly remains controversial.

The reciprocal interaction between tumor cells and the tumor microenvironment is a crucial topic in cancer research and therapy, as recently demonstrated by the finding that targeting stromal factors could improve efficacies of chemotherapy and prevent metastasis.

Our studies on tumor-infiltrating $\gamma\delta$ T lymphocytes from well controlled cohorts of patients with different types of solid tumors clearly show that both $\gamma\delta$ abundance and *IFNG* gene expression positively associate with better patient outcome in three different cancers , namely CRC, NMSC and melanoma. Moreover in CRC samples, this association appears significantly influenced by the tumor microenvironment, through yet unidentified suppressive molecules released from tumor cells and capable to inhibit $\gamma\delta$ T cell proliferation and IFN- γ production.

$\gamma\delta$ T cell-based immunotherapy represents an emerging therapeutic option for patients afflicted with different cancers, despite so far disappointing results in different small-scale clinical trials. It is possible that the tumor microenvironment contributes to limit their effi-

cacy. Therefore, the identification of immunosuppressive factors in the tumor microenvironment is of crucial importance when designing $\gamma\delta$ T cell-based therapy, either alone or in combination with other immunotherapies.

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CONFLICT OF INTEREST

All authors declare no conflict of interest with this review.

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LEGEND TO FIGURES

FIGURE 1.

The $\gamma\delta$ T lymphocytes in t-SNE map of a scRNAseq dataset from human PBMC. Cells are clustered according to transcriptomic similarity, constituting clouds of cells from the same lineage and subset. PBMC datasets typically comprise a group of more or less continuous T cell clusters neighbored by an NK cell cluster, a myeloid cluster encompassing monocytes and DCs, as well as a separate but compact cluster of B lymphocytes. Minor clusters of plasma cells, plasmacytoid DC, and scarce megakaryocytes or erythroid precursors are eventually observed in larger datasets. In t-SNE maps from such samples, most $\gamma\delta$ T lymphocytes are embedded between TCD4, TCD8, and NK cells, although with slight differences between cells of the TCRV δ 1 and TCRV δ 2 subset from CMV⁺ individuals. For visual clarity, the $\gamma\delta$ T cells are shown with larger symbols.

FIGURE 2.

The anti- and pro-tumor activities of $\gamma\delta$ T lymphocytes. The figure shows several different studies on the anti- or pro-tumor activities of human $\gamma\delta$ T lymphocytes in different types of cancer. Numbers inside each circle indicate refer to the reference number, while the size of the circle indicates the number of citations each study has received: for an estimation, see the lower box on the right hand side of the figure.

FIGURE 3.

$\gamma\delta$ T lymphocytes in the progression from IBD to CRC. V δ 1 T cells are the major $\gamma\delta$ T cell population in normal gut and a large fraction of intraepithelial V δ 1 T cells express Nkp46. They express IFN- γ and TNF- α and are equipped with cytolytic and anti-tumor activity.

Chronic IBD patients have a reduced frequency of gut-resident V δ 1 T cells which still maintain their effector functions, but in the gut of CRC patients V δ 1 T cells are almost completely depleted (including the NKp46+ population) and those few remaining V δ 1 T cells have lost the capacity to produce IFN- γ and TNF- α .

Gut V δ 2 T cells from healthy donors are less abundant than V δ 1 T cells, but similarly produce IFN- γ and TNF- α . Conversely, but V δ 2 T cells from the gut of chronic IBD patients show increased production of TNF- α and also produce IL-17. Finally, and similarly to V δ 1 T cells, gut V δ 2 T cells from CRC patients are massively depleted and have very limited cytokine-production capability.

The figure also illustrates the hypothesis that yet unknown soluble factors produced by several cells in the tumor microenvironment (including CAF and CSC) profoundly inhibit proliferation and cytokine production by tumor-infiltrating $\gamma\delta$ T cells.