

Tumor cell recognition by $\gamma\delta$ T lymphocytes

T-cell receptor vs. NK-cell receptors

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The dissection of the molecular mechanisms underlying tumor-cell recognition by $\gamma\delta$ T-cells is crucial to improve their performance in cancer immunotherapy. Here, we discuss the controversy around the relative contributions of the $\gamma\delta$ T-cell receptor (TCR) and natural killer receptors (NKRs) to tumor-cell targeting by $\gamma\delta$ T cells.

$\gamma\delta$ Cells: T Cells with an NK Character

$\gamma\delta$ cells constitute the prototype of unconventional T lymphocytes that are not restricted by classical MHC-mediated antigen presentation. Instead, these innate-like lymphocytes are thought to directly recognize molecular “indicators of stress” in dysfunctional cells (such as tumor cells), against which they exert potent cytolytic activity.^{1,2} This establishes a clear functional parallel between $\gamma\delta$ cells and their lymphoid relatives, natural killer (NK) cells.³ This parallel was also evident upon genome-wide expression analyses that highlighted the similarities between the transcriptional profiles of activated human V γ 9V δ 2 $\gamma\delta$ T-cell lines and NK cells.⁴ An additional key characteristic shared by these two lymphocyte subsets is the expression of a wide set of germline-encoded receptors that were initially described in NK cells and hence are collectively known as “NK receptors” (NKRs). These include killer-activating receptors (KARs), such as NKG2D, CD94/NKG2C, DNAX accessory molecule-1 (DNAM-1), NKp30 and NKp44^{5–7}; and killer-inhibitory receptors

(KIRs), like CD94/NKG2A, ILT2, CD161 or KIR2DL 1–3.^{5,8}

This said, there is a key difference between $\gamma\delta$ T and NK cells, i.e., the expression of a somatically rearranged TCR (which in this case is a heterodimer of γ and δ chains) by the former but not the latter. Alike its $\alpha\beta$ counterpart, the $\gamma\delta$ TCR was considered as the dominant receptor for tumor-antigen recognition by $\gamma\delta$ cells.⁵ This view has been challenged by a consistent set of reports highlighting the importance of activating NKRs in cancer-cell recognition by human and mouse $\gamma\delta$ cells. Here, we discuss this controversy and propose that $\gamma\delta$ cells rely on the TCR $\gamma\delta$ for the perception of “danger” (often pathogen)-associated molecular patterns and on NKRs for the actual discrimination between (“stressed”) tumor cells and their (“healthy”) non-transformed counterparts.

$\gamma\delta$ TCR-Mediated Tumor Cell Recognition?

In the early 1990s, the distinct patterns of cytotoxicity of human $\gamma\delta$ T and NK-cell clones from the same individuals was interpreted as suggestive of TCR-dependent tumor cell recognition by $\gamma\delta$ T cells.⁹ However, the global lack of success in identifying $\gamma\delta$ TCR ligands (including in the tumor context) has severely limited the credit given to this hypothesis.

It is known since the mid-1990s that the major $\gamma\delta$ T-cell subset in the human peripheral blood, V γ 9V δ 2 cells, are uniquely activated by non-peptidic prenyl-pyrophosphate antigens

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Abbreviations: NK, natural killer; IFN γ , interferon γ ; IL, interleukin

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(phosphoantigens) such as isopentenyl pyrophosphate, (IPP) (reviewed in ref. 10). In fact, this constitutes the basis of current $\gamma\delta$ T cell-based immunotherapeutic strategies against cancer.^{11,12} Phosphoantigen-activated V γ 9V δ 2 T cells can recognize and kill a large variety of tumor cell lines in vitro and in vivo (in xenograft models), including breast, colon and nasopharyngeal carcinoma, melanoma, pancreatic adenocarcinomas and a particularly large panel of hematological tumors.^{12–15}

As IPP constitutes an intermediate of the mevalonate pathway of isoprenoid biosynthesis that significantly increases upon malignant transformation, it might act as a “tumor-associated antigen” for V γ 9V δ 2 cells.¹⁶ Furthermore, since the reactivity of V γ 9V δ 2 T cells to phosphoantigens can be abolished with TCR-blocking antibodies and conferred by the transfer of V γ 9V δ 2 TCR-coding genes,¹⁷ phosphoantigens were postulated to act as V γ 9V δ 2 TCR ligands. However, no direct binding could ever be demonstrated in vitro between the V γ 9V δ 2 TCR and phosphoantigens, including those of microbial origin, such as (E)-4-hydroxy-3-methylbut-enyl pyrophosphate (HMBPP), which possess a much higher bioactivity (in the picomolar rather than in the micromolar range) than IPP.⁵

These important limitations raised the possibility that phosphoantigens trigger the V γ 9V δ 2 TCR by indirect means. In 2005, Scotet et al. proposed that the ecto- F_1 ATPase, a form of the mitochondrial ATP synthase ectopically expressed at the cell membrane, would form a complex with the serum protein apolipoprotein A1 (ApoA1) that would be recognized by the V γ 9V δ 2 TCR and would underpin the presentation of endogenous phosphoantigens.^{5,18} Consistent with this, F_1 ATPase-coated beads were later shown to stably bind an adenylated derivative of IPP, and to promote V γ 9V δ 2 TCR aggregation, cytokine secretion and cytotoxicity.¹⁹

More recently, Scotet and collaborators have identified a new potential link between phosphoantigens and V γ 9V δ 2 TCR activation.²⁰ This seems to require the conformational modification and/or clustering of CD277 (butyrophilin 3) molecules in target cells, which in turn depends on intracellular accumulation of

phosphoantigens. The effects of both agonistic and blocking anti-CD277 monoclonal antibodies on V γ 9V δ 2 TCR transductants indicate that the TCR is necessary for such a CD277-dependent activation process.²⁰ How V γ 9V δ 2 T cells detect phosphoantigen-induced changes of CD277 remains to be determined, since the authors have not detected cognate interactions between recombinant V γ 9V δ 2 TCR and CD277.

In sum, the currently available data places phosphoantigens as clear V γ 9V δ 2 TCR agonists, even if most likely they do not operate as direct ligands. In the context of tumor-cell recognition, this raises the key question whether any putative TCR ligand, somehow linked to phosphoantigens, might indeed account for the discrimination between tumor and healthy cells.

An important study has recently identified an unexpected MHC-like protein as a cognate ligand for a V γ 4V δ 5 clone isolated from a cytomegavirus (CMV)-infected patient.²¹ This new TCR ligand is the endothelial protein C receptor (EPCR), a key component of the protein C pathway, which has been linked to endothelial barrier protection during inflammation and hypoxia. Human EPCR expression is restricted to endothelial cells (which are key targets for CMV infection in vivo), and is upregulated after cellular transformation, in particular by carcinomas. The TCR/EPCR interaction allowed $\gamma\delta$ T cells to recognize both endothelial cells targeted by CMV and epithelial tumors.²¹ However, the recognition of target cells by $\gamma\delta$ T cells required a multimolecular stress signature composed of EPCR and co-stimulatory ligand(s). The presence of EPCR protein could thus “flag” target endothelial cells, but additional factors (such as NKG2D, ILT2 and others) are likely used by V δ 2 T cells to distinguish CMV-infected and tumor cells from healthy cells.

The involvement of molecules of the MHC family in tumor-cell recognition by $\gamma\delta$ T cells is ambiguous, as they also participate in T-cell activation through NKR. For example, the interaction of human intestinal epithelial V δ 1 T cells with MHC Class I polypeptide-related sequence A (MICA)⁺ and MHC Class I

polypeptide-related sequence B (MICB)⁺ target cells occurs through MIC recognition, which drives both TCR-dependent and NKG2D-dependent stimulatory signals. Both receptors compete for binding to MIC ligands, and interaction analyses showed that MIC binding by the two receptors is mutually exclusive.²² However, surface plasmon resonance-based interaction analyses revealed strikingly different binding kinetics and affinities for TCR/MIC vs. NKG2D/MIC interactions. MIC proteins bind to NKG2D receptors with affinities (submicromolar K_D) that are nearly 1,000-fold lower than those characterizing the TCR/MIC interaction (hundreds of micromolar K_D). These data suggest a temporally ordered model for the formation of hypothetical T cell/target cell synapses, with implications for signaling mechanisms. In this setting, initial interactions at the point of contact may be dominated by NKG2D/MICA binding, which may then give way to longer-lived $\gamma\delta$ TCR/MICA complexes.²²

From a more global standpoint, if we consider most of the molecules claimed to constitute $\gamma\delta$ TCR ligands (Table 1), many do not comply with the expression pattern of tumor-associated antigens. This has led us and other researchers to consider in more detail the potential role of NKR as determinants of tumor-cell recognition by $\gamma\delta$ T cells.

NKR-Mediated Tumor Targeting by $\gamma\delta$ Cells?

Our studies with hematological tumors have highlighted a major role for activating NKR in tumor-cell recognition by human $\gamma\delta$ T cells. This was observed for both V γ 9V δ 2⁺ and V δ 1⁺NKp30⁺ T-cell subsets, in which NKG2D and/or NKp30, but not the respective TCRs, mediated leukemia/lymphoma-cell recognition.^{7,23}

NKG2D is a C-type lectin receptor shared by NK, $\gamma\delta$ T and CD8⁺ $\alpha\beta$ T lymphocytes, which recognizes MICA, MICB and UL16-binding proteins (ULBP1–6) in humans as well as Rae, Mult and H-60 in mice.²⁴ NKG2D ligands are not expressed by most normal tissues but are upregulated by many tumor-cell types, as well as by virus- or bacteria-infected cells.^{2,24,25}

Table 1. Molecules described as $\gamma\delta$ TCR ligands

Molecule(s)	Biochemistry	$\gamma\delta$ cell subset	PubMed ID (references)
DRw53 + <i>C. tetani</i> peptide	MHC-II + peptide	V γ 9V δ 2	2469770, 1345917, 2524009
Staphylococcal enterotoxin A	superantigen	V δ 2	8144918, 2377230
Staphylococcal enterotoxin B	superantigen	V δ 1	8696008
Oxidative stress response regulatory protein (OXYS)	Bacillus Calmette-Guerin protein		21526117
Apolipoprotein A-I	Lipoprotein	V γ 9V δ 2	15664160
Ecto-F1-ATPase (+ Apppl)	Mitochondrial ATPase domain	V γ 9V δ 2	15664160, 20483757
Phosphoantigens (+ undefined presenting molecule)	Prenyl pyrophosphates (bacterial/ mammalian)	V γ 9V δ 2	7584140, 7529807, 18802083
MutS homolog 2 (hMSH2)	DNA repair protein		18321859, 22433851
Histidyl-tRNA synthetase	tRNA synthetases (bacterial/ mammalian)	V γ 1.3V δ 2	22549773
Heat shock protein 60 (HSP-60)	Heat shock protein (bacterial/ mammalian)	V γ 9V δ 2	2473405, 1978758, 8094731, 18321859
MICA	MHC-Ib protein	V δ 1 ⁺	12133944, 16297874, 9497295
ULBP-4	MHC-Ib protein	V δ 2 ⁺	19436053
CD1c	MHC-Ib protein	V δ 1 ⁺	10727456, 2477705, 1690662, 12486100
CD1d + sulfatide	MHC-Ib protein + lipid	V δ 1 ⁺	22829134
Endothelial protein C receptor (EPCR)	MHC-Ib protein	V γ 4V δ 5	22885985

List of molecules (with respective biochemical nature) proposed to bind directly to $\gamma\delta$ TCRs in a particular human $\gamma\delta$ T-cell subset or clone. The published evidence (PMID provided) was based on anti- $\gamma\delta$ TCR blocking antibodies, $\gamma\delta$ TCR transfection experiments, surface plasmon resonance or co-crystallization studies.

In line with this notion, various studies have emphasized the unique contribution of NKG2D for $\gamma\delta$ T cell-mediated tumor immunosurveillance both in humans²⁶ and in mice.²⁷ Mouse $\gamma\delta$ T cells respond rapidly in vivo to the self stress antigen Rae-1 that engages their activating receptor NKG2D.²⁷ Mice lacking $\gamma\delta$ T cells are highly susceptible to cutaneous carcinogenesis and this susceptibility appears to be regulated by NKG2D expressed on $\gamma\delta$ cells.²⁸ Moreover, *Nkg2d*^{-/-} mice exhibit an impaired immunosurveillance of epithelial and lymphoid malignancies in two transgenic models of de novo tumorigenesis.²⁹ Another study has shown that the sustained localized expression of the murine NKG2D ligand Rae-1 impairs T-cell cytotoxicity in vivo and reduce tumor immunosurveillance.³⁰ In our studies with human $\gamma\delta$ T cells, the NKG2D ligand ULBP1, which is abundant in $\gamma\delta$ T cell-susceptible hematological tumors,¹³ was both required and sufficient for leukemia/lymphoma cell-recognition by V γ 9V δ 2 T cells.²³ These findings feed the general concept of NK receptors, particularly NKG2D, being key molecular determinants for the immune recognition of “oncogenic stress.”²⁴

Although nearly all V γ 9V δ 2 T cells express NKG2D on their surface, the hierarchy between NKG2D and V γ 9V δ 2 TCR signals remains highly controversial. Some studies reported the ability of V γ 9V δ 2 T cells to trigger effector responses through NKG2D stimulation alone (i.e., similarly to NK cells).^{15,25,31} However, other authors have failed to evidence an NKG2D-induced V γ 9V δ 2 T-cell activation without coincident TCR stimulation.³² In this case, NKG2D would function in $\gamma\delta$ T cells like in CD8⁺ $\alpha\beta$ T cells, i.e., as an accessory (“co-stimulatory”) receptor to the TCR (reviewed in ref. 5). Future research should clarify this issue, together with the signaling pathways that are activated in $\gamma\delta$ T cells when TCR and NKG2D are triggered individually or simultaneously.

Another NKR implicated in tumor cell recognition by V γ 9V δ 2 T-cells is DNAM-1.^{6,15} DNAM-1 ligands Nectin-like-5 and Nectin-2 are expressed on most hepatocellular carcinoma (HCC) cell lines, and antibody-based masking experiments demonstrated that the cytotoxic response of, as well as the production of IFN γ by, $\gamma\delta$ T cells exposed to HCC cells

involve interactions between DNAM-1 and Nectin-like-5.⁶

We have recently characterized a V δ 1⁺ T-cell population capable of targeting hematological tumors that are highly resistant to fully activated V γ 9V δ 2 peripheral blood lymphocytes (PBLs).⁷ We have shown that this V δ 1⁺ subset owes its specialized killer function to an increased expression of the natural cytotoxicity receptors (NCRs) NKp30, NKp44 and NKp46, which had been previously regarded as NK-specific markers. Importantly, NCRs are also clearly implicated in tumor-cell recognition by human NK cells.^{33,34} Although neither V δ 1⁺ nor V δ 2⁺ cells express NCRs constitutively, these can be selectively upregulated in V δ 1⁺ cells by AKT-dependent signals provided synergistically by γ c cytokines (IL-2 or IL-15) and TCR stimulation.⁷ Thus, NCR induction in V δ 1⁺ T cells occurs downstream of TCR activation, which provides a link between the two types of receptor signals.

We have also demonstrated that NKp30 and NKp44 are both functional in NCR⁺ V δ 1⁺ T cells, and non-redundantly contribute to the targeting of

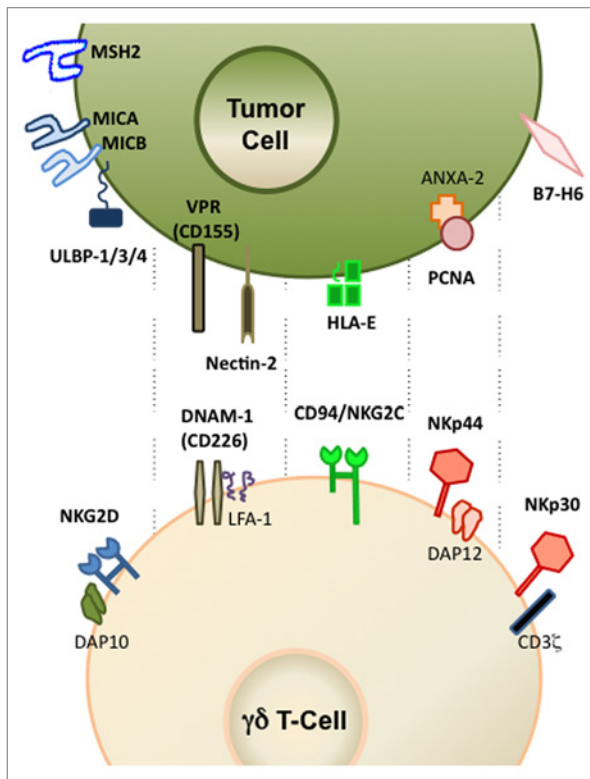


Figure 1. Activating NK receptors and corresponding ligands implicated in tumor cell recognition by human $\gamma\delta$ T cells. Depicted are also key signaling molecules associated with natural killer receptors (NKR). Additional details are provided in the main text.

lymphocytic leukemia cells, with NKp30 playing the most prominent role in this process.⁷ Of note, we tested three different $\gamma\delta$ TCR-blocking monoclonal antibodies and could not detect any reduction in tumor-cell killing by NCR⁺ V δ 1⁺ T cells. Thus, we suggest that while TCR signals are critically required for the differentiation and activation of NCR⁺ V δ 1⁺ T cells, these cells recognize tumor-cell targets through activating NK receptors, namely NKp30, NKp44 and NKG2D.

Other groups have suggested that $\gamma\delta$ T cells could recognize tumor targets through the interaction of their TCR with self-ligands that are overexpressed by tumor cells, and use NKR signals to fine-tune the cell-activation threshold (reviewed in Refs. 5, 10, 14, 35). In this scenario, the TCR-mediated activity would be tightly regulated by an interplay between activating and inhibitory NKRs.⁵ Of note, MHC Class I expression did not consistently segregate between $\gamma\delta$ T cell-susceptible and resistant tumor cell lines, thus excluding a direct “missing self” mechanism as the basis for $\gamma\delta$ T-cell

recognition of hematological tumors.¹³ This is also consistent with the observation that MHC Class I knockdown does not enhance the V γ 9V δ 2-mediated lysis of $\gamma\delta$ T cell-resistant Raji and B-cell chronic lymphocytic leukemia cells.¹⁸ Nevertheless, the contribution of inhibitory NKRs to $\gamma\delta$ T-cell activation and tumor targeting^{8,36} should be further evaluated in studies that mostly focus on activating NKRs.

Concluding Remarks

The current understanding of the role of $\gamma\delta$ TCRs in tumor-cell recognition is hampered by the limited number of tumor-associated antigens that are known to bind directly these unconventional TCRs. The fact that many of the identified ligands for human $\gamma\delta$ TCRs are molecules expressed by microbes (Table 1) suggests that $\gamma\delta$ TCRs were evolutionary selected to detect microbial molecules or metabolites. In this scenario, the sensing/recognition of self and “stressed self” components would be mainly mediated by NKRs. Building

on these considerations, our current working model propose two stages of $\gamma\delta$ T-cell activation/differentiation and tumor-cell recognition. First, $\gamma\delta$ cells are potently activated by (mostly unknown) $\gamma\delta$ TCR ligands in the presence of IL-2. This, which can be achieved for V γ 9V δ 2 cells using (microbial or synthetic) phosphoantigens (plus IL-2), endows them with potent cytolytic (and cytokine-secreting) functions, but requires a subsequent phase of target discrimination between tumor and healthy cells. We propose this is mainly determined by the binding of activating NKRs to stress-inducible proteins that selectively accumulate on the surface of tumor cells. Of note, the segregation of these two processes (activation vs. tumor cell recognition) in experimental systems requires the pre-activation of $\gamma\delta$ T cells (via their TCR) before their use against tumor targets. More importantly, we believe the integrated exploitation of these two phases will be the key for the clinical success of future $\gamma\delta$ cell-based therapeutic protocols (Fig. 1).

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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