The function and dysfunction of memory CD8⁺ T cells in tumor immunity 1 2 James L Reading*+1,2, Felipe Gálvez-Cancino*3, Charles Swanton4, Alvaro 3 Lladser³, Karl Peggs^{1,2} and Sergio A Quezada^{+1,2} 4 *Contributed equally. 5 *Corresponding author(s) 6 s.quezada@ucl.ac.uk (+44)20 7679 0743 7 J.reading@ucl.ac.uk 8 9 1. Cancer Immunology Unit, University College London Cancer Institute, 10 University College London, London WC1E 6DD, U. K. 11 2. Research Department of Haematology, University College London Cancer 12 Institute, University College London, London WC1E 6DD, U. K. 13 3. Laboratory of Gene Immunotherapy, Fundación Ciencia & Vida, Santiago, 14 Chile. 15 4. The Francis Crick Institute, London NW1 1AT, U. K. 16 17 18 19

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Abstract: The generation and maintenance of CD8⁺ T cell memory is crucial to longterm host survival, yet the basic tenets of CD8+ T cell immunity are still being established. Recent work has led to the discovery of tissue-resident memory cells and refined our understanding of the transcriptional and epigenetic basis of CD8+ T cell differentiation and dysregulation. In parallel, the unprecedented clinical success of immunotherapy has galvanized an intense, global research effort to decipher and derepress the anti-tumor response. However, the progress of immunotherapy is at a critical juncture, since the efficacy of immuno-oncology agents remains confined to a fraction of patients and often fails to provide durable benefit. Unlocking the potential of immunotherapy requires the design of strategies that both induce a potent effector response and reliably forge stable, functional memory T cell pools capable of protecting from recurrence or relapse. It is therefore essential that basic and emerging concepts of memory T cell biology are rapidly and faithfully transposed to advance therapeutic development in cancer immunotherapy. This review highlights seminal and recent reports in CD8+ T cell memory and tumor immunology, and evaluates recent data from solid cancer specimens in the context of the key paradigms from preclinical models. We elucidate the potential significance of circulating effector cells poised downstream of neoantigen recognition and upstream of T cell dysfunction and propose that cells in this immunological 'sweet spot' may prolong survival and serve as the substrate for checkpoint blockade.

Naïve T cell activation

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CD8+ T cell responses are initiated in secondary lymphoid organs (SLOs) when naïve 46 CD8+ T cells (Tn) are activated by migratory dendritic cells (DC) presenting antigen-47 derived peptides loaded on major histocompatibility complex (MHC) class I molecules. 48 Tn cells carrying epitope-specific T cell receptors (TCR) may undergo activation, 49 dysfunction, survival or deletion, contingent upon the following interdependent 50 variables: i) the cytokine/chemokine/metabolite milieu, ii) status of the dendritic cell 51 (DC) (e.g. activation, co-stimulatory/adhesion molecule profile, tissue of origin), iii) 52 53 TCR affinity for presented peptide, iv) epitope antigenicity (amino acid sequence, MHC binding affinity, concentration) v) presence/quality of CD4+ T cell help and vi) duration 54 and frequency of contact at the immunological synapse 1-5. During acute viral infection, 55 56 Tn recognize antigenic peptides presented by migratory DC that have sensed pathogen- or danger-associated molecular patterns (e.g. dsRNA via TLR3) and 57 subsequently expressed co-stimulatory molecules (e.g. CD80/CD86, CD40L, OX40L, 58 41BBL, CD70). After receiving sufficient signal 1 (TCR signaling), signal 2 (co-59 stimulation e.g. CD80/CD86) and signal 3 (inflammatory cytokine e.g. IFNα/β, IFNy, 60 61 IL-2, IL-12, IL-21, IL-33, TNFα), CD8+ T cells clonally expand and give rise to vast numbers of effector CD8+ T cells (Teff). Teff subsequently migrate to the infected 62 63 tissue through the bloodstream via chemokine receptor (e.g. CCR5) and adhesion 64 molecule (e.g. LFA-1) interactions where they recognize their cognate peptide:MHC-I complex on target cells and exert cytolytic functions (secretion of perforin, GZMb, 65 TNFα, IL-2, IFNy) to lyse infected cells. Following the effector phase, 90-95% of Teff 66 cells undergo apoptosis whilst a pool of clonally expanded, antigen-experienced cells 67 persist to provide durable immunological memory ⁶. Memory T cells are present at 10-68 100 times their precursor frequency, and bear a distinctive migratory, molecular, 69

epigenetic, metabolic, phenotypic and functional profile relative to Tn and Teff cells ⁶⁸. These properties enable memory T cells to traffic throughout the blood, SLOs and tissues in a quiescent state yet hyper-proliferate and elicit augmented effector responses during antigen re-encounter; thereby coordinating rapid pathogen elimination.

CD8⁺ memory T cell generation

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Several studies have suggested that T cells are programmed to become memory during the early stages of the priming phase 9. In vaccinated humans, memory CD8+ T cells arise from a rapidly dividing effector pool formed in the first 14 days post challenge, subsequent to re-engagement of naïve like chromatin landscapes 10. Similarly, in the lymphocytic choriomeningitis virus (LCMV) model, long-lived memory CD8⁺ T cells emerge from de-differentiation of fate-permissive Teff cells ¹¹. These findings concur with single cell RNAseq (scRNAseq) analysis of early CD8+ T cell specification during adoptive transfer in the LCMV model, in which Teff and memory differentiation emerge from an early burst of transcriptional activity followed by epigenetic refinement ¹². Work in the *Listeria monocytogenes* and LCMV models have previously classified subsets of Teff cells based upon their ability to give rise to memory CD8⁺ T cells. These precursor subsets are defined by differential expression of the IL-7 receptor (CD127) and the killer cell lectin-like receptor G1 (KLRG1). Memory precursor effector cells (MPEC; CD127^{hi}KLRG1^{neg}) are characterized by BCL2 expression, a longer lifespan and proliferative potential in response to homeostatic cytokines (IL-7/IL-15) or antigenic re-challenge, whilst short-lived effector cells (SLEC; CD127loKLRG1hi) have a shorter lifespan and reduced homeostatic proliferative capacity ¹³⁻¹⁵. The recent finding that effector differentiation precedes memory formation is complicit with this 'separate precursor' model, and the long-held knowledge that memory potential is non-equivalent amongst Teff cells, since certain effectors may preferentially re-engage naïve like programs that specify memory fate. Although not necessarily contradictory, it is also noteworthy that production of memory CD8+ T cells has also been reported to occur in the absence of an overt effector response ¹⁶.

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Data from several infection models have shown that SLEC differentiation is favored by increased signal 1 (prolonged antigen exposure, affinity/avidity/concentration low intraclonal competition) and signal 3 (elevated inflammatory cytokine burden, IFNy, IL-12 directly or via CXCR3-mediated trafficking to the infected site), whilst brief TCR stimulation, truncated infection periods (e.g. via administration of antibiotics), defects in inflammatory cytokine signaling, enhanced anti-inflammatory cytokine availability (e.g. TGFb, IL-10) or the presence of regulatory T cells promotes MPEC development or derivation of less differentiated memory subsets 15. Costimulation via CD28-CD80/CD86 is also required during priming to prevent anergy and adaptive tolerance, whilst ligation of TNF super family receptors (TNFSRs) on CD8⁺ T cells (CD27, OX40, 41BB, CD30) promotes proliferation, survival and enhances the quality of the recall response ¹⁷⁻²⁰. Similarly, ligation of HVEM receptor on CD8⁺ T cells by BTLA (on CD8α DC) is required for Teff cell survival and development of protective immune memory in response to bacterial and viral infection, in part via promoting MPEC persistence ²¹. Another key factor in the generation of memory CD8⁺ T cells is CD4⁺ T cell help. CD8⁺ T cells primed in the absence of CD4⁺ T cells have impaired long-term survival and display defective ability to respond against secondary challenge ²². The mechanisms behind the requirement of CD4+ T cells are not completely understood, however the interaction between CD40 on CD8+ T cells with CD40L on CD4+ T cells and the secretion of IL-15 from these cells have shown to be relevant in the generation Teff cells with enhanced ability to become memory ^{23,24}. More recently, CTLA-4 on CD4⁺ T regulatory (Treg) cells has been shown to force memory T cell quiescence, suggesting that helper and regulatory CD4⁺ T cell subsets may be required for optimal memory CD8⁺ T cell generation and homeostasis, respectively ²⁵.

Circulating memory CD8⁺ T cell subsets

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Memory CD8+ T cells are heterogeneous, and can be defined as one of four major subsets according to their surface markers, effector potential, stemness and ability to home lymphoid organs and non-lymphoid tissues (Figure 1). Circulating memory CD8+ T cells can be classified as stem central memory (Tscm), central memory (Tcm) and effector memory (Tem), whereas memory CD8+ T cells that become established within the infected/challenged tissue and do not re-circulate are termed tissue resident memory (Trm). Tscm cells are present in mouse, human and non-human primates and are endowed with the greatest stem potential of all memory subsets, allowing them to give rise to Tcm and Tem cell populations upon antigen stimulation²⁶. Tscm cells have a naïve-like phenotype with low expression of CD44 (mouse), high levels of CD62L and co-express antigen-experienced CD8+ T cells molecules such as CD122, the Stem Cell Antigen 1 (SCA-1), B cell lymphoma 2 (BCL-2), CXC-chemokine receptor 3 (CXCR3), and CD95 ²⁶. Tcm and Tem cells were originally described in mouse and human based on the expression of CD44, CCR7 and CD62L, and CD45RO and CCR7 respectively ²⁷. Tcm cells display reduced effector function and have a stem-cell-like phenotype given their ability to generate new Tem cells after antigen recognition ²⁸. In mice, Tcm cells are CD44+CD62L+CCR7+ while in human these cells are CD45RO+CCR7+ (and CD62L+). Expression of CCR7 and CD62L facilitate migration through the high endothelial venules (HEV) into secondary lymphoid organs, where

Tcm cells preferentially accumulate ²⁸. Tcm/Tscm cells show common transcriptomic, epigenetic and proteomic features (e.g. high basal STAT5) that cluster them separately from Tem cells ²⁹. In comparison, Tem cells are more differentiated, display a molecular fingerprint associated with Teff cell function (cytolytic Teff genes) and exhibit immediate effector function upon antigen re-encounter ³⁰. Mouse Tem cells have a CD44+CD62L- phenotype, whilst human Tem cells are defined by CD45RO+CCR7-, with KLRG1 expression being common to Tem in both species ³¹. In humans, the markers CD27 and CD28 can be used to further define circulating memory CD8+ T cells. Both markers are expressed by naïve, Tscm and Tcm cells, whereas Tem cells can be divided into Tem 1 (CD28+CD27+), Tem 2 (CD28+CD27- or CD28⁻CD27⁺), or Tem 3 (CD28⁻CD27⁻) that exhibit progressively enhanced effector potential ex vivo 32. Terminal differentiation of human CD8+ T cells is demarcated by re-expression of CD45RA within the Tem cell pool, giving rise to Temra cells (Terminally differentiated effector memory cells re-expressing CD45RA; CCR7-CD28-CD27⁻CD45RA⁺) ³³. Temra cells exhibit potent effector function, poor proliferative capacity, low IL-2 production and are enriched for phenotypic and functional (defective telomerase activity) traits of senescence ³³. One marker associated with Temra cells is CD57, which correlates with a history of extensive cell division, short telomeres, replicative senescence, ageing, cytomegalovirus (CMV) status, decreased ex vivo IFNy but enhanced cytotoxic function (i.e. GZMb and perforin expression) ³³. Temra cells may also (re)express KLRG1, which is enriched in populations specific for viruses with latency periods ³⁴. Interestingly, CD57+KLRG1⁻ and CD57+KLRG1+ CD8+ T cells retain effector function but the latter subset fail to proliferate and have diminished expression of CD27, CD28 and CD127, indicating more terminal differentiation ³⁴.

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Signals 1-3 form complex molecular circuitries, which enact key transcription factors (T-bet, Eomes, Blimp-1, Bcl-6, Tcf7, Foxo1) to determine precursor fate and memory CD8+ T cells subset differentiation. These findings have been expertly reviewed elsewhere ⁶. An oversimplified consolidation of this data is that strong TCR signals, IL-2 (inducing Tbet and BLIMP-1) and IL-12 (upregulating Tbet) favor Tem cell (and SLEC) differentiation, whilst abrupt signal 1, IL-21, IL-10, TCF7, FOXO1, EOMES and Bcl-6 support Tcm cell (and MPEC) specification, as summarized in ³⁵. Tcm cells express higher levels of the latter two transcription factors, require Bcl-6 and sustain Eomes expression via the Tcf-1-Wnt axis ³⁶. Together with augmented IL-7/IL-15driven Stat5 phosphorylation and induction of Bcl-2 this forms a module which confers enhanced survival and self-renewal to Tcm/Tscm cells relative to Tem cells ³⁷. Transcriptional networks downstream of increased inflammation and TCR signaling (which favor Teff cell development during priming) in contrast drive Tem/Temra cell differentiation ¹⁵. However, whether subset commitment depends on the malleability of a single naïve CD8+ T cell population via alterations in TCR stimulation (signal strength model) or successive rounds of antigen exposure (decreasing potential model) has been contended ^{6,38,39}. It is noteworthy that a model in which repetitive antigen exposure drives stepwise Tscm>Tcm>Tem>Temra cell differentiation is supported by recent functional, transcriptomic and proteomic data and the redistribution of these subsets following chronic immune stimulation 8,40-42. In accordance with this, CD8+ T cells in healthy human blood are predominantly of a naïve phenotype (40%), Tem and Temra cells are present at approximately equal proportions (20-25%) and a minority are of a Tcm cell phenotype ^{43,44}. However, this is highly variable between donors and changes with age or antigen experience such that Temra cells (but also to an extent Tem and Tcm cells) gradually increase at the

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expense of naïve pools ⁴⁴. This phenomenon of 'immunosenescence' is exemplified in chronic infection (e.g HIV), auto-inflammatory disease (e.g. Rheumatoid arthritis) and cancer, and can be tracked within antigen specific CD8+ T cells (e.g. HIV, CMV, EBV), where progressive differentiation may result in clonal deletion ³³. It should be noted that, despite the discrete properties and phenotypes of memory CD8+ T cell subsets observed in a variety of experimental and clinical settings, the concept of linear differentiation remains a framework imposed upon a likely fluid spectrum of cell fates; consequently, exceptions and regular revisions to this model are common and necessary. An additional layer of complexity is that phenotypes used to describe memory CD8+ T cell subsets derive largely from analysis of resting cells in the circulation. Since activation *in vitro* and *in vivo* drastically affects expression of the majority of markers used to define classical subsets, application of this nomenclature in the context of an ongoing or experimental immune responses can be challenging

Tissue resident memory CD8⁺ T cells

Tem cells within tissues were historically considered to be circulatory, however tissue-reident memory CD8+ T (Trm) cells were formally described in 2009 46 . Trm cells have been shown to stably reside in the skin, lung, intestine, brain, female reproductive tract, salivary glands and others, where they provide rapid and potent protective immunity against re-infecting pathogens $^{46-52}$. Trm cells are long-lived, mediate immediate protective immunity and are the most abundant T cell lineage in organisms with natural infection experience 53,54 . Phenotypically, Trm cells constitutively express CD69, integrin α E(CD103) β 7 (commonly referred to as CD103) and are devoid of CD62L and CCR7 55 . Given that CD103 is the ligand for E-cadherin, which is

expressed in epithelial cells, it has been proposed that CD103 is responsible for residency in epithelial tissues ⁵⁶. CD103 is also induced by TGFβ (which is key to Trm development) and competes for E-cadherin binding with KLRG1 creating a circuit in which TGFβ favors Trm cell abundance via induction of CD103 and interception of the KLRG1-E-cadherin axis ^{55,57}. CD69 upregulation abrogates tissue egress by degrading sphingosine 1-phosphate (S1P) receptor 1 (S1P1R), disabling CD8+ T cells to respond to S1P gradients, which is highly abundant in blood and lymph ⁵⁸. Interestingly, Trm cells from unrelated tissues share a core transcriptional program that is different from Tem, Tcm and Tn cells, but may also diverge on the basis of auxiliary, tissue-specific gene expression characteristics reflective of the site of origin ^{55,59-61}

Several transcription factors are involved in the generation and maintenance of Trm cells. Downregulation of Eomes during Trm cell development is necessary for CD103 induction, whereas low levels of T-bet are necessary for the expression of IL-15 receptor (a key signal for the maintenance of these cells in the tissues) ^{55,62}. Furthermore, the Trm cell differentiation program is controlled by the expression of Blimp-1 and the homolog of Blimp-1 in T cells (Hobit) transcription factors together with downregulation of the transcription factor Krüppel-like factor 2 (Klf2), which represses the expression of S1PR1 (receptor for S1P) thereby inhibiting tissue egress ^{63,64}. RUNX3 was also recently described as a transcription factor required for the establishment of Trm cells in different tissues and solid tumors, operating via induction of tissue-residency genes and the suppression of loci related to tissue egress ⁶⁵. Trm cell commitment appears to be two stage process (Bcl-2 and CD69 induction followed by CD103 expression), and Tem as well as Tcm cells can give rise Trm cells in different tissues ^{55,66,67}. It should be noted that, in a similar manner to their impact on

Tem cells, CD4⁺ T cell help has been shown to guide Trm cell formation ⁶⁸.

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Functionally, the positioning of Trm cells at sites of previous antigen encounter provides host organisms with a means of rapid response to reinfection and protection from reactivated latent viruses ⁶⁹. Upon antigen recognition, Trm cells likely mediate both immediate lytic activity via high constitutive production of GZMb and orchestrate an alarm state at the local tissue site, recruiting and activating NK cells, DC and other lymphocytes via secretion of IFNγ, IL-2 and TNFα ^{51,70,71}. Interestingly, Trm cells recruit Tem cells into the tissues in an IFNy-dependent manner, potentially inducing bystander activation since recruited populations are GZMb⁺ ^{51,72}. Two recent studies have extended these findings to show that Trm cell reactivation promotes their in situ local proliferation and the recruitment of new Trm cells into the tissues without displacement of pre-existing populations ^{72,73}. It is of relevance to tumor immunity and vaccination strategies that Trm cell induction is, intuitively, site specific. For example, cutaneous HSV infection establishes a virus-specific Trm cell pool at the challenge site, but not the contralateral flank, providing protection upon challenge in the former but not the latter ⁴⁶. Similarly heterosubtypic (cross strain) protection from influenza virus can be achieved by influenza-specific lung Trm cells generated through intranasal live attenuated influenza but not systemic administration of injectable inactivated or live attenuated influenza 74. Intriguingly, although Trm cells in various barriers sites are maintained by IL-15, their turnover and persistence also appears to be tissue and/or context-specific ⁵⁵. Trm cells in multiple target tissues have been reported to exhibit extended life spans ^{59,75}. However, unlike the skin, lung Trm cells undergo rapid turnover, with attrition after infection being partly counterbalanced by ongoing recruitment from the circulation ⁶⁶.

In humans, pioneering work to produce a spatial map of T cells in tissues using brain dead organ donors has illustrated that blood and lymph nodes have a diffuse distribution of naïve (most abundant)>Temra/Tem>Tcm (least abundant) subsets, whereas the spleen and lungs contain mainly Tem and Temra cells and in the Jejunum, Ileum and Colon are predominantly of a Temra cell phentoype (approx. 80%) ⁷⁶. Interestingly, CD103 expression was preferentially localized to the CD45RO⁺ fraction of CD8+ T cells (in the Jejunum, Ileum, colon and lung), whilst Temra cells were largely, but not entirely CD103⁻⁷⁶. Only a small fraction of Trm cells produce IFNy or IL-2 following stimulation with PMA and lonomycin (PMA/Io), thus the full scope and magnitude of effector function in human Trm cells is likely under appreciated ^{43,76}. Subsequent work by the same group demonstrated that a shift towards more differentiated phenotypes (Tem cells > Temra cells, increased %CD57⁺ cells) occurred as a function of viral specificity, age and /or CMV status in both Trm cell and circulatory compartments ^{76,77}. Of relevance, work in clinical samples unveiled that lung-derived Trm cells but not skin or circulating CD8+ T cells elicit polyfunctional responses to influenza challenge, confirming tissue-specific immunity of Trm cells seen in vivo is common to humans 78,79.

Memory CD8+ T cells and immune homeostasis

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Genetic, pharmacological or pathogen-derived memory CD8⁺ T cell deficiency or dysfunction renders the host susceptible to potentially fatal opportunistic infection and tumor development, whilst de-restricted Teff cell responses precipitate lethal autoimmunity, allergy or inflammatory tissue destruction. There is therefore strong evolutionary pressure to develop tightly regulated, multilateral mechanisms of immune homeostasis. In the memory CD8⁺ T cell pool, immune homeostasis is orchestrated

in several layers. The overall size of the CD8⁺ memory T cell pool is maintained by balancing attrition with compensatory homeostatic proliferation driven by IL-7 and IL-15 80,81. These cytokines reconstitute lymphopenic hosts by peripheral expansion which simultaneously converts naïve and Tcm cells to a Tem-like 'memory phenotype' with augmented effector potential 82,83. Memory CD8+ T cells are also restrained by a myriad of T cell intrinsic and extrinsic regulators of effector function including Treg cells, intracellular quiescence factors ^{25,84-87}, cell surface proteins involved in ATP hydrolysis (CD38, CD39, CD73) 88, antigen presenting cell-derived IFNy-inducible catabolic enzymes (i.e. IDO) 89, nitric oxide 90, arginase 1 91, prostaglandin E2 and anti-inflammatory cytokines (TGFβ, IL-10, VEGF, IL-35) 91,92 and T cell inhibitory receptors (TCIR), many of which are currently targeted or under investigation in immune oncology. The latter include well characterized receptors who's cognate ligands are expressed on various cells in the tumor microenvironment (TME) and lymph nodes, such as PD-1 (PD-L-1/PDL-2; antigen presenting cells (APC), tumor cells or epithelial cells), CTLA-4 (CD80/86 on professional APC), Tim-3 (galectin-9 on APC and tumor cells), and LAG-3 (MHC-II on APC) 93. The abundance of TCIRs is restricted to activated CD8+ T cells, and terminally differentiated Tem/Temra cells, whilst their ligands are found on activated APC or epithelial cells, illustrating spatial and temporal restriction to balance immunity and tolerance.

Memory CD8⁺ T cell dysregulation

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Perturbation of signals 1, 2 or 3 can dysregulate memory CD8⁺ T cell responses. This includes the onset of self-tolerance and anergy; two differentiation programs that share an overlapping molecular basis which manifests in hypo-responsiveness to self-peptide ⁹⁴. The deletion of autoreactive T cell clones during central tolerance is

incomplete. Therefore, peripheral self-tolerance is a necessary evolutionary strategy that prevents autoimmunity via inhibition of effector responses to cognate antigen following sub-optimal co-stimulation (i.e. in the absence of DAMP/PAMP signalling on APC). Context and system-dependent differences (including cytokine environment and TCR avidity) may bring about variable degrees of hyporesponsiveness, altering the requirement for antigen persistence, as well as the magnitude or co-occurrence of defects seen in cytokine production/proliferation, in some instances leading to T cell deletion ⁹⁴⁻⁹⁹. Self-tolerance may also result from induction of TCIRs, via suppression from immune regulatory cell populations (e.g. Treg cells) or the action of antiinflammatory cytokines/cc (e.g. IL-10) ^{94,98}. *In vivo*, tolerance can be rescued by IL-2, IL-7 or lymphopenia, but this occurs transiently with resumption of tolerance occurring in the absence of antigen, suggesting commitment to an epigenetically programmed tolerogenic cell fate 98. Similar to self-tolerance, stimulation of T cell clones with antigen or anti-CD3 in the absence of costimulation in vitro results in proliferative inhibition via a process termed anergy 100, which is rescuable via addition of exogenous cytokines 101,102. However, it has been suggested that anergy and tolerance can be discriminated on the basis of functional and molecular characteristics, despite overlapping features 94. Self-tolerance is engaged through a CD8⁺ T cell intrinsic gene expression profile distinct to naïve or memory CD8⁺ T cells. Relative to memory CD8⁺ T cells, tolerant CD8⁺ T cells exhibit enhanced expression of TCIRs (e.g. LAG-3), transcriptional repressors (EGR1/2, DUSP2), loss of key transcription factors (EOMES, T-BET, GATA-3), diminished expression of cytokine receptors and chemokine receptors (e.g. IL12RB1, CXCR3, CCR5) and crucially, lack of effector genes induction (e.g. IFNγ, PRF1) ⁹⁴. *In vitro* anergy induces NFAT in the absence of AP-1, leading to NFAT homodimers that induce Egr2, Ikaros, E2F

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transcription factors and the E3 ubiquitin ligase family which inhibit IL-2, TNF α , IFN γ and other effector genes ¹⁰³. Models of *in vivo* anergy are associated with defective calcium signaling and nuclear translocation of NFAT2 in the absence of NFAT1 leading to anergy-associated gene expression ¹⁰⁴.

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CD8+ T cells experience persistent antigen exposure in a range of pathologies and microenvironments resulting in the onset of an unconventional cell fate often described as T cell exhaustion ¹⁰⁵. During acute viral infection, host CD8⁺ T cell responses clear pathogen during the effector phase, contract and form functional memory CD8⁺ T cells. A failure to rapidly eliminate pathogen results in chronic infection, associated with unremitting antigen load and high levels of inflammation that drives exhaustion. Seminal studies using the LCMV clone 13 mouse model of chronic viral infection led to the prototypic description of exhaustion as a state of T cell hyporesponsiveness 106-¹⁰⁸. Despite common misconceptions, exhausted T (Tex) cells are not entirely devoid of effector function, since they contribute to viral control 109. Rather, Tex cells exhibit a broad spectrum of dysfunctional states, characterised by stepwise loss of i) IL-2 production ii) in vitro cytotoxicity iii) IFNγ/TNFα production, iv) degranulation and in some instances ultimately v) physical deletion ^{94,108,110,111}. Progression to a terminal Tex cell fate coincides with altered metabolism and broad expression of TCIRs including, PD-1, CTLA-4, LAG-3, CD160, BTLA and Tim-3 112-114. The severity of exhaustion has been further defined by altered transcription factor expression. In the LCMV clone 13 infection model, a circulating progenitor pool of TNFa, and IFNyproducing EOMES^{lo}PD-1^{int} Tex cells gave rise to a tissue homing, poorly proliferative, but cytotoxic EOMEShiTbetloPD-1hi Tex cell progeny upon antigen restimulation 115. Given that T-bet represses PD-1, LAG-3 and other TCIR in Teff cells, loss of this transcription factor marks transition into severe exhaustion that facilitates increased

negative signaling ¹¹⁵. Conversely, NFAT signaling enhances the expression of PD-1 and Tim-3 ¹¹⁶; thus, a balance between T-bet and NFAT may be crucial determinants of the TCIR profile of Tex cells. Interestingly BLIMP-1 and BATF also appear to display a distinct-context-dependent role in Tex cells; the former is correlated with TCIR expression but is necessary for GZMb expression, whilst the latter is induced by PD-1 signaling to suppress effector function ^{117,118}. Thus, in chronic viral infections there is a progenitor subset of Tex cells whose function is supported by T-bet which may stall severe exhaustion, whilst in progressively exhausted CD8+T cells BLIMP-1 and EOMES provide residual cytotoxic function whilst BATF and NFAT limit effector potential ¹¹⁹. It is also of note that the NFAT-EGR2 axis appears central in anergy, and thus may be a master regulator of T cell hyporesponsiveness ¹¹⁶. Targeting TCIRs with blocking antibodies has been suggested to reverse exhaustion in chronic infection and tumors, however this appears to be stage and to an extent system-dependent. In LCMV chronic infection, targeting Tim-3 and PD-1 synergistically restores effector function of CD8+ T cells 120. It has also been suggested that there is a differential sensitivity amongst TbethiPD-1intEOMESlo (reversible Tex cell phenotype) and Tbet^{neg}PD-1^{hi}EOMES^{hi} (irreversible Tex cell phenotype) subsets to PD-L1 blockade in LCMV chronic infection ^{115,121}. Similar to what has been proposed in tolerance, chronic infection appears to impose epigenetic re-programming associated with T cell exhaustion^{122,123}. In this module transcription factors, cytokine and TCR signaling loci appear in closed chromatin conformations at later stages of infection coincident with increased accessibility of the PD-1 locus 124,125. It has been suggested that this epigenetically fixed state of CD8+ T cell dysfunction is accountable for checkpoint blockade activity¹²⁶. In agreement with this, two recent reports showed that i) PD-L1 blockade in the LCMV infection model only transiently engaged effector transcriptional

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circuitry but did not alter the epigenetic landscape of Tex cells or induce functional memory T cells and ii) determined a specific epigenetic basis of Tex cells in murine and human chronic viral infections ^{122,123}. Indeed, Tex cells have been widely described in chronic viral infection of higher primates, including humans with Hepatits C virus (HCV) infection, Hepatitis B virus (HBV) induced-hepatitis and both simian immunodeficiency virus (SIV) and human immunodeficiency virus (HIV) infection ¹²⁷. CD8⁺ T cells in chronic SIV and HIV exhibit cardinal phenotypic (TCIR expression), functional and molecular features of exhaustion described above. HIV-specific resting and activated CD8+ T cells showed a TbetintEOMEShi population marked with multiple TCIRs, corresponding to the severely exhausted T cells found in LCMV chronic viral infection models ¹²⁸, whilst CMV-specific CD8⁺ T cells showed balanced EOMES and Tbet expression. HIV-specific TbetintEOMEShi CD8+ T cells exhibited a Tem1 cell phenotype with poor effector function, and persisted long after anti-retroviral therapy initiation suggesting that exhaustion was not reversed and that these cells may remain long after removal of high antigen load in humans ¹²⁸. Another report classified CD8⁺ T cells of HIV patients based on EOMES and CD57 expression showing that EOMES^{int}CD57⁺(Tbet^{hi}GZMb⁺PRF⁺) cells retained functionality and correlated with HIV control, whereas EOMEShiCD57+(TbetintGZMbintPRFlo) cells were dysfunctional ¹²⁹. A subsequent study showed that the frequency of activated/Tex cells (CD38+PD-1⁺) correlated with viral load in plasma and rapid clinical progression in HIV infection ¹³⁰. However, in line with findings in the LCMV model, it seems that Tex cells in chronic SIV and HIV infection may exert residual cytolytic function to contribute to viral control, since their depletion leads to virus rebound/disease progression in SIV ^{131,132}. CD8+ T cell exhaustion therefore appears to result from the convergence of chronic antigen stimulation and inflammation, leading to augmented TCIR signalling, de novo gene

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expression, dysregulation of CD8⁺ T cell transcription factor networks and epigenetic reprogramming.

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As mentioned above, over-differentiation or immunosenescence of the CD8+ T cell memory compartment is observed in ageing, chronic infection and cancer; resulting in elevated apoptosis in addition to increased frequencies of terminally differentiated memory CD8+ T cells (e.g. Temra cells) at the expense of progenitor pools (naïve CD8+ T cells, Tscm cells and Tcm cells) that manifests in defective immune memory ³³. This accelerated ageing of the immune system has been shown to accompany T cell senescence, a triphasic process of cell cycle arrest that occurs following DNA damage (either via insult such as irradiation or through exposure of DNA via telomere erosion) (Phase 1) and involves a DNA damage response (Phase 2) and growth arrest (Phase 3) ¹³³. In senescent CD8⁺ T (Ts) cells this process involves signaling via p53, MAPK, p38, and CDK inhibitors, and is linked to progressive differentiation as marked by CD57, KLRG1, loss of CD27 and CD28 expression and re-expression of CD45RA ¹³³. However, distinguishing highly polyfunctional, pre-senescent CD8⁺ T cells (including CD57+ cytotoxic CD8+ T cells and CD45RA re-expressing Temra cells) appears challenging and relies on KLRG1 and CD57 dual expression as a minimum ³⁴. Loss of telomerase, BCL-2 and phosphorylation of AKT^{Ser473} may also mark truly senescent CD8⁺ T cell populations ¹³⁴. Senescent CD8⁺ T cells are sustained by IL-15 to persist in vivo and home to inflamed tissues, through interaction with ICAM-1, the extracellular matrix and Fractalkine (CCR7-,CD62L-,CD11a+CD18+, CD49e+, CX3CR1+). Most crucially, when stimulated with appropriate APC/co-stimulatory signals (41BBL) these cells down regulate CD45RA, become activated, proliferate and mediate potent cytotoxic effector function including IFNγ, TNFα and a reduced amount of IL-2 ¹³⁵.

Similar to Tex cells, Ts cells share a loss of proliferation and IL-2 production accompanied by high TCIR expression but these programs differ in many features ¹³³. Ts differentiation is associated with CD45RA re-expression, expression of CD57 and KLRG1, the acquisition of enhanced IFNγ, TNFα, cytotoxicity, shortened telomeres and reduced telomerase activity (many of which are also linked to pre-senescence) ¹³³. In contrast, Tex cells have been described as CD57-, KLRG1- exhibiting progressive loss of effector function given by their low expression of IFNγ and TNFα. Finally, the epigenetic status of Tex and Temra cells is divergent, with the IFNγ locus being hyper and hypo-methylated, respectively^{33,105,133,136,137}.

The inception and inhibition of anti-tumor immunity

The unprecedented survival rates achieved with checkpoint blockade have fueled renewed optimism in cancer immunotherapy. However, only a minority of patients are sensitive to treatment and few experience durable clinical benefit ¹³⁸. Key correlates of a therapeutic response to checkpoint inhibition include high tumor mutational burden (TMB) and T cell infiltration; implying that mutation-encoded neoepitopes serve as a substrate for tumor specific Teff cells and that these neoantigen reactive T (NART) cells are actively suppressed by the targeted TCIRs ¹³⁹⁻¹⁴². However, the increasingly appreciated transience of Teff cell reinvigoration and prevalence of relapse collectively signify a defect in durable immune memory post checkpoint blockade. As a field, we have therefore failed to design immunotherapeutic strategies that reliably forge stable, functional memory T cell pools capable of protecting from recurrence, indicating a lack of essential knowledge in the ontogeny and dysregulation of anti-tumor T cell responses. Pioneering studies have shown that cross-presentation by tumor resident DC and direct presentation on tumor cells can prime CD8+T cell cells at the tumor site, eliciting an efficient anti-tumor immune response in the absence

of lymph nodes ¹⁴³. More recently however, it has been proposed that tumor antigens are most often presented in the tumor-draining lymph-nodes by migratory DC derived from the tumor site ^{144,145}. Following priming, formation of functional immune memory in the presence of chronic viral and tumor antigen is impaired, the basis of which remains only partly understood¹⁴⁶. T cell extrinsic barriers of Teff and memory CD8⁺ T cell function in anti-tumor immunity likely include i) inefficient priming (insufficient antigen load via low mutation rate, a high sub-clonal neoantigen burden and/or poorly expressed tumor antigens, similarity of tumor epitopes to self-peptides, inability of epitopes to bind HLA, lack of danger signals low levels of co-stimulation or inflammatory cytokines/chemokines, checkpoint ligand expression or tolerogenic function(s) of APCs and lack of CD4+ T cell help) ii) local regulatory cell suppression (Tregs, myeloid-derived suppressor cells, tumor associated macrophages, cancer associated fibroblasts), iii) soluble inhibitory factors in the TME (e.g. TGFβ, IL-10, reactive oxygen species) iv) tumor-intrinsic resistance (expression of anti-apoptotic molecules, mutations in tumor antigen processing/presentation machinery and IFNy signaling, down-regulation or loss of heterozygosity of MHC alleles), loss of neoantigens, inhibitors of cytolytic compounds, expression of FASL and checkpoint ligands) v) physical exclusion of T cells from the tumor vi) Metabolic and hypoxic constitution of the TME ¹⁴⁷⁻¹⁵⁰. T cell intrinsic hurdles to generate a functional tumor specific memory T cell pool include: i) the deletion of tumor-associated self-antigens and potentially NART cells by central tolerance ii) low avidity TCR-peptide:MHC interactions iii) increased sensitivity of T cells to apoptosis, iv) inability to migrate to the tumor site, v) TCIR expression and vi) T cell dysfunction (anergy, tolerance, exhaustion) ⁹⁴. The anti-tumor immune response therefore shares common features with those discussed above for chronic viral infection. This includes prolonged antigen

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stimulation, a predominance of T cell inhibitory networks, and regulatory cell expansion⁹⁴. Some key differences in anti-tumor immunity include priming conditions, where lower antigenicity of self- or modestly altered non-self peptides, the absence of danger signals to activate APC and the initial lack of inflammation, collectively there are reduced signals 1, 2 and 3 in cancers compared to viral infection. Thus, the context of tumor-specific T cell priming in early disease is similar to conditions conducive to tolerance, yet consequent antigen chronicity and increased inflammation thereafter recapitulate cardinal aspects of exhaustion^{94,98,151,152}. It is therefore unsurprising that T cells exhibiting TCIR expression, defective cytokine production, altered cytokine production, modulated TCR signalling and epigenetic reprogramming have been widely observed in experimental and clinical settings of cancer^{105,153}.

Memory CD8⁺ T cells in tumor immunity: Pre-clinical models

CD8⁺ T cells in pre-clinical cancer models exhibit profound TCIR expression and are typically unable to reject even highly immunogenic tumors. However, experimental interventions such as checkpoint blockade, adoptive cell therapy, vaccination or induced lymphopenia can lead to tumor regression via inhibition of suppressive signals, delivering agonistic co-stimulation or cytokine signals, depletion of Tregs or provision of Teff cells devoid of inhibitory receptors ^{154,155}. Given phenotypic, functional and transcriptomic similarities, it has been proposed that an overlapping program of T cell dysfunction occurs in tumors similar to T cell exhaustion seen in chronic viral infection. For example, the co-expression of PD-1 and Tim-3 has been used to define dysfunctional tumor infiltrating CD8⁺ T cells in colon and mammary mouse tumors, where the blockade of these two molecules restores the functionality of CD8⁺ T cells ¹⁵⁶. Another study has shown that co-blockade of TIGIT and PDL-1 can resurrect functionality of intratumoral CD8⁺ T cells ¹⁵⁷. However, targeting of different

checkpoints clearly elicits tumor regression via divergent mechanisms that may not always reflect reversal of dysfunction. Indeed, whilst α-PD-1 treatment specifically induces the expansion of PD-1^{hi}TIM-3⁺CD8⁺T cells inside the tumor (which may point to either transient rewiring of effector machinery or disengagement of CD8 T cell dysfunction), α-CTLA-4 treatment induces the proliferation of peripheral ICOS+ Th1 CD4+ and CD8+T cells and depletes Tregs, suggesting that these agents i) have vastly different mechanisms of action beyond antagonism ii) de-repress CD8+ T cells via disrupting CD8⁺ T cell intrinsic (PD-1) and/or CD8⁺ T cell extrinsic (Treg cell depletion) regulation iii) mobilize independent memory or Teff cell subsets and thus iv) may exhibit a differential impact on CD4+ and CD8+ T cell memory induction 155. Loss of effective CD8⁺ T cell responses in tumors also appears to involve transcription factor dysregulation. Rescue of T-bet and EOMES phosphorylation was seen concomitant with tumor clearance following α -PD-1 combined with α -CTLA-4 in a CT26 GVAX tumor model ¹⁵⁸. Ablation of the key anergy gene *lkaros* induced tumor rejection in a melanoma model and loss of the transcription factor MAF augmented anti-tumor responses in established melanoma ^{159,160}. More recently, the transcription factor Egr2 (implicated in T cell anergy) together with LAG-3 and 4-1BB expression was used to define dysfunctional CD8+ T cells in the tumor microenvironment that can be reactivated using blocking antibodies against these two molecules ¹²⁷. Furthermore, these dysfunctional LAG-3⁺4-1BB⁺CD8⁺ T cells expressed a wide range of inhibitory and stimulatory receptors including 2B4, TIGIT, CD160, CTLA-4, OX-40, GITR, NRP1 and ICOS and downregulated the IL-7 receptor which is essential for memory CD8+ T cell survival ¹³. The ATPase CD39 has been recently used to define exhausted CD8⁺ T cells in a mouse model as well as in melanoma and breast cancer patients. Tumorinfiltrating CD39hiCD8+ T cells produce less TNF-α, IL-2 and express more PD-1, Tim-

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3, LAG-3, TIGIT and 2B4 compared with the CD39^{int} and CD39^{neg} tumor infiltrating CD8+ T cells ¹⁶¹. In addition to TCIRs, several immunosuppressive and protumorogenic factors, including adenosine, indoleamine 2,3 dyoxigenase (IDO), vascular endothelial growth factor (VEGF), type I interferons, glucose, Treg cells and myeloid-derived suppressor cells (MDSC) have been implicated in CD8+ T cell exhaustion or dysfunction ¹⁵³. However, direct evidence for the role of these factors in mouse tumor models is scarce. VEGF has been shown to induce an exhausted phenotype in tumor infiltrating CD8+T cells characterized by the expression of several inhibitory receptors including PD-1, CTLA-4 and TIM-3. Interestingly, VEGF blocking antibodies synergize with α-PD-1 antibodies promoting CD8+ T cell reinvigoration and slowing tumor growth ¹⁶². Treg cells induce a dysfunctional state of tumor-infiltrating DC, promoting the induction of PD-1+TIM-3+ exhausted CD8+ T cells that produced lower amounts of IFN-y and TNF-α inside the tumor ¹⁶³. Thus, TCIR expression appears to identify tumor reactive T cells that experience negative TCIR signaling, transcription factor dysregulation, loss of cytokine-mediated homeostasis and extrinsic regulation, with checkpoint inhibition (CPI) eliciting anti-tumor responses by inducing heterogeneous effector T cell pools via interception of several pathways. However, this evidence does not elucidate the inception of tumor specific T cell dysfunction.

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Several recent studies have used inducible experimental neoantigen expression in tissues to model the physiology of tumorigenesis. Elegant work demonstrated that chronic neoantigen stimulation induced biphasic tumor-specific T cell dysfunction that is initiated in early tumorigensis. Using an inducible SV40 T antigen, it was shown that neoepitope exposure resulted in first a plastic (Day 8) then irreversibly fixed (day 35) state which could not be rescued *in vitro* via IL-2 or anti-PD-1 ¹⁵². More specifically, *in*

vivo, at day 35 post neoantigen induction, neoantigen-specific T cells showed enhanced T-BET and Ki67 following anti-PD-1/PDL-1 but no reinvigoration of IFNy or TNFα production ¹⁵². Importantly, immunization of mice with epitopes for two TCRtransgenic CD8⁺ T cell clones elicited comparable effector responses and migration to the TME for corresponding adoptively co-transferred cells. However, cells specific for the persistently (but not transiently) expressed neoantigen selectively developed dysfunction; demonstrating that chronic neoantigen exposure rather than elements of the TME were the key drivers of dysfunction ¹⁵². Molecular analysis of these cells illustrated that an overlapping but not identical transcriptional profile existed for chronic viral infection and tumor-specific dysfunctional cells. However, importantly, contextspecific differences were evident and tumor-specific CD8+T cells also shared common gene signatures with tolerised CD8+ T cells. The molecular basis of the aberrant response showed that, relative to Teff cells, late dysfunctional cells exhibited diminished key effector and memory transcription factors (Eomes, Tbet), with progressive loss of genes involved in memory differentiation (Tcf7, Foxo1) and attenuated expression of regulators of Trm cell fate commitment (Klf2, S1pr1) whilst at day 8 Teff cells up-regulated anergy or hypofunction related loci (*Egr*2, *E2f*1, *E2f*2) ^{152,164}. At Day 34 memory CD8⁺ T cells upregulated multiple genes that were also enriched in late stage patient melanoma samples. These included transcription factors (e.g. Blimp-1, Batf, Dusp1), TCIR (Ctla4, Lag3, CD137) and down regulation of memory and quiescence factors (Tcf7, Foxo1, Bach2) 152. Another difference to the LCMV chronic infection model was the progressive loss of both *Tbet* and *Eomes* expression in the tumor-specific dysfunction setting, which differed from the switch of TbethiPD-1int into Tbetlo EOMEShiPD-1hi discussed in previous sections of this review ^{115,152}. Given that loss of EOMES and T-bet are necessary for CD103 and IL-15R

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expression in Trm development (see **Tissue resident memory CD8**+ **T cells** section above), this observation may reflect activity of the Trm program in solid tumors.

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Since CD8+ T cells in inducible neoantigen cancer models exhibit a truncated effector phase, it remains possible that memory CD8+ T cell generation and CD8+ T cell dysfunction occur in the absence of canonical fate commitment, and that memory cells are formed without complete effector de-differentiation ¹¹. Results from these models suggest that tumor-specific CD8+ T cell dysfunction represents a unique program of differentiation, distinguishable from acute/chronic infection, or tolerance that is caused by chronic neoantigen exposure in the TME. How this molecular program of dysfunction is altered in models testing neoepitopes derived from mutated selfproteins (that may have a broad range of affinities) remains to be seen. Work from Schietinger's group has subsequently shown that the irreversible dysfunction in this model is linked with epigenetic reprogramming and a fixed chromatin state ¹⁵¹. In this report, changes in epigenetic landscape occur during the first 14 days (plastic state) and not thereafter (fixed state), whilst PD-1 expression steadily increases. The fixed state was consistent with inaccessible enhancer regions at the *Ifng* and *Tcf* family loci whilst accessibility to the *Pdcd1* locus and predicted NFATC1- binding sites of anergyinducing (Egr1/2) or TCIR-encoding loci was increased ¹⁵¹. A crucial finding in this report was that adoptively transferred memory CD8+ T cells also underwent rapid dysfunction upon neoantigen exposure, implying that even the development of functional memory may not overcome tumor-specific CD8+ T cell dysfunction. The fixed chromatin state was also seen in human tumor infiltrating lymphocytes (TIL) from melanoma and NSCLC (a common feature between species being altered Tcf7 accessibility) and correlated with the presence of surface markers, including coexpression CD38 and CD101, which marked cells unable to respond to stimulation,

although a minor subset in these cultures were still able to produce cytokine (i.e. the CD38-CD101- cells). Treatment of dysfunctional CD8⁺ T cells with IL-15 *in vitro* did not reverse dysfunction, however it has been shown that IL-15 only epigenetically altered specific loci (*Tcf7*) in CD8⁺ T cells that convert from a Tscm/Tcm to Tem cell phenotype during homeostatic proliferation ³⁰, and thus intuitively would be insufficient to completely reverse dysfunction. In line with both of these findings, IL-15 has been shown to sustain rather than reverse exhausted CD8⁺ T cell pools at the tumor site

A combined inference of work in mouse models of cancer is therefore that chronic antigen stimulation and negative co-inhibitory signaling appear to produce a positive feedback loop reinforcing tumor specific CD8+ T cell dysfunction to a stabilized epigenetic state of CPI non-responsiveness. Moreover, where effective, the antagonism of single or multiple negative signaling cascades (e.g. the PD-1:BATF module) may not re-shape Tex cells *per se* but offer transient reprieve from one of the central orchestrators of the dysfunctional program, without altering remodeled chromatin, as demonstrated in the mouse model of LCMV ¹²². This theme may be imperative to improving long-term memory T cell responses. It is perhaps of crucial relevance that murine dysfunctional NART cells had gene expression profiles that showed considerable overlap with MART-1 specific CD8+ T cells isolated from late stage human cancers ¹⁵². This speaks to a vast amount of data attesting that tumor specific CD8+ T cell dysfunction is also a major feature and therapeutically critical facet of T cells in human cancer.

Memory T cell subsets in tumor immunity: Studies in clinical samples

TILs isolated from colon, renal, lung, ovarian, bladder and melanoma tumors have been phenotyped using various combinations of markers to define activation status (e.g. HLA-DR, CD38, Ki67), cytotoxicity (PRF, GZMb), transcription factor profile (EOMES, Tbet), tissue residency (CD69, CD103) and linear differentiation (CD45RA, CCR7, CD27, CD28) ^{166,167}. The majority of tumor infiltrating CD8⁺ T cells exhibit dysfunction-associated phenotypes, including broad and intense TCIR expression (e.g.PD-1, LAG-3, TIM-3 and TIGIT) ¹⁰⁵. For example, in clear cell renal cell carcinoma TILs exhibited increased markers of residency (CD69), activation (CD38) and TCIR (ICOS, LAG-3, PD-1, TIM-3) relative to T cells in normal tissue ¹⁶⁷. In non-small cell lung cancer (NSCLC) the frequency of GZMb+CD8+ T cells in early lung adenocarcinoma was decreased relative to adjacent lung, whilst CD8+PD-1+ T cell frequency was increased ¹⁶⁶. A separate study in early stage NSCLC revealed that relative to adjacent tissue, tumor lesions contained increased activated (HLA-DR+), Tem cells that co-expressed PD-1, Tim-3, CTLA-4, LAG-3 and TIGIT that were largely KLRG1⁻CD127⁻, with PD-1⁺ cells specifically enriched for activation markers and TCIRs (TGIT, TIM-3, CD137, CD38 and Ki67), but displaying lower EOMES expression ¹⁶⁸. In this investigation, increased activation of CD8⁺T cells was observed relative to normal tissue, and to a greater extent in current or ex-smokers compared to never smokers. Despite TCIR expression, CD8+ T cells appeared capable of synthesizing IFNy and IL-2 in response to synthetic stimuli (PMA/Io) and IL-2 in response to autologous tumor antigens, suggesting that CD8+ T cells may be preferentially activated in response to mutagens but that functional competence is retained or can be recovered at the tumor site by at least a subset of cells ¹⁶⁸. In terms of linear differentiation Kargl et al. showed that CD8+ TIL in NSCLC were predominantly Tem, with a smaller population of Temra cells and that lung

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adenocarcinoma (LUSC) had a higher Temra to Tem cell ratio compared to LUSC ¹⁶⁹. CD8+T cells from NSCLC in a second report were shown to be of a Tem or Temra cell phenotype and able to produce IFNy and IL-2 upon PMA/Ionomycin stimulation following IL-2 pre-treatment ¹⁷⁰. In melanoma, two reports showed that CD8+ T cells were largely CD45RO+CCR7-CD27+CD28+ (Tem1) though a smaller Temra cell population were present 171. Moreover, in patients with advanced melanoma, NY-ESO-1-specific memory CD8+ T cells displayed a dysfunctional phenotype (CD45RO+CCR7-TIM-3+PD-1+) and lower *in vitro* production of IFN-y, TNF-α and IL-2 compared to TIM-3⁻PD-1⁺ and TIM-3⁻PD-1⁻ CD8⁺ T cells ^{172,173}. In clinical specimens, activation markers, TCIRs expression and a Tem cell phenotype therefore appear to be associated with exposure to, or specificity for tumor antigens. Intriguingly, a report by Baitsch et al, showed that virus-specific and vaccine-induced CD8+ T cells specific to Melan-A/MART-1 melanoma antigens in the periphery exhibited small but significant differences (higher expression of TIM3 and CTLA4 but lower XCL1 in the latter) though both were noted to be late differentiated effector cells. Tumor-specific CD8+ T cells in the tumor infiltrated lymph nodes however, showed preferential overlap with LCMV-derived Tex cells, suggesting that tumour specific T cell exhaustion or dysfunction is localised to the tissue site, but not a feature of cells within the circulation ¹⁷⁴. Two articles form Rosenberg's lab identified that PD-1⁺ CD8⁺ T cells contained tumor-specific pools in melanoma. Firstly, it was discovered that Melan-A/MART1 specific CD8+ T cells were predominantly (though not exclusively) PD-1⁺. In this report, PD-1 expression tracked with signs of ongoing activation (HLA-DR, CTLA-4, Ki67) and ex vivo dysfunction (lower IFNy and IL-2 production) ¹⁷⁴. In the second, report PD-1+CD45RO+CD8+ Tem cells in the blood were found to contain circulating tumor-reactive CD8⁺T cells that recognize neoantigens in the tumor ¹⁷⁵. In

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688 agreement with this we have also identified NART cells in the tumor of NSCLC patients, and found these cells to be largely PD-1+, with heterogenous expression of 689 LAG-3, GZMb and CTLA-4 ¹⁴⁷. These findings therefore confirm that PD-1 expression 690 691 coincides with tumor reactivity in humans and extends this to include NART cells. In NSCLC it was shown that the level of co-expression of TCIRs on memory CD8+ T 692 693 cells associates with stage of disease and loss of functional competence, but that CD8+ T cells expressing intermediate levels of TCIRs may retain function ¹⁷⁶. Merad's 694 group showed that CD8+PD-1+ T cells correlated with TCR clonality, whilst Karql et al 695 696 demonstrated that tumor-specific (private) clonal expansion was correlated with in vitro reactivity to autologous tumor cells ^{166,169}. Collectively, these findings imply that 697 activation and/or exhaustion correlates with clonal expansion to tumor antigens ¹⁶⁹. 698 699 Recently, scRNAseq analysis was used to deconvolute the multicellular ecosystem of the TME in melanoma in a report by Garraway's group. In this study, TCR expansion 700 was associated with enrichment of an exhaustion molecular signature, further 701 underlining that clonal expansion may predispose commitment to a dysfunctional state 702 ¹⁷⁷. An in-depth scRNAseq and TCRseq profile from PBMC, adjacent tissue and TILs 703 704 of six patients with hepatocellular carcinoma has supported this model where 705 expanded clonotypes enrich for exhaustion and suggested a cell fate trajectory from naïve > Tem > Tex cells may occur in liver cancer ¹⁷⁸. Interestingly, this report paid 706 707 attention to two subsets of CD8+ T cells that have been ill defined in human tumors; mucosal associated invariant T (MAIT) cells and an intermediate subset of GZMK-708 expressing cells positioned between the effector and Tex state 178. The study of MAIT 709 710 cells in tumors remains in its infancy, but has been recently reviewed elsewhere 179. 711 Clearly much work is required to reconcile these potential pathways of differentiation

with programs of gradual dysfunction observed in pre-clinical data. Two important

conclusions can be drawn from the data on memory CD8+ T cells in human samples; i) Tumor reactivity is linked to a Tem cells expressing TCIRs (but not TEMRA cells, which have lower TCIR expression) ii) Clonal expansion or disease progression predicts T cell dysfunction. However, this does not explain the multitude of other dynamic states that memory CD8+ T cells appear to adopt within human TILs, especially those unveiled by recent scRNAseq studies. Indeed, the co-existence of phenotypically diverse, antigen experienced CD8⁺ T cells is a common observation in human TILs. Whilst a consistent finding is the presence of dysfunctional CD8⁺ T cells, less attention has been paid to tumor-specific CD8+ T cells within the TME and blood that retain ex vivo cytotoxicity consistent with functional Teff or Tem cells. Hallmarks of these cells are i) an ability to circulate in the periphery ii) more primitive states linear of differentiation (e.g. CD27⁺ or CD28⁺), ii) lower degrees of dysfunction, as shown by decreased TCIRs expression, iii) the presence of activation markers and iv) ex vivo cytolytic or Teff cell function ^{167,168,171,176,180}. These studies and others, therefore suggest that, like viral infections, tumor-specific memory CD8+T cells may be present in solid cancers at multiple stages of differentiation and that an earlier stage of differentiation may predict function. This paradigm is consistent with mouse models of checkpoint blockade discussed above, where less differentiated (plastic) cells, comprised the subset responsive to anti-PD-1 therapy compared to stably dysfunctional cells 121,152. The enhanced activity of less antigen-experienced T cells can be extrapolated to the

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The enhanced activity of less antigen-experienced T cells can be extrapolated to the setting of adoptive transfer. Results of pre-clinical experiments using Tcm and Tem cell subsets (generated by IL-15 or IL-2 in vitro, respectively) showed that less differentiated (lymph node-homing Tcm cells) had superior anti-tumor activity, suggesting that expansion of a progenitor population is required to supply the anti-

tumor response (possibly by retaining non-exhausted pools) 181. Consistent with this, infusions of human Teff cells bearing ectopic TCRs were inferior to Tcm cells of the same specificity in vivo, with the latter giving rise to Teff and memory CD8+ T cells ¹⁸². Furthermore, in a T cell competent patient-derived xenograft (PDX) mouse model, adoptively transferred Tcm and Tem cells derived from breast cancer infiltrate and rejected tumors 183. In vitro generated Tscm cells transferred into lymphodepleted mice have also showed enhanced capacity to mediate rejection of melanoma tumors compared to Tcm and Tem cells ²⁶. In this report, the authors suggest that, given their lower TCR signaling upon antigen recognition, Tscm cells survive better in environments with persistent antigen stimulation such as tumors, potentially resisting entry into a dysfunctional state. In the clinic, TIL therapy of metastatic melanoma showed that infusions of polyclonal TIL with superior T cell persistence correlated with better clinical outcome ¹⁸⁴, and that TIL retaining a 'young' (CD27+CD28+ expression, longer telomeres) phenotype can mediate regression in melanoma ¹⁸⁵. On aggregate, these data indicate that less differentiated, circulating memory CD8+T cell subsets of humans and mice exhibit favorable anti-tumor activity in vivo. Remarkably, it has also been shown that peripheral activation of effectors may be integral for the success of immunotherapy. Recent data from Nolan and Engleman's laboratories demonstrated that sustained systemic immunity across different tissues is required for tumor rejection in a range of immunotherapy models ¹⁸⁶. These preclinical data, and the transient rewiring of Tex cells described by Pauken et al. may explain the temporary clinical response observed in an anti-PD-1 treated NSCLC

patients, decline of which coincided with the contraction and dysfunction of NART cells

in the blood ¹⁴¹. Intratumoral expansion of Tem cells also was seen to associate with

response to anti-PD-1 therapy in clinical samples, however it is not evident whether

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these cells were dysfunctional prior to therapy or emerged from increased migration of newly primed cells into the tumor ¹⁸⁷. Of note, a high frequency of CD27⁺CD28⁺ Tem cells in the blood of late stage Ipilimumab-treated patients also correlated with response rate and overall survival whilst Temra cells frequency negatively associated with overall survival ¹⁸⁸. Furthermore, in clear cell RCC CD8⁺ T cells with lower levels of activation markers and TCIR (termed immune silent or activated) in the tumor were linked to disease-free survival, whilst cells exhibiting co-expression of multiple TCIR (immune regulated) were associated with worse outcome ¹⁶⁷. Work from Wherry's group additionally suggested that activation or reinvigoration of circulating cells is associated with clinical response to anti-PD-1 ¹⁶⁷. Several correlative *in silico* studies further support that intratumoral Tem cells or activated Teff cells may offer protection in primary disease as well as following CPI treatment. Charaentong et al. have made in silico predictions that suggest activated CD8+T cells could be major substrates for immune checkpoint inhibition (CPI) in solid tumors, whilst Tem cells could be important for control of primary disease ¹⁸⁹. This is in accord with previous work highlighting a correlation of Tbet expression and Tem cell signatures with clinical outcome in solid tumors ^{190,191}. These data therefore suggest that i) Tscm and Tcm cells capable of differentiating into Teff cells are the most potent memory T cell subsets for tumor rejection in adoptive cell therapy (due to their enhanced persistence, expansion, lymph-node homing and resistance to dysfunction). ii) T cell subsets associated with survival in primary disease and CPI are Teff, Tem and activated CD8+ T cells. iii) Dysfunctional CD8⁺ T cells and Temra cells may appear later in disease or negatively associate with outcome.

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The current body of T cell profiling data from solid cancer specimens raises several central questions, especially when considered in the context of basic T cell immunology and murine tumor models. Firstly, what are the cellular, molecular, clinical and tumor-associated factors which determine T cell differentiation in the anti-tumor response in humans? The current data suggest that clinical stage, clonal T cell expansion, metastasis, stromal architecture (e.g. presence of tertiary lymphoid structures) histological subtype or mutagen exposure may influence the level of dysfunction or activation, but beyond that there is little evidence 166,169,171,176. A second question is whether T cell differentiation links with immune editing? Clonal expansion in melanoma and liver cancer TIL was linked to an 'exhausted' molecular profile by scRNAseq or high PD-1 expression, whilst loss of heterozygosity at HLA alleles in non small cell lung cancer (NSCLC) associated with an increased cytolytic score, suggesting that tumor antigen recognition exerts selection pressure to alter the tumor genomic landscape and synchronously shapes co-evolution of memory CD8+ T cell differentiation ^{149,177,178}. Moreover, therapeutic NART cell infusion clearly causes loss of neoantigen presentation by tumors, demonstrating that selection pressure can drive evolutionary tumor escape ¹⁴⁹. Thus, existing evidence supports that clonal expansion and immune editing likely co-evolve, associated with increased PD-1 expression. Related to this it is worth considering that CD8+ T cells specific for edited or lost neoantigens may persist in the TME. Indeed, although Tex cells in viral infections are maintained after antigen withdrawal, the turnover of tumor reactive cells in humans is uncertain, and tissue resident populations such as those in the lung in fact experience rapid attrition ⁶⁶. This becomes particularly cogent when considering the impact of surgery on immune memory and in the context of clinical decisions to offer adjuvant or neoadjuvant CPI, i.e. will removal of the main source of antigen impede formation

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of memory following treatment and/or will Tex cells recover? Longitudinal studies will likely determine this conundrum. Thirdly does the nature of antigen shape the T cell response? T cells in cancer may recognise tumor-associated, tumor-specific or viralderived and mutation-encoded neoantigens. However, whether T cells recognising these antigens adopt phenotypes consistent with divergence of tolerance induction (i.e. due to degrees of self-similarity, or resemblance to viral epitopes) or chronicity/level/dosage of exposure (i.e. ubiquitous truncal neoantigens present in every tumor cells and thus appearing early in tumor development compared to branch, sub clonal antigens that may appear later in tumor evolution) remains to be seen ^{147,150,192}. In this regard it is interesting that the burden of clonal neoantigens and high affinity frameshift insertion and deletion encoded neoantigens associate with response to checkpoint blockade, yet how the pool of cells fostered by these favourable genomic landscapes differs from low mutational burden patients is largely unknown ^{147,193}. Fourthly, what is the differentiation program, ontogeny and fate of tumor reactive memory CD8+ T cells in humans? The limited data on phenotypes of NART cells and MART-1/Melan-A in humans suggest high TCIR expression but also heterogeneity, provoking the idea that specific tumor reactive clonotypes may differentiate from functional and dysfunctional states ^{147,174}. In acute viral infection and vaccination, we have discussed that memory CD8⁺ T cells emerge from effector de-differentiation ¹¹. *In vivo*, NART cells appear to become activated then rapidly and progressively adopt dysfunctional states 152. In human TILs we find Tem, Temra and Teff cells and phenotypically dysfunctional cells some of which may be connected by clonotype. Thus, there appears to be a cell fate trajectory in tumor specific cells that is vastly different cells differentiating in optimal conditions of immune memory (acute viral infection) that leads to a spectrum of differentiation whereby less antigen experienced

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cells (e.g. those recently migrated to the TME) are functional and those with prolonged antigen exposure gradually acquire high TCIRs expression. The multitude of phenotypes emerging from high dimensional flow cytometry and scRNAseg analysis may also arise from different priming environments (tumor or APC in situ vs lymph node) have different specificities (for tumor versus common pathogens) and/or be interconvertible. Regardless of the pathway of differentiation, the ultimate cell fate of tumor specific T cells in humans requires better definition. Tumor driven T cell dysfunction appears to be distinguishable from classical T cell exhaustion in viral infections, consequently the level of assumed dysfunction in these cells requires full clarification. Fifth, connected to this is whether there such thing as a tumor-reactive T cell phenotype? There is certainly a predisposition of pathogens to evoke responses dominated by specific T cell subsets. For example, in humans, the majority of respiratory syncytial virus (RSV), influenza (Flu) and Epstein bar virus (EBV) specific CD8+ T cells show a Tem1 (CD45RA-CCR7-CD28+CD27+) profile, whilst HIV-specific CD8⁺ T cells tend to be Tem 2-3 and CMV-specific CD8⁺ T cells split between Tem1 or Temra ¹⁹⁴. Furthermore, clonal dominance may influence this hierarchy, since CMVspecific CD8⁺ T cells show a different phenotype in healthy vs HIV infected individuals (increased Temra cells in the latter) 42. For tumor specific T cells this is less clear, multimer technologies are an immensely powerful tool, being implemented widely and expertly in the study of NART cells and other tumor specific T cell populations, but the current data does not provide a consensus on a tumor reactive phenotype ¹⁹⁵. Despite PD-1 and TCIR co-expression proving useful to enrich for tumor specificity, these markers are also expressed on activated cells ¹⁷⁵. Co-expression of multiple TCIR, the presence of CD38 and CD101 or high levels of PD-1 expression perhaps may be the most accurate predictors of tumor reactivity, since these are a feature of chronic

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stimulation, not likely to be shared by bystander cells ¹⁹⁶. However, these phenotypes likely only enrich for a subset of tumor reactive cells which are dysfunctional. Recently primed or functional anti-tumor Teff cells and circulating Tem cells present in the TME, blood, adjacent tissue or LN may be more challenging to distinguish given that such phenotypes are common to viral specific T cell populations. Indeed, although pathways of differentiation may be gleamed from coupled TCRseq and scRNAseq analysis of CD8⁺ T cells in human TlLs, an integral missing component to these data is antigen specificity. Finally, which T cell subset elicits therapeutic responses to CPI? This will clearly depend on the TCIR targeted and the context. For anti-PD-1/PD-L1 evidence suggests that intratumoral T cells with high TCIR expression expand in the TME ¹⁸⁷. On the other hand the most exhausted PD-1^{hi} cells in tumor and chronic infection settings appear to be refractory to rescue and responses in the clinic and in *vivo* rather associate with peripheral effector cell expansion ^{140,185,121,151,152}. It remains possible therefore that several subsets are mobilised in response to anti-PD-1, but that de-repression of a key non-exhausted effector pool facilitates durable clinical benefit.

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Whilst functionally relevant TCRs may be recovered from cells expressing high TCIR levels, the intrinsic dysfunction of such populations may limit their utility in adoptive cell transfer. This limitation would be evident both when preventing *in vitro* expansion and by an inability to induce a response *in vivo* via compromised persistence or inability to recirculate to the LN to serve as progeny. Efforts to reverse exhaustion may assist in generation of functional TIL products from such populations, and may include cytokines (e.g. IL-21), agonistic antibodies or epigenetic modifiers ^{126,197,198}. Although potentially not as efficient, reversal of exhaustion *in vitro* may be possible with current methods of rapid expansion, given the ability of several groups to detect neo-antigen

reactivity in expanded products, though it is uncertain if these cells were Tex or functional *ex vivo* ¹⁹⁹. Engineering of exhaustion-resistant TILs (i.e. use of CRISPR technology to remove TCIRs) for adoptive cell therapy, or combining adoptive cell therapy with checkpoint blockade may avoid recrudescence of T cell dysfunction and improve the efficacy of cellular cancer therapeutics ²⁰⁰. Whilst these findings underline the crucial contribution of circulating CD8+ T cell in anti-tumor immunity, emerging evidence also points towards a key role for Trm cells in some cancers.

Tissue resident memory cells in anti-tumor immunity

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The role of Trm cells in tumor protection is yet to be fully discerned. Two reports in mouse models of melanoma indicate these cells may have anti-tumor activity. Trm cells driven by autoimmune vitiligo were shown to protect from melanoma in a CD103dependent manner ²⁰¹ and OVA-encoding vaccinia virus was shown to generate Trm cells that delayed growth of OVA-expressing melanoma ⁶⁷. The prevalence, if not relevance of Trm cells in clinical specimens however, is clear. Tumor samples from patients with ovarian, endometrial, breast and lung cancers exhibit infiltration of CD8+CD103+ TIL, the abundance of which correlates with prolonged survival and better prognosis 202-206. Counterintuitively, in ovarian and lung tumors, the CD103⁺CD8⁺ TIL subset express the highest levels of inhibitory immune checkpoints such as PD-1, TIM-3, CTLA-4 and LAG-3, indicating that Trm cells may preferentially adopt a dysfunctional phenotype, likely due to chronic antigen stimulation ²⁰⁷. However, it is not certain whether a subset of Trm cells in tumors retain functionality ^{204,206}. Although a CD103⁺CD8⁺ T cell signature associated with prolonged survival in NSCLC, and total CD8+ T cells from CD103hi TIL produced increased GZMb, no difference was observed between CD103⁺ and CD103⁻ CD8⁺ T cells in the production of GZMb, IFNy or CD107, and PFN expression was lower in CD103⁺ cells ²⁰⁶. This

implies that CD103⁺CD8⁺ T cell accumulation may, like intense PD-1 expression, reflect a history of cells with previous effector function that have converted to Trm/ Tex cells, or that Trm cells confer a survival advantage through indirect mechanisms. Interestingly, a major function of Trm cells is recruitment of cells from the circulation ^{51,72,73}. Given the significant role of circulating Teff or Tem cells in anti-tumor immunity, it remains possible that Trm cells confer protection via recruitment of bystander circulating, tumor-specific T cells. Indeed, this mechanism may contribute to heterosubtypic immunity in influenza models and may facilitate the immigration of recently primed effectors from the tumor draining lymph nodes ⁷⁴.

In melanoma tumors, nearly 60% of all CD8+T cells have a CD45RO+CD69+CCR7-phenotype with nearly 50% being CD103+ ²⁰⁷. However, the presence of Trm cells in melanoma tumors has not been correlated with enhanced survival or better prognosis, suggesting an unknown mechanism by which a Trm cell phenotype is associated with good prognosis and survival in some types of tumors while not in others ²⁰⁷. This could be accounted for by a difference in subsets of Trm cells and their relative ability for cytotoxicity, dysfunction retention/ turnover and recruitment at different sites. Both mouse Trm cells in the lung and Trm cells of NSCLC samples were shown to have increased sensitivity to apoptosis, a feature of lung Trm cell biology linked to maintenance of antigen diversity and prevention of autoinflammatory tissue damage at this sensitive host site ^{66,208}. Direct, *ex vivo* analysis of lung Trm cells has shown that IL-2 can selectively induce cytotoxic features in CD103+ Trm cells, and that blocking CD103 reduced *in vitro* lysis of autologous targets in the context of PD-1/PD-L-1 blockade, suggesting that in the appropriate cytokine environment or following CPI. Trm cells become potent anti-tumor effectors ²⁰⁸.

A recent report examining the TCR diversity between metastatic lesions of melanoma patients suggests that Trm in tumors are less competent (e.g. lower IFNγ, IL-2) than circulating populations, and that TCR diversity in Trm cells among lesions exceeds that expected by changes in genomic landscape (although this prediction may be challenging) ²⁰⁷. It was suggested by the authors of the article that the interlesional diversity in TCR sequences may explain differential responses to checkpoint inhibitors and therefore that Trm cells are a major target of these therapies. Whether Trm cells contribute directly or indirectly to tumor destruction during checkpoint blockade in the clinic is currently unknown. The data above propounds that Trm cells may indirectly or directly promote anti-tumor immunity yet may be selectively prone to TCIRs linked dysfunction, and that the relative contributions of these features may be context and possibly tissue specific.

A potential disadvantage of a stable pool of Trm cells in the TME is the retention of cells with a reduced capacity for anti-tumor function, competing for trophic factors with *de novo* primed or functional circulating Tem/Teff cells pools. This may occur due to either cumulative antigen-driven dysfunction, or through maintenance of CD8+ T cells with specificity for epitopes that have been edited, down-regulated or lost. A recent report in a breast cancer model suggests that recent arrivals in the tumor exhibit functionality, but that Trm cells established previously are dysfunctional ¹⁶⁵. Tumor-reactive Trm cells in this model persisted at the tumor site independent of antigen and were sustained by TAM-derived IL-15, where Trm cells act as a 'sink' for cytokine. This is in keeping with the persistence of Tex cells in the absence of antigen in viral infection *in vivo* and in the clinic. Furthermore, in line with this it is likely that induction of a Trm cell profile in the tumor may both allow recruitment of functional circulating cells, and facilitate direct anti-tumor responses but as these cells become

dysfunctional or relevant epitopes are eliminated in later phases, Trm cells may exert a negative impact by occupying the niche and preventing accommodation of more functional or relevant cells (Figure 2). Indeed, it is possible that enforcing the Trm program, which incurs loss of T-bet and EOMES transcription factors and ostensibly reduced Teff potential may be a mechanism of tumor immune evasion^{47,62,76,77}. Two reports this year have shown that existing Trm cells proliferate and give rise to secondary Trm cells upon re-challenge, and that initial seeding populations are not replaced upon recruitment of antigen-specific and bystander populations- implying once more that irrelevant cell specificities may be accrued in the tumor, harnessing cytokine resources at the expense of functional recent arrivals ^{72,73}. Furthermore, the second generation of Trm cells in the TME would presumably inherit the inhibitory chromatin landscape of their progenitors, further expanding the dysfunctional pool. Interestingly, a major molecular mechanism of anti-PD-1 is the increase of cell motility, it is thus a possibility that mobilization of Trm cells may favor enhanced intratumoral responses by permitting entry to the niche ²⁰⁹. However, the turnover and attrition of Trm cells is site-specific and this may have crucial implications of local anti-tumor responses in different malignancies. Evidence from pulse-chase experiments in the influenza model shows that Trm cells in the lung have a short half-life 66,210, and that the gradually waning numbers after infection reflect the net effect of this loss partly counterbalanced by continual reseeding from circulating memory CD8⁺ T cells pools ⁶¹. Whether this is also true in lung cancer is unknown.

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Similar to circulating tumor specific-cells, the origin of tumor reactive Trm cells is undefined, though this subset is likely to emerge from the Tem or Tcm cell pool. Whether Trm cells acquire dysfunctional characteristics or whether tumor reactive cells acquire dysfunction and a Trm cell gene expression signature synchronously is

also not clear. It is possible that the high concentration of TGFβ inside the tumor induces CD103 on cells that do not bear transcriptional hallmarks of Trm cells, or equally that TGFβ driven *bona fide* Trm cell formation is directly accountable for increased frequency of Trm cells in solid tumors relative to adjacent tissue ^{55,206,208,211}. Further research to converge the nascent fields of Trm cell biology and T cell dysfunction is required to better define this process and the role of Trm cells in tumor immunity. In keeping with the 'streetlight hypothesis', our current attention may be guided to analysis of effector functions common to circulating CD8+ T cells, whilst thus far under-appreciated facets of Trm cell biology may be more significant in the antitumor response.

Conclusion

The generation and maintenance of CD8⁺ T cell memory subsets is crucial to host survival. Dysregulation of the central orchestrators in these networks leads to defective immune memory and host pathology. Recent work has made evident the complexity of memory T cell ontogeny, epigenetic reprogramming and the fundamental role that Trm cells play in immediate protection at portals of pathogen entry. Transposing our evolving knowledge of anti-tumor immunity onto this framework is a demanding but essential challenge, given the promise of immunotherapy and clinical need to broaden and optimize its application. The recent pre-clinical data suggest that following immune checkpoint inhibitors in the clinic i) the inability to revert the dysfunctional state and ii) the onset of fixed dysfunction in existing or *de novo* memory cells may both contribute to a lack of durable immune memory ^{122,152}. However, TIL therapy can lead to durable and complete responses and a minority of

patients receiving immune checkpoint inhibitors experience long-term clinical benefit, suggesting either or both of these limitations may be overcome. It will be imperative to monitor memory T cell function in this sub group of patients to decipher the requirements for generation of functional tumor specific memory.

The reversal of T cell dysfunction and the availability of neoepitopes represent two recently defined hurdles for tumor reactive memory CD8+ T cell maintenance and generation, respectively. Together with an inhibitory TME and lack of infiltration we now have four major hurdles to overcome for the development of effective immunotherapy in solid cancers. Therefore, combinatorial treatments providing i) a stimulatory priming environment (e.g. TLR agonists) ii) source of antigen (personalised neoepitope or tumor specific/associated antigen vaccines) or antigen-specific T cells (e.g. targeting neoepitopes) iii) enhanced infiltration (e.g. anti-TGFb, or anti-VEGF) and iv) a means to prevent exhaustion and/or regulation (e.g. CPI) may ultimately be fruitful if proven economically and clinically feasible 212-214. Correspondingly, a high frequency of endogenous NART effector cells in an immunological 'sweet-spot' that are effectively primed, but non-exhausted may provide these benefits to prolong survival during primary disease or enhance responses to CPI. This is consistent with the mounting evidence which supports a major contribution of systemic activation and circulating Tem cells in effective anti-tumor responses. Unveiling the mechanisms which can form and maintain functional, tumor specific effector and memory cells remains key to the success of next generation immunotherapeutic strategies in solid cancers.

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Figure legends

Figure 1. Linear differentiation refreshed.

A composite of seminal work that has defined the lineage relationships of human CD8 memory T cells. The conversion of naïve cells to Teff and consequent dedifferentiation gives rise to diverse memory cells subsets with specific migratory potential. Re-stimulation of T subsets gives rise to progeny later in the scheme. See main text for a detailed description.

Figure 2. A putative model of co-evolution of T cell dysfunction and tumor genomics within the TME: Phase I, Circulating tumor-specific Teff or Tem migrate to the tumor alongside bystander cells via chemotactic and inflammatory signaling. Teff/Tem convert to Trm and elicit cytotoxic effector function whilst experiencing chronic antigen stimulation. Selection pressure from T cell responses drives tumor evolution, including loss of class I presentation. Phase II, Tumor-specific cells undergo clonal expansion, consume IL-15 and experience progressive dysfunction. IL-15 resources for incoming circulating Tem/Teff are depleted as dysfunctional T cells with specificity to lost antigen dominate the niche, facilitating tumor escape and disease progression.

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