

Research paper

The tumor microenvironment: Thousand obstacles for effector T cells

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ARTICLE INFO

Keywords:

Effector T cells
Immune check point
Tumor microenvironment

ABSTRACT

The immune system is endowed with the capability to recognize and destroy transformed cells, but even in the presence of an immune infiltrate many tumors do progress. In the last decades new discoveries have shed light into (some of) the underlying mechanisms. Immune effector cells are not only under the influence of immune suppressive cell subsets, but also intrinsically regulated by immune check point molecules that under physiological condition avoid attach of healthy tissue. Moreover, tumor cells are modifying the surrounding micro-environment through secretion of immune modulators as well as via their own metabolism, thus further impairing the development of immune effector functions. Different approaches are currently being evaluated in the clinic to overcome those regulatory mechanisms and to unleash effector T cells.

1. Introduction

Since the demonstration that T cells can recognize tumor associated antigens (TAA), which lead to the eradication of cancer cells, efforts have been made to increase the understanding of the interaction between T cells and tumor cells and to improve the use of this knowledge not only to enhance the ability to cure cancer patients with novel immune based therapies, but also to select the best therapy for each tumor patient.

During the last two decades different strategies have been identified through which tumor cells can protect themselves against antigen specific CD8⁺ cytotoxic T lymphocytes (CTLs). Some of them are “normal” negative feedback mechanisms of the immune system, which are required under physiologic conditions to shut down a successful immune response in order to avoid damage to bystander healthy tissues. These include the induction of negative regulators on the effector cells to inhibit their response, but also the recruitment/polarization of immune suppressive cells. In addition, the tumor is converting the microenvironment into a hostile environment for T cells and their ability to perform effector functions, which is related to the tumor metabolism that not only deplete important nutrients for the T cells, but

also induce accumulation of “waste products”, which could further impair T cell function.

In the following sections we will discuss in more detail all these distinct mechanisms summarized in Fig. 1 and the implementation of this information to improve immunotherapeutic strategies in preclinical experimental models and in the clinic (Fig. 2).

2. Immune check point as an intrinsic shut down mechanism

In order to keep a balance between the elimination of dangerous entities and protection of healthy tissues, different negative feedback mechanisms exist in the immune system. Thus, directly after recognizing their target structure and performing their effector activity, T cells upregulate one or more negative feedback process(es) leading to a shut-down of the response, once the danger is eliminated. The prototype of this mechanism encompass immune check point (ICP) molecules or co-inhibitory receptors that are upregulated upon T cell stimulation and when engaged by their ligand impair different signaling pathways resulting in a reduced proliferation, secretion of cytokines and/or development of cytotoxic activity. Evaluation of tumor infiltrating lymphocytes (TILs) highlights an upregulation of many of these ICP

Abbreviations: A, anti; Ab, antibody; ACT, adoptive cell therapy; AML, acute myeloid leukemia; APC, antigen presenting cell; CAR, chimeric antigen receptor; CEACAM1, carcinoembryonic antigen related adhesion molecule 1; CPI, check point inhibitor; CTL, cytotoxic T lymphocyte; CTLA-4, cytotoxic T lymphocyte associated protein-4; CXCL, CXC-motiv chemokine; EC, endothelial cell; gal, galectin; DC, dendritic cell; GITR, glucocorticoid induced TNF-receptor related gene; HCC, hepatocellular carcinoma; HMGB1, high mobility group protein B1; ICOS, inducible T-cell co-stimulator; ICP, immune check point; IDO, indoleamine 2,3 dioxygenase; IFN, interferon; IHC, immunohistochemistry; IL, interleukin; iNOS, inducible nitric oxide synthase; LAG-3, lymphocyte activation gene-3; MDSC, myeloid derived suppressor cell; MHC, major histocompatibility complex; MSI, multispectral imaging; NK, natural killer; PBMNC, peripheral blood mononuclear cell; PD-1, programmed death-1; PD-L, programmed death ligand; ROS, reactive oxygen species; TAA, tumor associated antigen; TAF, tumor associated fibroblast; TAN, tumor associated neutrophil; TCR, T cell receptor; TIL, tumor infiltrating lymphocyte; Teff, T effector cell; TGF, transforming growth factor; TIGIT, T cell immunoglobulin and immunoreceptor tyrosine-based inhibitory motif; Tim-3, T-cell immunoglobulin domain and mucin domain-3; TME, tumor microenvironment; Treg, regulatory T cell; VISTA, V-domain Ig suppressor of T cells activation

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<https://doi.org/10.1016/j.cellimm.2017.12.004>

Received 17 August 2017; Received in revised form 4 December 2017; Accepted 7 December 2017
Available online 08 December 2017

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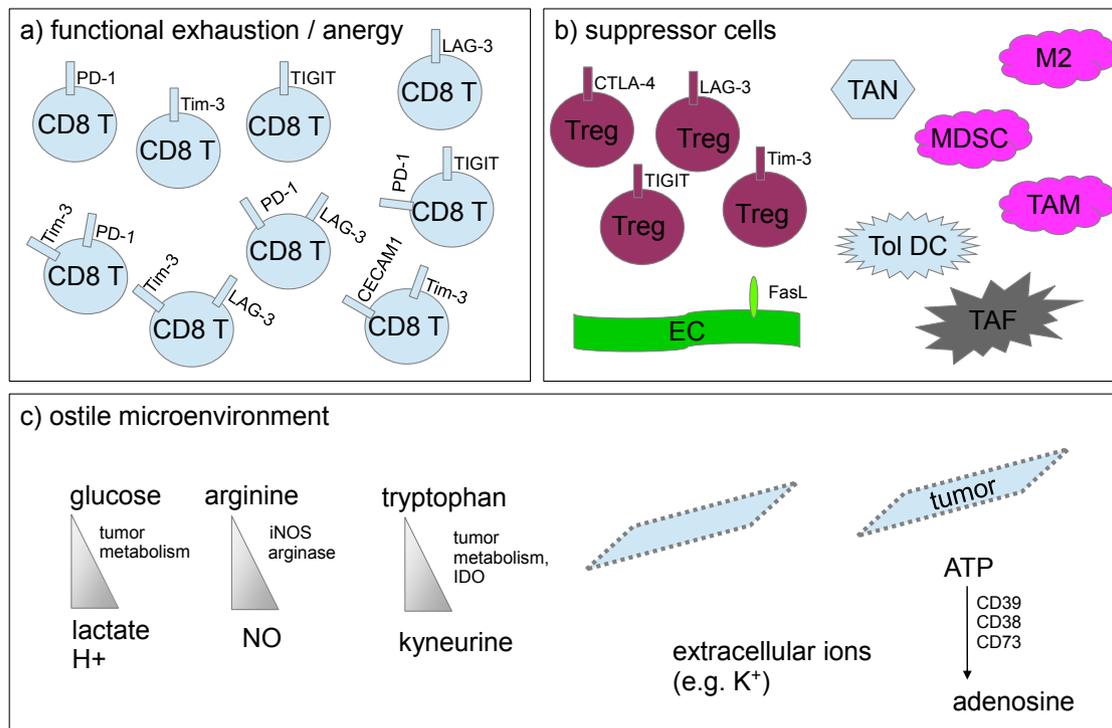


Fig. 1. Multiple mechanisms inhibit antigen specific effector cells within the tumor microenvironment. Antigen specific CD8⁺ T cells that infiltrate the tumor are characterized by an enhanced expression of co-inhibitory receptors, either alone or in combination, and by low levels of co-stimulatory molecules, a phenotype correlating with functional exhaustion or energy. In addition to an intrinsic impairment, the TME is also characterized by the presence of many immune and stromal cells that can directly suppress Teff functions in a cell contact dependent and independent manner as well as by a depletion of nutrients and accumulation of metabolites that further impair their activity and/or survival.

molecules on antigen specific T cell, which is accompanied by an either reversible or irreversible dysfunctional state. In the next sections the basic data on these ICPs, their relation to cancer progression and therapeutic targeting are outlined.

2.1. CTLA-4

The first identified co-inhibitory receptor has been CTLA-4 (cytotoxic T lymphocyte associated protein-4 or CD152) that is upregulated shortly after T cell receptor (TCR) triggering and due to its higher affinity for CD80/B7.1 and CD86/B7.2 than CD28 it can dampen its co-stimulatory signal and thus turn off T cell activation. In light of the absence of an own intracellular signaling domain and the difficulties in identifying a signaling partner, such inhibition might be mainly due to competition and not to direct signaling of CTLA-4. Moreover, the effect can also be cell extrinsic, since CTLA-4 can induce a depletion of co-stimulatory molecules from professional antigen presenting cells (APCs) via trogocytosis [1]. High CTLA-4 expression levels have been found on CD4⁺ regulatory T cells (Tregs), which are frequently used as a marker together with CD25^{hi} to identify Tregs when intracellular staining of Foxp3 cannot be performed. Furthermore, CTLA-4 is not exclusively expressed on T cells, since its expression was found on a sub population of suppressive dendritic cells (DCs) in hepatocellular carcinoma (HCC) [2].

Being the first identified negative regulator of T cell responses, it was also the first one to be targeted in the clinic with an approval of the anti-(a)CTLA-4 antibody (Ab) ipilimumab in 2011 by the Food and Drug Administration for the treatment of unresectable or metastatic melanoma, whereas the second aCTLA-4 antibody tremelimumab was

approved in 2015 for the treatment of mesothelioma, but both antibodies have been also tested in other tumor histotypes. In addition to the direct promotion of effector cell functionality [3], aCTLA-4 therapy works by depleting Tregs [4] and can also possibly influence migration of effector cells [5].

2.2. PD-1

PD-1 (programmed death-1 or CD279) is an inhibitory receptor that is transiently upregulated after TCR triggering and that upon binding to PD-L1 (B7-H1 or CD274) or PD-L2 (B7-DC or CD273) block the TCR signaling and T cell effector functions. Constitutive expression of the receptor is associated with conditions of chronic and/or suboptimal antigen stimulation and correlate with a state of functional exhaustion. High levels of PD-1⁺ T cells in the tumor infiltrate can have a good prognostic value since they postulate the presence of an existing antigen specific immune response [6]. Different antibodies targeting either PD-1 (nivolumab and pembrolizumab, to cite the most used) or its major ligand PD-L1 (avelumab, atezolizumab and durvalumab) have been implemented in clinical trials in order to “remove the brake” and unleash the immune response against the tumor resulting in an increased clinical outcome in different tumor settings [7].

Evaluation of the response to aPD-1 therapy in relation to the expression of PD-L1 in the tumor biopsy has provided contrasting results. Indeed, despite patients with PD-L1⁺ tumors have a higher probability to respond to the therapy, there are some responding patients that lack PD-L1 expression suggesting a role of PD-L2 [8] or even a direct effect of the antibody on a small population of PD-1⁺ melanoma cells [9]. Alternative explanations can also be related to technical issues, like the

clone of antibody implemented for the staining, the cut off value used to define a tumor as positive and/or the discrimination between membrane versus cytosolic staining or the expression by tumor versus infiltrating cells. Finally, distinct mechanisms leading to the expression of PD-L1 could be responsible. In some cases PD-L1 is constitutively expressed as a result of oncogenic signaling and is not associated with the immune infiltrate that can be targeted by the blocking antibody. Similarly, even when PD-L1 expression is induced as escape mechanism against an immune response, its expression can vary over time, and a “one time point” evaluation can provide a misleading value (reviewed in [10]).

2.3. Tim-3

Tim-3 (T-cell immunoglobulin domain and mucin domain-3) expression was originally described on activated CD4⁺ and CD8⁺ type 1 effector cells [11], but it was also detected on Tregs [12,13], where it plays an important role in their suppressive function [14]. Mechanistically, it has been demonstrated that chronic exposure to interleukin (IL)-12 or stimulation with IL-27 are responsible for the induction of Tim-3 expression and the dysfunctional phenotype [15,16].

Triggering by its canonical ligand galectin (gal)-9, expressed by tumor cells and also by Tregs, induce impaired T cell responses and can also lead to cell death [17]. In addition, Tim-3 can bind to the “danger associated molecule” high mobility group protein B1 (HMGB1) thereby suppressing immune responses by limiting its availability [18] and to carcinoembryonic antigen related adhesion molecule 1 (CEACAM1) that, when expressed in *cis*, can promote Tim-3 surface expression and mark cells with a more dysfunctional effector status [19,20].

In tumor patients infiltrating lymphocytes are enriched in Tim-3⁺ cells when compared to peripheral counterparts and can also co-express PD-1 [21–23]. Analogous to PD-1, Tim-3 expression is considered as a marker for antigen specific T cells and a target for tumor immunotherapy. Therefore, different phase I clinical trials using Tim-3 blocking Abs are currently ongoing in patients with solid tumors as well as with acute myeloid leukemia (AML) (NCT02817633, NCT03099109, NCT02608268, NCT03066648 on www.clinicaltrials.gov).

Clinical targeting of Tim-3 can have also effects independent of the adaptive immunity. Different tumor cells have been shown to express Tim-3, which is directly involved in their tumorigenic potential *in vitro* [24–26]. Furthermore, cells from the innate immunity, like natural killer (NK) cells, express Tim-3, which could lead by gal-9 triggering to inhibition of their cytotoxic activity, but also to improved secretion of interferon (IFN) γ [27,28]. The secreted IFN γ can have positive anti-tumor effects, but can also induce an upregulation of other inhibitory feedback mechanisms. The role of Tim-3 on APC is more complex. On monocytes/macrophages it favors their polarization toward a tumor promoting M2 phenotype [29] and can boost immune suppression via interaction with gal-9⁺ Tregs [30]. Due to its ability to bind to phosphatidylserine, Tim-3 plays also a role in the removal of apoptotic bodies and can induce antigen cross presentation in murine DC [31].

2.4. LAG-3

LAG-3 (lymphocyte activation gene-3 or CD223) is upregulated on activated CD4⁺ and CD8⁺ T cells in response to treatment with different cytokines [32]. It shares homology with CD4, but displays a higher affinity to major histocompatibility complex (MHC) class II molecules and therefore can act as a decoy receptor impairing CD4 mediated TCR co-stimulation. Despite its interaction with MHC class II molecules LAG-3 is able to directly inhibit CD8⁺ T cells in a CD4⁺ T

cell independent manner [33]. LAG-3 plays an important role in the suppressive activity of Tregs [34] as well as in the sensitivity of naïve cells toward their suppressive activity [35].

Upregulated expression of LAG-3 in CD8⁺ TILs was found in different tumor settings, both alone [36,37] and in combination with PD-1 [38,39], Tim-3 [40] or 4-1BB [41].

Binding of LAG-3 to MHC class II antigen can induce a reverse signaling into accessory cells, whose effect seems to depend on the “form” of LAG-3. While soluble LAG-3 can promote DC maturation [42,43], the interaction with transmembrane LAG-3 expressed by Tregs induce a semi-mature, and thus tolerogenic DC phenotype [44,45]. A reverse signaling by LAG-3 has also been described for MHC class II positive melanoma cells that became resistant to apoptosis upon interaction with a soluble as well as cell associated LAG-3 [46].

Immunotherapeutic approaches aiming at blocking the LAG-3 signaling use either classical inhibitory Abs or a soluble form of LAG-3. Whereas for the former no published results yet exist, absence of toxicity and some hints of functional activity have already been demonstrated for the latter [47–49].

2.5. TIGIT

TIGIT (T cell immunoglobulin and immunoreceptor tyrosine-based inhibitory motif [ITIM] domain) is a co-inhibitory receptor that bind to nectin molecules like CD155 (or Polio virus receptor), nectin-2 (CD112) and nectin-3 (CD113) and thus can directly transduce inhibitory signals into the effector cells as well as compete with DNAM-1 (CD226) and CD96 for their binding to these ligands and thus dampen their signaling pathway. It is highly expressed on Tregs and cells expressing TIGIT are also more prone to become regulatory cells characterized by the ability to secrete IL-10 and induce M2 polarization of macrophages [50].

In melanoma a direct role of TIGIT in inhibiting killing of CD155 overexpressing cells was reported *in vitro* [51] and in patients it is frequently co-expressed with PD-1 and can thus be responsible for the impaired response to ligand positive tumors [52]. A phase I clinical trial (NCT03119428) using a TIGIT blocking Ab is currently recruiting patients.

2.6. VISTA

VISTA (V-domain Ig suppressor of T cell activation, or programmed death-1 homolog, PD-1H) is a co-inhibitory molecule belonging to the CD28/B7 family that is expressed both on APC and on naïve T cells, leading to an inhibition of effector T cells (Teffs) and the induction of Foxp3⁺ Tregs [53]. In the human setting its expression has been found in patients with gastric cancer but with no correlation to their survival [54], whereas in oral squamous carcinoma high VISTA expression levels combined with paucity of CD8⁺ T cells is a predictor of poor survival [55]. Preclinical evaluation in mouse models suggests potential synergy with the blockade of PD-1 and/or CTLA-4 [56,57], and the increase of VISTA⁺ cells in ipilimumab treated patients [58] suggests that these combinations might be required also in the human setting. Currently, two ongoing clinical trials are targeting VISTA either with an Ab (NCT02671955) or with the small molecule inhibitor CA-170, which target VISTA, PD-L1 and PD-L2 (NCT02812875).

3. Co-stimulatory molecules

Comparison of the phenotype of Teffs and Tregs from TILs and peripheral blood mononuclear cells (PBMCs) as well as from cancer patients and healthy donors highlights low levels of co-stimulatory

molecules on effector cells, whereas higher levels are found on Tregs [59]. Since in most cases triggering of the co-stimulatory molecule on Tregs reduces their suppressive activity and/or induces their depletion, different clinical attempts are utilizing agonists of such co-stimulatory molecules to reduce the immune suppression rather than boosting effector cells [60,61]. In the following paragraph basic information on the various co-stimulatory molecules and their possible implementation for tumor immunotherapy are provided.

3.1. OX40

OX40 (or CD134) is a co-stimulatory receptor expressed transiently on activated T cells, but constitutively expressed on Tregs. Experiments performed *in vitro* indicated that OX40 triggering on Tregs reduces the expression of Foxp3 and their suppressive activity [62,63]. In experimental murine models, combination of OX40 triggering with blockade of CTLA-4 [64,65] or PD-1 [66] as well as with triggering of other co-stimulatory molecules like 4-1BB [67] or ICOS [68] is currently being investigated. OX40 triggering can also induce regression of murine sarcoma in the absence of T cells via the activation of endothelial cells and endogenous DCs [69] further promoting the implementation of OX40 for tumor immunotherapy.

After a first clinical trial with a single dose of a murine Ab [70], many humanized Abs have been produced [71,72] and phase I clinical trials are currently recruiting patients.

3.2. GITR

GITR (glucocorticoid induced TNF-receptor related gene or CD357) is expressed in infiltrating Tregs at higher levels than in the circulating PBMCs and upon triggering with soluble ligand *in vitro* their suppressive activity is reduced [73]. *In vivo* experiments using mice as well as humanized NSG mice indicate that the GITR-specific Ab induces tumor regression by inhibition of Tregs and activation of Teffs [74,75].

As for the other co-stimulatory molecules, combinations with IFN α [76] or aPD-1 therapy, with or without additional chemotherapy or peptide vaccination [77–79] are currently evaluated in mouse models, whereas a combination with aCTLA-4 therapy has been tested in mice as well as *in vitro* with PBMCs from cancer patients [80,81].

Different triggering antibodies like MK4166 [82], but also AMG228, TRX518 and INCAGNO1876 as well as a trimeric form of the extracellular domain of GITR-L, MEDI1873 [83] are currently studied in various phase I clinical trials.

3.3. 4-1BB

CD137 (or 4-1BB) is a co-stimulatory receptor upregulated shortly after TCR triggering and is thus considered a marker of antigen specific activation [84]. A 4-1BB mAb has been used in the setting of adoptive cell therapy (ACT) both to purify [85] and to specifically stimulate antigen specific cells *in vitro* [86–89].

The receptor is also expressed on Tregs, but in contrast to the other co-stimulatory molecules, its *in vitro* triggering with the soluble ligand induces expansion of Tregs without affecting their suppressive capacity [90]. Furthermore, stimulation of CD4⁺ and CD8⁺ Teffs via 4-1BB renders them less susceptible to Treg suppressive activity [90,91].

While also new antibodies are being developed and tested in phase I clinical trials, the first results obtained by administering *in vivo* the same antibody that has been used for *in vitro* expansion, Urelumab or BMS663513, displayed limited toxicity together with some immunological functions as indicated by the induction of different cytokines in the patients sera [92].

3.4. ICOS

ICOS (inducible T cell costimulator or CD278) is a co-stimulatory receptor belonging to the family of CD28. Cancer patients harbor high levels of ICOS⁺ Tregs that can be expanded both by the tumor cells themselves and by ICOS-L⁺ plasmacytoid DC and their presence can correlate with poor prognosis [93–96]. In contrast, high levels of ICOS expression on effector cells are found in patients responding to treatment with aCTLA-4 [97–101] but for example not to treatment with anti PD-1 [101]. Furthermore, mouse experiments suggest a direct role of such effectors for tumor rejection [102] thus paving the way for the preclinical combination of blocking aCTLA-4 mAb and a cell vaccine overexpressing ICOS-L [103]. In the murine setting an important role of ICOS⁺ effector cells has also been found in response to OX40 agonist therapy [68]. Currently, two different phase I trials are evaluating ICOS triggering Abs in lymphoma (NCT02520791) and in solid cancer (NCT02723955).

4. Immune suppressive cells

Tumor cells are able to subvert immune cells and to polarize them toward tumor-promoting and/or immune suppressing types. In addition, cellular components of the tumor microenvironment (TME), like tumor associated fibroblasts (TAFs), endothelial cells (ECs) and tumor associated neutrophils (TANs) can be manipulated by the tumor for protection against an immune response.

4.1. CD4[±] and CD8[±] regulatory T cells

T lymphocytes have a high degree of functional plasticity and include also cells with immune regulatory/suppressive activities whose function is to maintain self-tolerance and avoid immune toxicity on bystander healthy cells. Tregs can act either in a contact dependent way via an APC bridge by downregulating immune responses in an antigen specific way or via the secretion of immune suppressive cytokines, like e.g. IL10, that dampen immune responses independently of contact and antigen specificity.

Despite most of the studies in the end of last century have focused on CD4⁺ Tregs the existence of CD8⁺ Tregs has been re-proposed in the last decade and their presence has been identified in the infiltrate of different tumor histotypes [104–107]. The induction and/or expansion of those suppressive cells can be directly mediated by the tumor or via the induction of tolerogenic APCs [94,108].

4.2. Accessory cells

In addition to lymphocytes, many other immune cells can infiltrate the tumor, where they can be subverted to a pro-tumorigenic phenotype not only directly promoting tumor cell proliferation and metastasis formation, but also protecting them from an immune response. Indeed, tumor derived factors can promote the differentiation of monocytes versus myeloid derived suppressor cells (MDSC) [109] and the polarization of macrophages and neutrophils toward a type 2, immunosuppressive phenotype [110]. Moreover, myeloid as well as plasmacytoid DCs infiltrating the TME have a semi-mature or tolerogenic phenotype [111,112]. All those pro-tumorigenic accessory cells are characterized by expression of low levels of co-stimulatory molecules together with the upregulation of different suppressive mechanisms. As further discussed below, those cells can upregulate different enzymes like inducible nitric oxide synthase (iNOS), indoleamine 2,3 dioxygenase (IDO) and arginase that deplete the microenvironment from nutrients required for the cytotoxic function of effector cells. Moreover,

they can also upregulate ligands for different immune checkpoints. Indeed, myeloid cells can increase PD-L1 in response to co-culture with T cells [113] and such expression can protect a PD-L1 negative tumor from immune-mediated rejection [114]. Similarly, myeloid cells, and in particular MDSC express the highest levels of VISTA and are thus the major mediators of T cells inhibition [115].

4.3. Stromal cells: endothelial cells and fibroblasts

One of the first obstacles for anti-tumor T cells is to penetrate into the tumor mass. This is frequently caused by the missing vasculature and the abnormal pressure flow, but also by delimiting ECs, which are modified by the tumor itself. ECs not only express low levels of adhesion molecules, thus impairing adhesion and extravasation, but they can also upregulate death ligands like FasL thus inducing CD8⁺ T cell death [116]. Due to this fact, attempts to combine immunotherapy with a normalization of the tumor vasculature have been implemented [117].

TAFs composing the stroma within the tumor mass also exhibit immune suppressive activity. They can directly suppress Teff function via the transforming growth factor (TGF) β and their ability to penetrate into the tumor via the CXC-motiv chemokine (CXCL)-12 [118,119]. Moreover, TAF can foster the immune suppressive condition by induction of regulatory DCs and M2 polarized macrophages [120,121]. In experimental mouse models different strategies have been implemented to eliminate such TAFs, but with discrepant results reporting either a positive or a negative outcome on tumor growth, respectively [122–124]. In the human setting strategies targeting TAFs are still under evaluation. Interestingly, TAFs obtained from lung cancer patients were neither affected in their suppressive activity nor in their survival by radiation therapy *in vitro* [125].

5. Ostile microenvironment

In addition to the above mentioned immune mechanisms, also other “general” aspects of the TME modulate the composition of the tumor infiltrating immune cell repertoire as well as the activity of immune cells.

5.1. Metabolic competition

Whereas the tumor metabolism has a long history with the description of the so called “Warburg effect”, a link between different metabolic pathways and immune cell subset differentiation and functional activity has only recently started to be dissected.

While Tregs mainly depend on oxidative phosphorylation and the availability of fatty acids, Teffs rely on glycolysis and thus on glucose to mount their effector functions. Since the tumor is depleting the TME of glucose to sustain its energetic requirement, different metabolic sensors or check points induce a functional inactivation of T cells in response to glucose deprivation [126,127]. This link between the inability to shift to mitochondrial respiration and exhaustion of Teffs, which has been also described upon virus infection [128], is currently re-evaluated, since experiments performed with human PBMCs comparing glycolysis inhibition via 2-deoxy-glucose (with which most of the previous studies were performed) with real glucose deprivation highlighted a level of metabolic plasticity that might be important in therapeutic settings [129]. To further sustain the role of metabolic competition between tumor and immune cells, an inverse correlation between tumor metabolism and T infiltration was found both in renal and in squamous cell carcinoma [130,131].

In addition to glucose, the TME is also depleted of different amino acids. On one side tumor cells utilize them for their anabolism, not only for building up proteins, but also as precursors for nucleotide

biosynthesis, while on the other side immune suppressor cells, like MDSCs, are upregulating IDO or arginase enzymes that induce the degradation of tryptophan and arginine, respectively, thereby further reducing the availability of such amino acids [132].

5.2. Suppressive “waste products”

The metabolism of tumor cells not only deprives the TME of nutrients, but it also fills it with degradation or by-products, some of which display immune suppressive activities.

Degradation of glucose into lactate results not only in high concentration of extracellular lactate, but also in an acidification of the microenvironment that further suppresses Teff functions [133–136], whereas Tregs are less affected [137].

Similarly, the enhanced degradation of tryptophan by IDO results in the release of 3-hydroxyanthranilic acid that inhibits T cells either directly or via DC inhibition [138,139]. Moreover, despite glycolysis produces less oxygen reactive species (ROS) than the mitochondrial respiration, there is also an increase in various ROS species within the TME. Once the detoxifying mechanisms have been saturated, ROS can induce downregulation of functional proteins like the CD3zeta chain, but also cell death [140,141].

5.3. Released cellular content

Upon cell death different compounds are released, which negatively interfere with Teff functions. This includes e.g. ATP, which is characteristic of immunogenic cell death due to its ability to enhance DC maturation. On the contrary, its release can have immune suppressive effects in the TME, since Tregs, MDSCs, but also stromal and tumor cells could express CD39 and/or CD73, two enzymes that progressively degrade ATP into adenosine that can then trigger the inhibitory receptors Adora2A and Adora2B. This directly affects T cells and their migratory capabilities [142], but also inhibits APCs like DCs and promotes induction of Tregs [143]. Different compounds targeting those receptors are being evaluated in the clinic.

Upon cell death there is also release of intracellular ions resulting in alterations of the gradient between intracellular and extracellular space. For example excessive extracellular levels of potassium impair T cell functions if they are not able to keep the required gradient [144] and in the TME T cells with the highest levels of the Kv1,3 channel are the most functional ones [145].

6. Clinical translation

Against all the above described mechanisms of immune evasion exploited by the cancer, different attempts to overcome them therapeutically have been undertaken (Fig. 2). As stated above, therapy with CPIs has provided some good responses, but only in 20–40% of patients and some of them develop resistances during treatment [146–148]. Therefore the search for criteria to stratify patients (see below), but also to develop even more potent treatment options are urgently required. Recently, combinations among different CPIs have been employed, such as the combination of CTLA-4 and PD-1, but despite an improvement [149] the side effects and the associated costs led to the evaluation of other combinations, mostly based on the inhibition of the PD-1/PD-L1 axis [52,150]. CPIs have also been combined with vaccinations [151–153], chemotherapy [154], radiation [155] and with modulators of the TME [132,156].

The increased knowledge has also been translated in ACT. Studies performed on the role of different co-stimulatory molecules in influencing T cell metabolism and fate decision are translated into second and third generation chimeric antigen receptors (CARs) that are endowed with different signaling domain(s) [157,158], whereas cytokine

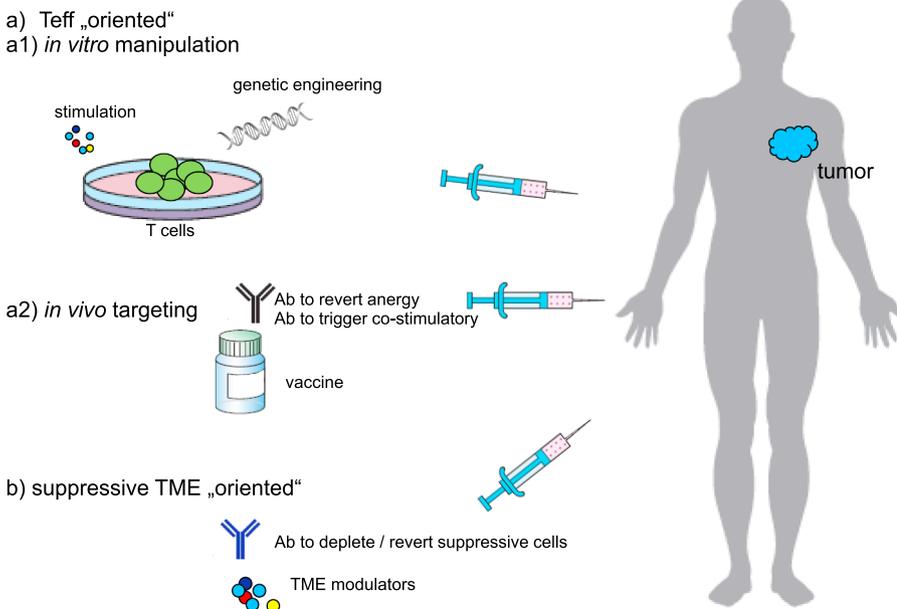


Fig. 2. Therapeutic strategies to rescue tumor infiltrating effector cells. Different immunotherapeutic approaches have been developed to fight cancer, either focusing directly at the antigen specific effector cells or on other components of the TME. The first approach includes ACT, vaccination and CPI that act by blocking the inhibitory signal in the Teffs and thus by reversing their exhaustion or anergy, while the latter comprises antibodies or small molecules that can deplete or reverse the polarization of the immune suppressor cells as well as those that act on the mediators of immune suppressive conditions of the TME like cytokines and metabolites.

induced killer cells have been transfected with the full ICOS co-stimulatory receptor [159]. Similarly, CAR or TCR transgenic cells are further modified with genes that will render them less susceptible to immune suppressive pathways [160–163], high levels of ROS [164,165] or also to cope better with the nutrient situation of the TME [158,166].

7. The quest for the holy grail: immune markers with prognostic and/or predictive value

The above data demonstrate that just the presence of an immune cell infiltrate cannot be a sufficient marker for cancer patients. For that reason many laboratories have taken/are undergoing the difficult task of identifying biomarkers correlated with disease progression and patients' survival, both spontaneous (i.e. prognostic markers) and in response to therapy (i.e. predictive markers), in order to stratify patients accordingly and thus being able to perform a personalized therapy, selecting for each patient the most promising therapeutic approach, and/or to quickly evaluate if the therapy is working or the patient is developing resistances to the treatment regimen.

For this purpose the immune system of tumor patients with many different cancer types has been deeply characterized and correlated with clinical parameters, such as tumor grading, staging, and patients' outcome. Different approaches have been used for such characterization, like immunohistochemistry (IHC), flow cytometry and deep sequencing, each with advantages and disadvantages.

IHC requires a highly invasive intervention to obtain the tumor biopsies, and is therefore mainly used as one time evaluation, but can provide information about the localization of the immune cells within the tumor. This has been shown to be of relevance and led to the development of the immunoscore or immune contexture [167]: evaluation of the presence of combinations of immune markers like CD3, CD8, CD45RO, CD103 and/or CD163 in the invasive margin and/or the core of the tumor can identify patients with better survival chances [55,168–174]. Recently, with the technical improvement both in the staining techniques that allow multiple parameters to be analyzed in parallel and in the software for imaging evaluation, multispectral imaging (MSI) could be employed to evaluate the reciprocal location

and even the topology and distance between different cell types, like Teffs and Tregs within the tumor, which is of potential value for prognosis as shown for oral squamous carcinoma [175]. Evaluation by conventional flow cytometry allows the analysis of a higher number of parameters in parallel (up to 32), a number that can be further expanded by mass cytometry due to the introduction of isotope- instead of fluorochrome-labeled Abs. On the downside, these analyses give only information about the cellular composition and their activation status, but all information on the cellular localization are lost, since they are performed in cell suspension. However, a huge advantage of the implementation of these flow cytometric based technologies is their application on liquid biopsies like PBMCs or ascites that can be obtained with less invasive techniques than tumor biopsies and thus allow multiple evaluations over time that are essential for the determination of predictive biomarkers for responsiveness to therapy, such as e.g. the enhanced levels of ICOS⁺ effector cells or the reduction in MDSC found following aCTLA-4 therapy [176–178]. Despite the increased knowledge obtained using these technology on liquid biopsies, it is noteworthy that circulating cells are not a faithful representation of TILs and that small changes in the TME correlating with therapy response might be lost when peripheral lymphocytes are evaluated.

More recently, with the advances in sequencing techniques, tumor biopsies have also been characterized from the genomic and transcriptomic point of view not only to evaluate the mutation load of the neoplastic cells, that can correlate with its immunogenicity and have prognostic value, but also to characterize its cellular composition and thus the “status” of the immune infiltrate. For example, response to aPD-1 therapy has been positively associated with the presence of an IFN γ signature in the pre-operative biopsy [179], whereas a negative correlation was found with high expression levels of metabolic enzymes [180]. Similarly, expression levels of genes associated with antigen processing, immunomodulatory molecules and effector as well as suppressor cells has been converted into an immunophenoscore that when applied to biopsies from clinical trials with aCTLA-4 or aPD-1 blockade was able to predict response to therapy [181]. An additional tool that has been “created” to help stratifying patients for therapy selection is the immunogram. Initially theorized by Blank et al. [182] on the basis

of the cancer immunity cycle [183] it has then been “created” and experimentally applied to lung cancer patients by Karasaki and co-authors [184].

8. Conclusion

In the last decade a greater understanding of the interaction between tumor and immune cells has been obtained and its translation into clinical practice has resulted in some great clinical responses. Despite this improvement, a long way has still to be undertaken in order to expand the patients that can really take advantages from such therapies, both by enhancing their efficacy and by finding reliable markers to initially select the best therapy for each patient and for monitoring the possible development of resistance(s) in order to change the therapeutic approach to be applied. In this way it will be possible not only to reduce the side effects to the patients, but also to better use the economical resources by (quickly) selecting the best possible therapeutic strategy(ies) for each patient.

Acknowledgment

The work was supported by a grant the Mildred Scheel Stiftung to CM and BS (111105).

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