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## Genetically retargeting CD8<sup>+</sup> lymphocyte subsets for cancer immunotherapy

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### Summary

The extraordinary sensitivity and specificity of T cells for their cognate antigen make them a highly attractive cancer therapeutic. However, the rarity of tumor-reactive T cells in cancer patients, the difficulty isolating them in sufficient numbers for adoptive immunotherapy, and the unpredictable persistence of transferred cells have been significant obstacles to broad application. Technologies that enable genetic modification of T cells have been refined and are being used to redirect the specificity of T cells to tumor antigens. An issue the field is now grappling with is how the diverse phenotypic and functional heterogeneity in T cells that could potentially be genetically modified can be capitalized upon to enhance the efficacy, safety, and reproducibility of cancer immunotherapy.

### Introduction

Gene transfer to redirect the specificity of any human T lymphocyte is a rapidly developing area in cancer immunotherapy. This approach relies on introducing genes into T cells that encode T cell receptors (TCR) specific for a tumor associated antigen, or chimeric antigen receptors (CAR) that typically consist of a single chain Fv constructed from a monoclonal antibody specific for a tumor cell surface molecule and linked to one or more T cell signaling moieties [1–3]. The initial clinical applications of adoptive immunotherapy with genetically retargeted T cells have primarily employed unselected T cells from the patient's peripheral blood for gene transfer, which ignores the considerable phenotypic diversity of T lymphocytes that have been programmed for distinct functions by previous experience [4–7]. Here, we will review the strategies being used to engineer therapeutic T cells, and discuss how the phenotypic and functional diversity of human CD8<sup>+</sup> T cells may provide opportunities to enhance cancer immunotherapy with genetically modified cells.

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## Genetic modification of T cells to confer tumor specificity

The potential for adoptively transferred T cells to eradicate human malignancies is illustrated by the graft versus leukemia effect of allogeneic T cells administered as part of a stem cell transplant [8], and by the dramatic tumor regressions that can occur in melanoma patients who receive autologous T cells derived from the tumor infiltrate and expanded *ex vivo* prior to transfer [9]. Although culture methods have improved, it is still not possible to rapidly derive tumor-reactive T cells from the blood or tumor infiltrates of most patients with cancer. Even when T cells are isolated from the endogenous repertoire, expanded, and adoptively transferred, their ability to persist and mediate antitumor activity *in vivo* has been unpredictable [10]. An approach to overcome the low frequency of tumor-reactive T cells in patients and potentially ensure predictable behavior after adoptive transfer is to redirect the specificity of T cells using gene insertion (Figure 1). Vector systems to deliver transgenes into primary human T cells have been developed and the advantages and disadvantages of the various gene delivery methods have been reviewed [11,12].

### T cell receptor gene transfer

Tumor antigens are predominantly derived from non-mutated self-proteins that are either cell lineage specific, aberrantly expressed, or overexpressed in tumor cells; and most T cells that express TCRs with high affinity for such self-determinants are eliminated by thymic selection. Although rare, moderate and high avidity T cells specific for self-antigens can occasionally be cloned from patients or healthy individuals. These T cells provide a source of TCR  $\alpha$  and  $\beta$  genes that can be used *de novo* or after mutation to increase affinity, as “off the shelf” reagents that confer tumor reactivity to T cells from any patient with the appropriate HLA restricting allele. TCR genes have been cloned that redirect specificity to several tumor antigens including MART-1, gp-100, WT-1, NY-ESO-1, and CEA [13–17].

A problem with TCR gene transfer is mispairing of the introduced TCR chains with the endogenous TCR chains, creating potentially deleterious reactivity with normal host tissues [18]. Such off-target toxicity has not been definitively observed in the small clinical trials that have been performed thus far [19,20], however studies in animal models have clearly demonstrated the potential for toxicity resulting from acquired self reactivity as a consequence of mispairing in TCR gene-modified T cells [21]. The potential for toxicity can be minimized by modifications to the design of TCR transgenes that promote appropriate pairing of the introduced chains [18], and by the selection of defined T cells as recipients of TCR gene transfer, such as TCR $\gamma\delta$  cells that lack endogenous  $\alpha\beta$  chains, or virus-specific T cells that utilize a very limited endogenous TCR repertoire [21,22].

### Chimeric antigen receptor gene transfer

Redirecting T cells to recognize tumor antigens through TCR gene transfer is inherently constrained by the requirement for MHC restricted peptide presentation by tumor cells. Chimeric non-MHC restricted artificial receptors that recognize tumor cell surface molecules have been developed to overcome this limitation. A CAR is typically comprised of a fusion gene that encodes monoclonal antibody-derived single chain variable fragments (scFv), consisting of heavy ( $V_H$ ) and light ( $V_L$ ) chains joined by a flexible linker, and then fused through a transmembrane domain to cytoplasmic signaling moieties consisting of CD3 $\zeta$  alone, or CD3 $\zeta$  combined with activation domains from costimulatory molecules [2]. As with TCRs, CARs have been constructed for many tumor-associated molecules including CD19, CD20, EGFR, Her2neu, GD2, PSMA, CAIX and ROR1 [23–29].

## Heterogeneity of peripheral blood CD8<sup>+</sup> T cells

Several clinical trials in which polyclonal T cells are obtained from the peripheral blood, genetically modified with either a TCR or a CAR, expanded, and re-infused into the patient are in progress. Impressive antitumor activity has been observed in some trials, but inconsistent T cell persistence and serious toxicities that are often not fully explained have also been reported [17,30,31]. A factor that is emerging as an important variable is the potential for vast differences in the composition of T cell products if unselected T cells are used for genetic modification. For brevity, this review will focus on heterogeneity in human CD8<sup>+</sup> T cell subsets and the implications for deriving genetically modified T cells for adoptive therapy, however the issues discussed are equally germane for redirecting CD4<sup>+</sup> T cells for tumor reactivity.

A variety of phenotypic and functional subsets of CD8<sup>+</sup> T cells are present in peripheral blood, and this heterogeneity ensures appropriate responses to neo-antigens and to antigens to which the host has been previously exposed (Figure 2). CD8<sup>+</sup> T cells are broadly divided into CD45RA<sup>+</sup> antigen inexperienced naïve T cells (T<sub>N</sub>) that contain the greatest diversity of endogenous T cell receptors [32], and express CD62L<sup>+</sup> and CCR7<sup>+</sup> to enable their transit through lymph nodes where they survey for foreign antigens; and CD45RO<sup>+</sup> memory T cells that have clonally expanded in response to prior antigen encounter, and can be subdivided into CD62L<sup>+</sup> central memory (T<sub>CM</sub>) and effector memory (T<sub>EM</sub>) subsets [33]. In humans, the CD45RO T<sub>CM</sub> and T<sub>EM</sub> subsets have recently been shown to contain a major population of distinct CD161<sup>hi</sup>, IL-18R $\alpha$ <sup>hi</sup> T cells that remain to be fully characterized but differ significantly in functional properties from their CD161<sup>lo</sup> counterparts [35–37]. A subset of memory T cells with a CD44<sup>lo</sup>CD62L<sup>hi</sup>Sca-1<sup>hi</sup>CD122<sup>hi</sup> bcl-2<sup>hi</sup> phenotype that is intermediate between that naïve and memory cells was identified in a murine model of graft versus host disease (GVHD) and suggested to represent a “memory stem cell” based on the ability to self-renew, and give rise to effector (T<sub>E</sub>), and T<sub>CM</sub> and T<sub>EM</sub> subsets [34]. A counterpart for this memory CD8<sup>+</sup> T cell has not been reported in viral infections in mice or in humans, and whether specialized CD8<sup>+</sup> T cells with stem cell qualities develop after antigen exposure remains unproven.

An important consideration for genetic modification of T cells is that the proportion of each of the T<sub>N</sub>, and CD161<sup>hi</sup> and CD161<sup>lo</sup> T<sub>EM</sub> and T<sub>CM</sub> subsets in the blood of normal individuals and cancer patients can vary dramatically depending on age, pathogen exposure, and prior chemotherapy [5,35,37]. This heterogeneity poses a potential variable that could impact safety and efficacy of cancer immunotherapy if polyclonal unselected cells derived from the blood are genetically modified with TCR or CAR genes. Indeed, recent data suggests that depending on the clinical situation it may prove valuable or even essential to select T cells for therapy from a defined subset, or of singular antigen specificity.

### Properties of effector cells derived from CD8<sup>+</sup> T<sub>CM</sub> and T<sub>EM</sub>

The longevity of T cell memory is a cardinal feature of adaptive immunity, and the cell intrinsic and extrinsic mechanisms that determine memory cell differentiation and survival continue to be intensively studied [38,39]. Adoptive transfer studies in humans demonstrated that virus-specific T<sub>E</sub> cells could be isolated and expanded from the memory pool of immune hematopoietic stem cell donors, expanded in vitro as clones or polyclonal populations and transferred to transplant recipients to restore durable immunity [40,41]. However, whether T<sub>E</sub> cells from the T<sub>CM</sub> or T<sub>EM</sub> subsets contributed more or less to reconstitution was unknown.

Studies using gene-marked virus-specific T<sub>E</sub> cells in non-human primates have now demonstrated that T<sub>E</sub> cells derived from the CD62L<sup>+</sup> T<sub>CM</sub> subset rather than the T<sub>EM</sub> subset

possess a markedly superior capacity to survive in vivo, revert to a memory phenotype, and establish long-lived immunity that is capable of responding to antigen challenge [42,43]. In these studies, the transferred T<sub>E</sub> cells were clonally derived and had uniformly upregulated granzyme B and perforin, and downregulated CD62L, CCR-7, CD127 and CD28. Despite the similarities in differentiation markers at the time of infusion, only T<sub>E</sub> cells derived from T<sub>CM</sub> reacquired memory markers and established reservoirs of CD62L<sup>+</sup> CCR-7<sup>+</sup> CD28<sup>+</sup> T<sub>CM</sub> that largely resided in lymph nodes, and CD62L<sup>-</sup> T<sub>EM</sub> in the blood and bone marrow. This result suggested that T<sub>CM</sub>-derived T<sub>E</sub> retain a cell-intrinsic capacity to revert to a quiescent memory cell through cloning, effector differentiation, and long-term culture [42]. A similar analysis of polyclonal human T<sub>CM</sub>- and T<sub>EM</sub>-derived T<sub>E</sub> cells has been performed using NOD/SCID/ $\gamma$ c<sup>-/-</sup> (NSG) mice as recipients of the transferred T cells. Here again, T<sub>CM</sub>-derived T<sub>E</sub> exhibited vastly superior engraftment and antitumor activity [44]. Moreover, analysis of the TCR V $\beta$  repertoire of persisting human T cells in the NSG mice suggest that longevity is a general property of T<sub>CM</sub>-derived T<sub>E</sub>, and not confined to a rare subset of cells [44].

### Gene transfer into virus-specific memory T cells

While animal model data has identified superior in vivo persistence of T<sub>CM</sub>-derived T<sub>E</sub>, it is premature to conclude that virus-specific or polyclonal CD8<sup>+</sup> T<sub>CM</sub> should be selected for introducing tumor-targeting receptors for adoptive therapy in all circumstances. However, this strategy may improve safety and be necessary in some clinical settings. For example, genetic modification of unselected T cells from an allogeneic stem cell donor with a TCR or CAR to direct specificity to leukemia and augment the graft versus leukemia effect after allogeneic stem cell transplant is likely to be complicated by GVHD mediated by T cells in the product that have an alloreactive endogenous TCR. Donor CMV and EBV-specific T cells do not cause GVHD in the allogeneic transplant setting, thus selecting such virus-specific cells from T<sub>CM</sub> to genetically modify with a CAR or TCR to treat leukemia should improve safety. As previously discussed, selecting virus-specific T cells for TCR gene transfer will also limit the endogenous TCR repertoire available for cross-pairing of the introduced TCR. Furthermore, stimulation through the endogenous virus-specific TCR during episodes of viral reactivation or by vaccination could promote selective activation, survival and expansion of the transferred cells, and potentially overcome tolerance mechanisms [45].

Modifying virus-specific memory cells rather than unselected T cells may also have advantages for autologous cell therapy. In a clinical trial performed by Brenner et al, eleven neuroblastoma patients were treated with cell products that contained both EBV-specific T cells and anti-CD3 activated T cells that were retrovirally transduced with a GD2-specific CAR [46]. Sequence differences in the vectors used to transduce EBV-specific or  $\alpha$ CD3-stimulated T cell preparations enabled measurement of persistence of the two products, which suggested that EBV-specific CAR-transduced T cells were better equipped to survive after transfer.

### CD161<sup>hi</sup> CD8<sup>+</sup> memory cells

Several recent papers have shed light on the function of a specialized subset of CD45RO<sup>+</sup> CD8<sup>+</sup> memory cells characterized by high levels of CD161 expression. In the course of studies analyzing chemotherapy resistance of human T cells, we identified CD8<sup>+</sup> T cells that rapidly effluxed fluorescent dyes based on high levels of ABC transporter activity and found that these effluxing cells were distinguished by the expression of high levels of CD161 and IL-18R $\alpha$  [35]. CD161<sup>hi</sup> CD8<sup>+</sup> T cells represent a significant fraction of the total circulating CD8<sup>+</sup> memory pool in normal donors, and are characterized by uniform expression of CD28 and CD27, and high levels of bcl-2 and bcl-xl. In a series of elegant papers, Lantz and

colleagues have shown that CD161<sup>hi</sup> CD8<sup>+</sup> T cells comprise an innate-like subset that expresses a semi-invariant TCR V $\alpha$ 7.2-J $\alpha$ 33 that confers specificity for undefined bacterial ligands presented by the MHC class Ib MR1 molecule [37,47,48]. CD161<sup>hi</sup> cells also express tissue homing integrins and preferentially localize to liver and gastrointestinal tract [37]. Analysis of the functional properties of this subset of CD8<sup>+</sup> T cells remains incomplete but in addition to IFN- $\gamma$ , CD161<sup>hi</sup> CD8<sup>+</sup> T cells produce IL17 after PMA/ionomycin stimulation [35–37]. Because these T cells have enhanced resistance to certain chemotherapy drugs, they may be further enriched in the blood of cancer patients. Thus, if peripheral blood T cells from cancer patients are genetically modified in bulk, the expression of tumor-targeting receptor in these peculiar but prevalent memory T cells is likely to occur to some degree, with uncertain clinical consequences. Infiltration of normal colon with CD8<sup>+</sup> T cells and serious colitis was observed in 3/3 patients treated with autologous T cells modified with a CEA-specific TCR for metastatic colorectal cancer [17]. This was presumed to be due to recognition of CEA on normal colonic cells by the transferred gene modified cells raising the interesting possibility that the preferential gut-homing properties of certain subsets of CD8<sup>+</sup> T cells might contribute to toxicity.

### CD8<sup>+</sup> naïve T cells

As noted above, T<sub>N</sub> have clear disadvantages for immunotherapy in the allogeneic stem cell transplant setting because this subset has been shown to be primarily responsible for GVHD [49]. However, T<sub>N</sub> exhibit many traits that could be advantageous when genetically modifying autologous T cells for adoptive therapy. Elegant cell transfer studies in mice have indicated that a single T<sub>N</sub> can give rise to T<sub>E</sub>, T<sub>CM</sub>, and T<sub>EM</sub> cells, illustrating both the proliferative and differentiation potential of this subset [50]. In a murine TCR transgenic model, superior tumor elimination was demonstrated after transfer of engineered T<sub>E</sub> derived from T<sub>N</sub> compared to those derived from T<sub>CM</sub> and T<sub>EM</sub>, and this was linked to less upregulation of KLRG-1, which is a marker of a terminal effector cell [51]. The properties of human T<sub>E</sub> cells derived from T<sub>N</sub>, T<sub>CM</sub>, and T<sub>EM</sub> and modified with a tumor-specific TCR have thus far only been compared in vitro. These studies demonstrated that T<sub>N</sub> cells were easily transduced, and the derived T<sub>E</sub> cells exhibited greater proliferation without acquiring markers of late effector differentiation, and retained longer telomeres -- traits that would be preferred in therapeutic T cell products [52]. However, in the absence of in vivo experiments, it remains uncertain whether T<sub>N</sub> that are expanded and differentiated in vitro will have the cell-intrinsic properties that have been convincingly demonstrated to confer long-term survival of adoptively transferred CMV and EBV-specific T<sub>E</sub> cells. The answer to this critical question will require carefully designed clinical adoptive transfer studies.

A potential advantage of T<sub>N</sub> is their plasticity, which could enable modifications of culture conditions to direct cell fate decisions. For example, an in vitro counterpart of the memory stem cell identified in murine GVHD studies has been generated by chemical augmentation of Wnt signaling during in vitro priming of murine TCR transgenic CD8<sup>+</sup> T cells, which led to upregulation of Tcf-1 and Lef-1 and arrested the acquisition of effector function [53]. After adoptive transfer, these T cells exhibited enhanced in vivo recall responses and antitumor activity in murine models compared with T<sub>CM</sub> and T<sub>EM</sub>. In vivo pharmacologic manipulation of mTOR activation and fatty acid metabolism has also been demonstrated to augment the generation of memory T cells during priming in animal models [54,55]. These results suggest that altering signaling pathways involved in directing cell fate decisions might be used in vitro during genetic modification to derive T cells with selected qualities that promote in vivo persistence and function.

## Conclusions

The past decade has seen an apparent coming of age of T cell adoptive immunotherapy for cancer, due in large part to the success in melanoma where the use of lymphodepleting therapy before T cell transfer led to improvements in the in vivo persistence of transferred cells and therapeutic efficacy, and to advances in T cell genetic engineering. Our understanding of the fundamental properties of heterogeneous subsets of T cells is also evolving and suggests that selection of defined populations for gene modification may be necessary to capitalize fully on the opportunities for adoptive immunotherapy for cancer. Clinical investigation of distinct cell populations will require the development of improved cell sorting and selection technologies that enable cell manipulation without compromising function, and current approaches have serious limitations in this regard. It is also imperative that future clinical trials incorporate detailed characterization of the cell products that are infused and sophisticated monitoring of their fate, migration and function in vivo, to provide insight into the basis for therapeutic success and toxicity, and direct subsequent investigation.

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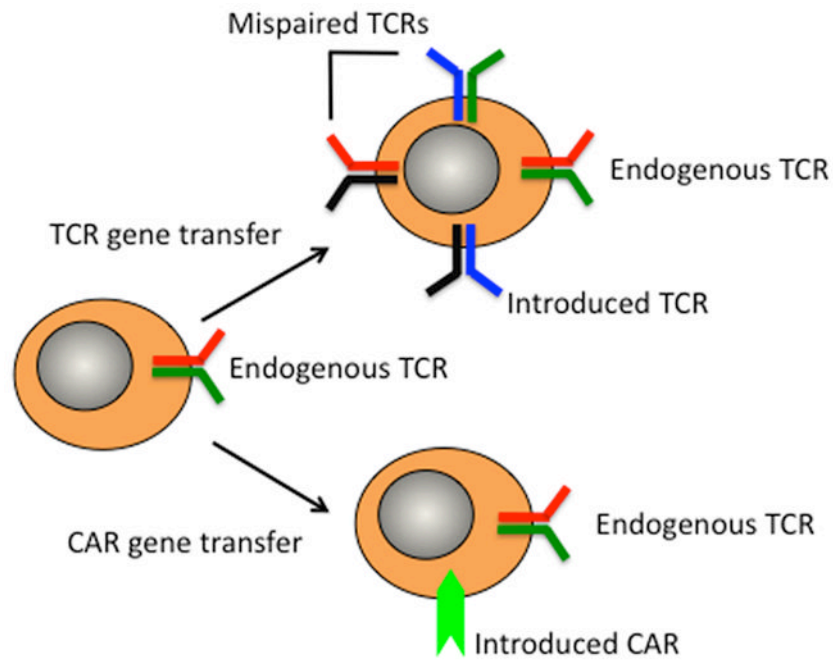
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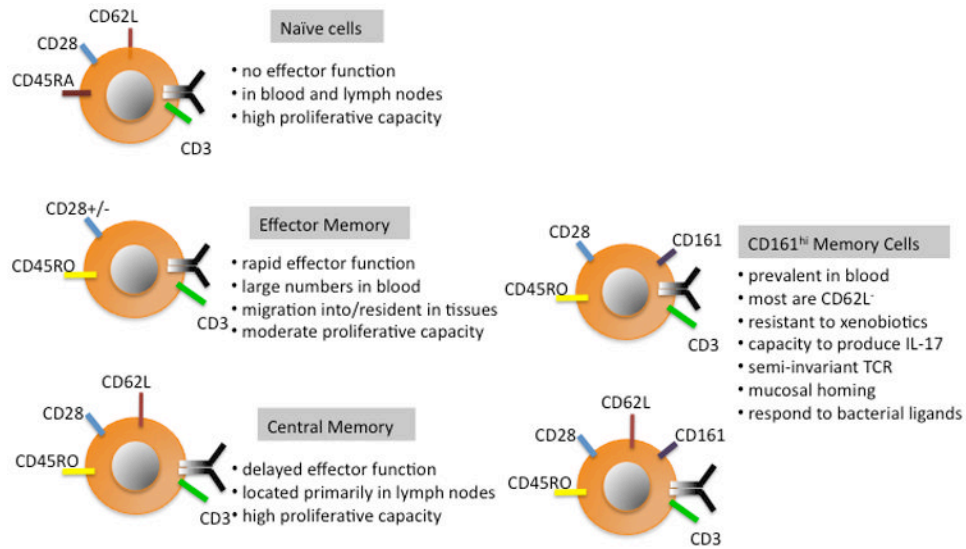
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**Figure 1. Redirecting T cell specificity by insertion of genes encoding a TCR or CAR**  
Peripheral blood T cells (or selected subsets) are activated and exposed to a gene delivery vector to introduce a tumor targeting T cell receptor (TCR) or chimeric antigen receptor (CAR). In the case of TCR introduction, the possibility of mispairing with endogenous  $\alpha$  and  $\beta$  chains leads to the potential for four receptors to be expressed on the transduced cell.



**Figure 2. Surface markers and functional attributes of major subsets of CD8<sup>+</sup> T cells in peripheral blood**

CD8<sup>+</sup> T cells can be identified as naïve or memory based on the acquisition of the CD45RO isoform on memory cells. Memory cells can then be broadly subdivided into CD161<sup>hi</sup> and CD161<sup>lo</sup> subsets. Within the CD161<sup>lo</sup> pool of memory cells, the expression of CD62L distinguishes functionally disparate central (T<sub>CM</sub>) and effector memory (T<sub>EM</sub>) subsets, although it should be noted that there are cells with an overlapping phenotype. The CD161<sup>hi</sup> memory cells are predominantly CD62L<sup>-</sup> and differ in specificity and function from CD161<sup>lo</sup> memory cells. The functional properties of the small subset of CD62L<sup>+</sup>CD161<sup>hi</sup> cells have not been separately evaluated.