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DEPARTMENT OF ONCOLOGY-PATHOLOGY
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**TO KILL TWO BIRDS WITH ONE
STONE: TARGETING MYELOID CELLS
IN CANCERS**

Yumeng Mao

毛郁萌



**Karolinska
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About the cover:

This photo was taken by photographer/pharmacist Henry Jager, who blended milk with cream at adjusted proportions and poured the mixture into the salted water. The stunning effects were captured within a minute. In my view, this photo offers a visual interpretation of the extreme heterogeneity (the colors) and plasticity (the shapes) of myeloid cells.

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To Kill Two Birds with One Stone: Targeting Myeloid Cells in Cancers

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By

Yumeng Mao

毛郁萌

Principal Supervisor:

Professor, Rolf Kiessling, M.D., Ph.D.
Karolinska Institutet
Department of Oncology-Pathology

Co-supervisors:

Docent, Andreas Lundqvist, Ph.D.
Karolinska Institutet
Department of Oncology-Pathology

Dr. Isabel Poschke, Ph.D.

German Cancer Research Center (DKFZ)
Department of Translational Cancer Research
Division of Molecular Oncology of
Gastrointestinal Tumors

Opponent:

Professor, Suzanne Ostrand-Rosenberg,
Ph.D.
University of Maryland
Department of Biological Sciences
Baltimore, U.S.A.

Examination Board:

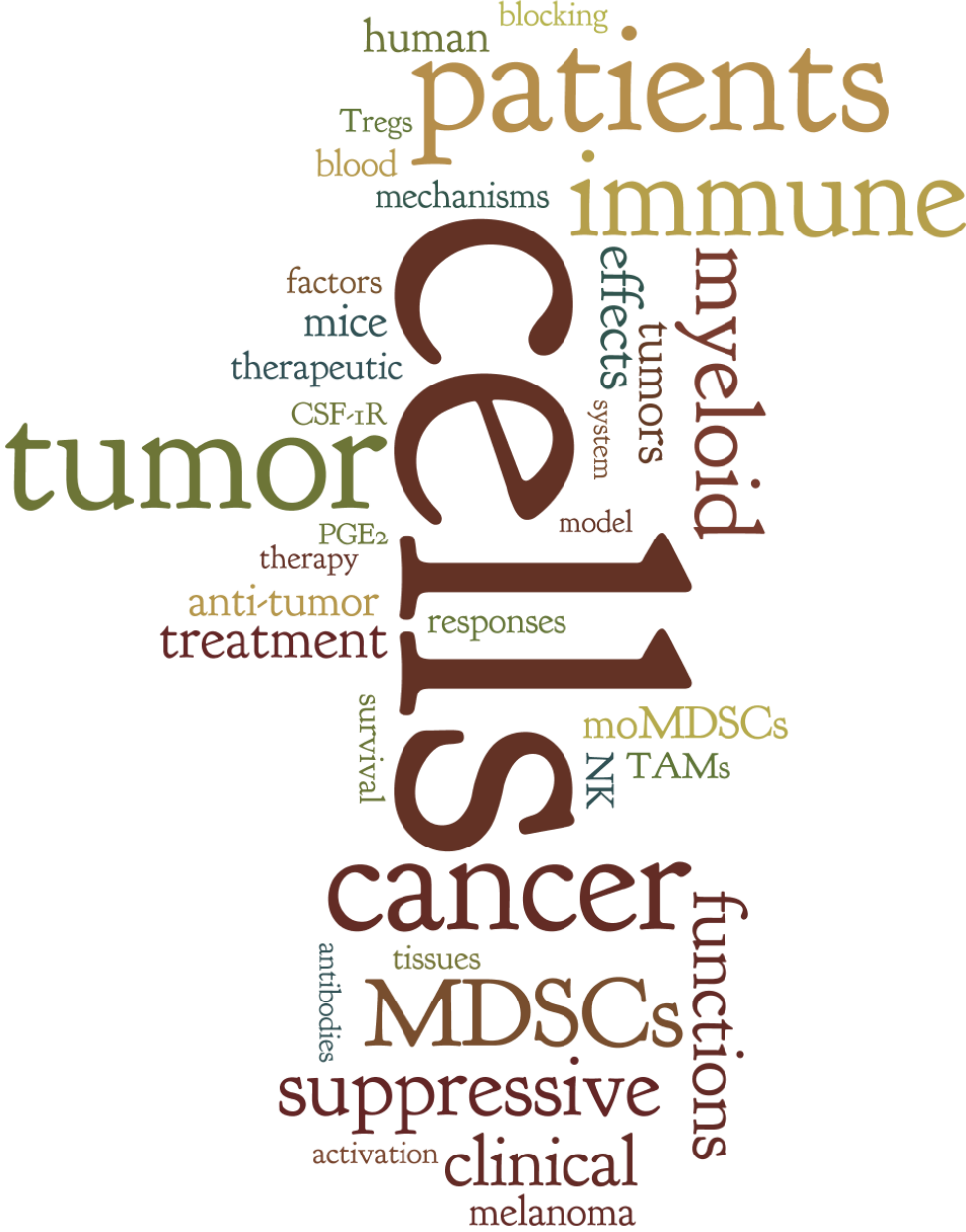
Docent Susanne Gabrielsson, Ph.D.
Karolinska Institutet
Department of Medicine

Docent Angelo De Milito, Ph.D.
Karolinska Institutet
Department of Oncology-Pathology

Docent Karin Leandersson, Ph.D.
Lund University
Department of Laboratory Medicine

To my beloved grandmother, a cancer survivor since 1998

KEY WORDS



*: The graph was created using an online word cloud tool (<http://www.wordle.net>). It was based on the text content of this thesis, excluding acknowledgements, references and the constituent research articles.

MY PERSONAL VIEW OF THE IMMUNE SYSTEM

The few of you that might have visited my hometown, Xi'an (China), must have been impressed by the spectacular scene of the 'Terracotta Army'. However, as a local kid breathing the city's air, my favorite has always been the rectangular-shaped city walls, which has been offering security to the inner city for more than 600 years*.

Not until when I have learned more about the immune system, I started to realize how perfectly the structure of ancient Xi'an city could explain the sophisticated design of the human body. The walls, just like the skins, frequently reject life-threatening invading enemies (microbes and viruses). Within these walls, vital facilities (brain, heart, lungs etc.) and civilians (normal tissues) could function well under the protection of the highly-skilled watchmen of the city (immune system).

In general, this protecting force comprises of military troops that have large numbers of soldiers (T and B lymphocytes) as well as specialized, fast-responding fighters (NK cells) and special agents (myeloid cells). Once there is a break-in at any point of the fortification, guards will light up the beacon tower (inflammation) and the special agents will be summoned immediately. They could release explosive weapons to kill the invaders and report first-hand information to initiate military operations later on (antigen presentation).

In comparison to microbes and viruses, cancer initiation is more similar to a gangster group started within the city. In most cases, this kind of activity is quickly detected by the watchmen and terminated on the spot. However, gangster groups could use many tricks, for example fake identities or acting undercover, to avoid being recognized. When these groups have gained enough power, they could even corrupt the city's watchmen and receive assistance to spread their influences to other functioning parts (metastasis).

The special agents, myeloid cells as we mentioned earlier, normally are among the first ones to notice the gangster activities. Part of their job is to gather intelligence by infiltrating these outlawed groups and collect key information that enables effective military executions. However, due to their constant presence in the gangs, they often betray their duties and participate in illegal activities that support growth of the gangster groups.

Investigations conducted in this thesis focus on clarifying main channels that the gangster groups (tumors) employ to convert these special agents (**Study I, II and IV**). In detail, I aim to understand how these converted members of the immune system could slow down efficient cancer clearance (**Study I and II**) and block smooth information transfer to the authorities (**Study III**).

The goal of these investigations is to develop counteractive tactics that could regain the loyalty of these 'double-agents' and ultimately work from both ends to efficiently eliminate threats of the gangster groups within the city (**Study IV**).

*: The city walls in Xi'an are the most well-preserved city fortification among all Chinese cities. Its construction started in 194 B.C. and the existing part was built by the Ming Dynasty in 1370. Nowadays it is approximately 14 km long and on average 12 meters in height and 18 meters wide on the base.

ABSTRACT

Cancer progression is often accompanied by chronic inflammation and severe impairment of the immune system. In recent years, therapies eliciting tumor-specific immunity have resulted in striking tumor control and survival benefits in cancer patients. However, establishment of effective and durable immune responses is hampered by various tumor-dependent mechanisms. Besides the direct suppression mediated by tumor cells, a number of immune cell types, including regulatory T cells (Tregs), myeloid-derived suppressor cells (MDSCs), 'M2-biased' tumor-associated macrophages (TAMs) and regulatory dendritic cells, occur in the periphery and tumor microenvironment. These cells conduct potent inhibition of anti-tumor immunity and are associated with poor prognosis in patients. Studies included in this thesis aim to elucidate the molecular machinery that tumor cells utilize to induce suppressive functions from healthy myeloid cells (**Study I, II and IV**) and how the resulted suppressive myeloid cells could limit functions of T cells (**Study I**), natural killer (NK) cells (**Study II**) and differentiation of the immune-stimulating dendritic cells (DCs) (**Study III**). Finally, we tested the role of a myeloid-specific chemical inhibitor in antagonizing the induction of these suppressive myeloid cells *in vitro*. In a transgenic murine model developing highly aggressive spontaneous tumors, treatment with the inhibitor elicited robust control of established tumors and potentiated the anti-tumor effects of checkpoint blocking antibodies (**Study IV**). In summary, this thesis provides mechanistic insights for the induction of suppressive myeloid cells and demonstrates the therapeutic potential of targeting these cells for the treatment of solid tumors.

LIST OF INCLUDED STUDIES

- I. **Mao Y.**, Poschke I., Wennerberg E., Pico de Coaña Y., Hansson J., Masucci G., Lundqvist A., Kiessling R.[#], Melanoma-educated CD14⁺ cells acquire a myeloid-derived suppressor cell phenotype and are potent inhibitors of T cells via COX-2/PGE2-dependent mechanisms, *Cancer Research* 73 (13): 3877-87, 2013.
- II. **Mao Y.**^{*}, Sarhan D.^{*}, Steven A., Seliger B., Kiessling R., Lundqvist A.[#], Inhibition of tumor-derived prostaglandin-E2 blocks the induction of myeloid-derived suppressor cells and recovers natural killer cell activity, *Clinical Cancer Research*, 2014 Aug 1;20(15):4096-106.
- III. Poschke I.[#], **Mao Y.**, Adamson L., Salazar-Onfray F., Masucci G., Kiessling R., Myeloid-derived suppressor cells impair the quality of dendritic cell vaccine, *Cancer immunology, immunotherapy : CII* 2012;61(6):827-38.
- IV. **Mao Y.**^{*#}, Eissler N.^{*}, Le Blanc K., Johnsen J.I., Kogner P., Kiessling R.[#], Targeting CSF-1R potentiates checkpoint inhibitors to control spontaneous neuroblastoma growth through modulating suppressive myeloid cells, *Manuscript*, 2015.

SUPPORTING RESULTS

Research Articles

1. Sarhan D., Palma M., **Mao Y.**, Adamson L., Kiessling R., Mellstedt H., Österborg A. and Lundqvist A., Dendritic cell regulation of NK-cell responses involves lymphotoxin- α , IL-12 and TGF- β , *Eur. J. Immunol.*, *accepted*, 2015.
2. Poschke I., **Mao Y.**, Kiessling R., de Boniface J., Tumor-dependent increase of serum amino acid levels in breast cancer patients has diagnostic potential and correlates with molecular tumor subtypes, *J. Transl. Med.*, *11(1):290*, 2013.
3. Pico de Coaña Y., Poschke I., Gentilecore G., **Mao Y.**, Nyström M., Hansson J., Masucci G., Kiessling R., Ipilimumab treatment results in an early decrease in frequencies of granulocytic MDSCs as well as their arginase-1 production, *Cancer Immunol. Res.*, *1(3): 1-5*, 2013.
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Reviews and Commentaries

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Manuscript

1. **Mao Y.**, *et al.*, Interleukin-15 potentiates human natural killer cells to acquire resistance against tumor-induced immune suppression through mTOR-regulated metabolic control, 2015.

*: *Equal contributions*

CONTENTS

Foreword	1
1 Snapshots of the Immune System	2
1.1 Introduction	2
1.2 The Fast-responding Immunity	2
1.3 The Three Signals	2
1.3.1 Antigen Presentation to T Lymphocytes.....	2
1.3.2 Co-stimulation	3
1.3.3 Cytokines	3
1.4 The Secondary Immunity	3
1.4.1 T lymphocytes	3
1.4.2 Humoral Responses	3
2 Immune Responses in Controlling Cancers	4
2.1 Historical Overview.....	4
2.2 Barricades for Anti-tumor Immunity.....	4
2.2.1 Regulatory T Cells	4
2.2.2 Immune Checkpoints	4
2.2.3 Enzymatic Machinery.....	5
2.3 Immunoscore	5
3 New Trends in Cancer Immunotherapy	7
3.1 ‘Check-point’ Inhibitors	7
3.1.1 Unleashing T Cells by CTLA-4 Blockade	7
3.1.2 PD-1/PD-L as a Therapeutic Target.....	7
3.1.3 Unique Clinical Properties of Check-point Inhibitors	8
3.2 Adoptive Cell Transfer.....	9
3.2.1 Tumor Infiltrating Lymphocytes (TILs).....	9
3.2.2 Creating Anti-tumor T Cells through Genetic Modifications	9
3.2.3 NK Cell Therapy.....	10
3.2.4 DC-based Therapy	10
3.2.5 Sustaining Infused Cells <i>In Vivo</i>	10
4 The ‘Double Agents’: Myeloid Cells in Cancers	12
4.1 Background	12
4.2 Myeloid Cells as Biomarkers	13
4.3 Driving Forces for Suppressive Myeloid Cells.....	15
4.3.1 Established Soluble Factors	15
4.3.2 Emerging Inflammatory Factors.....	17
4.3.3 Hypoxic and Metabolic Control.....	18
4.3.4 The ‘Jemaa el-Fnaa’	18
4.4 Targeting Suppressive Myeloid Cells.....	19
4.4.1 Anti-cancer Treatments and Suppressive Myeloid Cells.....	19

4.4.2 Alleviating Inflammation	23
4.4.3 Restraining Induction Signals	23
4.4.4 Blocking Mobility	24
4.4.5 Reprogramming Activation	25
4.4.6 To Kill Two Birds with One Stone	25
5 Immunotherapy: Where Are We Heading?	26
5.1 Introduction	26
5.2 Combination Therapy	26
5.2.1 Restoration of Immune Functions.....	26
5.2.2 Correction of Vasculature	26
5.2.3 Multi-tasking Therapeutics.....	27
5.2.4 Risk Analysis.....	28
5.3 Technological Advances	28
5.3.1 Biomaterials and Immunotherapy.....	28
5.3.2 Mega-analysis of Immune Responses	29
5.3.3 Precise Genome Editing	29
5.4 Interdisciplinary Framework for Cancer Immunotherapy	30
6 Summary of the Major Findings	31
6.1 Tumor-driven Induction of MDSC is Mediated by COX- 2/PGE2	31
6.2 MDSCs Suppress NK Cells Through TGF- β	31
6.3 MDSCs Impair the Maturation of Dendritic Cells.....	32
6.4 CSF-1R Inhibition as a Potent Approach to Boost Anti-tumor Immunity	33
6.5 Technical Details	34
6.5.1 <i>In Vitro</i> Models to Study Suppressive Myeloid Cells in Humans and Mice....	34
6.5.2 TH-MYCN Neuroblastoma Murine Model.....	35
6.5.3 The R2 Database.....	35
7 Acknowledgements.....	37
8 Cited Articles	40

ABBREVIATIONS

ADCC	Antibody-dependent cellular cytotoxicity
ALL	Acute lymphoblastic leukemia
ATP	Adenosine triphosphate
CLL	Chronic lymphocytic leukemia
CCL-2	Chemokine (C-C motif) ligand 2
CCR-2	C-C chemokine receptor type 2
cGMP	Cyclic guanosine monophosphate
COX-2	Cyclooxygenase-2
Cas	<i>CRISPR</i> -associated genes
CRISPR	Clustered regularly interspaced short palindromic repeats
CTLA-4	Cytotoxic T lymphocyte antigen-4
CXCR-2	CXC chemokine receptor type 2
DCs	Dendritic cells
FoxP3	Forehead box P3
GM-CSF	Granulocyte-macrophage colony-stimulating factor
HIF-1 α	Hypoxia induced factor-1 alpha
HMGB-1	High-mobility group box protein B-1
IDO	Indoleamine 2,3-deoxygenase
JAK	Janus Kinase
M-CSF	Macrophage colony-stimulating factor
MDSCs	Myeloid-derived suppressor cells
MHC	Major histocompatibility complex
mPGES-1	Membrane-associated PGE synthase-1
NKG2D	Natural-killer group 2, member D
NOS	Nitric oxide synthase
PBMC	Peripheral blood mononuclear cells
PD-1	Programmed cell death-1
PDE-5	Phosphodiesterase type-5
PDGF	Platelet-derived growth factor
PD-L1 or -L2	Programmed cell death ligand-1 or -2

PGE2	Prostaglandin E2
RAG-2	Recombinase-activating gene-2
RAGE	Receptor for advanced glycation endproducts
RNS	Reactive nitrogen species
ROS	Reactive oxygen species
ScFv	Single-chain variable fragment
STAT	Signal transduction and transcription
TAA	Tumor-associated antigen
TAM	Tumor-associated macrophages
TGF- β	Transforming growth factor-beta
TLR	Toll-like receptor
TRAIL	TNF-related apoptosis-inducing ligand
Treg	Regulatory T cells
VEGF	Vascular endothelial growth factor

FOREWORD

Since the beginning of my scientific training in 2009, I have frequently heard the strong doubts about cancer immunotherapy just a few years ago. One of the common arguments that discredited the ability of the immune system in controlling established tumors was based on observations that tumors continued to progress despite being 'surrounded' by immune cells. In the clinic, boosters for the immune system, such as interleukin-2 (IL-2) or interferon- γ (IFN- γ), caused severe systemic adverse events but only showed therapeutic effects in a small number of patients. On the other hand, less toxic approaches, such as cancer vaccines, struggled to achieve satisfactory clinical responses against established solid tumors.

Recently, success stories of the uprising immunotherapies, such as 'check-point' blocking antibodies and various adoptive cell transfer strategies, have energized the research in cancer immunology once again. Massive eradication and durable tumor control have been documented in patients who have failed to respond to existing treatments. More importantly, these new approaches have 'revived' an array of classic anti-cancer drugs, to be tested at lower doses as part of the combinational approaches.

However, for anti-tumor immunity to operate optimally in a larger number of patients, we cannot avoid challenges from the extremely hostile environment in cancer patients. Some argue that this problem could be sufficiently overcome once dominant strength of the immune responses are introduced, for example by pumping in trillions of tumor-reactive T cells. This option is potentially risky due to collateral damages against healthy tissues caused by this 'unleashed' T cell army. Thus, it is reasonable to hypothesize that we may achieve a ' $1+1>2$ ' situation, when immune-activating reagents are wisely combined with approaches that disarm resilient mechanisms utilized by tumor cells, such as abnormal vasculature, immune suppression, hypoxia or acidity.

The immune system is a vastly complicated network involving many distinct cell types. Therefore, we are still in great needs of in-depth knowledge on how the immune system functions in cancer patients, for example how immune cells could interact with tumor cells and regulate each other. Identification of these 'missing pieces', facilitated by refined technological advances, could help us identify new targets and develop approaches that could not only generate sufficient clinical efficacy, but also improve the quality-of-life for cancer patients.

1. SNAPSHOTS OF THE IMMUNE SYSTEM

1.1 INTRODUCTION

The textbook model divides the immune system into innate and adaptive arms. The former includes a variety of cell types that quickly respond to invading pathogens. In contrast, the latter refers to responses directed by selected fragments of pathogens and is thought to be the exclusive effectors for the establishment of immunological memory. However, as emerging evidence points towards the memory properties of certain innate immune subsets [1], it is becoming increasingly challenging to utilize the classic definitions to address current immunological questions. Thus, instead of categorizing immune cell subsets following the framework, I will try to explain the immune response as a process and introduce key elements involved in every major step.

1.2 THE FAST-RESPONDING IMMUNITY

The principle of immune protection is largely based on the 'danger signal hypothesis', which was a concept first suggested by Burnet in 1949 and refined by numerous subsequent studies [2]. In simple words, the evolutionary force has shaped the immune system to detect common features of dangerous pathogens, known as the pathogen-associated molecular patterns (PAMPs). Once healthy cells are infected, they will express the 'kill-me' signals, or damage-associated molecular patterns (DAMPs), in order to initiate immune recognitions. A group of immune cells, known as the antigen-presenting cells (APCs), bear receptors that specifically bind to PAMPs or DAMPs. Upon detection of PAMPs or DAMPs, APCs can capture the infected cells and extract antigens, which are small peptide fragments that are essential for eliciting further immune responses. Generally, this process initiates within hours after infections and the antigen-carrying APCs will migrate to lymph nodes and activate the residing T and B lymphocytes. We will have a closer look at this process in the sections below.

Besides APCs, other immune cells are also playing pivotal roles in the immediate control of invading pathogens. NK cells constitute approximately 5 to 15% of the immune cells in human peripheral blood and rapidly respond to cells lacking MHC class I surface molecules, which is often caused by viral infections [3, 4]. Previous studies have revealed that development and effector functions of NK cells are fine-tuned by a panel of inhibitory and activating molecules [5]. Recently, a hotly debated topic underlines the memory property of NK cells in an antigen-specific manner [6-9], which is traditionally considered to be exclusive for secondary immune effector cells [10]. Moreover, the complement system, which comprises a multitude of circulating or membrane-associated proteins with enzymatic activities, plays a rapid defensive role through lysis of microbes. In many cases, the fast-responding immunity is not sufficient to eradicate invading pathogens. Therefore, secondary immunity, which takes a few days to reach its maximal capacity, needs to be recruited.

1.3 THE THREE SIGNALS

1.3.1 Antigen presentation to T lymphocytes

T cell receptors (TCRs) are unique surface molecules that are essential for the activation and functions of T lymphocytes. Every TCR has a specific reactivity towards a short peptide sequence, which is presented by MHC molecules on the cell surface. Ligation between peptide-containing MHCs on APCs and TCRs can induce intracellular signal transduction cascades, which are required for the activation and expansion of T cells. There are two types of MHCs involved in the antigen recognition,

MHC class I and II. TCRs on CD8+ cytotoxic T cells (CTLs) binds to MHC class I-peptide complexes, whereas MHC class II-peptide complexes are responsible for the activation of CD4+ helper T cells.

1.3.2 Co-stimulation

For T cells to reach the full activation capacity, it is necessary to engage signal transduction mediated by co-stimulatory molecules on professional APCs. Represented by the B7 family members, for example B7.1 (CD80) and B7.2 (CD86), these molecules could bind to various receptors such as CD28 on T cells. This ligation induces vital signals for the survival and expansion of T cells. In addition, together with other adhesion molecules, binding to co-stimulatory molecules could enhance T cell activation by stabilizing immune synapses between APCs and T cells. As opposed to the co-stimulatory molecules, there are also co-inhibitory molecules that function through similar principles but negatively regulate T cells functions. This mechanism is essential to maintain immune homeostasis after infections and forms a major barrier for tumor-reactive immune responses. I will mention this pathway and its therapeutic potential for cancer treatment in later sections.

1.3.3 Cytokines

Cytokines are proteins that regulate cell functions through binding to their matching receptors. APCs can release a panel of cytokines that potentiate various functions of T cells. For example, IL-12 produced by APCs during antigen presentation could stimulate production of IFN- γ from T cells, which is a key regulator for immune defense [11]. Moreover, cytokine environment during antigen presentation could shape the functions of activated T cells, especially in the CD4⁺ subset.

1.4 THE SECONDARY IMMUNITY

1.4.1 T lymphocytes

As a result of the three signals, large numbers of pathogen-reactive T cells are produced through clonal expansion. These cells will then migrate to the infection sites and eliminate invading pathogens or infected host cells. CD8⁺ CTLs recognize cells presenting peptides by the MHC class I molecules and induce apoptosis of target cells through a variety of mechanisms, including perforin, granzymes, granulysin or membrane-bound molecules such as FasL or TRAIL. On the other hand, the classic model describes CD4⁺ T cells to function mainly by producing cytokines. Based on the cytokines that activate them and those released by these CD4⁺ T cells, they can be categorized into the Th1 or Th2 subsets. Th1 cytokines, such as IFN- γ , IL-2 and TNF- α , promote immune functions of CTLs, macrophages or NK cells. In contrast, Th2 cells produce distinct cytokines, for example TGF- β , IL-10 and IL-4, and are thought to mainly regulate humoral immune responses. The balance between Th1 and Th2 cells has been proposed to be critical in autoimmunity, allergy and cancer.

1.4.2 Humoral responses

Humoral responses are featured by the activation of B lymphocytes and production of antibodies. B cell receptors (BCRs) are membrane-bound immunoglobulins (IgG) that recognize specific antigens. Thus, different from TCRs, BCR signaling does not require the presence of MHC-peptide complexes. Instead, BCRs could directly recognize microbial surfaces. Consequently, this recognition will result in proliferation of B cells with pathogen-specific BCRs and promote their maturation into antibody-producing plasma cells. This process will lead to increased concentrations of antibodies which will bind to the pathogens and result in clearance through antibody-mediated cellular cytotoxicity (ADCC). In addition, B cells are equipped with MHC and co-stimulatory machinery and could activate and amplify antigen-specific T cells.

2. IMMUNE RESPONSES IN CONTROLLING CANCERS

2.1 HISTORICAL OVERVIEW

In 1909, Enrich proposed that immune surveillance was engaged in the eradication of transformed cells [12] and this hypothesis was elaborated by Burnet a few decades later [13, 14]. However, several lines of experimental evidence argued that immune surveillance was not involved in limiting spontaneous or chemically induced tumors because tumor growth was comparable between immunodeficient athymic nude mice and wild-type controls [15-18]. It was later shown that the development of NK cells, $\gamma\delta$ -T cells and some subsets of T cells were still present in athymic nude mice [19, 20]. In addition, wild-type mice indeed demonstrated substantially lower tumor incidence when the chemical carcinogen dosage was carefully titrated [21]. Similar results were obtained from RAG-2-deficient mice [22] that lack functional B and T cell populations [18, 23]. More recently, animal models created by gene-targeting technologies allowed mechanistic analysis of immunological pathways in controlling tumor development, including TCR signaling of T, NKT or $\gamma\delta$ -T cells [24-26], synthesis of type I IFNs [27-29] and perforin [26, 30]. On the other hand, tumor progression is often accompanied by a panel of mechanisms that hamper effective clearance mediated by the immune system (section 2.2). Collectively, these observations delineated the dynamic dialogues between tumor cells and the immune system during cancer occurrence and development [31, 32].

2.2 BARRICADES FOR ANTI-TUMOR IMMUNITY

As briefly discussed in the earlier section, tumor-induced immune suppression attenuate effective anti-tumor immune responses. Even though many different cell types mediate these effects, the molecular basis of the suppression is overlapping. Below I will introduce some key aspects of these mechanisms.

2.2.1 *Regulatory T cells*

Regulatory T cells (Tregs) naturally occur in the thymus and are important to maintain self-tolerance in physiological conditions [33]. In malignancies and inflammation, Tregs could be induced in response to various inflammatory signals, such as IL-10, TGF- β and PGE2 [34]. Tregs belong to the CD4⁺ helper T cell subsets and express CD25 (IL-2R α) on the surface and transcriptional factor FoxP3 intra-cellularly. Moreover, low expression of CD127 (IL-7R α) was used to define Tregs in humans [35]. Numerous *in vivo* studies have demonstrated that Tregs form a substantial barrier for anti-tumor immune responses. Due to the high expression of CD25, Tregs are able to deplete IL-2 from effector T cells, therefore hamper their activation and functions [35]. In addition, Tregs are potent producers for immune-regulatory cytokines such as IL-10 or TGF- β [36, 37]. Further, Tregs could be more resistant to apoptosis in the tumor microenvironment by releasing antioxidant thioredoxin-1 [38]. These factors conduct multi-faceted effects and facilitate tumor growth and metastasis. Indeed, depleting Tregs by low-dose cytoxin potentiated the therapeutic effects of cancer vaccines in the HER2/neu transgenic mice [39].

2.2.2 *Immune checkpoints*

Sufficient antigen presentation requires co-stimulatory signals triggered by APCs. However, co-inhibitory molecules, also known as immune checkpoints, also exist in order to restore homeostasis after immune clearance [40]. The most well-characterized immune checkpoint to date is CTLA-4 [41, 42], which expresses at high levels on activated T cells and binds to CD80/86 with an affinity that was superior to CD28 [43], which is a T cell-activating receptor that also binds to CD80/CD86. In

addition, CTLA-4 could remove CD80/86 from APCs through trans-endocytosis [44]. Similarly, PD-1 emerges when T cells are activated [45] and can negatively regulate T cell functions and induce T cell apoptosis through ligation to PD-L1 [46, 47] or PD-L2 [48, 49]. Other co-inhibitory ligands such as B7-H3 and B7-H4 [50, 51] were also identified, but their matching receptors on T cells and detailed functions remain elusive. Expression of these immune checkpoints on tumor or immunosuppressive cells is known to be important protective mechanisms that facilitate tumor growth [52, 53] and have proven to be one of the most promising therapeutic targets for the treatment of human cancers (section 3.1).

2.2.3 Enzymatic machinery

Tumor tissues are featured by high levels of energy consumption and altered metabolic profile. Thus, production of various enzymes exhausts crucial amino acids that could support anti-tumor immunity. For example, L-arginine is extremely important for maintaining TCR signaling and T cell functions [54]. Activation of myelomonocytic cells by tumor-derived factors could lead to massive production of ARG and inducible NOS (iNOS) that results in T cell anergy by rapid depletion of L-arginine [55] and release of NO [56, 57]. However, since production of NO was shown to be one of the defending mechanisms mediated by macrophages against cancer cells [58], the role of NO on anti-tumor immunity is still not clear. A recent study showed low-dose irradiation promoted macrophage-mediated tumor rejection through the NOS pathway [59]. Even though ARG and iNOS regulate independent catalytic pathways, co-expression of these two enzymes are often observed, which leads to challenging situations for designing treatment strategies.

Another important enzyme is IDO, which catalyzes tryptophan to N-formyl-kynurenine [60]. It is an important regulatory channel for APCs to modulate T cell functions during antigen presentation through calibrating tryptophan levels [61, 62]. Tumor cells and many types of immunosuppressive cells also utilize this pathway to sabotage T cell responses [63]. Besides the direct effects, IDO activity could control other regulatory schemes in the tumor micro-environment, including COX-2/PGE2 pathway [64, 65], TGF- β or IL-10 production [66, 67]. Thus, it is becoming therapeutically appealing to target IDO activity due to the potential effects on both tumor cells and the immune system. Certainly, pharmacological inhibitors of IDO activity have demonstrated anti-tumor effects [68] and boosted chemotherapy [69] and checkpoint inhibitors [70, 71] in murine models.

2.3 IMMUNOSCORE: Creating Immunological Signatures for Cancer Classification

Observations of inflammatory immune cells in human tumor tissues date back to 1863 by pathologist Rudolf Virchow. Nowadays, it is well-documented that density of CD8+ CTL could independently predict the clinical outcome in various types of human

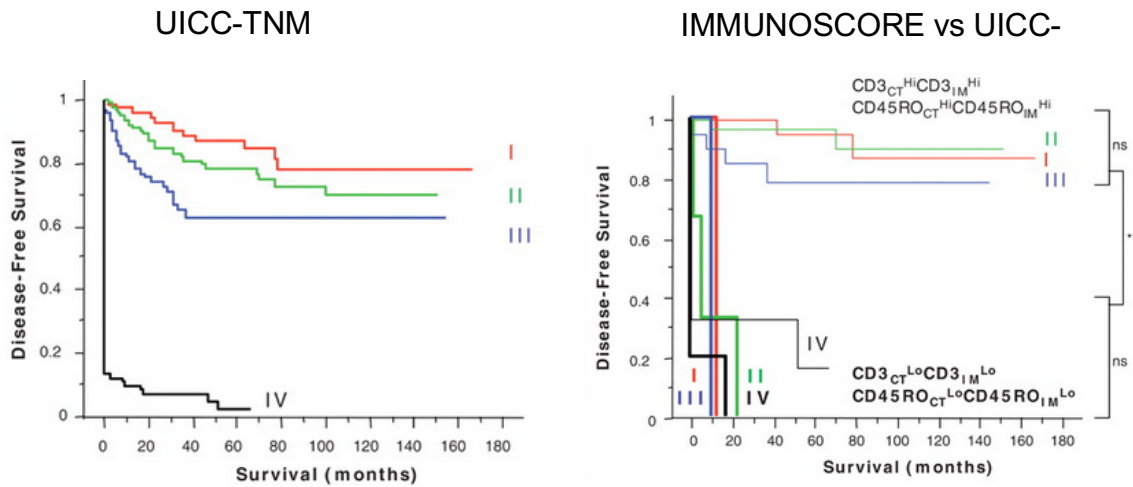


Figure 1, Cancer classification based on immune contexture. CT: Center of the tumor; IM: Invasive margin; CD3: T cell marker; CD45RO: Memory T cell

marker. Adapted from Galon *et al.* *Science* 2006 **313**(5795): p 1960-4. Reprinted with

cancers [72-74]. Infiltration of NK cells has also been reported to be a positive factor in human cancers [75-77]. In contrary, the prognostic role of suppressive immune cells has been inconsistent. In some reports, 'M2-biased' macrophages [78-81] or Tregs [82-84] are associated with poor clinical outcome but correlated with better patient survival in other studies [85-87].

In a study published by Galon *et al.* [88], a large quantity of immune-related genes were screened and candidate genes were validated by tissue microarray in colorectal cancer tissues. Strikingly, it revealed that density of CD45RO+ memory T cells in the tumors provided an independent predictive factor that was complementary to the traditional histopathological classification system (**Figure 1**). In particular, late-stage tumors crowded with memory T cells may have more favorable survival than early-stage patients lacking T cell infiltration [89]. In a recent study, the intratumoral 'landscape' of 28 immune cell types was illustrated in colorectal cancer patients and different immune cells demonstrated distinct localization in the tumor [90]. Based on these findings, Immunoscore, which uses the immune contexture in human tumors as staging criteria, is proposed to be implemented in addition to the TNM classification method [91, 92]. Initiated by a few researchers focusing on colorectal cancer patients, it is to date a worldwide, multi-center investigation for various cancer types. The value of Immunoscore has provided solid evidence advocating the importance of immune surveillance during the occurrence and progression of human cancers. Particularly, these findings may have a profound future impact on the diagnosis and treatment decisions in cancer patients.

3. NEW TRENDS IN CANCER IMMUNOTHERAPY

For decades, immunotherapy struggled to prove its therapeutic efficacy in cancer patients and was never widely-accepted to be useful as a treatment option. Nowadays, therapeutic interventions eliciting tumor-reactive immunity are proven to be clinically effective even in patients with multiple metastatic lesions. In this section, I will highlight the major approaches that have shown success in clinical trials. However, it is important to point out that this is an extremely fast-evolving field that is powered by research talents across all scientific disciplines. Thus, new treatment concepts or technical advances may further improve our current view on this topic in the near future.

3.1 'CHECK-POINT' INHIBITORS

3.1.1 *Unleashing T cells by CTLA-4 blockade*

Immune checkpoint molecules negatively regulate immune effector cells by binding to the matching receptors. As discussed in section 2.2.2, CTLA-4 and PD-1 are two well-characterized receptors on T cells and their therapeutic potentials have been evaluated in preclinical models and clinical studies. In preclinical animal models, blocking CTLA-4 signaling effectively limited tumor growth in mice through activation of T cells [93-96]. Ipilimumab, an anti-human CTLA-4 blocking antibody, was approved by the FDA in 2011 for the treatment of metastatic melanoma and is now under investigation in patients with non-small cell lung carcinoma, small cell lung carcinoma, bladder cancer and prostate cancer. This approval was motivated by results of the landmark phase III clinical trial, which has generated durable survival advantages in metastatic melanoma patients who have failed existing therapies [97-99]. Apart from attenuating negative signals transduced, blocking antibody for CTLA-4 has demonstrated potent ability to remove Tregs in animal models by ADCC mediated by immune cells expressing FcγR [100-102]. Thus, adjusting Fc binding properties of therapeutic antibodies according to the clinical purposes may boost the *in vivo* efficacies in patients [103].

3.1.2 *PD-1/PD-L as a therapeutic target*

Remarkable clinical responses induced by ipilimumab have accelerated the investigation and approval of blocking antibodies against PD-1 pathway. In melanoma patients, both nivolumab (Bristol-Myers Squibb) and pembrolizumab (Merck) generated durable survival benefits [104, 105]. As a result, FDA granted permissions to these antibodies for treating human melanoma recently. Notably, clinical outcome after ipilimumab treatment did not appear to predict the efficacy of PD-1 blockade, since nivolumab enabled substantial clinical responses in patients who failed to respond to prior ipilimumab treatment [106-108]. Importantly, sequential but not concurrent administration of the two antibodies appeared to be clinically favorable because the latter resulted in severe immune-related adverse events [109]. This could be explained by the distinct regulatory role of PD-1 and CTLA-4 on the immune system [110]. Specifically, mice lacking PD-1 protein experienced tolerable autoimmune reactions [111, 112], but CTLA-4 deficiency resulted in devastating autoimmunity [113, 114]. Thus, it has been postulated that PD-1 functions through fine-tuning the threshold of T cell priming, whereas interfering CTLA-4 signaling leads to a broad activation of non-specific T cells. Even though ADCC-mediated removal of Tregs could contribute to the effects of CTLA-4 blockade, it remains to be clarified whether similar mechanisms are involved in PD-1 blocking agents.

Further therapeutic opportunities lay within PD-1 ligands PD-L1 and PD-L2, which are often expressed on tumor cells or immunosuppressive cell types. Results from several clinical trials revealed that PD-L1 blocking antibody was well-tolerated and led to promising clinical responses in patients with various solid cancers [115-117]. Existing evidence indicated that expression of PD-L1 in tumor tissues could be used as a predictive marker for the check-point blocking antibody treatment [118]. Nonetheless, it should be noted that this observation remains controversial since PD-L1 expression is not exclusive to tumor cells, but could also be expressed by fibroblasts, endothelial cells and immune cells. Expression of PD-L1 could also be controlled by external factors such as IFN- γ [119, 120], which is a cytokine produced by activated tumor-infiltrating lymphocytes (TILs) [71, 121]. Thus, expression of PD-L1 might be dynamically regulated by different treatment strategies or pathological conditions in patients.

Expression of PD-L2 was initially identified on APCs but was later demonstrated to be inducible on immune or non-immune cell types by a range of soluble factors [49, 122, 123]. It is well-documented to be a second ligand for PD-1 and transmits negative signals to T cells. Paradoxically, previous findings using PD-L2-deficient animals or blocking antibodies have implied the activating role of PD-L2 on the immune system [52, 124, 125]. In preclinical tumor models, most results available to date included PD-L2 blockade as an addition to the anti-PD-1/PD-L1 antibodies [126, 127]. Even though blocking PD-L2 indeed enhanced anti-tumor effects of other check-point blocking agents [128], PD-L2 knock-out mice conversely demonstrated more aggressive tumor progression [129]. Due to its unclear biological functions, clinical approaches towards PD-L2 are currently scarce. In a recently completed phase I study (NCT01352884), a PD-L2-IgG1 fusion protein was well tolerated and induced promising clinical responses in advanced cancers (abstract 3044, 2013 ASCO meeting). Nonetheless, it is yet to be revealed in a larger cohort of patients how this agent could potentiate anti-tumor immunity.

In order to achieve thorough blockade of the PD-1 pathway, it might be of necessity to combine anti-PD-1 and anti-PD-L1 approaches. On one hand, both PD-L1 and PD-L2 could diminish T cell activation through PD-1 signaling. On the other hand, PD-L1 was shown to inhibit proliferation and expansion of PD-1-deficient T cells [43], indicating multiple receptors could be coupled to PD-L1.

In summary, immune check-point blockers have generated encouraging clinical responses and elicited durable tumor control in patients with advanced solid tumors. However, current clinical trials are predominantly focusing on melanoma or smoking-related lung cancers, which are believed to be more immunogenic due to their high mutation rates. Thus, clinical efficacy of these agents in other cancer types remains to be explored. Taken into account that CTLA-4 and PD-1 are two of the many members in the immune check-point family, novel targets may emerge as the fundamental mechanistic landscape of these proteins is depicted.

3.1.3 Unique clinical properties of check-point inhibitors

Currently, clinical efficacy of anti-cancer treatments is mainly evaluated according to the Response Evaluation Criteria in Solid Tumors (RECIST) criteria, which measure decrease of tumor volumes after drug administration. However, immune-activating agents have demonstrated very unique response patterns in cancer patients. In certain cases, enlargement of tumor lesions or appearance of new lesions have been documented before the onset of a late clinical response after ipilimumab treatment [130, 131]. This could be explained by the distinct kinetics for establishing effective immune responses and infiltration of immune cells into tumor tissues may result in

increased tumor volumes. Therefore, it is critical to adjust the evaluation criteria for cancer immunotherapy.

Recent clinical experiences with ipilimumab revealed that check-point inhibitors may induce severe immune-related adverse events in cancer patients [132, 133]. This is a direct indicator for the potency of these agents in activating the immune system, but it also has posed challenges for clinical care of the patients. Emerging results demonstrated that blocking PD-1 or PD-L1 was associated with more tolerable toxicity. It is in line with the magnitude of autoimmunity observed in animals lacking CTLA-4 or PD-1 expressions. Consequently, in-depth knowledge of the biological functions of immune check-point pathways may be of essential for the development of novel immunotherapeutics.

3.2 ADOPTIVE CELL TRANSFER

Given that immune responses are capable of controlling tumor growth, it is reasonable to hypothesize that adoptive infusion of highly functional tumor-reactive immune cells could be effective as a therapeutic approach. Numerous investigations have been conducted and many have shown stunning anti-tumor effects. In this section, I will briefly summarize treatment strategies utilizing activated T cells or NK cells in human solid and hematological malignancies.

3.2.1 Tumor-infiltrating lymphocytes (TILs)

Solid tumor tissues are often infiltrated with T lymphocytes, which is an independent prognostic factor for clinical outcome in various types of cancer as discussed earlier. Moreover, it is generally believed that T cells in tumor tissues are recruited due to their tumor-targeting properties. Proven to be effective in human melanoma in 1988 [134, 135], TILs retrieved from surgically removed tumor tissues followed by activation with high-dose IL-2 have become an attractive treatment option. Even though not validated in the original report, it was later shown that ability of TILs to kill autologous tumor cells *in vitro* could strongly predict the response rate in patients [135, 136]. Further, transferring TILs containing both CD4⁺ and CD8⁺ T cells [137, 138], as well as lymphodepletion in patients prior to adoptive T cell transfer [138, 139] were demonstrated to be key factors for clinical efficacy. This could be due to clearance of suppressive Tregs and retention of available T cell stimuli, such as IL-2, IL-7 and IL-15 *in vivo*. These findings have introduced valuable modifications to the TILs treatment procedures. In an updated report containing 93 metastatic melanoma patients, the overall response was up to 72% and 36% of the patients treated with TILs achieved survival longer than 3 years [140]. However, this approach is only possible when sufficient amount of TILs could be generated from the same patient. To overcome this issue, alternative strategies using genetically engineered T cells were developed.

3.2.2 Creating anti-tumor T cells through genetic modifications

TCRs that recognize tumor-associated antigens (TAAs) are required for T cells to lyse tumor targets. Thus, genetic engraftment of such TCRs (TCR-T) into T cells enables their specific killing against tumor cells presenting peptides derived from TAAs [141-143]. When the TAA-specific TCR-T cells were infused, it resulted in shrinkages of tumor burdens in patients with various types of cancers [141, 144-146]. In a recently reported clinical trial, T cells equipped with TCRs specific for the tumor antigen NY-ESO-1 induced tumor regression in patients with metastatic sarcoma and melanoma [147]. Even though TAA-specific CD8⁺ CTLs are important for the cytolytic effects, TCR-engineered CD4⁺ T cells also play indispensable roles when infused simultaneously [148, 149]. This could result from their ability to produce T cell supporting cytokines.

Alternatively, T cells could be engineered to express chimeric antigen receptors (CAR-T). In these structures, the extracellular antigen specificity of a monoclonal antibody is coupled to the intracellular T cell-activating signaling domains through trans-membrane spacer molecules. Since the initial discovery, several improvements have been introduced, mainly through fine-tuning the contents of intracellular signaling domains [150, 151]. In comparison to TCR-Ts, cytolytic function of CAR-Ts does not require presence of the MHC-peptide complexes on tumor cells and T cells are sustained by multiple activating signals coupled to the CAR complexes. Therapeutic strategies using CAR-Ts targeting CD19 (CD19-CAR) have achieved remarkable success in treating refractory B cell malignancies [152-155]. In an updated report with a small patient cohort, 90% (27 out of 30) of relapsed or refractory ALL patients reached complete remission after CD19-CAR therapy and the overall survival rate was 78% at 6 months [156]. In solid tumors such as ovarian cancer [145, 157], renal cell carcinoma [158-160] and neuroblastoma [161, 162], CAR-expressing T cells were less effective in controlling tumor progression. This could be explained by the impaired persistence and survival of infused T cells caused by hostile environment both in the blood and tumor microenvironment. Currently, many ongoing clinical trials are exploring the therapeutic potential of CAR-expressing T cells as a treatment for solid and hematological malignancies [163].

3.2.3 NK cell therapy

In contrast to T cells, lysis of tumor cells mediated by NK cells is primarily based on the mismatches between killer cell Ig-like receptors (KIRs) on NK cells and MHC class I molecules on target cells. This important feature allows recipients to accommodate NK cells derived from a haploidentical family member. In addition, NK cells express FcγR on the surface and could contribute to ADCC effects triggered by tumor-binding antibodies. Moreover, death receptors on NK cells could induce apoptosis of the tumor cells through activating caspase pathways [164]. Therefore, highly-activated NK cells are suitable for treating patients with cancers. To date, most promising results with adoptive NK cell transfers were observed in patients with hematological malignancies who received allo-reactive haploidentical NK cells [165-167]. Influenced by similar resilient mechanisms as the T cells, this approach is yet to be improved in controlling tumor growth in patients with solid tumors [168-170].

3.2.4 DC-based therapy

Dendritic cells are professional APCs and are important for providing the 'three signals' during T cell priming (see 1.3). Even though a few reports acknowledged their cytotoxic functions [171, 172], DC therapy in general is thought to mediate tumor killing through enriching tumor-reactive T cells. Since most of the treatment procedures involve generating and infusing clinical grade DC products into patients, I will here categorize it as one of the cellular therapies.

In principle, DC-based therapeutics require generation of functional DCs followed by decoration with TAAs. Even though blood-derived monocytes are most frequently used, CD34+ hematopoietic progenitor cells have also been tested as precursors for maturing DCs [173, 174]. To introduce TAAs, various methods, including direct pulsing of synthetic peptides, recombinant proteins, tumor lysates or transfection-based methods have been implemented [175]. Some investigative results in small numbers of cancer patients have shown promising clinical responses [173, 174, 176-178]. As the first FDA-approved cellular therapy in 2010, Sipuleucel-T (Provenge) was one of the milestones in the history of cancer immunotherapy. This DC-based product was used to treat patients with refractory prostate cancer and could prolong overall survival for 4.1 months [179, 180]. In general, DC-based treatments are well-tolerated and

toxicity is minimal. Recently, the clinical values of naturally occurring DC subsets, such as plasmacytoid DCs have also been evaluated [181, 182]. Even though infused at low numbers, these cells were able to generate favorable immune responses in patients with melanoma.

3.2.5 Sustaining infused cells *in vivo*

Current protocols implemented for adoptive cell therapy require rapid activation and expansion of patient-derived T or NK cells using high-dose cytokines or agonistic antibodies. The resulted cells are extremely potent in killing tumor cells *in vitro*. Nevertheless, a marked decrease of cell numbers was observed after infusion (from one T cell in 580 PBMC one day post infusion to 1 T cell per 35.400 PBMC after 2 weeks [137]). Some argue that this reflected trafficking of the infused T cells to various organs and tumor sites. But others proposed that it was mainly due to *in vivo* apoptosis induced by cytokine withdrawal or shortened telomere length [183].

In comparison, infused at as low as 1.5×10^5 cells per kilogram body weight, CD19-CARs proliferated *in vivo* and potently controlled tumor progression in leukemia patients [152, 184]. However, when similarly designed CAR-T cells were tested in patients with solid tumors, infused cells rapidly diminished from the peripheral blood and failed to limit tumor growth efficaciously [161]. By analyzing intratumoral CAR-T cells in a preclinical animal model, recent findings suggested that inhibition of T cell signaling, rather than loss of CAR expression or antigen-carrying tumor cells could contribute to this result [185].

Thus, sustaining anti-tumor capacity of the effector cells after infusion might be the key to a successful adoptive cell therapy. This goal could be achieved through a number of approaches. Firstly, early clinical trials using anti-viral CD4+ CAR-T cells have demonstrated *in vivo* persistence of CAR-expressing T cells for almost a decade [186]. This implies that presence of antigen-specific **central memory T cells** (T_{CM}) may help prolong *in vivo* anti-tumor immunity [187]. Given the central role of IL-15 in activating memory T cells and NK cells in cancer patients [188], this cytokine holds substantial promise to extend the *in vivo* life-span of transferred T or NK cells. This point has been consolidated in experimental animal models, where tumor-specific T cells persisted *in vivo* when activated with IL-15, possibly through recruiting antioxidant mechanisms [189] or preventing loss of telomere [190]. Secondly, it is rational to use **combinational approaches** to sustain T cell activities. Results of a phase I clinical trial combining DC vaccines with TIL therapy in a small number of melanoma patients have been recently released [191]. The combination was safe and generated promising clinical responses and the updated protocol will include prior lymphodepletion in patients. Based on similar principles, various **protective mechanisms** could be introduced to prevent tumor-induced immune suppression. For example, co-transduction of IL-12 into CAR-T cells improved anti-tumor activity in mice by potentiating macrophage functions [192] and resisting suppression mediated by Tregs [193]. Lastly, opportunities for improving the *in vivo* persistence of adoptively transferred immune effector cells may underlie **novel regulatory mechanisms**. In a recent report, pre-activated antigen-specific T cells were infected with shRNA libraries that silenced greater than 1500 T cell regulatory genes. After infusion, T cells were retrieved from tumor sites and spleens and compared for the enrichment of shRNAs [194, 195]. This approach allowed the authors to identify genes that were important for T cell functions and survival, particularly in tumor microenvironment. These results highlighted that loss of *Ppp2r2d*, a gene without previously known functions in T cells, contributed substantially to survival and proliferation of transferred T cells in melanoma tumors. Therefore, manipulating these novel pathways may optimize longevity of transferred effector cells in patients with solid tumors.

4. THE 'DOUBLE AGENTS': MYELOID CELLS IN CANCERS

4.1 BACKGROUND

For decades, the dynamic interactions between chronic inflammation and cancers have been carefully dissected [196]. It has been well-documented that non-steroidal anti-inflammatory compounds, such as aspirin, prevent occurrence of various types of human cancers [197]. Local inflammation in tumor tissues is represented by increased infiltration of leukocytes, elevated levels of cytokines or chemokines and abnormal angiogenesis. Emerging evidence depicts that tumor-driven inflammation also has a systemic impact on the peripheral immune system and tumor-free organs.

In cancer patients, circulating monocytes are recruited to tumor tissues by various chemokines, such as CCL-2, and skewed into 'M2-biased' TAMs [67, 198]. In contrast to their 'M1-like' counterparts, TAMs are inefficient in producing pro-inflammatory factors such as IL-12 and TNF- α . Instead, they hamper tumor eradication through release of TGF- β , IL-10, PGE2 or activation of regulatory T cells. In addition, TAMs are an important source of VEGF and PDGF, which support abnormal vasculature in tumor tissues. Visualization tools revealed that TAMs were the chaperones for intravasation of tumor cells during cancer metastasis [199].

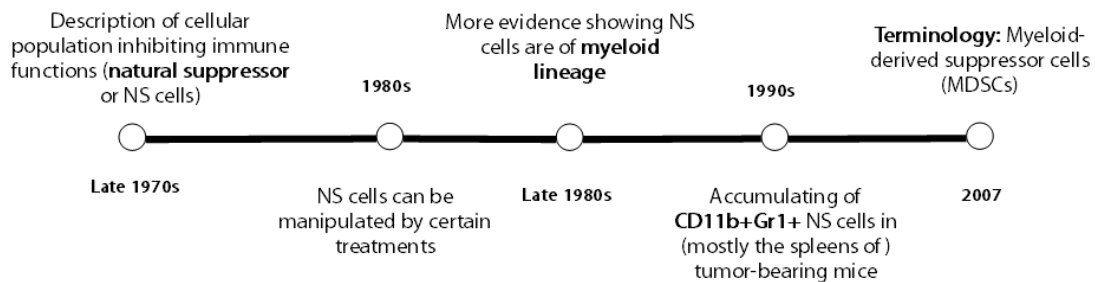


Figure 1, Brief history of myeloid-derived suppressor cells (MDSCs) in cancers.
Modified from: Talmadge and Gabrilovich, *Nat. Rev. Cancer*, 2013 Oct;13(10):739-52

Recently, the role of myeloid-derived suppressor cells (MDSCs) in cancers has been highlighted. Although the description of immature 'natural suppressor' cells dated back to 1970s, it was not until 2007 that the scientific nomenclature of these cells could be agreed (**Figure 1**) [200]. In tumor-bearing mice, MDSCs are defined by co-expression of CD11b and Gr1 and could be further divided into monocytic (moMDSCs) and granulocytic (grMDSCs) lineages based on the expression levels of Ly6C and Ly6G [201]. In cancer patients, phenotypic definition of MDSCs remains challenging. Several myeloid markers including CD34, CD33, CD11b, CD14, HLA-DR, CD16, CD15 or CD66b have been suggested as individual marker or in combination to detect MDSCs [202] in peripheral blood of cancer patients. Thus, the general consensus for MDSC definition emphasizes the immature phenotype and immune-suppressive functions. Due to the complex leukocyte composition in tumor tissues, functions of intratumoral MDSCs stay controversial. Previous study showed that MDSCs isolated from melanoma tumor tissues lack immune suppressive functions in comparison to the ones in the blood [203]. Conversely, later reports demonstrated that MDSCs in tumors were more potent in exerting suppression on T cells [204, 205].

In summary, TAMs and MDSCs are both heterogeneous populations that bear overlapping surface markers and employ similar immune-regulatory mechanisms in cancer patients. Since the phenotypic signatures and suppressive functions of TAMs [67, 198, 206] and MDSCs [200, 202, 207] have been extensively reviewed elsewhere,

I will instead focus on the clinical implications and targeting strategies of these cells in patients with cancers.

4.2 MYELOID CELLS AS BIOMARKERS

As mentioned in section 2.3, immune contexture in tumor tissues is a powerful prognostic indicator in cancer patients. It has been widely reported that frequencies of TAMs predicted survival of cancer patients [78-81]. In a newly proposed evaluation system (TMEM) for predicting risk for metastasis in breast cancer patients, infiltrating CD68+ cells were included as one of the essential criteria [208]. However, other studies demonstrated the positive prognostic values of TAMs [85, 209, 210]. These discrepancies could be explained by the highly tissue-dependent and versatile nature of macrophages, particularly in tumor tissues. Thus, it is becoming increasingly attractive to explore the prognostic potential of monocytic and granulocytic MDSCs in peripheral blood of cancer patients (summarized in **TABLE 1**).

Many studies have reported that levels of moMDSCs in the blood correlated well with cancer stages and predicted survival in patients with melanoma [211, 212], breast [213, 214], ovarian [215], colorectal [216], lung [217] and various types of other cancers [218, 219]. This was recently supported by the observation that increased numbers of moMDSCs reversely associated with numbers of antigen-specific CD8+ CTLs in melanoma patients [212, 220].

It is widely accepted that MDSCs form one of the main hurdles for sufficient anti-tumor immune responses. Presence of moMDSCs, but not Tregs, was observed at higher levels in colorectal cancer patients who failed to respond to an anti-cancer vaccine [221]. In addition, CD14⁺HLA-DR^{low/neg} moMDSCs were proposed to be a biomarker in patients who received a multi-epitope peptide vaccine [222]. In accordance, grMDSCs diminished from the peripheral blood in patients undergoing ipilimumab treatment [223] and frequencies of pre-treatment moMDSCs appeared at higher levels in non-responders [220, 224]. However, it should be noted that blood-derived moMDSCs and grMDSCs have distinct properties during experimental procedures *ex vivo*. While moMDSCs are present in PBMCs after gradient centrifugation, high numbers of arginase-producing grMDSCs could only be co-purified from blood of cancer patients [225]. Since cryopreservation of human PBMC could drastically change the frequencies and suppressive functions of grMDSCs [226], evaluation of this population might be limited if only frozen materials are available.

TABLE 1: Prognostic values of suppressive myeloid cells in cancer patients

Patients	Prognostic values	Other findings	Ref
Melanoma	Frequencies of moMDSCs and Tregs, but not the grMDSCs, correlated with the stage and poor prognosis in melanoma patients	Inflammatory factors, IL-1 β , IFN- γ and CXCL10 in the sera correlated with the Tregs and MDSCs	[211]
	Lower moMDSCs predicted better responses to ipilimumab	No changes of moMDSCs during ipilimumab treatment	[224]
	moMDSC numbers at week 6 after ipilimumab treatment correlated with overall survival	moMDSCs were inversely associated with CD8 ⁺ T cell frequencies	[220]

	Frequencies of moMDSCs, but not Tregs, predicted poor survival	moMDSCs reversely correlated with NY-ESO-1 and Mart-1 specific T cells	[212]
	Low TAM infiltration predicted better survival in uveal melanoma	TAMs associated with higher density of microvasicles	[227, 228]
Breast cancer	CD68/CD4/CD8 in tumor tissues predicted patient survival	Paclitaxel treatment increased M-CSF production and TAM levels	[229]

TABLE 1 (continued)

Patients	Prognostic values	Other findings	Ref
	CD14 ⁺ Arg ⁺ cells in the blood correlated with the stage of the patients	High numbers of CD14 ⁺ Arg ⁺ cells were detected in tumor tissues and draining lymph nodes	[213]
	Circulating MDSCs correlated with the stages of the disease	MDSC increased after doxorubicin and cyclophosphamide treatment	[214]
	CD68+ TAMs were used to predict metastasis (TMEM)		[208]
	TAMs were an independent prognostic factor for survival	TAMs correlated with angiogenesis and VEGF in tumors	[79]
	Higher CD163+ and CD68+ cells predicted poor survival	Localization in tumor stroma but not tumor nest was important	[230]
	Proliferative TAMs correlated with higher grade tumors	TAMs did not correlate with tumor sizes or metastasis	[81]
Ovarian Cancer	Blood MDSCs correlated with primary tumors and metastasis	MDSCs maintained the stemness of cancer cells by miRNA101	[215]
Colorectal and breast	Blood-derived MDSCs correlated with poor prognosis	Lineage ^{neg} cells in bone marrow were the suppressive cells	[216]
Colorectal	TAMs increased with stages and predicted poor survival	Chemokine expression, especially CCL-2 correlated with stage	[80]
	Non-responders to an anti-cancer vaccine had high blood MDSCs	Treg did not predict response	[221]
Neuroblastoma	Infiltration of inflammatory myeloid cells negatively correlated with survival	Independent from MYCN or stage	[231] Study IV
Non-small cell lung cancer	High moMDSCs in cancer patients and correlated with metastasis	moMDSCs suppressed T cells through ROS	[217]
Renal cell carcinoma	CD14 ⁺ HLA-DR ^{lo/neg} MDSCs strongly correlated with the survival of patients after cyclophosphamide and IMA901 treatment	Treg numbers before treatment also predicted responses	[222]

Various solid tumors	Common myeloid progenitors correlated with the stage of cancers	Myelopoiesis skewed towards granulocytic lineage	[218]
	Increased MDSCs and Tregs in cancer patients and MDSCs predicted poor outcome	MDSC levels correlated with higher Th2 cytokines, especially IL-13	[219]
Hodgkin's lymphoma	TAMs were associated with poor prognosis	Frequencies of TAMs predicted treatment failure rate	[78]

4.3 DRIVING FORCES FOR SUPPRESSIVE MYELOID CELLS

Tumor-driven inflammatory mediators are the most frequently cited mechanism to induce myeloid cells with suppressive functions. The majority of published studies employ well-designed *in vitro* model systems, where human or murine immune (progenitor) cells are exposed to tumor-derived factors. These findings are then validated using *in vivo* models or primary immune cells sorted from cancer patients. Even though most research articles emphasize the importance of a particular pathway, it is likely that multiple aspects are involved in regulating the diversified inflammatory network. Besides, environmental factors such as hypoxia and acidity have recently been revealed to shape the functions of myeloid cells (**TABLE 2**).

4.3.1 Established soluble factors

GM-CSF

Under physiological conditions, GM-CSF is one of the driving forces for myelopoiesis and maturation of APCs. Early studies showed the potent anti-tumor effects of GM-CSF-based vaccines in preclinical models [232]. The mechanisms of action include enhanced maturation and infiltration of 'M1-like' macrophages and dendritic cells. In humans, GM-CSF as an adjuvant therapy was shown to be clinically favorable in various types of cancer patients [233-235]. When GM-CSF was delivered to melanoma patients by an oncolytic vector (OncoVex), it decreased numbers of MDSCs as well as Tregs efficiently, and raised antigen-specific T cell responses [236]. In contrast, one clinical study using GM-CSF as an adjuvant therapy increased moMDSCs levels in melanoma patients and these cells could inhibit lymphocytes by producing TGF- β [237]. These controversial findings could be explained by the dose-dependent immune modulatory effects of GM-CSF *in vivo* [238]. In an animal model, high-dose GM-CSF, but not intermediate or low-doses, hampered efficient tumor-reactive immunity by inducing MDSCs [239]. This was supported by a recent clinical study, where low-dose GM-CSF adjuvant treatment did not increase MDSCs in pancreatic cancer patients [240]. The direct link between tumor-derived GM-CSF and induction of suppressive myeloid cells was dissected by a number of experimental models. Together with other factors including G-CSF or IL-6, recombinant GM-CSF enabled suppressive functions of human CD34+ hematopoietic stem cells [218] or primary human monocytes [216, 241, 242]. In a *Kras*-driven pancreatic tumor model, neutralization of GM-CSF abolished the induction of suppressive myeloid cells *in vivo* [243].

COX-2/PGE2

Prostaglandins (PGs) are lipids that play multifaceted roles during inflammation, autoimmunity and cancer. Cyclooxygenase-2 (COX-2) is an inducible enzyme that regulates the production of PGE2. It is often over-expressed in human cancers and indicated to be a parameter associated with poor prognosis in cancer patients [244]. Even though PGE2 initially was thought to be important in stimulating dendritic cells [245, 246], recent studies have revealed its alternative role in inducing suppressive functions in myeloid cells. In human ovarian cancer patients, the COX-2/PGE2 pathway was demonstrated to be the master regulator for suppressive functions of MDSCs via a positive feedback loop [247]. Specifically, PGE2 could activate a panel of suppressive mechanisms in human myeloid cells, including IDO, ARG1, TGF- β , PGE2 and IL-10 [247-252]. Since PGE2 is a strong activator for the JAK-STAT signaling, it is likely that this is the main pathway controlling these events [205, 253].

Interleukin-1

IL-1 is another widely reported factor in driving the induction of suppressive myeloid cells in cancers. In a recent study, IL-1/IL-1R interaction was significantly enhanced on monocytes isolated from patients with kidney malignancies and drove molecular

mechanisms to support angiogenesis and cancer invasion [254]. In preclinical models, tumor-derived IL-1 β could augment mRNA expression of iNOS and ROS in myeloid cells, and could therefore be a potential target for cancer immunotherapy [254-257].

TABLE 2: Induction mechanisms of suppressive myeloid cells in cancers

Methods	Tumor types	Essential factors	Suppressive mechanisms	Ref
Patients	Malignant melanoma	GM-CSF (adjuvant therapy)	TGF- β	[237]
		STAT-3 (AG490)	ROS, ARG1	[253]
	Ovarian	PGE2	PGE2, IDO, IL-10, ARG1 (mRNAs)	[247]
	Renal cell carcinoma	IL-1/IL-1R	Angiogenesis and invasiveness	[254]
	Head and neck	STAT-3 (Static or siRNA)	ARG1	[205]
In vitro tumor co-culture	Human early-passage melanoma tumor cells	COX-2/PGE-2 (Celecoxib)	PGE2, ROS	[250]
	Various human solid tumor cell lines	GM-CSF, IL-1 β , IL-6, VEGF, TNF α	ARG1, ROS	[258]
	Pancreatic human tumor cell lines	COX-2/PGE2	ARG1 (expression)	[259]
	Human glioblastoma tumor cell lines	Not tested	PD-L1 (higher expression)	[260]
In vitro cytokine mixture	Seven human tumor types	GM-CSF, G-CSF and IL-6 (used on CD34 ⁺ progenitor cells)	Not tested	[218]
	Human ovarian cancer	PGE2	PGE2, IDO, IL-10, ARG1 (mRNAs)	[251]
	Human solid tumors	GM-CSF+G-CSF	ARG1 (higher expression)	[216]
	Various human cancers	PGE2	TGF- β , ROS	[248]
		GM-CSF+G-CSF	IDO, Tregs	[241]
		GM-CSF+IL-6 (Possible other factors)	iNOS, TGF- β , ARG1, VEGF (mRNAs)	[242]
In vivo murine models	Breast cancer (4T1)	COX-2/PGE2 (shRNA, inhibitor)	Not tested	[248, 261]
		IL-1 β	iNOS, ROS (higher expression)	[255-257]
		S100A8/A9	Arginase (high expression)	[262]

	Various tumors	HMGB-1	IL-10	[263]
	Colon and lymphoma (CT26 and EL-4)	S100A9 (silencing and transgenic)	ROS (expression)	[264]
	Lymphoma (EL-4)	Hypoxia, HIF-1 α	Arginase (expression)	[265]
		SIRT-1/HIF-1 α , Glycolysis	Arginase, IL-10, TGF- β (expression)	[266]
	Neuroblastoma (NXS2)	ATP-P2X7R	ROS, ARG1, TGF- β 1 (expression)	[267]
	Melanoma (B16F10)	GM-CSF	ARG1, iNOS	[268]
	Melanoma (MT-RET-1)	VEGF, iNOS	ROS, STAT-3 (higher expression)	[269]
	Melanoma (B16F10), Lung cancer (LLC)	Hypoxia, HIF-1 α	PD-L1	[270]
		Lactic acid, HIF-1 α	ARG1 (mRNA)	[271]
	B cell lymphoma (A20) Melanoma (B78H1)	GM-CSF (vaccine)	iNOS	[239]
	Pancreatic cancer (KRAS-driven model)	GM-CSF (antibody or silencing)	ARG1, iNOS	[243]
	Lymphoma (EL-4)	Retinoblastoma-1 (<i>Rb-1</i>) (in moMDSCs)	Not tested	[272]

4.3.2 Emerging inflammatory factors

Other mediators involved in inflammation and autoimmunity also take part in cancer-induced modulation of the immune system. S100 proteins are conserved among vertebrates and possess calcium-binding properties [273]. Among all 21 members, S100A8 and S100A9 are by far the most investigated in suppressive myeloid cells [274]. These two proteins can form heterodimers (S100A8/9) and skew myelopoiesis towards a suppressive phenotype by binding to TLR4 and RAGE [262, 264]. Accordingly, higher levels of soluble S100A8/9 were observed in blood of cancer patients and correlated with MDSC frequencies [275, 276]. Quinoline-3-carboxamide is a clinically validated compound for the treatment of autoimmunity and inflammatory disorders. A recent study identified that it directly interacted with S100A9, engaging both Zn⁺⁺ and Ca⁺⁺ [277]. Provided that S100A9 was strongly associated with poor clinical outcome in prostate cancer patients [278], tasquinimod has been tested in randomized clinical trials [279, 280] and is currently under phase III clinical investigation as a treatment of metastatic prostate cancers (NCT01234311).

Another pro-inflammatory protein that interacts with TLR4 and RAGE is HMGB-1 [281]. It was originally recognized for its regulatory functions on DNA conformation but later shown to be released by macrophages during sepsis [282, 283]. In tumor-bearing mice, HMGB-1 could potentiate the production of IL-10 via NF κ B pathway in MDSCs and directly inhibit functions of T cells [263]. In addition, post-surgical removal of colon cancer tumor masses in mice resulted in elevated production of HMGB-1, which

facilitated the recruitment of MDSCs [284]. This could partially contribute to cancer recurrence after surgery in patients with solid tumors. In addition, human tumor cells can produce HMGB-1 in an autocrine fashion to sustain their survival and proliferation [285], potentially through modulating mitochondrial activities [286]. Conversely, radiotherapy or irradiation were reported to induce immunogenic cell death by triggering release of HMGB-1 and antigen presentation mediated by TLR4 on DCs [287-289]. These findings imply the dual role of HMGB-1 in regulating the interplay between tumor cells and the immune system. During cancer progression, HMGB-1 is released as a mechanism to prevent immune surveillance. When tumor masses are assaulted by anti-cancer agents, massive production of HMGB-1 in combination with other pro-inflammatory factors and tumor-associated antigens promote activation of APCs and T cell priming. However, retention of HMGB-1 after the anti-cancer treatments recruits immune cells with tumor-promoting properties and contributes to a favorable environment for cancer recurrence.

4.3.3 Hypoxic and metabolic control

Cancer cells are highly proliferative and can avoid programmed cell death. Consequently, the abnormal metabolic and acidic landscape in the tumor tissues creates a hostile environment for anti-tumor immune effectors. In normal tissues, HIF-1 α is maintained at low levels in myeloid cells, but could be elevated in MDSCs or TAMs by tumor-induced hypoxia [265, 270, 290] or lactic acid [271, 291]. This activation subsequently results in enhanced immune expression of suppressive factors such as arginase and immune check-point PD-L1 on myeloid cells. Moreover, fast-growing tumor cells feature high concentrations of ATP in the adjacent tissues and the P2X7 receptor on myeloid cells could capture the available ATP and promote synthesis of arginase, ROS and TGF- β [267]. In line with these findings, differentiation of MDSCs was shown to be powered by mTOR/HIF-1 α -regulated glycolytic activity [266]. Even though the metabolic alterations in cancer cells have been extensively discussed [292], it is only recently that mTOR-mediated metabolic control was shown

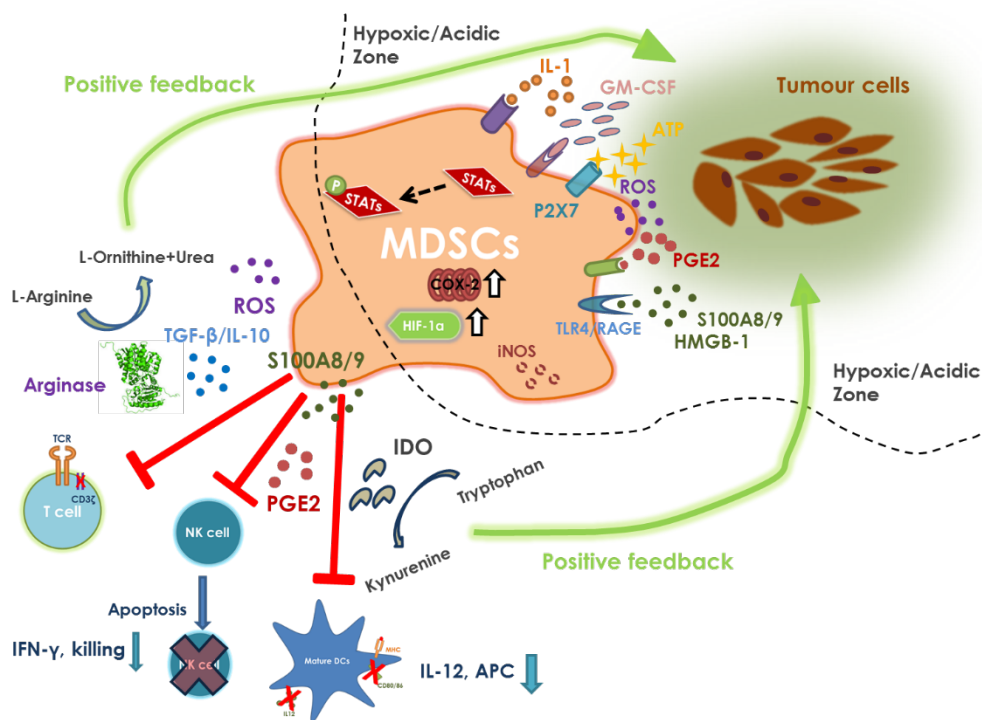


Figure 2, Functional overview of interactions between MDSCs and tumors.

Updated from: Mao, Poschke and Kiessling, *J. Intern. Med.*, 2014 Aug;276(2):154-70.

to regulate the development of immune cells [293, 294]. Thus, it is reasonable to hypothesize that tumor-induced metabolic rearrangements may have a great impact on the immune composition in cancer patients. In-depth understanding of these mechanisms could reveal novel targets for therapeutic interventions in cancer treatment.

4.3.4 The 'Jemaa el-Fnaa'

The activation and differentiation of suppressive myeloid cells are guarded by interconnected mechanistic networks (**Figure 2**). Tumor-induced metabolic and oxidative changes promote myeloid cells to acquire suppressive functions through a HIF-1 α -mediated machinery. Meanwhile, a variety of tumor-derived factors, such as GM-CSF, PGE2, IL-1 and IL-6, are potent inducers for JAK-STAT signaling pathways, which in turn activate production of suppressive factors from myeloid cells. Through STAT signaling, TNF α , TGF- β , VEGF [295], PGE2 [296, 297] or the hypoxic environment [298] also enhance the production of pro-inflammatory HMGB-1 or S100 protein family members. On the other hand, suppressive myeloid cells release soluble factors such as microRNAs, ROS or various inflammatory mediators and deplete essential metabolites from the adjacent areas. This collectively reinforces the abnormal metabolic and oxidative milieu, which facilitates tumor invasion and migration. Even though less discussed in this thesis, interactions among immune cells, or between immune cells and endothelial cells or fibroblasts, amplify the cellular complexity in the solid tumor microenvironment. Thus, instead of illustrating this network as many independent one-to-one dialogues, it resembles my experience in the seemingly 'chaotic' night market 'Jemaa el-Fnaa' in Marrakesh (Morocco). Thousands of vendors and customers are entering and exiting the market and simultaneously interacting with each other. Even though people bargain for different goods, the negotiation methods and tactics are largely overlapping.

4.4 TARGETING SUPPRESSIVE MYELOID CELLS

Suppressive myeloid cells in cancers are extremely heterogeneous and characterized by the production of inhibitory factors but lacking immune-stimulatory potential. Because they often share surface antigens with immune-stimulatory myeloid cells, it remains challenging to specifically target these cells for the treatment of human cancers. In general, existing results support that blockade of tumor-induced inflammation is an efficient way to decrease the numbers and functions of suppressive myeloid cells. Standard therapies, such as surgery or radiation, also have an impact on the suppressive myeloid cells. Even though certain chemotherapeutics have been reported to ameliorate the expansion of suppressive myeloid cells, other cytostatic agents have demonstrated a promoting role. While the detailed mechanisms remain to be revealed, recent findings suggest that targeted therapy or immunotherapy also reduce suppressive myeloid cells in cancer patients. In this section, I have summarized the recently reported *in vivo* modulatory effects of anti-cancer treatments on suppressive myeloid cells, especially in cancer patients (**TABLE 3**).

4.4.1 Anti-cancer treatments and suppressive myeloid cells

Standard surgical procedure or cytostatic drugs have recently demonstrated their role on suppressive myeloid cells in cancer patients. Removal of tumor burdens by surgery decreased the number of arginase-producing CD14⁺ cells in the blood of breast cancer patients [213]. Chemotherapeutics, such as gemcitabine, capecitabine [240], or trabectedin [299], reduced circulating MDSCs in cancer patients, possibly by inducing selective cell death through the caspase-8 pathway [299]. In contrary, treatments

using doxorubicin, cyclophosphamide [214] or paclitaxel [229] have resulted in elevated numbers of MDSCs in cancer patients. These observations were in agreement with observations in tumor-bearing mice [229, 299-302]. Paradoxically, paclitaxel [303-305] and doxorubicin [306] could reduce accumulation of MDSCs in preclinical models. This could be explained by the distinct dosing and concurrent treatment agents used in humans or mice. Although not yet shown in humans, 5-fluorouracil specifically deleted MDSCs and recovered anti-tumor T cell responses in mice [307]. Furthermore, low-dose irradiation enabled re-activation of TAMs to an anti-tumor phenotype that was featured by high production of iNOS and potently controlled tumor growth in mice [59].

Novel anti-cancer agents, such as targeted therapy or immunotherapy, have also shown modulatory roles on suppressive myeloid cells in patients with cancers. Vemurafinib, an inhibitor targeting a *BRAF* mutation in cancer cells, could decrease moMDSCs and grMDSCs in peripheral blood of melanoma patients [308]. However, it remains to be elucidated whether this effect was directly on myeloid cells or resulted from rapid tumor shrinkage. The checkpoint inhibitor ipilimumab also induced a marked decrease of grMDSCs in the blood of melanoma patients within weeks [223]. Even though moMDSCs frequencies were unchanged during the antibody therapy, pre-treatment levels of moMDSCs were associated with treatment outcome [224]. Additionally, adoptive transfer of highly activated lymphocytes reduced MDSCs in the peripheral blood of cancer patients, but it did not seem to predict treatment outcome in these patients [309].

TABLE 3: Modulation of suppressive myeloid cells in preclinical and clinical studies

Subjects	Tumor types	Treatments	Key effects	Ref
HUMAN	Breast cancer	Surgery	Decreased levels of CD14 ⁺ Arg ⁺ cells in the blood	[213]
		Doxorubicin, cyclophosphamide	Higher levels of circulating MDSCs	[214]
		Paclitaxel prior to surgery	Increased levels of CD11b ⁺ CD14 ⁺ cells in the blood	[229]
	Pancreatic cancer	Gemcitabine, Capecitabine, vaccine and GM-CSF	Reduction of MDSCs in the blood	[240]
	Diffuse-type giant cell tumor	Anti-CSF-1R mAb	Reduction of CD68 ⁺ CD163 ⁺ cells and tumor regression	[310]
	Various solid tumors	VEGF-Trap	No effects on MDSCs but enhanced DC maturation	[311]
	Metastatic prostate cancers	Anti-CCL-2 mAb (Calumab, Phase II)	No responses, probably due to insufficient neutralization	[312]
	Soft tissue sarcoma	Trabectedin	Selective depletion of blood monocytes through caspase-8 pathway	[299]

		Adoptive T and NK therapy	Reduction of MDSCs in blood	[309]
	Renal cell carcinoma	Sunitinib	Reduction of MDSCs but no correlation to tumor burden	[313]
			Reduced immature myeloid cells but better CD1c+ DCs	[314]
		All-trans-retinoic acid (ATRA)	Reduction of MDSCs and maturation to DCs	[315, 316]
	Small cell lung cancer	All-trans-retinoic acid (ATRA)	Decreased MDSCs and improved antigen-specific response to p53	[317]
	Head and neck	25-hydroxyvitamin D3	Decreased CD34 ⁺ cells in the blood and increased HLA-DR	[318]
		Tadalafil (PDE-5 inhibitor)	Significant reduction of MDSCs in the tumor and blood at intermediate doses	[319]
	Advanced stage melanoma	Vemurafinib (<i>BRAF</i> inhibitor)	Decrease of both moMDSCs and gr MDSCs in the blood	[308]

TABLE 3 (continued)

Subjects	Tumor types	Treatments	Key effects	Ref
HUMAN	Advanced stage melanoma	Ipilimumab (anti-CTLA-4 mAb)	Reduced numbers of Arginase-producing grMDSCs, but no effects on moMDSCs	[223]
		Denileukin Diftitox (ONTAK)	Induction of STAT-3 ^{hi} toleragenic DCs and Tregs	[320]
		GM-CSF vaccine (OncoVex)	Decreased MDSC and Tregs in vaccinated patients	[236]
		GM-CSF adjuvant	Expansion of CD14 ⁺ HLA-DR ^{lo/neg} moMDSCs	[237]
		DC vaccine	Induction of IDO in the vaccine production and higher IDO ⁺ FoxP3 ⁺ cells after infusion	[321]
MOUSE	Glioblastoma (inducible) Cervical (transplantable)	CSF-1R inhibitor (BLZ945)	Repolarization of M2-like macrophages to M1-like; delayed tumor growth	[301, 322]
	Neuroblastoma (MYCN-driven)	CSF-1R inhibitor (BLZ945)	Reduction of MDSCs and M2-like macrophages, significant control of established tumors	Study IV
	Breast cancer (MMTV-PyMT)	Paclitaxel (PTX) +CSF-1R inhibitor	PTX induced TAM infiltration and CSF-1R blocking increased the anti-tumor effects	[229, 301]

		(PLX3397 or BLZ945)		
		Anti-CCL2 mAb	Reduced macrophage infiltration to metastases in lungs	[323]
	Breast cancer (4T1, EMT6)	Doxorubicin (DOX) +T cell transfer	Depletion of MDSCs and decrease of IDO production	[306]
	Prostate cancer (RM-1, -3)	Radiotherapy +CSF-1R inhibitor (PLX3397)	Blocking CSF-1R improved anti-tumor immunity mediated by irradiation by depleting TAMs and moMDSCs	[324]
	Pancreatic cancer (orthotopic)	Checkpoint antibody +CSF-1R inhibitor (PLX3397)	CSF-1R blockade eliminated TAMs and moMDSCs and potentiated better response of anti-PD1/CTLA4 mAb	[325]
	Melanoma (B16, SM-1)	T cell transfer +CSF-1R inhibitor (PLX3397)	CSF-1R inhibition improved efficacy of antigen-specific adoptive T cell transfer	[326]
	Lewis lung carcinoma (3LL)	Anti-VEGFR-2 mAb (DC101) +CSF-1R inhibitor (GW2580)	Decreased MDSCs in tumors; best tumor control when combined	[327]
		Sunitinib	Reduction of MDSCs and improve mIL12+anti-4-1BB activation	[328]

TABLE 3 (continued)

Subjects	Tumor types	Treatments	Key effects	Ref
MOUSE	Lymphoma (EL-4)	Pepti-body (against S100A9)	Peptide-Fc fusion protein depleted MDSCs by binding to membrane S100A9	[329]
		5-Fluorouracil	Selective depletion of MDSCs and improved T cell response	[307]
	B cell lymphoma (A20HA)	Various chemotherapies	Cyclophosphamide, doxorubicin and melphalan induced MDSCs; Gemcitabine reduced MDSCs	[302]
	Melanoma (B16, LLC)	Dopamine	Depletion of CD115+Gr1+ moMDSCs and improved anti-tumor immunity	[330]
	Prostate (CR Myc-Cap) Melanoma (B16-h5T4)	Tasquinimod (S100A9 inhibitor)	Decrease of MDSCs and M2-like macrophages; increase of T cell infiltration	[331]

Melanoma (MT-RET-1)	L-NIL (iNOS inhibitor)	Reduction of MDSCs and loss of suppressive functions	[269]
Melanoma (<i>Ret</i> transgenic) or colon cancer (CT-26)	Sildenafil (PDE-5 inhibitor)	Reduction of MDSCs and inflammatory factors	[332, 333]
	Paclitaxel	Reducing MDSCs by promoting maturation	[303-305]
	Cyclophosphamide	Induction of MDSCs	[300]
Pancreatic cancer (RT-5)	Low-dose irradiation	Promotion of iNOS ⁺ M1-like macrophages and increased T cell response	[59]
Human RCC (Xenograft A498)	IL-1R antagonist	Abrogated tumor promoting TAMs and delayed tumor growth	[254]
Fibroma (MN/MCA1)	Trabectedin	Depletion of MDSCs and TAMs; delayed tumor growth	[299]
Neuroblastoma (MYCN transgenic) Glioma (inducible) Mesothelioma	COX-2 inhibitor (Aspirin, Celecoxib, SC58236)	Decreased TAMs and MDSCs, delayed tumor growth	[261, 334-336]
Fibrosarcoma, Lymphoma (EL-4)	Gr-1 antibody	Complete tumor protection by eliminating MDSCs	[329, 337]
Melanoma (B16F10)	Depletion of CCR2 ⁺ MDSCs (antibody)	Blocked monocyte trafficking to tumors and improved CD8 ⁺ T cell therapy	[268]
Sarcoma (RMS)	Depletion of CXCR2 ⁺ MDSCs (antibody)	Enhanced T cell activation and effects of anti-PD-1 mAb	[338]
Colon cancer (<i>APC</i> ^{min/+})	CXCR2 pepducin	Blocked the formation of spontaneous tumors	[339]

4.4.2 Alleviating inflammation

Given that chronic inflammation is tightly intertwined with cancer progression, agents with anti-inflammatory properties have been extensively explored in patients with cancer. The preventive effects of COX-2 inhibitors on cancer incidence have been proven in large numbers of patients [197]. Besides the direct limiting effects on tumor cells, modulation of suppressive myeloid cells could contribute to this protection. In experimental settings, genetic ablation of tumor-derived COX-2 [248] or pharmacological inhibition of COX-1/2 [261, 334-336] efficiently limited the accumulation of suppressive myeloid cells in tumor-bearing animals and translated into slower tumor growth *in vivo*. However, it should be noted that COX-2 inhibitors often are associated with cardiovascular toxicity [340]. A recent study using genomic analysis of COX-2 deficient mice revealed that more than 1000 genes were differentially expressed in the kidney, which caused dysregulation of nitric oxide synthase [341]. Therefore, inhibitors targeting alternative checkpoints of the COX-2 pathway, for example the enzyme mPGES-1 [342], should be explored.

Other inflammatory pathways could also be drugable targets for blocking suppressive myeloid cells. A chemical inhibitor, tasquinimod, specifically binds to S100A9 and was able to enhance the anti-tumor T cell response in animal models by removing MDSCs and TAMs [331]. It is currently being validated in a phase III clinical trial in metastatic prostate cancer patients (NCT01234311). Recently, a novel ‘pepti-body’ mediated potent deletion of MDSCs *in vivo* through ligation to membrane-bound S100A9 [329]. In addition, antagonizing IL-1R signaling could block TAM functions and attenuate human tumor invasiveness in a xenograft model [254].

A few pharmacological compounds that were originally designed to resolve physiological inconveniences have demonstrated anti-tumor capacity by re-shaping tumor-induced inflammatory landscape. PDE-5 inhibitors, such as tadalafil or sildenafil, which antagonize cyclic GMP degradation and induce release of NO, efficiently controlled tumor growth by blunting induction of suppressive myeloid cells in head and neck cancer patients [319] and pre-clinical models [332, 333]. This is in line with another study, where low-dose irradiation potentiated the functions of iNOS-producing myeloid cells [59]. On the other hand, an inhibitor blocking iNOS activity was shown to be effective in controlling tumor progression by attenuating suppressive myeloid cells [269]. These findings may reflect the dual role of NO production during progression and treatment of solid tumors.

4.4.3 Restraining induction signals

As described in section 4.3, the precise induction pathway for suppressive myeloid cells is still unclear. In mice, depletion methods using antibodies targeting Gr-1 are commonly used [329, 337]. However, Gr-1 is not expressed in humans and myeloid cells quickly recover once the antibody treatment is discontinued. Thus, restraining induction signals of suppressive myeloid cells is clearly more beneficial as a therapeutic option.

Among all the key pathways, antagonizing M-CSF receptor (CSF-1R) has to date demonstrated the most profound therapeutic potential. RG7155, an antibody developed by Roche showed consistent effects to eliminate TAMs in pre-clinical murine models, non-human primates and cancer patients [310]. Data from a phase I clinical trial (NCT01494688) in patients with pigmented villonodular synovitis (PVNS) disclosed during the ASCO annual meeting in 2014 (abstract 10504) confirmed the safety of the treatment and 9 out of 10 patients showed progression-free survival for up to 17 months. In addition, chemical inhibitors against the tyrosine kinase associated with CSF-1R signaling, such as BLZ945 (Novartis) or PLX3397 (Roche) also demonstrated encouraging results in a number of studies, as monotherapy [301, 322] or in combination with radiotherapy [324], chemotherapy [229, 301], checkpoint inhibitors [325], adoptive T cell transfer [326] or anti-angiogenic antibody [327]. However, in a phase II clinical trial, PLX3397 did not show benefits for the progression-free survival in patients with recurrent glioblastoma (abstract 2023, 2014 ASCO annual meeting). Starting from January in 2015, the first clinical trial combining the anti-PD-1 mAb (Bristol-Mayer Squibb) and anti-CSF-1R mAb (Five Prime) was initiated in 6 different types of human solid tumors.

It is worth pointing out that the *in vivo* mechanisms of action of CSF-1R blockers are yet to be clarified. In a few pre-clinical tumor models, CSF-1R inhibition as a monotherapy only resulted in moderate tumor control, despite efficient *in vivo* depletion of TAMs [301, 324, 326, 327]. In contrast, other studies [301, 322] including **study IV** in this thesis showed potent therapeutic effects of CSF-1R blockade, potentially through re-programming myeloid cells in the tumors. Of note, the CSF-1R blocking antibody depleted TAMs but elevated numbers of MDSCs in the tumors [310].

Besides the distinct inflammatory nature of each murine tumor model, the *in vivo* stability, permeability or kinetics of the compound in various organs may greatly influence the treatment outcome. In all of the studies, notably, CSF-1R inhibition enabled superior synergistic effects in the respective combinatorial settings. This confirms that suppressive myeloid cells form one of the major resistance mechanisms towards anti-cancer therapies and could be utilized as a therapeutic target.

Based on the similar principle, sunitinib inhibits multiple receptor tyrosine kinases including CSF-1R, CD117, flt3, and could also block the induction of suppressive myeloid cells. In patients with renal cell carcinoma, sunitinib efficiently decreased the numbers of immature MDSCs [313, 314] and enhanced the maturation of CD1c+ DCs [314]. In addition, sunitinib could potentially elicit similar effects in lung cancer patients, as indicated in an *in vivo* murine model [328].

4.4.4 Blocking mobility

Leukocyte trafficking is guided by a variety of chemokines and often skewed by tumor-derived factors. In malignant conditions, suppressive myeloid cells are recruited in response to the inflammatory milieu in the tumor microenvironment. Chemokine (C-C motif) ligand 2 (CCL-2), released by tumors is key to the infiltration of inflammatory

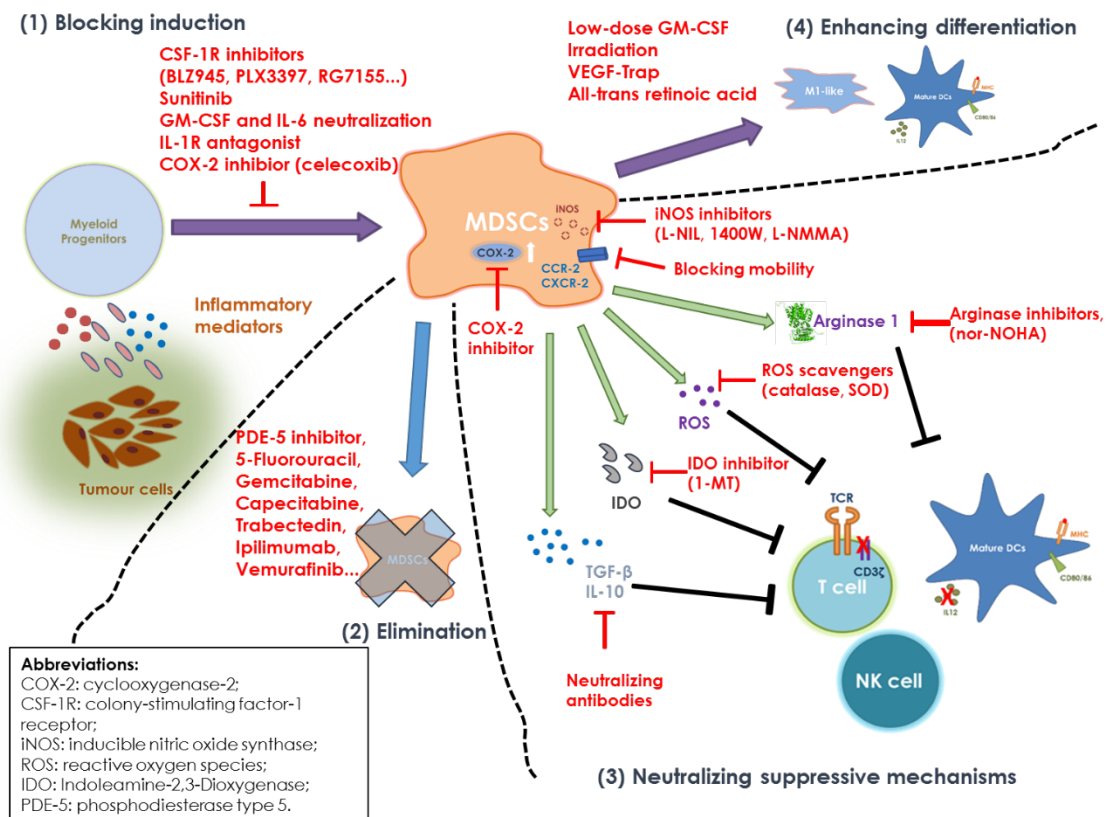


Figure 3, Targeting strategies for suppressive myeloid cells in cancers.

myeloid cells [323]. A therapeutic antibody (Calumab) against CCL-2 has been tested in a phase II clinical trial in metastatic prostate cancer patients. The response rate was poor, which could be due to the insufficient neutralization of CCL-2 in patients [312]. To overcome this problem, CCR-2, the receptor for CCL-2 has been evaluated as an alternative target. Indeed, blocking CCR-2 with a therapeutic antibody depleted MDSCs from tumor-bearing mice and synergized with adoptive CD8+ T cell transfer [268].

Another important migratory molecule is CXCR-2, which is essential for recruiting myeloid cells during inflammation-driven tumorigenesis [343]. In mice, limiting CXCR-2 functions on circulating myeloid cells greatly prevented their infiltration into tumor tissues [339] and boosted the anti-tumor effects of anti-PD-1 blockade [338].

4.4.5 Reprogramming activation

Myeloid cells are extremely plastic and their functions are substantially influenced by the surrounding factors. Monocytes isolated from blood could be primed *in vitro* to immune-stimulatory DCs for cancer treatment or acquire tolerogenic properties for combating autoimmune diseases. Thus, an appealing approach for cancer treatment is to promote the re-activation of suppressive myeloid cells *in vivo*. To some extent, this could be achieved by using GM-CSF, which enabled the maturation of MDSCs to DCs [236]. However, it should be carefully calibrated since high-dose GM-CSF may support the expansion of MDSCs *in vivo* [237]. Another agent that has potent reprogramming function of suppressive myeloid cells is all-trans-retinoic acid (ATRA), which is structurally similar to vitamin A and is used to treat various malignancies [344]. It could induce a DC-like phenotype and trigger IL-12 production from monocytes *in vitro* [345] and enhance *in vivo* efficacy of cancer vaccines [346]. When tested in patients with renal cell carcinoma or lung cancers, MDSCs were diminished from the blood, potentially due to maturation towards functional DCs [315-317] mediated by the intra-cellular accumulation of glutathione [347]. Moreover, a VEGF blocker (VEGF-trap) [348] has also promoted the maturation of DCs in cancer patients, but it did not decrease the numbers of MDSCs [311].

4.4.6 To Kill two birds with one stone

Suppressive myeloid cells possess multi-faceted functions in sustaining cancer occurrence, progression and metastasis and are one of the major barriers for successful therapeutic interventions in cancer immunotherapy. To date, tremendous efforts have been invested to design and validate pharmacological compounds that could efficiently target these mechanisms. In brief, four main strategies, including **1)** blocking the induction, **2)** eliminating the presence, **3)** disarming the suppressive machinery and **4)** facilitating the maturation, have been proposed (**Figure 3**). From my point of view, it is risky to unselectively neutralize immune modulatory factors, since many of them, such as TGF- β , ROS, PGE2 or iNOS, also play pivotal physiological roles in humans. Although elimination of suppressive myeloid cells has been observed in patients receiving certain anti-cancer agents, the mechanistic details are yet to be clarified. Therefore, it might be more plausible to combine approaches that limit tumor-driven induction of suppressive myeloid cells, with stimulatory signals that potentiate their functional maturation. Together, this may not only remove immunosuppressive barricades, but also create an environment that is favorable for anti-tumor immunity, both in the periphery and in the tumor microenvironment.

5. IMMUNOTHERAPY: WHERE ARE WE HEADING?

5.1 INTRODUCTION

Combating cancers with the patient's own immune system is being gradually acknowledged as an attractive therapeutic option. However, a range of hurdles need to be overcome for achieving curative effects in patients with advanced solid tumors. Throughout this thesis, I have highlighted the challenges and opportunities posed by myeloid cells with immunosuppressive properties. However, it is important to keep in mind that this is only one of the many mechanisms that tumor cells employ to prevent effective immune clearance. We also cannot ignore that different cancer types may have distinct inflammatory profiles, leading to diversified immune landscapes. Here, I will handpick some emerging aspects that hold promises towards improved efficacy of cancer immunotherapy.

5.2 COMBINATION THERAPY: Going Beyond the Immunity

5.2.1 Restoration of immune functions

The unprecedented success of cancer immunotherapy has raised excitement in redesigning current cancer treatment regimens. One general notion is to pursue a '1+1>2' scenario, where the existing therapeutics that trigger anti-tumor immunity could be used simultaneously to boost the effects of immunotherapy.

Chemotherapeutics and radiation therapy are known to modulate immune cell functions including the myeloid compartment (section 4.4.1). In addition, these treatments are thought to increase the permeability of solid tumor tissues and directly regulate molecular properties of cancer cells, making them more sensitive to immune cell mediated lysis [349]. Indeed, synergistic effects could be achieved when chemotherapy or radiation was combined with checkpoint blocking antibodies [350-353]. Because high-dose cytostatic drugs or radiotherapy could limit immune cell functions by inducing cell death, it may be more reasonable to implement the 'metronomic dosing' [354] of the agents in such combinations. This notion was supported by observations in preclinical models, where fractionated radiotherapy, but not a single high dose, boosted the anti-tumor effects of anti-CTLA-4 treatment [355]. These synergistic effects of fractionated radiotherapy with checkpoint blockade, particularly for the PD-1/PD-L1 axis could be explained by the modulation of PD-L1 expression on tumor cells [350].

Besides suppressive myeloid cells, many players in the cancer-induced immunosuppressive network could be targeted in the combinatorial approaches [356]. For example, immunosuppressive regulatory T cells (Tregs) may cause the failure of efficient immune surveillance against cancer cells. Depletion of Tregs has long been investigated as a potential treatment strategy for cancers [357-359]. The anti-tumor effects of anti-CTLA-4 mAb in mice were partially due to removal of Tregs by ADCC. Moreover, inhibitors for key suppressive mechanisms, such as IDO, have also generated additive effects as part of combinational approaches in preclinical models [70, 71, 360].

5.2.2 Correction of vasculature

Initially, anti-angiogenic therapy was believed to function through exhausting nutrient supplies for cancer cells by destroying their blood supplies. However, later evidence indicated that normalization of vascular architecture in the solid tumor microenvironment might be more beneficial [361], possibly due to the repolarization of M2-like macrophages and enhanced destruction through infiltrating immune cells [362, 363]. VEGF was previously shown to have a direct role on T cell development

and induced exhaustion of CD8⁺ T cells in tumors [364-366]. In accordance, blocking VEGF potentiated anti-tumor effects of DC vaccines [367] and adoptive T cell therapy [368] in murine models and supported significantly longer patient survival when combined with chemotherapy [369]. In melanoma patients, anti-angiogenic antibody could enhance immune cell infiltration after ipilimumab treatment [370]. Similar effects could be expected when VEGF blockade is combined with inhibition of the PD-1/PD-L1 pathway. In a recent report, tumor-derived VEGF collaborated with IL-10 and PGE2 to induce death ligand expression on endothelial cells, which resulted in apoptosis of infiltrating CD8⁺ T cells [371]. Consequently, combining COX-2 inhibitor with anti-VEGF antibody abolished these mechanisms and restored anti-tumor immunity.

5.2.3 Multi-tasking therapeutics

Antibody engineering technology allows production of artificial proteins that merge two antigen specificities. Typically, one part of the 'bi-specific' antibody recognizes tumor-associated surface proteins, while the other part could trigger T cell activation, for example through CD3 signaling. In addition, some products contain the Fc domain, which engages ADCC mediated by NK cells or macrophages. Therefore, bi-specific antibodies are extremely potent in directing tumor-specific killing through multiple cytotoxic machineries [372]. The first bi-specific antibody approved for clinical usage was catumaxomab, which recognized EpCAM and simultaneously triggered T cell activation through CD3 signaling [373]. Based on similar concepts, a collection of bi-specific antibodies were designed and investigated for cancer treatments [372].

However, severe adverse events induced by bi-specific antibodies hamper the clinical application in a wider range of cancer patients. This is partially due to the anti-CD3 fragment, which elicits excessive T cell activation *in vivo*. Decreased dosing could alleviate toxicity but also jeopardize the anti-tumor efficacy. In a preclinical model, this issue could be compensated by combining low-dose anti-GD2 bi-specific antibody with DC vaccines [374]. Alternatively, such toxicity might be attenuated if the anti-CD3 domain is replaced by fragments that liberate tumor-reactive T cells from inhibitory pathways, such as PD-1 or PD-L1 signaling. This approach may facilitate an antigen-directed activation of T cells in the proximity to tumor cells, which could be further supported by effector cells engaged through ADCC. For cancer types that lack common antigens, multiple immune checkpoint blocking fragments, or fragments potentiating reprogramming of suppressive myeloid cells, such as anti-CSF-1R, could be collaborated.

Another novel concept that is currently under clinical development is the production of high-affinity, antigen-specific monoclonal TCRs. These proteins recognize defined epitopes of tumor-associated antigens presented by MHC class I molecules. The linked anti-CD3 ScFv could attract and activate T cells to conduct specific lysis of the tumor cells [375, 376]. In comparison to monoclonal antibodies, this approach could target antigens that are derived intra-cellularly. It also circumvents the laborious preparation procedure of TCR-transduced T cells required for adoptive T cell therapy.

Besides engineered biological products, some naturally existing proteins could also play multi-faceted roles in directing immune responses. CD80 provides co-stimulation through CD28 during T cell priming, which is often interrupted by immune checkpoint molecules in the tumor microenvironment. Thus, the soluble form of CD80 protein is likely to restore T cell functions by blocking immune checkpoint interactions, as well as offering additional co-stimulatory signals. Indeed, a CD80-Fc fusion protein improved functions of human and murine T cells, even more pronounced than blocking antibodies against the PD-1/PD-L1 axis [377, 378]. This indicates that previously unidentified receptors are involved in CD80 ligation. However, CD80 has been

reported to be expressed at high levels on the surface of MDSCs in cancer patients [253] and tumor-bearing mice [379], and has been proposed to be one of the suppressive mechanisms against T cells. Of note, the CD80-Fc fusion protein activated, rather than inhibited human and murine T cell functions *in vitro*. This suggests that membrane-bound CD80 may have distinct biological functions to the soluble proteins. Even though the *in vivo* efficacy remains to be seen, the CD80-Fc fusion protein may amplify anti-tumor capacity via elimination of Tregs or PD-L1+ cells by ADCC.

5.2.4 Risks analysis

Novel concepts of combination therapy are accompanied with previously unrecorded concerns and clinical complications. For example, concurrently administrating blocking antibodies for CTLA-4 and PD-1 amplified the autoimmune toxicity associated with either antibody alone [109]. In another case, devastating liver toxicity was reported when inhibition of *BRAF* oncogene mutation was combined with ipilimumab [380]. These cases restate the necessity of conducting risk assessments while new combinatorial approaches are being clinically investigated, even if the individual treatments have been approved separately by the regulatory agencies.

5.3 TECHNOLOGICAL ADVANCES

Currently, the enthusiasm towards cancer immunotherapy is immense. However, we still cannot underestimate challenges from immune suppression and the potential risk in using immune-stimulatory agents that elicit immune responses unselectively. Thus, we need to be able to improve exclusively tumor-specific immunity and accurately manipulate immunosuppressive mechanisms. To reach this goal, we need technical advances that enable comprehensive analysis of the human immune system and precise modulation of immune cell subsets.

5.3.1 Biomaterials and immunotherapy

Advances in biomedical material research hold great promises in improving clinical efficacy and safety of cancer immunotherapeutics. Encapsulation of biological products, for example cytokines or antibodies, into engineered nanoscale vehicles, could optimize their *in vivo* stability and pharmacokinetics. This is particularly attractive for agents that have severe systemic adverse effects. In a proof-of-principle study, a nanoporous material supported gradual release of the anti-CTLA-4 mAb *in vivo* and the anti-tumor effects were improved [381]. It is also possible to equip nanoparticles with multiple immune stimulatory properties, creating controllable doses of personalized therapeutic 'cocktails'. For example, nanoparticles conjugated with co-stimulatory anti-CD137 mAb and IL-2 induced profound anti-tumor effects in tumor-bearing mice [382]. When decorated with 'anchors' recognizing surface molecules on tumor cells, it is possible for the systemically injected nanoparticles to locally deliver agents that otherwise induce systemic adverse events. Similarly, nanoparticles could be used to maintain *in vivo* activity of adoptively transferred anti-tumor effector cells by specific delivery of immune activating factors [383, 384]. Moreover, it is possible to specifically and more efficiently target or reprogram suppressive myeloid cells using these approaches.

Some naturally occurring nanoscale vesicles could also be used as novel therapeutic approaches. Exosomes are released as 'messengers' from biologically functional cells and encapsulate contents that could conduct versatile properties on the immune system. Tumor-derived exosomes have been shown to induce suppressive myeloid cells by delivering factors such as PGE₂, TGF- β [385] or membrane-bound Hsp72 [386]. On the other hand, exosomes shed from DCs carry co-stimulatory molecules

and are able to stimulate antigen-specific immune responses. Therefore, it has economically attractive to utilize these exosome as the DC-surrogates in treating cancer patients [387]. Several studies have proven that exosomes derived from DCs were immune stimulatory and potentiated *in vivo* protective effects in tumor-bearing mice [388, 389], through activation of T and B cells [390, 391].

Currently, the majority of cancer vaccines inject peptides, proteins or DNA plasmids that contain potential T cell epitopes directly into patients. In most cases, this approach elicits protective immune responses against the given antigen(s), but has modest therapeutic effects against established tumors [392]. Thus, encapsulating tumor-associated antigens into biomedical materials may be advantageous for cancer vaccine approaches by prolonging *in vivo* exposure, specific delivery to APCs or enabling co-delivery of adjuvants [393]. A number of studies focused on delivering antigens and adjuvants to residing DCs in lymph nodes [394, 395]. An emerging perspective is to program dendritic cells *in situ* by implanting nano-scaffolds containing tumor-associated antigens [396]. A recent update from the same group utilized nano-scaffolds with self-assembling properties after implantation. This allowed formation of a 3D mesoporous structure, where immune cells from the host animal could be primed against tumor-associated antigens [397]. This resulted in controlled and durable release of immune activating contents and recruited substantial tumor-rejecting humoral and cellular immune mechanisms.

5.3.2 Mega-analysis of immune responses

The immunological response to cancer occurrence or therapeutic interventions is a fine-tuned network of numerous parallel events. Contents in the extracellular matrix, cell surface proteins or intracellular signaling pathways collaboratively govern the success of treatment strategies. Therefore, a comprehensive overview of these components and the subsequent signaling cascades has substantial prognostic and therapeutic implications in guiding the development of cancer immunotherapy.

Development of multi-color flow cytometry was a milestone achievement and this method is currently widely used for analyzing immunological profile in cancer patients. Using fluorochrome-conjugated antibodies, a sophisticatedly designed flow cytometry platform allows detection of 10 to 15 proteins simultaneously. When appropriate lineage markers are included, the results reflect cellular properties of a defined immune cell subset at a given time. However, immune cell populations are extremely heterogeneous and analysis of large numbers of functional pathways are also required to accurately dissect major disease- or treatment-related cellular alternations. Therefore, technological advances empowering massive data-recording and processing are in great demand.

Cytometry by Time-of-Flight (CyToF) is a powerful cell detection method with significantly improved protein detection capacity. Instead of fluorophores, antibodies are labeled with element isotopes and recorded by subsequent mass spectrometry [398, 399]. This approach potentiates measurement of up to (theoretically) 100 parameters at the same time and circumvents the compensation step, a procedure that is required for correcting spectral overlaps among different fluorochromes. In one of the first studies using this technology, 34 parameters were characterized by CyToF, in order to depict the hematopoietic hierarchy and response to pharmacological inhibitors [400]. A later study analyzed the virus-specific CD8⁺ T cells and identified previously less appreciated complexity within the population [401]. Application of CyToF technology has also been extended for imaging tumor tissues. Recently, 32 parameters were measured simultaneously in breast cancer tumor tissues and the extremely heterogeneous sub-populations in the tumor microenvironment could be

delineated [402]. Although these platforms are not currently applicable to fulfill routine clinical demands, they hold great potential to reveal vital information towards in-depth understanding of the anti-tumor immunity.

Given the heterogeneity of myeloid compartment, CyToF platform may offer a powerful tool to scrutinize the regulatory network during the development and activation of suppressive myeloid cells. In addition, anti-tumor T cell responses after immunotherapy could be better illustrated not only in the peripheral blood, but also in solid tumor tissues. This may allow us to uncover novel therapeutic targets and prognostic markers that facilitate our understanding on tumor-induced immune suppression and guide the development of novel treatment strategies.

5.3.3 Precise genome editing

The CRISPR-Cas9 system is a natural defensive mechanism utilized by bacteria and archaea, in order to prevent incorporation of foreign DNAs into their own genomes [403]. Guided by a short RNA sequence, the Cas9 endonuclease could use molecular scissors to cut on a precise point and disable the functions of invading DNAs. With appropriate engineering, the CRISPR-Cas9 system could be used as a tool to modify genome on the desired locations accurately [404]. It has shown promising clinical implications, particularly for correcting genetic flaws in human stem cells [405, 406]. For the treatment of cancers, some studies encourage direct injection of CRISPR-Cas9 *in vivo*, which targets and corrects cancer-driven mutations. However, this approach should be carefully evaluated since the injected agents could be neutralized by the host's immune system, thus may have low penetration into the tumor tissues.

Seattle-based corporation Dendreon, known to develop the first FDA-approved DC vaccine approach, claimed bankruptcy at the end of 2014. The high treatment cost and the modest clinical benefits might be the main hurdles for Provenge, their prostate cancer vaccine, to be commercially appealing for a large number of patients. It definitely does not discredit the clinical efficacy of DC-based therapies. Rather it reflected the challenges of implementing cell-based therapies in the real-life scenario.

Alternatively, RNA-guided genome editing may be utilized to improve immune cell functions against human cancers. After acquisition of the GMP facilities from Dendreon, pharmaceutical giant Novartis is leading the way to evaluate CD19-CAR T cells for the treatment of hematological malignances in a phase II clinical trial. It is now becoming clear that the CRISPR-Cas9 technology will be incorporated into this treatment. Even though the detailed applications are not yet disclosed, a few potential modifications could be speculated. Firstly, the current treatment strategy of CD19-CARs requires isolation and transduction of autologous T cells for each individual patient. It is a labor-intensive procedure that requires tremendous amounts of dedication and expertise. Therefore, if the HLA class I molecules and the intrinsic TCRs could be silenced from the CAR-transduced T cells, it will be possible to prepare universal CD19-CAR T cell products that are not destroyed by the host's immune system or perturb graft-versus-host reactions. This could be a key step to implement the treatment in a more standardized and cost-effective manner. Secondly, certain molecules hampering *in vivo* functions of the adoptively transferred T cells, for example PD-1 or CTLA-4, could be removed using the CRISPR-Cas9 system. This step restricts the functional enhancement to tumor-reactive T cells, avoiding unselective activation of T cells often induced by checkpoint blocking antibodies. Furthermore, upon establishment, the genome-editing tools could modify genes that are crucial for the *in vivo* durability of the adoptively transferred T cells, such as *Ppp2r2d*. This might be less critical for the success of CD19-CAR T cells but could have substantial implications for adoptive cell therapies against solid tumors.

5.4 INTERDISCIPLINARY FRAMEWORK FOR CANCER IMMUNOTHERAPY

In the modern day cancer research, the rigid boundaries among research disciplines are diminishing. Although studies of cancer genetics are still the mainstay for many cancer types, associations between genomic instability and inflammation have been elucidated. Powerful next generation sequencing platforms are now employed to pinpoint mutations that may contain neo-epitopes that guide potent T cell responses. Moreover, development of high through-put analytical approaches, such as CyToF, requires specialists in bioinformatics for reliable data interpretation and validation. Rapid advances in biotechnology and molecular biology have broadened the genetic editing arsenal with superior accuracy and specificity. Nano-technology inventions promise greater future potency and safety for today's medicine. Although these are just very few examples, it is evident to me that tumor immunologists can no longer dissect complicated research questions and develop effective anti-cancer therapies without key contributions from other research disciplines. The interdisciplinary framework that marries a wide range of expertise and know-how today, is the foundation for an improved patient survival tomorrow.

6. SUMMARY OF THE MAJOR FINDINGS

The central aim of this thesis is to elucidate how tumor-derived factors could induce suppressive functions from healthy myeloid cells. The detailed interactions between patient-derived MDSCs and T cells, NK cells and DCs were analyzed in **study I, II and III**, respectively. **Study IV** extended this evaluation to the myelopoiesis process of human hematopoietic stem cells and suppressive myeloid cells were explored as a therapeutic target in mice developing aggressive spontaneous tumors.

6.1 **Study I: TUMOR-DRIVEN INDUCTION OF MDSC IS MEDIATED BY COX-2/PGE2**

Motivation

Human melanoma is believed to be one of the cancer types that is responsive to immunotherapy due to its high mutation rates associated with UV-induced damages. We and many other groups have noted the accumulation of suppressive MDSCs in the peripheral blood of melanoma patients and these cells may hamper effective anti-tumor immunity. However, the mechanisms of their induction remain unclear. Thus, we sought to analyze the precise pathways that regulate the induction of MDSCs.

Experimental Design

To dissect the detailed mechanisms, I established a co-culture model, where primary human monocytes from healthy donors were exposed to early-passage melanoma tumor cell lines expanded from fresh patient biopsies. Next, the tumor-educated monocytes were retrieved from cultures and their phenotype and T cell inhibitory functions were evaluated. A variety of pharmacological inhibitors were added during the co-culture, to analyze the key regulators driving tumor-induced alterations.

To assure that our *in vitro* findings were clinically relevant, we purified monocytes from blood of patients with advanced melanoma. These cells were subsequently added to autologous T cells and the suppressive mechanisms were compared to those obtained from *in vitro* induced MDSC-like cells.

Main Findings

After *in vitro* co-culture with early-passage melanoma tumor cells, healthy monocytes acquired a phenotype resembling CD14⁺HLA-DR^{low/-} moMDSCs in melanoma patients. In addition, MDSC-like cells and patient-derived monocytes potently inhibited

T cell effector functions. Mechanistically, COX-2/PGE2 pathway was involved both during the induction of MDSC-like cells and inhibition of T cells because a selective COX-2 inhibitor (Celecoxib) or a PGE2 neutralizing antibody could restore T cell functions. Finally, adding synthetic PGE2 to monocytes increased their ability to inhibit T cells.

Outlook of the Study

One major limitation of the co-culture model was that it did not reflect the impact of tumor-derived factors on myelopoiesis, which may directly contribute to the immobilization of progenitor cells and production of immature myeloid cells in the peripheral organs. In addition, we utilized a panel of inhibitors, in order to dissect the main channels that led to the induction of MDSCs. However, selection of these inhibitors were based on previously reported pathways. Thus, a comprehensive comparison between control monocytes and MDSC-like cells by genomic or proteomic screening may identify novel pathways that are involved in this process.

6.2 **Study II:** MDSCS SUPPRESS NK CELLS THROUGH TGF- β

Motivation

NK cells play an important role in modulating tumor growth and metastasis and could be used as a therapeutic approach to treat human cancers. Although interactions between MDSCs and T cells have been frequently reported, the effect of MDSCs on NK cells is controversial. Therefore, we aimed to analyze the precise interplay between these two immune cell types in patients with melanoma.

Experimental Design

We utilized PGE2-treated human monocytes and autologous NK cells as an *in vitro* model to study their interactions. To validate the mechanisms, we performed experiments using moMDSCs and NK cells isolated from blood of advanced stage melanoma patients. Further, we inoculated control or COX-2-silenced murine tumors in mice and compared the frequencies of MDSCs by flow cytometry and *in vivo* cytolytic capacity of NK cells by live imaging in tumor-bearing mice.

Main Findings

We demonstrated that PGE2 could trigger the production of soluble TGF- β from healthy monocytes through the PGE2 receptors EP2 and EP4. This was the major NK suppressive mechanism utilized by PGE2-treated monocytes and moMDSCs from melanoma patients. *In vivo*, COX-2 silencing resulted in a marked decrease of MDSCs in the spleens and a concurrent increase of cytotoxicity mediated by NK cells in the tumor-bearing mice.

Relevance of the Study

Currently, the impact of cancer-driven MDSCs on NK cells in tumor-bearing mice is controversial. MDSCs were reported to suppress NK cells [407] through membrane-bound TGF- β [408]. However, another report indicated the stimulatory role of MDSCs on NK cells in a NKG2D-dependent manner [409]. In melanoma patients, interplay between MDSCs and NK cells, particularly the molecular mechanisms, are much less investigated.

Our results demonstrate how tumor-derived PGE2 could drive the induction of MDSCs that suppress NK cells in patients with advanced melanoma. It revealed a previously unknown connection between PGE2 and the release of TGF- β from human primary monocytes. COX-2 inhibitors may have off-target effects or a direct impact on the suppressive functions of MDSCs. Thus, our approach using tumor cells with genetic ablation of COX-2 *in vivo* allowed specific analysis of the impact of tumor-derived COX-2/PGE2 on the induction of MDSCs and inhibition on NK cells. In summary, this study expanded our current understanding on the multi-faceted role of tumor-derived PGE2, which recruited MDSCs to suppress NK cells in cancer patients. Thus, targeting COX-2/PGE2 pathway could synergize with the anti-tumor effects of adoptive NK cell therapy.

6.3 **Study III:** MDSCS IMPAIR THE MATURATION OF DENDRITIC CELLS

Motivation

Currently, DC-based therapy often relies on maturation of monocytes purified from blood of cancer patients. Inevitably, moMDSCs, with known ability to suppress various types of immune cells, will be present during the process. Thus, it is important to evaluate the role of moMDSCs and how their presence could influence quality of the resulting DC vaccines.

Experimental Design

The clinical materials were obtained from stage IV melanoma patients who were enrolled in a phase I clinical study (MAT01) [191], where DC vaccines were combined with adoptive T cell transfer. Patients underwent leukapheresis and monocytes and lymphocytes were enriched in different cell fractions by elutriation. Monocytic MDSCs were isolated based on the low surface expression of HLA-DR and HLA-DR+ cells from the same donor were used as controls. Next, moMDSCs were mixed with HLA-DR+ cells at escalating ratios, to evaluate their influence on the quality of DC maturation.

Main Findings

We found that the presence of moMDSCs did not alter the yield of DCs but had a negative impact on DC quality. In detail, high frequency of moMDSCs at the beginning of DC maturation procedure blocked the up-regulation of activation markers and co-stimulatory signals on DCs and impaired the ability of DCs to take up antigens, to migrate and stimulate T cell functions.

Relevance of the Study

This study is part of an ongoing clinical trial, where patients received cellular therapy combining DC vaccines and adoptive T cell therapy. Our data provided critical information regarding the impact of moMDSCs on the overall quality of DC-based vaccines. Even though moMDSCs could be matured upon stimulation, their performance was sub-optimal in comparison to the HLA-DR+ cells. In addition, their presence had a 'by-stander' effect, which negatively affected the maturation of HLA-DR+ cells. Based on these results, there is an ongoing research project in our group, where optimized protocols for DC maturation are being tested.

6.4 **Study IV: CSF-1R INHIBITION AS A POTENT APPROACH TO BOOST ANTI-TUMOR IMMUNITY**

Motivation

Neuroblastoma is one of the most common solid cancer type among infants. Despite the aggressive therapies, high-risk patients still suffer from poor survival and there is a great need for novel treatments. Inflammation-driven expansion of suppressive myeloid cells play pivotal roles in neuroblastoma-mediated immune suppression and these cells could independently predict worse clinical outcome in neuroblastoma patients [231]. Thus, it might be a suitable cancer type for therapeutic interventions by targeting these cells.

As mentioned in earlier sections, it is challenging to target suppressive myeloid cells specifically due to their heterogeneous nature. CSF-1R signaling is important for the survival and development of myeloid cells and we sought to inhibit this pathway to limit the induction of suppressive myeloid cells.

Experimental Design

To evaluate the immune system in neuroblastoma patients, in particular the myeloid compartment, we analyzed publically available expression datasets by searching the R2 database (see 6.5.3). In order to elucidate the impact of neuroblastoma-derived factors on the differentiation of myeloid cells, we established 3 *in vitro* models (**Figure 4**), where human CD34+ hematopoietic stem cells, primary monocytes and murine bone marrow cells were cultured in the presence of neuroblastoma tumor-conditioned medium (TCM). In addition, inhibitors of CSF-1R signaling were added into these cultures and the subsequent phenotypic and functional changes of myeloid cells were evaluated. To test the therapeutic potential of CSF-1R inhibition *in vivo*, we employed a mouse model, in which human oncogene *MYCN* drives the development of highly

aggressive spontaneous neuroblastoma from adrenal medullas. Mice bearing palpable abdominal tumors were treated with a selective CSF-1R inhibitor, BLZ945, or in combination with checkpoint blocking antibodies against the PD-1/PD-L1 axis. After 10 days, tumor weights and the immunological profiles were compared among groups.

Main Findings

In comparison to benign neurofibroma tissues, we found that neuroblastoma tissues expressed higher levels of M-CSF and CSF-1R. Indeed, both M-CSF and CSF-1R+ myeloid cells predicted poor survival in patients without prior treatments. These findings were validated using *in vitro* culture models, where CSF-1R signaling was proven to modulate myelopoiesis of human CD34+ hematopoietic stem cells and murine bone marrow cells and enabled suppressive functions from primary human monocytes. When mice were treated with CSF-1R inhibitor in the therapeutic setting, the progression of highly aggressive tumors was efficiently controlled. This was mainly due to the specific effects on suppressive myeloid cells *in vivo*. To our surprise, checkpoint blocking antibodies against PD-1/PD-L1 had no impact on the suppressive myeloid cells and failed to control tumor growth in the TH-*MYCN* mice. Combining CSF-1R inhibition with checkpoint inhibitors enabled striking anti-tumor effects that were superior to either treatment alone.

Relevance of the Study

It is well-appreciated that tumor-derived factors facilitate the engraftment of hematopoietic stem cells in the periphery, leading to splenic production of immature myeloid cells in mice [410]. However, these effects were less understood in humans. In this study, we comprehensively elucidated the impact of CSF-1R signaling on early differentiation and local activation of suppressive myeloid cells in humans and mice. These models could be potentially applicable to dissect myeloid cell functions in various types of solid tumors.

According to published findings using the TH-*MYCN* murine model of high-risk human neuroblastoma, it is extremely difficult to achieve meaningful therapeutic effects due to the known short treatment window and rapid disease progression once the tumors are established and palpable [411]. Although targeting suppressive myeloid cells have long been considered as an attractive option to improve cancer immunotherapy in other cancer types, our study is the first documentation of the *in vivo* synergistic potency between a small molecule CSF-1R inhibitor and checkpoint blocking antibodies in controlling aggressive progression of spontaneous tumors. In fact, the relative success in novel treatment of these animals resulted in prolonged survival but none of the animals was cured or even showed shrinkage of tumors contrasting our current results [412, 413]. Therefore, the study has a unique strength in that the combination therapy resulted in outstanding curative effects in 75% of the treated mice and prevented the aggressive progression of large tumors among the remaining ones.

Given that the therapeutic efficacy of PD-1 blockade and the prognostic values of suppressive myeloid cells are being tested in various human cancers, this study may have a broad implication for the therapy of human cancers.

6.5 TECHNICAL DETAILS

6.5.1 *In vitro* models to study suppressive myeloid cells in humans and mice

To investigate the induction of suppressive myeloid cells, three *in vitro* models were established, where human primary monocytes, cord blood-derived CD34+ hematopoietic progenitor cells or murine bone marrow cells were cultured in the presence of tumor-derived factors (**Figure 4**).

The model co-culturing primary human monocytes with tumor cell lines reflected how differentiated myeloid cells could gain suppressive functions under the influence of tumor-derived factors. To maximize the physiological relevance, freshly isolated melanoma tumor cells were expanded from lymph node metastases of advanced stage melanoma patients and utilized at early passages (<7 passages).

The monocyte-tumor co-cultures have limited power to reflect the influence of tumor-derived factors on myelopoiesis, which may result in accumulation of immature suppressive myeloid cells in the periphery. To overcome this issue, I established an *in vitro* model, where CD34+ hematopoietic stem cells purified from cord blood were matured in the presence of tumor-conditioned medium. This allows us to more accurately dissect the impact of tumor-derived factors on the early differentiation of the myeloid compartment.

Based on several previously published reports [243, 414], we utilized an additional *in vitro* model, where murine bone marrow cells were cultured in the presence of tumor-conditioned medium. This essential model offered a time effective method that allowed us to select myeloid-modulating compounds before testing in the *in vivo* models.

Collectively, these three independent approaches enabled us to gain in-depth understanding of the induction and functions of suppressive myeloid cells in cancer patients and tumor-bearing animals. More importantly, we were able to select compounds in a cost- and time-efficient manner that may have a greater *in vivo*

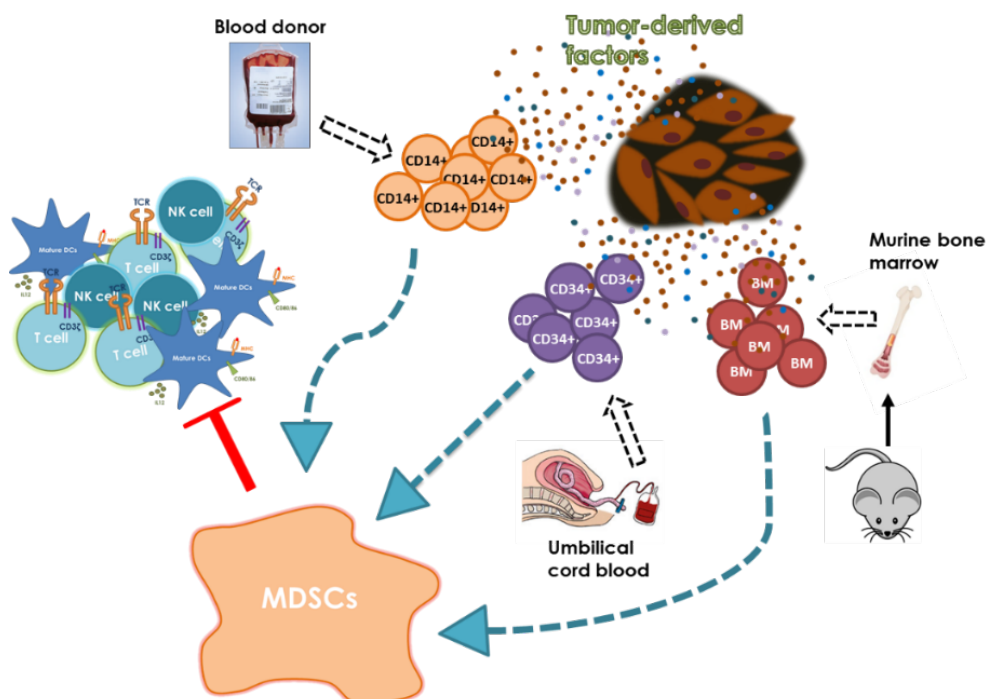


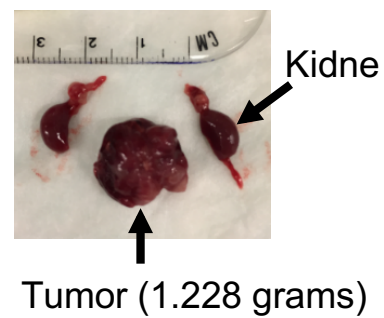
Figure 4, *In vitro* models to study tumor-induced differentiation of suppressive myeloid cells.

impact.

6.5.2 The TH-MYCN neuroblastoma murine model

The transgenic murine model that spontaneously develops neuroblastoma was established by Weiss *et al.* in 1997 [415]. In this model, human proto-oncogene *MYCN* is controlled by tyrosine hydroxylase promoter (TH-*MYCN*), which is active during early development of migrating cells in the neural crest [416]. Thus, TH-*MYCN* transgenic mice express high levels of human *MYCN* protein in the adrenal gland and paraspinal ganglia, which results in induction of spontaneous neuroblastoma tumors that resemble the aggressive growth pattern of high-risk neuroblastoma patients. Following the tumor incidence and treatment window suggested by a previous study [417], mice received 3 abdominal palpations per week and spontaneously arising tumors were harvested 10 days after detection. As shown in **Figure 5**, large spontaneous tumors arise from the adrenal gland in these mice and situate between kidneys in the abdominal cavity. The non-treated control mice on average developed tumors weighing 1.5 grams, approximately 7.5 % of the body mass (20 grams).

Figure 5, Representative



6.5.3 The R2 database

The 'R2: microarray analysis and visualization platform (<http://r2.amc.nl>)' is a public database containing enormous amounts of valuable expression datasets extracted from various types of healthy tissues, tumor tissues or cell lines. The purpose of this database is to create a user-friendly environment for biologists to test relevant hypotheses using existing datasets. In certain patient datasets, additional pathological information or clinical outcome of the patient cohorts are also available. Thus, this platform provides an extremely efficient tool for researchers who lack immediate access to clinical samples. In **study IV** of this thesis, we have retrieved key clinical information supporting the relevance of targeting CSF-1R+ myeloid cells in human neuroblastoma datasets. However, given that genomic information cannot completely reflect dynamic changes of the biological network, we have extensively validated the results by protein detection methods or assays enabling functional evaluations at the cellular level or in the *in vivo* environment.

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Key contributors to study II and IV

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The tumor immunology society on the CCK floor 01

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