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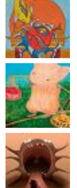

Three years ago, Cell Press launched the "Best of" reprint collections across a number of our journals, including *Immunity*. We proudly welcome you to the 2014 edition of *Best of Immunity*. In looking back at the papers published during 2014, we wanted to provide our readers with a sense of the various topics and findings in which they and their colleagues have shown significant interest. *Immunity* is published monthly in two volumes each year, with each volume covering 6 months. In order to account for the amount of time since publication, we have selected 11 of the most-accessed articles from volumes 40 and 41, which cover the first and second halves of 2014, respectively. We use the number of requests for PDF and full-text HTML versions of a given article up until the end of March 2015 to determine the "most-accessed" articles. We acknowledge that no single measurement can truly be indicative of "the best" research papers over a given period of time. This is especially true when sufficient time has not necessarily passed to allow one to fully appreciate the relative importance of a discovery. That said, we think it is still informative to look back at our readers' interest in the immunology that *Immunity* published over the course of 2014.

In this reprint collection, we present for your consideration four review articles and seven research articles from throughout 2014. You will see a range of the exciting topics that have widely captured the attention and enthusiasm of our readers, including a deep look at tumor-associated macrophages from mechanisms to therapies, an examination of the gut microbiota and antibody responses to seasonal influenza vaccination, and a review of innate lymphoid cells' roles in inflammation and immunity.

Additionally, we present a pair of *Immunity*'s SnapShots on nucleic immune sensors. To access the complete collection of SnapShots, visit snapshots.cell.com.

We hope that you will enjoy reading this special collection and that you will visit www.cell.com/immunity to check out the latest findings that we have had the privilege to publish. Also be sure to visit www.cell.com to find other high-quality papers published in the full collection of Cell Press journals.

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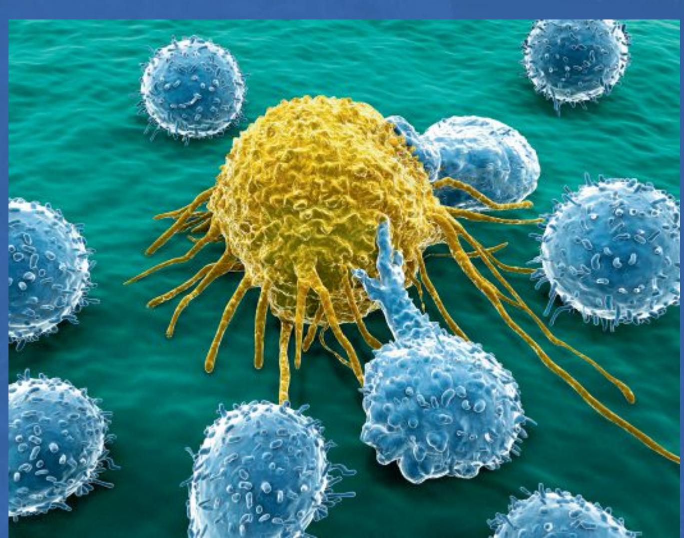

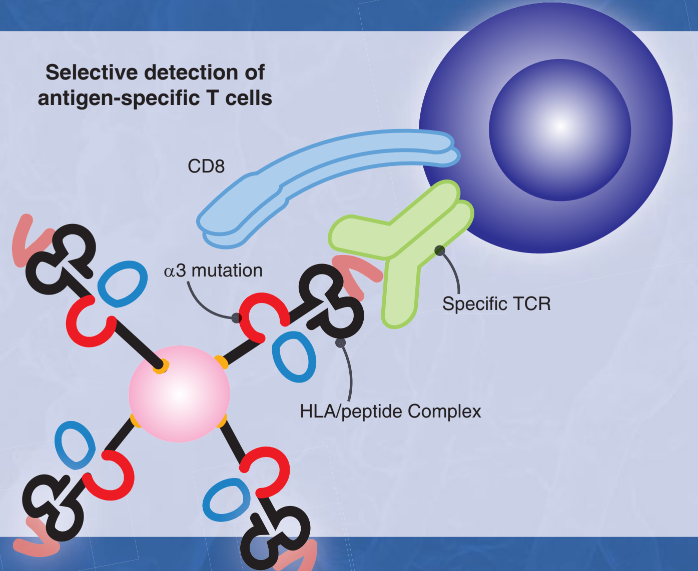


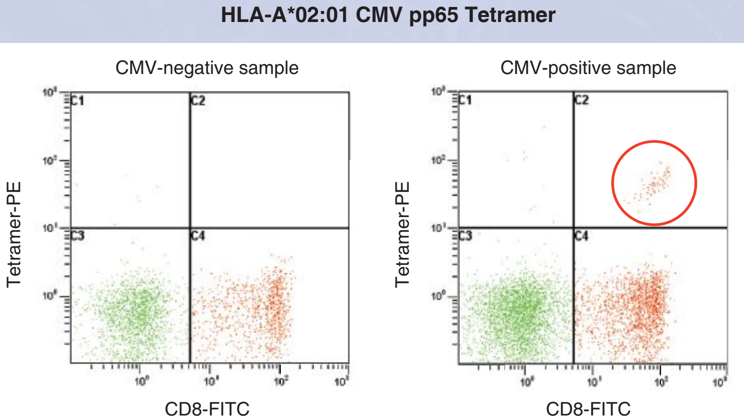


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Best of 2014

## SnapShots

**Nucleic Acid Immune Sensors, Part 1 and Part 2** — *Veit Hornung*

## Perspective

**Macrophage Activation and Polarization: Nomenclature and Experimental Guidelines** — *Peter J. Murray, Judith E. Allen, Subhra K. Biswas, Edward A. Fisher, Derek W. Gilroy, Sergij Goerdt, Siamon Gordon, John A. Hamilton, Lionel B. Ivashkiv, Toby Lawrence, Massimo Locati, Alberto Mantovani, Fernando O. Martinez, Jean-Louis Mege, David M. Mosser, Gioacchino Natoli, Jeroen P. Saeij, Joachim L. Schultze, Kari Ann Shirey, Antonio Sica, Jill Suttles, Irina Udalova, Jo A. van Ginderachter, Stefanie N. Vogel, and Thomas A. Wynn*

## Reviews

**Tumor-Associated Macrophages: From Mechanisms to Therapy** — *Roy Noy and Jeffrey W. Pollard*

**Development, Differentiation, and Diversity of Innate Lymphoid Cells** — *Andreas Diefenbach, Marco Colonna, and Shigeo Koyasu*

**Innate Lymphoid Cells in Inflammation and Immunity** — *Andrew N.J. McKenzie, Hergen Spits, and Gerard Eberl*

## Articles

**Small-Molecule RORγt Antagonists Inhibit T Helper 17 Cell Transcriptional Network by Divergent Mechanisms** — *Sheng Xiao, Nir Yosef, Jianfei Yang, Yonghui Wang, Ling Zhou, Chen Zhu, Chuan Wu, Erkan Baloglu, Darby Schmidt, Radha Ramesh, Mercedes Lobera, Mark S. Sundrud, Pei-Yun Tsai, Zhijun Xiang, Jinsong Wang, Yan Xu, Xichen Lin, Karsten Kretschmer, Peter B. Rahl, Richard A. Young, Zhong Zhong, David A. Hafler, Aviv Regev, Shomir Ghosh, Alexander Marson, and Vijay K. Kuchroo*

**Alterations in the Microbiota Drive Interleukin-17C Production from Intestinal Epithelial Cells to Promote Tumorigenesis** — *Xinyang Song, Hanchao Gao, Yingying Lin, Yikun Yao, Shu Zhu, Jingjing Wang, Yan Liu, Xiaomin Yao, Guangxun Meng, Nan Shen, Yufang Shi, Yoichiro Iwakura, and Youcun Qian*

**Embryonic and Adult-Derived Resident Cardiac Macrophages Are Maintained through Distinct Mechanisms at Steady State and during Inflammation** — *Slava Epelman, Kory J. Lavine, Anna E. Beaudin, Dorothy K. Sojka, Javier A. Carrero, Boris Calderon, Thaddeus Brija, Emmanuel L. Gautier, Stoyan Ivanov, Ansuman T. Satpathy, Joel D. Schilling, Reto Schwendener, Ismail Sergin, Babak Razani, E. Camilla Forsberg, Wayne M. Yokoyama, Emil R. Unanue, Marco Colonna, Gwendalyn J. Randolph, and Douglas L. Mann*

*(continued)*

**T-Cell-Receptor-Dependent Signal Intensity Dominantly Controls $CD4^+$ T Cell Polarization In Vivo**
*Nicholas van Panhuys, Frederick Klauschen, and Ronald N. Germain*

**Oral Tolerance Can Be Established via Gap Junction Transfer of Fed Antigens from $CX3CR1^+$ Macrophages to $CD103^+$ Dendritic Cells**
*Elisa Mazzini, Lucia Massimiliano, Giuseppe Penna, and Maria Rescigno*

**TLR5-Mediated Sensing of Gut Microbiota Is Necessary for Antibody Responses to Seasonal Influenza Vaccination**
*Jason Z. Oh, Rajesh Ravindran, Benoit Chassaing, Frederic A. Carvalho, Mohan S. Maddur, Maureen Bower, Paul Hakimpour, Kiran P. Gill, Helder I. Nakaya, Felix Yarovinsky, R. Balfour Sartor, Andrew T. Gewirtz, and Bali Pulendran*

**Interleukin-10-Producing Plasmablasts Exert Regulatory Function in Autoimmune Inflammation**
*Masanori Matsumoto, Akemi Baba, Takafumi Yokota, Hiroyoshi Nishikawa, Yasuyuki Ohkawa, Hisako Kayama, Axel Kallies, Stephen L. Nutt, Shimon Sakaguchi, Kiyoshi Takeda, Tomohiro Kurosaki, and Yoshihiro Baba*

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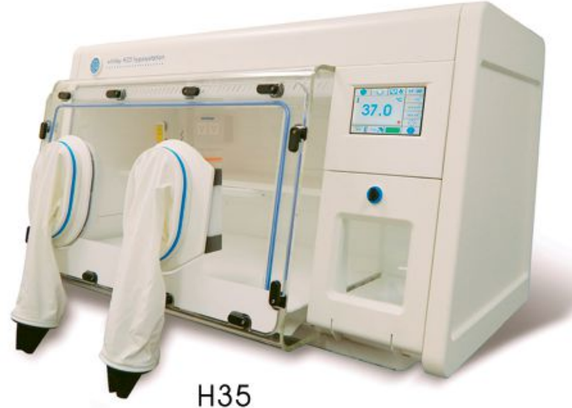

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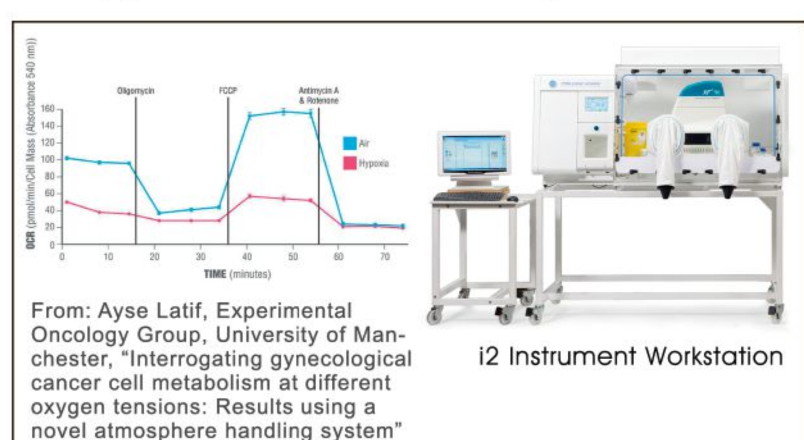


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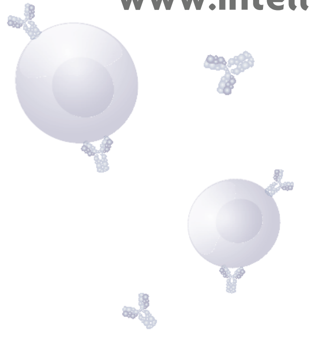

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# SnapShot: Nucleic Acid Immune Sensors, Part 1

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Veit Hornung
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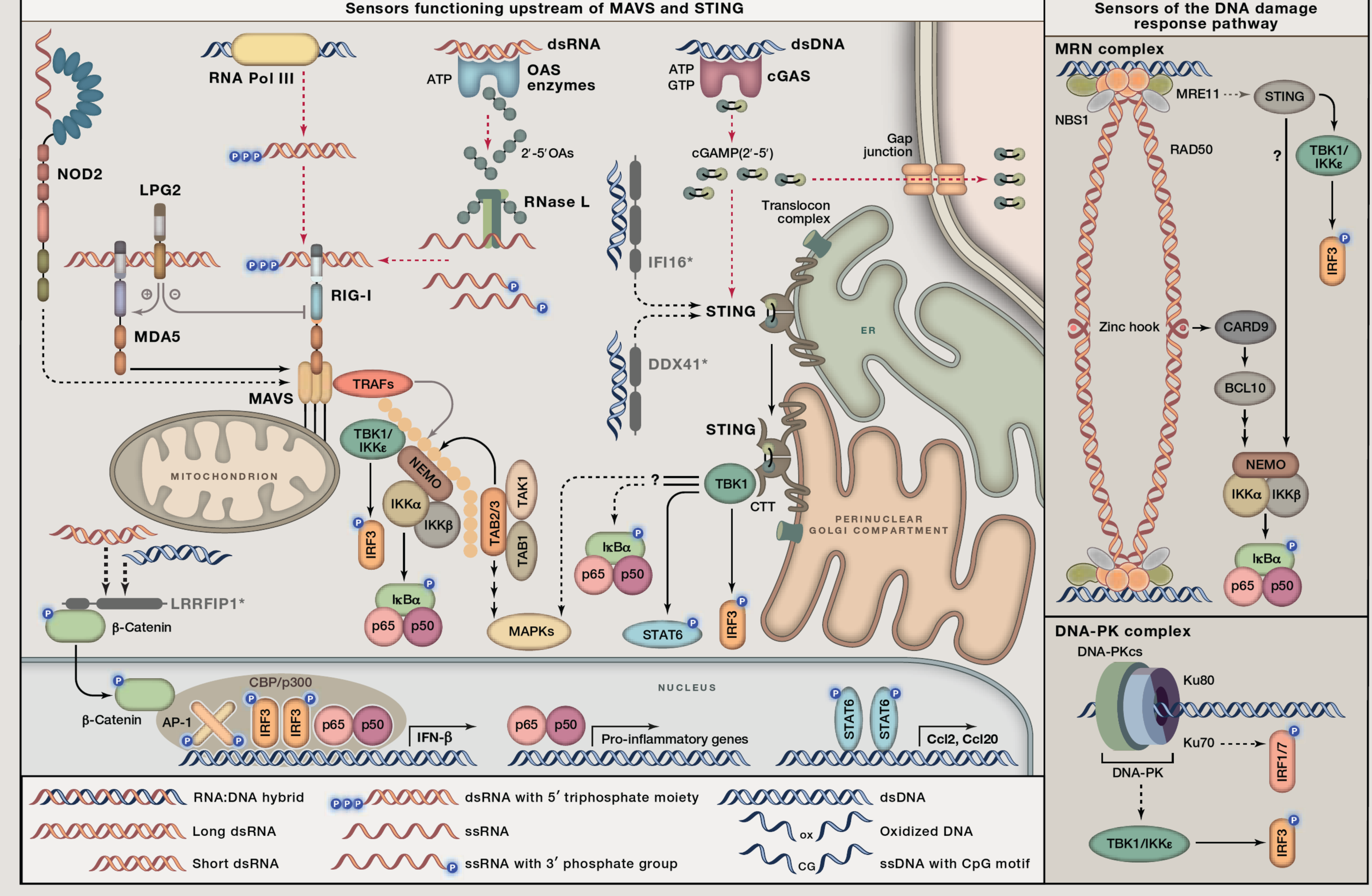


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# SnapShot: Nucleic Acid Immune Sensors, Part 2

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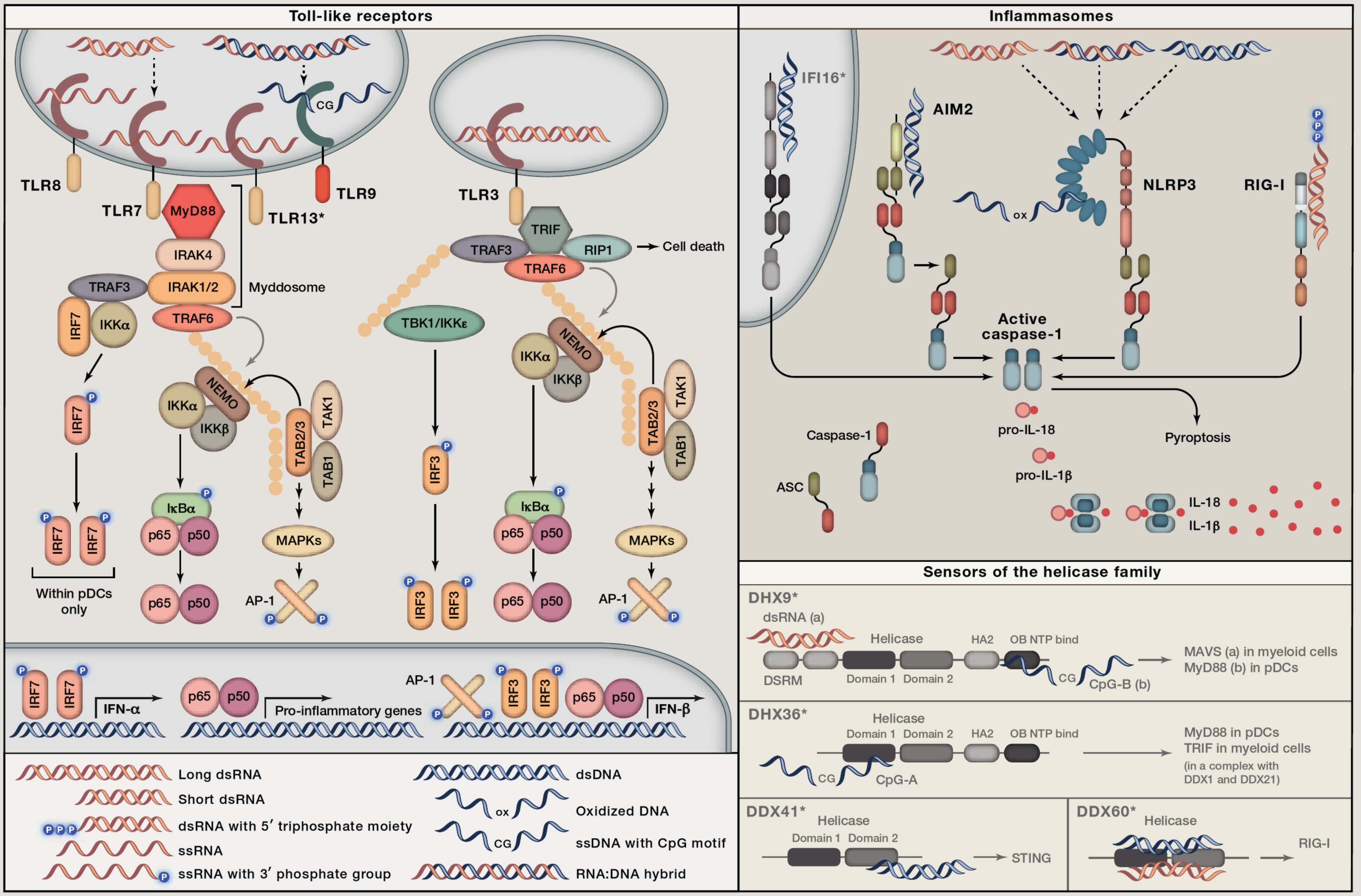


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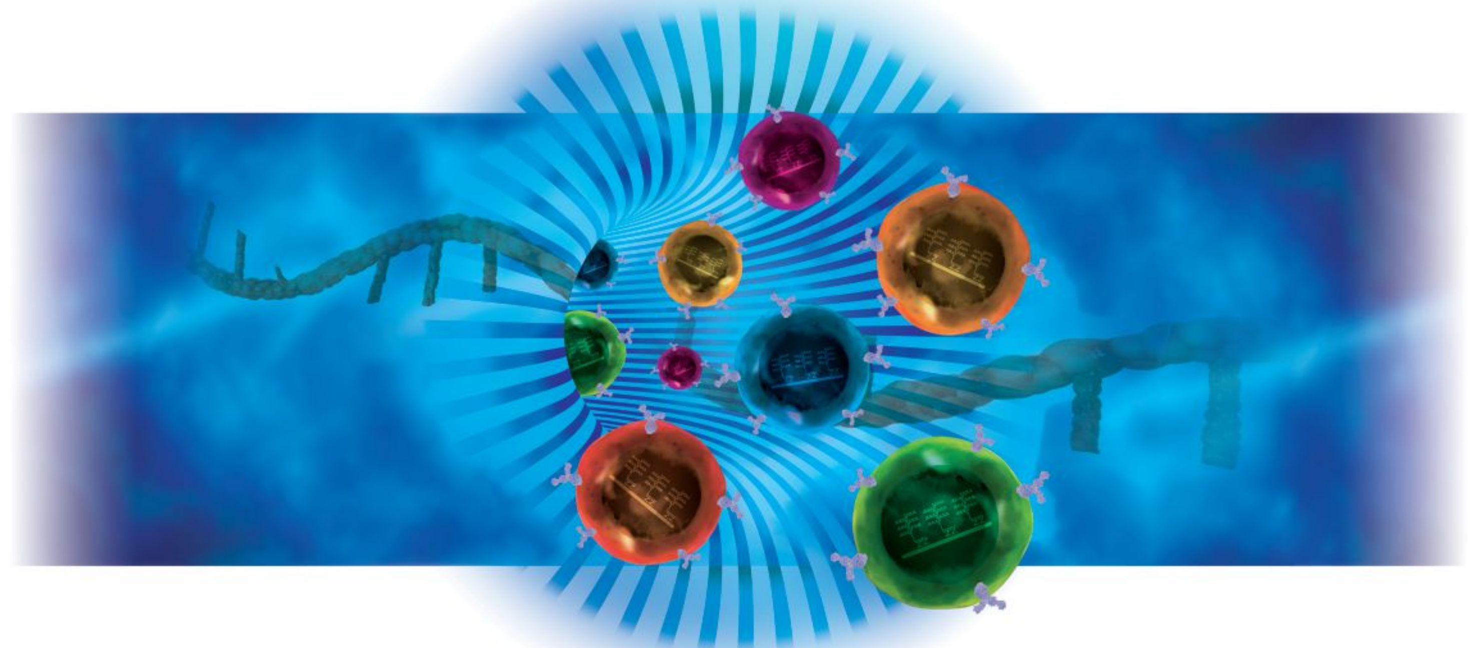

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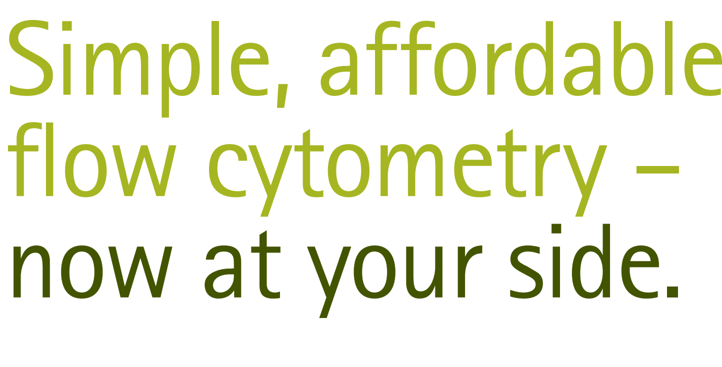


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Perspective

# Macrophage Activation and Polarization: Nomenclature and Experimental Guidelines

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**Description of macrophage activation is currently contentious and confusing. Like the biblical Tower of Babel, macrophage activation encompasses a panoply of descriptors used in different ways. The lack of consensus on how to define macrophage activation in experiments in vitro and in vivo impedes progress in multiple ways, including the fact that many researchers still consider there to be only two types of activated macrophages, often termed M1 and M2. Here, we describe a set of standards encompassing three principles—the source of macrophages, definition of the activators, and a consensus collection of markers to describe macrophage activation—with the goal of unifying experimental standards for diverse experimental scenarios. Collectively, we propose a common framework for macrophage-activation nomenclature.**

## Overview

Activation of macrophages has emerged as a key area of immunology, tissue homeostasis, disease pathogenesis, and resolving and nonresolving inflammation (Biswas and Mantovani, 2010; Gordon and Martinez, 2010; Lawrence and Natoli, 2011; Mantovani et al., 2008; Mantovani et al., 2005; Martinez et al., 2008; Murray and Wynn, 2011b; Nathan and Ding, 2010; Wynn et al., 2013). Over the last several years, diverse terms have been applied to macrophage activation and "polarization," where a stimulus such as a cytokine or toll-like receptor (TLR) agonist produces distinct patterns of gene and protein expression. Here, we use the term "activation" to mean the perturbation of macrophages with exogenous agents in the same vein as many use "polarization." We also note the ability of macrophages to change their activation states in response to growth factors (e.g., CSF-1 and GM-CSF) and external cues, such as cytokines, microbes, microbial products, and other modulators, including nucleotide derivatives, antibody-Fc receptor stimulation, glucocorticoids, infection, phagocytosis, and potentially any other entity capable of being recognized by macrophages. Because macrophage activation is involved in the outcome of many diseases, including metabolic diseases, allergic disorders (such as

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airway hyperreactivity), autoimmune diseases, cancer, and bacterial, parasitic, fungal, and viral infections, we need to establish a common language for describing the properties of the macrophages under investigation.

## Background to the Problem

We note widespread use of at least four definitions of macrophage activation, including terms such as M1 and M2, alternative and classical activation, "regulatory" macrophages, and subdivisions originating from the parent terms. The origins of these terms originated in the early 1990s when differential effects of interleukin-4 (IL-4) in comparison to those of interferon γ (IFN-γ) and/or lipopolysaccharide (LPS) on macrophage gene expression were described (Martinez and Gordon, 2014; Stein et al., 1992). Compared to IFN-γ, IL-4 was described to induce "alternative activation." It should be noted that the term "classical" activation, which originally referred to macrophages stimulated with IFN-γ, is now interchangeably used with IFN-γ and TLR stimulation (Martinez and Gordon, 2014). The second definition came several years later when Mills proposed the M1-M2 terminology (Mills et al., 2000). Mills's idea originated from the differential metabolism of arginine between macrophages from C57BL/6 and macrophages from Balb/c mice, an effect he correlated with differences between T helper 1 (Th1) and Th2 cell responses in the same strains. Mills and colleagues went further and proposed that the M1-M2 dichotomy was an intrinsic property of macrophages associated with transitions from inflammation to healing, would occur in the absence of an adaptive immune response, and arose early in evolution (Mills, 2012). Several lines of evidence suggest that this theory requires rethinking. First, C57BL/6 mice bear a deletion in the promoter of *Slc7a2*, encoding the key arginine transporter in macrophages, causing large differences in arginine utilization between C57BL/6 and BALB/c mice. This genetic difference between the strains was not known at the time that Mills's hypothesis was published and was therefore not taken into account (Sans-Fons et al., 2013). Second, although Mills's notion on "innate" shifts in macrophage activation might be true, most immunologists are concerned with immunity in the presence of lymphocytes, which profoundly affect the activation state of macrophages through cytokine secretion. Third, no molecular definition has yet accounted for an "innate" M1-to-M2 transition, although new information from epigenetics and metabolism (see below) might provide a means of dissecting intrinsic macrophage activation states.

The third set of nomenclature (M2a, M2b, etc.) expanded the M1-M2 definitions to account for different activation scenarios and was balanced by the idea that activation exists on a spectrum and cannot be easily binned into defined groups (Biswas and Mantovani, 2010; Edwards et al., 2006; Mantovani et al., 2005; Martinez and Gordon, 2014; Stout et al., 2005; Stout and Suttles, 2004). The fourth definition refers to macrophages grown in GM-CSF-1 as M1 and macrophages grown in CSF-1 as M2 (Joshi et al., 2014). Notably, significant differences have been documented in the transcriptomes of macrophage populations primarily generated with the use of CSF-1 or GM-CSF, with and without exogenous perturbation (Fleetwood et al., 2009), but there is no compelling evidence to assign CSF-1- or GM-CSF-derived macrophages as M1 or M2.

The diversity of terminology and inconsistent use of markers to describe macrophage activation impedes research in several ways. First, researchers entering the field encounter confusion about which terms to use and which markers are representative of their experimental or human-based system; many researchers might erroneously consider there to be only "two types of macrophages." Second, established researchers in the field have yet to agree on nomenclature or standards for describing activation. Third, grant and manuscript writers and their reviewers, funding and regulatory agencies, and journal editors can be exasperated at the breadth of terminology in use. Fourth, the lack of experimental standards impedes studies where comparisons are required (e.g., microarray and proteomic data sets). Fifth, deployment of therapeutic macrophage modulators requires that standards be translatable across disciplines so that pharmaceutical and regulatory bodies can draw meaningful comparisons in terms of diagnostic or efficacy metrics. A sixth and final issue is the diversity in macrophage activation across species (discussed briefly below).

To address the obstacles and pitfalls in describing macrophage activation and in achieving experimental standards, a small group of macrophage biologists met informally at the International Congress of Immunology in Milan in August 2013. We discussed the issues surrounding terminology and set out to provide an initial set of nomenclature and experimental guidelines. A draft letter was then circulated to a broader group of researchers active in this area. In this perspective, we do not attempt to capture everyone who has published on macrophage activation and polarization; rather, we aim to attain consensus about the problems within the field and to propose solutions. As such, discussion and revision will be essential for refining the properties and mechanisms of macrophage polarization.

## Recommendations

### *A Reproducible Experimental Standard*

We concluded that a starting point was to frame a nomenclature system within a reproducible in vitro experimental standard. CSF-1-cultured macrophages from murine bone marrow and human peripheral-blood monocytes remain the predominant in vitro systems used for generating macrophages and therefore will be used as references (Figure 1A). Other commonly used macrophage sources are peritoneal macrophages (resident or elicited) from mice and GM-CSF-cultured macrophages from murine bone marrow (Figure 1A), and each of these can be perturbed to generate activated populations of macrophages with gene-expression profiles overlapping those of CSF-1-generated cells. On this basis, the culture conditions for generating the two paradigmatic in vitro M1 and M2 populations are straightforward, i.e., postdifferentiation stimulation with IFN-γ or IL-4. IL-4 and IFN-γ often exert clear-cut antagonistic effects on macrophage polarization mediated by STAT6 and STAT1, respectively. Furthermore, IL-4 and IFN-γ induce defined and comprehensively investigated macrophage subpopulations (Lawrence and Natoli, 2011; Mills, 2012; Rutschman et al., 2001; Taub and Cox, 1995; Wynn et al., 2013).

### *Recommendation for Minimal Reporting Standards*

Incomplete descriptions of how macrophages are isolated, stimulated, and analyzed are contrary to the value of replication and reproducibility across laboratories. To this end, macrophages

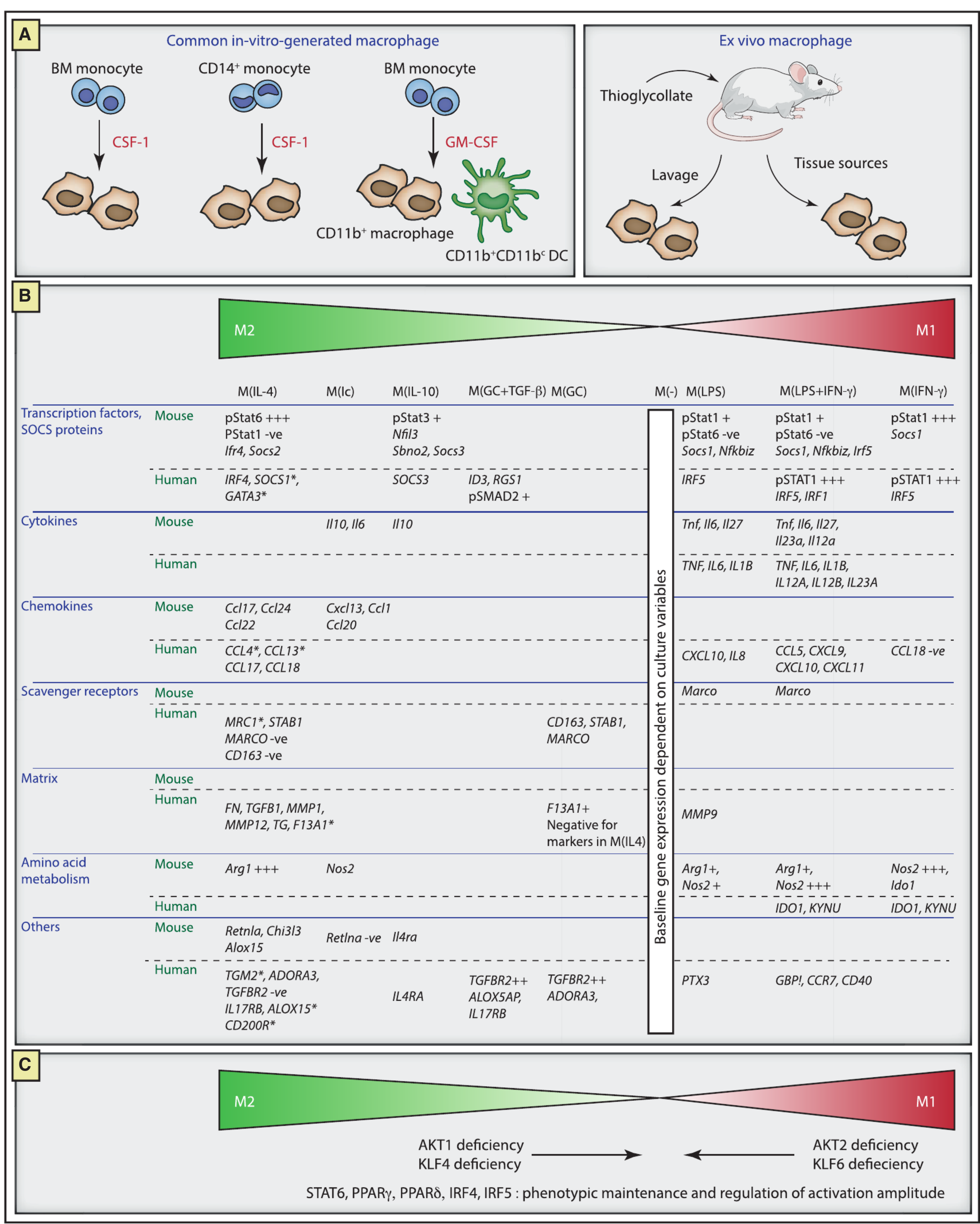


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**Table 1. Reporting Standards for In Vitro Experiments**

| Parameter | Notes |
|---|---|
| Mouse strain | how the bone marrow is isolated and processed |
| Starting cell number, media, and supplements | media (DMEM versus RPMI) have substantial effects of growth rate, development, and activation status |
| Tissue-culture conditions | different types of plastic affect macrophage growth and activation; tissue-culture conditions should be documented for reproducibility |
| Time of culture | the precise conditions used and whether cytokines and/or media are supplemented during the culture period |
| Source and concentration of differentiation cytokines | the source and concentration of CSF-1 |
| Macrophage yield | the yield relative to the starting number should be recorded |
| Activation conditions | variables include whether macrophages are rested prior to activation and how, whether CSF-1 is present in the activation cultures, the source and concentrations of the activating agents, and the time to assay |
| Processing and analysis | how the cells are processed and what marker readouts are used |

isolated from in vitro and in vivo systems require, at a minimum, reporting standards encapsulated in Table 1. With these standards as a guide, in vitro experiments from different laboratories can be directly compared. Finally, we favor the use of purified endotoxin-free recombinant CSF-1 rather than L-cell-conditioned medium as the source of CSF-1 to generate bone-marrow-derived macrophages because the latter is not readily defined and can vary from batch to batch. For example, L-cell-conditioned medium contains variable amounts of type I interferons that could cause confounding effects in subsequent activation experiments (Warren and Vogel, 1985).

### *Define the Activator*

In general, given that diverse mediators have been used alone or in various combinations for the generation of polarized macrophage populations, we propose that researchers describe stimulation scenarios and adopt a nomenclature linked to the activation standards, i.e., M(IL-4), M(Ig), M(IL-10), M(GC), M(IFN-γ), M(LPS), and so forth (Figure 1B). Such a system avoids the complexity of M2a, M2b, etc., where one laboratory might experimentally define activation differently than another, and allows new activation conditions to be compared and contrasted with these core examples. Figure 1 also depicts the concept of a "spectrum" of activation to denote activation "states" commonly observed (Mosser and Edwards, 2008; Stout et al., 2005; Stout and Suttles, 2004; Xue et al., 2014). The employment of the spectrum concept is useful where ambiguity exists or when researchers are operating outside the in vitro CSF-1 schema described above. In summary, we note that standards need to be simple for adoption but at the same time not cause sudden conceptual shifts. Therefore, researchers should consider harnessing the terminology and markers for CSF-1-grown macrophages activated under defined conditions as a reference standard (Xue et al., 2014). Where ambiguity exists—for example, in a macrophage population isolated from an in vivo system—researchers should emphasize the marker combinations used and state the closest relative(s) along the spectrum shown in Figure 1 (discussed below).

### *Terms to Avoid*

We propose that the term "regulatory" macrophages should be avoided because all macrophages are regulatory in some capacity. The use of macrophages derived from mice with specific targeted mutations that prevent development of an M(IL-4) profile (e.g., through the use of IL-4Rα- or STAT6-deficient macrophages) is recommended to confirm a specific phenotype. Some researchers often ascribe the subset terminology M1 and M2 to GM-CSF- and CSF-1-generated macrophages, respectively; such terminology should be abandoned. When CSF-1 or GM-CSF is used for generating activated macrophage populations, it should be clearly indicated. A further complication is that GM-CSF cultures contain substantial numbers of $CD11c^+$ cells with distinct antigen-presenting activities that need to be accounted for in gene profiling or functional analyses.

### *Markers of Activation*

CD4 defines $CD4^+$ Th cells. Within $CD4^+$ cells, Foxp3 defines regulatory T cells. These are just two examples of markers defining cell lineages. By contrast, macrophage activation is

**Figure 1. Framework for Describing Activated Macrophages**

(A) Examples of widely used macrophage preparations. CSF-1-grown mouse adherent macrophages from bone marrow (BM) or $CD14^+$ monocytes are used as the exemplars for marker evaluation and standardized activation conditions. Macrophages can also be generated with GM-CSF, where a $CD11c^+$ dendritic cell (DC) population is also present depending on the culture conditions. In mice, thioglycollate injection followed by peritoneal lavages is used for generating macrophage populations with differing yields and properties, whereas many organ systems in mice and humans are sources of tissue-infiltrating macrophages.
(B) Marker systems for activated macrophages. Shown are functional subdivisions according to stimulation of mouse CSF-1 macrophages or human monocyte-derived CSF-1 macrophages with the existing M1-M2 spectrum concept (Martinez and Gordon, 2014; Mosser and Edwards, 2008; Stout and Suttles, 2004). Stimulation conditions are IL-4, immune complexes (Ic), IL-10, glucocorticoids (GC) with transforming growth factor β (TGF-β), glucocorticoids alone, LPS, LPS and IFN-γ, and IFN-γ alone. Marker data were drawn from a wide range of published and unpublished data from the authors' laboratories and represent a starting consensus (Edwards et al., 2006; Fleetwood et al., 2009; Gratchev et al., 2008; Gundra et al., 2014; Krausgruber et al., 2011; Lang et al., 2002; Shirey et al., 2008; Shirey et al., 2014; Shirey et al., 2010; Xue et al., 2014). An asterisk indicates corroboration of human IL-4 genes by deep sequencing (K.A.S. and S.N.V., data not shown).
(C) Using genetics to aid in macrophage-activation studies. Mutations in *Akt1* and *Klf4* cause a "switch" to M(LPS)- and M(IFN-γ)-associated gene expression, whereas mutations in *Akt2* and *Klf6* show the reverse phenotype. Mutations in *Stat6*, *Ppard*, *Pparg*, and *Irf4* and IRF5 depletion are involved in the maintenance and/or amplitude of activation.

associated with substantial shifts in gene expression (hundreds of genes) depending on the specific stimuli, but none define a sublineage or activation state of macrophages. To the researcher outside the macrophage sphere, marker use probably appears confusing because immunologists are accustomed to tight marker-lineage association. An example of problematic marker use is expression of Arginase-1 (Arg1) as a "marker" for M2 or M(IL-4) spectrum macrophages, which has led to interpretive problems because Arg1 is also induced in M1 spectrum macrophages, expressed in some resident macrophage populations, and highly induced in mycobacteria-infected macrophages, further emphasizing the need for criteria encompassing multiple markers (El Kasmi et al., 2008). Accordingly, we favor an approach using combinations of markers (or a lack of marker expression) to ascribe activation outcomes as outlined in Figure 1B. Clearly, there is significant scope to expand upon marker assignment such as transcription factor and cell-surface marker combinations within the standardized experimental framework proposed here, and this should serve as a starting cartography for the field.

### Translation to In Vivo Experiments

When isolating macrophages from tissue and analyzing their activation state, each laboratory will confront a familiar problem: what do we call them? What if there are different populations present? Our recommendation is to acquire sufficient evidence to place a given population within the framework shown in Figure 1. It seems unlikely that a particular in vivo scenario will fall exactly within the groups in Figure 1. However, as more macrophage populations are dissected ex vivo, more information will accumulate to help us understand the general and specific nature of in vivo macrophage activation.

#### *Ex Vivo Characterization of Macrophage Activation*

Each laboratory has individualized macrophage isolation procedures. Because of the breadth of conditions used, we favor describing in detail how macrophages are isolated, which tissue and pathological or homeostatic condition they are from, and which marker combinations are used for ascertaining macrophage activation. All authors stress the need for rapid isolation techniques to preserve the underlying phenotype quickly and without additional ex vivo culture. Advances in technologies for in situ gene expression within individual tissues and cells will most likely advance the understanding of spatial macrophage activation. Regardless of the technology employed, combinations of markers need to be applied to the populations being analyzed, and a full description of the isolation techniques needs to be provided. For example, the Immgen Consortium has a mandate for isolation and sorting conditions for immune cells, and we favor their degree of descriptive rigor for ex vivo macrophages (Gautier et al., 2012). Another complication from ex vivo analysis of macrophage activation is plasticity across different disease stages. For example, in obesity research, macrophages residing in adipose tissue are thought to become more proinflammatory as fat accumulates and thus fall toward the M1 end of the activation spectrum (Wynn et al., 2013). In atherosclerosis, resolution of lesions is associated with the reverse: macrophage populations on the M1 spectrum convert to the M2 part of the spectrum without evidence of local STAT6 activation by IL-4 or IL-13 (Moore et al., 2013). One solution to the problem of describing macrophage activation in scenarios in vivo is to begin with an explicit description of the populations under investigation and how they were isolated (as Immgen defines, for example). Markers can then be used to reflect the perturbations they have encountered. For example, $Arg1^{hi}Retnla^{hi}pSTAT6^{+}pSTAT1^{-}$ could be used to enhance the description of a specific lung macrophage population isolated from a Th2-cell-type-driven disease and thus be reasonably related to the M(IL-4) cells (Figure 1B). Reporting the time points of ex vivo macrophage isolation and analysis are therefore mandatory in the description of tissue- and disease-associated macrophage populations.

#### *Translation to Human Macrophages*

How can we define and categorize activated human macrophages? This question continues to confound researchers in part because human macrophages are generally isolated from blood monocytes as opposed to bone marrow or tissues commonly used in murine studies. This distinction is particularly important with the new knowledge that many tissue-resident populations are not of bone marrow origin (Sieweke and Allen, 2013). Many of the markers used for murine macrophages have not translated to human macrophages. Plausible reasons for these discrepancies have been discussed (Murray and Wynn, 2011a), but it is worth emphasizing that no study has systematically compared the responses of blood-monocyte-derived macrophages from mice and humans in a side-by-side manner. We expect a range of interspecies variability on macrophage activation to reflect different evolutionary outcomes sculpted by different pathogens, diets, longevity, etc. Despite the variables involved, experimental rigor can be used in the search for information about human (and any other species) macrophage biology according to the principles and practices outlined here. Recently, systematic studies have begun to explore the conservation between macrophages from different species, including swine, where large numbers of different tissue macrophages can be isolated (Fairbairn et al., 2011; Martinez et al., 2013; Schroder et al., 2012; Xue et al., 2014). Therefore, researchers should describe how they generate their macrophages and subsequently stimulate them. When microarray, deep sequencing, and proteomic studies are combined to interrogate human macrophages, a consensus will emerge about which pathways of human macrophage activation are amenable to new drug discovery.

#### *Genetics to Alter Activation States*

Recent work has identified genetic modifications producing shifts in activation phenotype. For example, deletion of transcription factor IRF4 or KLF6 fails to make M(IL-4) macrophages, whereas PPAR$\gamma$ and PPAR$\partial$ are required for the amplitude of the M(IL-4) state (Chawla, 2010; Date et al., 2014; Ivashkiv, 2013). Ablation of proteins involved in anabolic growth, such AKT2 and PTEN, enhances an activation state where gene expression is linked to M(IL-4) macrophages, whereas deletion of TSC1, an inhibitor of mTOR, causes the opposite effect (Arranz et al., 2012; Byles et al., 2013; Yue et al., 2014). Other mutations in the mTOR pathway have produced disparate results. However, using the principles described here for systematic investigation of mTOR pathway mutants will most likely resolve why rapamycin-treated macrophages and macrophages from Raptor, Rictor, and TSC1 mutants have diverse phenotypes (Ai et al., 2014; Byles et al., 2013; Festuccia et al., 2014; Weichhart et al., 2008). Some of

these mutants are summarized in Figure 1C. We contend that these and related mutants will be increasingly useful for defining activation states. Finally, it is important to recognize the effect of timing on altering the activation state. Several parameters can affect activation state across time; these include (1) removal of the stimulus, (2) enforcement of feedback and feed-forward signaling loops, including autocrine production of cytokines, and (3) epigenetic and/or developmental effects built into the life history of a macrophage (Ivashkiv, 2013; Lawrence and Natoli, 2011; Porta et al., 2009). This would go back to Mills's notion of an activated-to-healing transition.

## Perspectives and Conclusions

Understanding macrophage behavior is a keystone of deciphering disease pathogenesis. It is straightforward to isolate and propagate macrophages, facilitating their links to disease. By contrast, nomenclature and standardization issues are stunting progress because a lingua franca has yet to be established and accepted. We hope our attempts are a starting point to resolve some of the immediate issues. We emphasize that our goal is to initiate dialog rather than act as arbiters of language and experiment. In doing so, we hope scientists new to macrophage biology, established researchers, pharmaceutical companies, and regulatory agencies can appreciate the history of our field and the need for a common framework open to frequent revision.

### ACKNOWLEDGMENTS

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# Tumor-Associated Macrophages: From Mechanisms to Therapy

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**The tumor microenvironment is a complex ecology of cells that evolves with and provides support to tumor cells during the transition to malignancy. Among the innate and adaptive immune cells recruited to the tumor site, macrophages are particularly abundant and are present at all stages of tumor progression. Clinical studies and experimental mouse models indicate that these macrophages generally play a protumoral role. In the primary tumor, macrophages can stimulate angiogenesis and enhance tumor cell invasion, motility, and intravasation. During monocytes and/or metastasis, macrophages prime the premetastatic site and promote tumor cell extravasation, survival, and persistent growth. Macrophages are also immunosuppressive, preventing tumor cell attack by natural killer and T cells during tumor progression and after recovery from chemo- or immunotherapy. Therapeutic success in targeting these protumoral roles in preclinical models and in early clinical trials suggests that macrophages are attractive targets as part of combination therapy in cancer treatment.**

## Introduction

Tumors engage the immune system from their inception. Initially, this mainly involves cells of the innate system such as macrophages and mast cells with their prevalence dependent on tumor type. However, even early on, there is also engagement of cells of the acquired system—particularly T cells (Gajewski et al., 2013). Nevertheless, despite this adaptive response and data that suggest better prognosis with CD8$^+$ T cell infiltration in some cancers, there is little evidence of immune rejection in established tumors, arguing that the local tumor microenvironment is immunosuppressive (Gajewski et al., 2013). Macrophages are among the most abundant normal cells in the tumor microenvironment. Substantial evidence indicates that macrophages, rather than being tumoricidal as suggested after their activation in vitro (Fidler, 1988), adopt a protumoral phenotype in vivo both in the primary and metastatic sites (Biswas et al., 2013). Indeed in lung cancer, macrophages are polarized to a protumoral phenotype at the time of tumor initiation (Redente et al., 2010). These activities include suppression of T cell responses (Coussens et al., 2013; Qian and Pollard, 2010). In addition, macrophages promote many important features of tumor progression including angiogenesis, tumor cell invasion, motility, and intravasation as well as at the metastatic site, stimulation of tumor cell extravasation and persistent growth (Qian and Pollard, 2010). Each of these activities is delivered by an identifiable subpopulation of macrophages (Qian and Pollard, 2010). These data, together with experimental studies showing inhibition of tumor progression and metastasis by ablation of macrophages, argue that immune cell engagement by tumors is essential for their acquisition of a malignant phenotype. Consequently, this cell type might represent an important therapeutic target for cancer treatment. Here we discuss the function of diverse macrophage subpopulations and their dynamic interplay with tumor cells that confer these protumoral activities and give particular emphasis to the immunoregulatory role of these cells. We suggest that ablation of or redifferentiation of macrophages within the tumor microenvironment will become an important prong of combination therapies designed to cure cancer.

## Macrophages in the Primary Tumor: Cancer Initiation

Tumors acquire mutations in oncogenes or tumor-suppressor genes that permit them to progress to malignancy. Although most cancer research has focused upon these changes and most therapeutics are directed against these tumor cells, it is now apparent that the nonmalignant cells in the microenvironment evolve along with the tumor and provide essential support for their malignant phenotype (Joyce and Pollard, 2009). In fact both the systemic and local environment play a tumor-initiating role through the generation of a persistent inflammatory responses to a variety of stimuli (Balkwill and Mantovani, 2012). For example, obesity is associated with increased risk of many but not all cancers (Grivennikov et al., 2010) and is characterized by an enhanced systemic inflammatory response and locally, for example in the breast, to an increased number of inflammatory crown-like structures consisting of macrophage and adipocytes whose number strongly correlates with breast cancer risk (Howe et al., 2013). Similarly persistent inflammation referred to as "smoldering inflammation" caused by chronic infection with viruses such as Hepatitis B virus in liver, bacteria like *Helicobacter pylori* in the stomach, or due to continuous exposure to irritants such as asbestos in the lung is casually associated with cancer initiation (Balkwill et al., 2005; Brown et al., 2008). Furthermore, inflammatory conditions such as Crohn's disease dramatically increase the risk of colorectal cancer (Balkwill et al., 2005; Balkwill and Mantovani, 2012; Coussens and Werb, 2002; Grivennikov et al., 2010). Inflammation always has a substantial macrophage involvement through their production of molecules such as interleukin-6 (IL-6), tumor

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necrosis factor-α (TNF-α), and interferon-γ (IFN-γ) (Brown et al., 2008; Grivennikov et al., 2010). To support this correlative data between macrophage-mediated inflammation and cancer induction, Deng and colleagues found that genetic ablation of the anti-inflammatory transcription factor *Stat3* in macrophages results in a chronic inflammatory response in the colon that is sufficient to induce invasive adenocarcinoma (Deng et al., 2010). In addition, loss of the anti-inflammatory cytokine IL-10 that acts through STAT3 enhances carcinogen-induced tumorigenesis in the intestine (Jobin, 2013). Mechanistically, this inflammation can cause tumor initiation by creating a mutagenic microenvironment either directly through free radical generation or indirectly via alterations in the microbiome and barrier functions that allow access of genotoxic bacteria to the epithelial cells (Dedon and Tannenbaum, 2004; Jobin, 2013). Furthermore, Langerhans cells, a type of macrophage and/or dendritic cell (DC), can promote skin carcinogenesis by metabolic conversion of carcinogens to their activated mutagenic state (Modi et al., 2012). Macrophages also produce growth factors and/or cytokines that stimulate growth of epithelial cells that have spontaneously acquired cancer-associated mutations (Grivennikov et al., 2010). These mutations in turn might cause recruitment of inflammatory cells resulting in a vicious cycle that drives cancer progression (Balkwill and Mantovani, 2012; Qian and Pollard, 2010). Significant data therefore exists showing a causal role for macrophages in cancer initiation because of their central status as mediators of inflammation. However, it is unclear whether macrophages in some inflammatory situations can kill aberrant cells before they become tumorigenic and thus be antitumoral.

Macrophages involved in these cancer-initiating inflammatory responses are immune activated (Balkwill and Mantovani, 2012). However, once tumors are established, the macrophages are educated to become protumoral (Pollard, 2004; Qian and Pollard, 2010). During this transition from benign growth to an invasive cancer, the microenvironment appears to be dominated by cytokines and growth factors that cause a bias away from this T helper 1 (Th1)-like inflammatory response to create a Th2-type immune environment. This bias results in the polarization of macrophages by a number of factors including IL-4 synthesized by $CD4^+$ T cells and/or tumor cells (Coussens et al., 2013; Gocheva et al., 2010) and growth factors produced by tumor cells such as colony stimulating factor-1 CSF1 (Lin et al., 2002) and GM-CSF (Su et al., 2014). This Th2 environment is characterized by transforming growth factor-β1 (TGF-β1) and Arginase 1, as well as increased numbers of $CD4^+$ T cells (DeNardo et al., 2009). It could be argued therefore that for tumors to prosper they need to acquire mutations and/or epigenetic changes that result in the synthesis of such factors that repolarize resident macrophages or more likely recruit new monocytes (see below) so that they become differentiated into tumor-promoting cells and act as their handymen.

## Origins of Tumor-Associated Macrophages

It has recently been demonstrated that the historic description of adult resident tissue macrophages as being solely derived from bone marrow (BM) is not correct. In fact, most tissue macrophages although with some exceptions such as the intestine, arise from yolk sac progenitors. In contrast, macrophages involved in pathogen responses appear to come from circulating BM monocytes (Wynn et al., 2013). These different embryonic origins challenge the assumption that tumor-associated macrophages (TAMs) in the primary tumor originate from the BM. Evidence for different origins and responses has recently been shown in a mouse model of glioma with the presence of resident yolk-sac derived microglia and recruited BM-derived TAMs in the tumor microenvironment behaving differently to antimacrophage therapies based on inhibition of the lineage regulating growth factor CSF1 signaling. In this case, the recruited TAMs appear to survive in response to another macrophage lineage regulating growth factor, granulocyte-macrophage colony stimulating factor (GM-CSF) (Pyonteck et al., 2013). Nevertheless, several recent studies suggest that most TAM subpopulations arise from the $Ly6C^+$ population of circulating mouse monocytes in grafted tumors (Movahedi et al., 2010), primary mouse mammary tumors (Franklin et al., 2014), and in lung metastases (Qian et al., 2011). There has also been discussion about the origins of these monocytes with the suggestion that instead of coming directly from the BM they arise from extramedullary hematopoiesis, particularly in the spleen. It is claimed that this gives a reservoir of monocytes that allows rapid mobilization to the tumor (Cortez-Retamozo et al., 2012). However, recent elegant experiments using photoconvertible fluorescent lineage tracing of spleen and BM monocytes suggest that the splenic contribution is minor and that BM is the primary source of monocytes that generate TAMs at least in the Lewis Lung carcinoma syngeneic transplant model (Shand et al., 2014).

CSF1 is the major lineage regulator of most populations of macrophages whether they derive from the yolk sac or BM, but in addition, it is a chemotactic factor for macrophages (Chitu and Stanley, 2006). High CSF1 concentrations in tumors are associated with poor prognosis, and expression is often found at the leading edge of tumors (Laoui et al., 2011; Qian and Pollard, 2010). In endometrial cancer, its synthesis by tumor cells is an independent predictor of poor overall survival (Smith et al., 2013). Consistent with these clinical observations, deletion of CSF1 genetically from several models of cancer results in delayed initiation (cervical), progression (breast, pancreas), and metastasis (breast) associated with the loss of TAMs. Similarly, the use of neutralizing antibodies, small molecule inhibitors, or antisense RNA strategies to inhibit CSF1R signaling also affected tumor malignancy in both xenograft and GEM models of cancer (Abraham et al., 2010; Lin et al., 2001; Qian and Pollard, 2010; Quail and Joyce, 2013). Most of these strategies however, will have had systemic effects as well as local ones, making it difficult to determine whether the therapeutic effects are on the macrophage lineage and/or directly affecting the recruitment and survival of TAMs in the tumor. Direct evidence for CSF1 recruiting macrophages was provided in the mouse model of breast cancer caused by the mammary epithelial-restricted expression of the Polyoma Middle T oncoprotein (PyMT). In these studies, organ-autonomous gain-of-function experiments whereby CSF1 was expressed in the mammary epithelium resulted in local macrophage recruitment and an acceleration of tumorigenesis in wild-type mice and also the rescue of the loss-of *Csf1* function mutation that had resulted in delayed tumor progression and reduced metastasis (Lin and Pollard, 2007; Wyckoff et al., 2007). Genetic gain-of-function of VEGFA over

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a loss-of function of CSF1 in the PyMT mouse model also resulted in a dramatic recruitment of macrophages and a rescue of angiogenesis that resulted in an acceleration of tumor progression to malignancy (Lin et al., 2007). VEGFA also recruits macrophage progenitors that then differentiate to TAMs under IL-4 influence in a xenograft model of skin cancer (Linde et al., 2012). Loss of these VEGF-recruited TAMs inhibited tumor growth, angiogenesis, and invasion (Linde et al., 2012). These data indicate that CSF1 and VEGFA can be independent recruiters of macrophages to tumors in mouse models. This effect could be via recruitment of monocytes and/or through proliferation of recruited or resident cells. These growth factors probably act collaboratively with locally synthesized chemokines to reinforce recruitment or retention. For example, CCL2 acting via its receptor CCR2 is a direct mediator of monocyte recruitment to the primary tumor and to metastases in the PYMT model (Cortez-Retamozo et al., 2012; Franklin et al., 2014; Qian et al., 2011) even though this recruitment requires CSF1 (Lin et al., 2001; Qian et al., 2011). Another example of chemokine-mediated TAM recruitment collaborating with GM-CSF is CCL18 acting via its receptor PITPNM3 in human breast cancer models (Su et al., 2014). Furthermore CCL9 acting through its receptor, CCR1, recruits immature myeloid cells in colon cancer models (Kitamura et al., 2010; Kitamura et al., 2007). In each case, ablation of these chemokines resulted in loss of monocytes and/or TAMs and a resultant inhibition of malignancy with effects particularly on tumor cell invasion and occasionally growth.

The origins of macrophages in many cancers particularly in early stages is still uncertain and, further, this recruitment and differentiation is likely to be different and more complex in those cancers exposed to microbial products such as in colon cancer than those in sterile sites. Nevertheless, while the understanding the origins of TAMs and their methods of recruitment, retention, and differentiation is in its infancy, understanding the mechanisms offers the tantalizing possibility of therapies targeted to recruited subpopulations of protumoral macrophages that spares antitumoral ones and the resident macrophages associated with homeostasis.

## Protumoral Mechanisms of TAMs

Among the ways in which the microenvironmental support to tumors is the acquisition of a vasculature that provides oxygenation, as well as the nutrition and waste disposal required for growth above a certain size in a process often referred to as the "angiogenic switch" (Hanahan and Weinberg, 2011). CSF1-regulated macrophages regulate this switch in the PyMT model in part through production of VEGF (Lin and Pollard, 2007). In this model, macrophage-synthesized WNT7b targets vascular endothelial cells, stimulating their production of VEGF, resulting in the angiogenic switch (Yeo et al., 2014). Macrophages also promote neoangiogenesis in glioblastoma models (Du et al., 2008) Characterization of angiogenic TAMs show that they express TIE2. Genetic ablation of this population inhibits angiogenesis in a variety of models including glioblastoma and the PyMT model (De Palma et al., 2005). These Tie2$^+$ macrophages are often aligned along the abluminal surface of blood vessels through endothelial cell expression of the TIE2 ligand ANG2. Targeting ANG2 or Tie2 releases this macrophage-vessel association and inhibits angiogenesis in the PyMT and RIP1-TAG models of breast and pancreatic cancer (Mazzieri et al., 2011). Interestingly, CSF1 upregulates TIE2 on TAMs (Forget et al., 2014) indicating a link between CSF1, TIE2$^+$ macrophages, and the induction of the angiogenic switch. There are numerous additional reports of TAMs affecting angiogenesis in a wide range of models, mostly xenograft ones, and for further information the reader is referred to recent reviews on this topic (Coffelt et al., 2009; Nucera et al., 2011).

This population of TIE2$^+$ macrophages aligned along the vessels also promotes another phenotype of malignancy, tumor cell intravasation into the circulation (Wyckoff et al., 2007). In fact, macrophages promote directional tumor cell migration and invasion via a paracrine loop that consists of tumor-cell-synthesized CSF-1 and macrophage-derived epidermal growth factor (EGF) or EGF family ligands. This causes tumor cells and macrophages to rapidly stream along collagen fibers in lock-step, ending up in tumor cells clustering around blood vessels (Condeelis and Pollard, 2006; Wyckoff et al., 2007) (Figure 1). Upon arrival at the blood vessels, macrophages open up a gate for the tumor cells to escape. Macrophages also produce several other molecules that advance tumor cell invasion, including Osteonectin (also known as SPARC) that increases tumor cell-ECM interaction and thus migration (Sangaletti et al., 2008), Cathepsin proteases that remodel the matrix and release sequestered growth factors (Laoui et al., 2011; Quail and Joyce, 2013) and TGF-$\beta$ that promotes EMT of the invading tumor cells (Bonde et al., 2012). Thus these protumoral macrophages not only increase the invasive capacity of tumor cells but also increase the density of blood vessels giving a double whammy that increases the number of circulating tumor cells and thus metastasis (Figure 1). Consequently, ablation of TAMs for example by genetic depletion of their major growth factor, CSF-I, diminishes the number of circulating tumor cells and reduces metastasis (Wyckoff et al., 2007). Importantly, an anatomical structure consisting of macrophages, endothelial, and tumor cells named the tumor microenvironment for metastasis (TMEM) is recognizable in histological sections and is predictive of metastatic potential in primary human breast cancers (Rohan et al., 2014).

Once the barrier of the angiogenic switch has been surmounted, tumors rapidly become invasive and thus characterized as malignant. This correlates with enhanced engagement of the acquired immune system indicating antigen recognition probably because the immune system has access to the products of mutated genes and/or recognizes tissue damage caused by invasion (Coussens and Pollard, 2011; Gajewski et al., 2013). However, despite data that suggest better prognosis with early T cell infiltration of some cancers, successful tumors that progress to kill the patients clearly are not rejected. This immunosuppression is at least in part mediated by macrophages or their progenitors (Figure 2) but also involves regulatory T cells, as well as tumor-cell-mediated immune evasion (Coussens and Pollard, 2011; Gajewski et al., 2013; Movahedi et al., 2010). In this context and importantly, the combination of macrophages and a high ratio of CD4$^+$ regulatory versus CD8$^+$ T cells in human breast cancer is predictive of poorer survival (Ruffell et al., 2011).

Macrophages and DCs express classical and nonclassical MHC-I molecules, and this is normally associated with the presentation of antigens to T cells. However macrophages can also express HLA molecules such as HLA-C (classical), HLA-E,

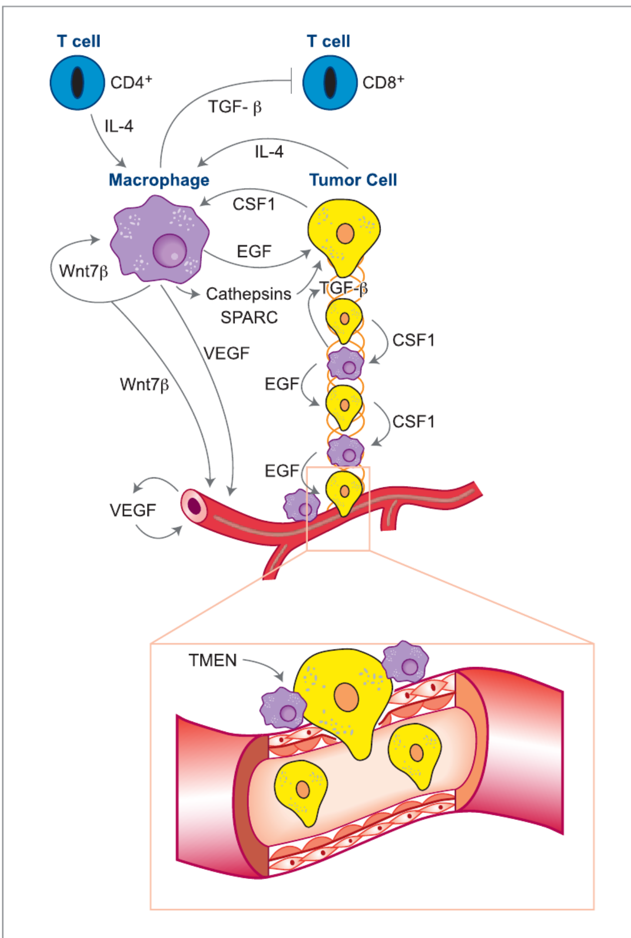


**Figure 1. Tumor-Associated Macrophages in the Primary Tumor Promote Malignancy**

In the primary tumor, microenvironment macrophages under the influence of IL-4 produced by $CD4^+$ T cells and tumors and WNT7b promote tumor cell invasion. This invasion is mediated via a paracrine loop involving tumor-synthesized CSF1 and macrophage-produced EGF that drives migration of tumor cells in lock-step with macrophages along collagen fibers that act as highways toward blood vessels. This process also requires TGFβ that drives an epithelial-mesenchymal transition (EMT) in the tumor cells that promotes migration and matrix remodeling via Cathepsins and matrix adhesion of tumor cells via SPARC. This streaming of tumor cells results in their pileup on the vessels where macrophages promote their intravasation into the circulation through a structure named the "Tumor Microenvironment of Metastasis" (TMEN). In addition to effect on tumor cell migration and invasion, $TIE2^+$ macrophages produce VEGF and WNT7b that stimulates angiogenesis in the tumor. Thus, there is an additive effect caused by macrophages of increased migration of tumor cells toward vessels and increased vascular targets that results in a large number of circulating tumor cells and thus increased malignancy. Macrophages also suppress cytotoxic T cell responses through the mechanisms described in Figure 2.

and HLA-G (nonclassical) membrane bound or soluble forms that can inhibit the activation of natural killer (NK) cells and a subsets of activated T cells upon their ligation to killer cell immunoglobulin like receptor CD94 (also known as NKG2) (Borrego et al., 1998) or the inhibitory leukocyte immunoglobulin-like receptors LIT-2 (HLA-E and HLA-G respectively). While some tumors express HLA-G (membrane bound or soluble) as part of their evasion mechanisms from NK and T cell lysis, others do not. These HLA-G negative tumors might rely on myeloid cell HLA-G expression as an effector of inhibitory mechanisms. An example of this is in glioblastoma and neuroblastoma where high concentrations of soluble HLA-G can be found in patient's serum. In this case, microglia and circulating monocytes are the source of this secreted HLA-G (Kren et al., 2010; Morandi et al., 2007). The inhibition of effector $CD8^+$ T cell activation in the lymph nodes by HLA-G expressing monocytes, macrophages, or DCs might also be indirect. For example, it has been shown that INF-γ secretion by activated NK cells that have migrated to the lymph node is an important mediator of $CD8^+$ T cell activation and that HLA-G and HLA-E inhibits this NK cells migration and INF-γ secretion (Kelly et al., 2002). In addition, HLA-G-transfected APCs can inhibit $CD4^+$ T cell activation and induce immunosuppressive differentiation in vitro (LeMaoult et al., 2004). Moreover, trogocytosis of HLA-G by activated $CD4^+$ and $CD8^+$ T cells during interaction with HLA-$G^+$ APCs leads to rapid generation of T cell's suppressor functions (LeMaoult et al., 2007). Monocytes and macrophages can themselves express members of the LILRB inhibitory receptors family (LIT-2 and LIT-4) that upon binding HLA-G causes them to acquire immunosuppressive phenotype through the secretion of IL-10 and TGF-β1 (Brown et al., 2004; McIntire et al., 2004). However, the expression of inhibitory receptors and their HLA ligands by TAMs and their effect on TAMs immunosuppressive function are yet to be determined.

In addition to these MHC molecules, macrophages express the ligands of the inhibitory receptors programmed cell death protein 1 (PD-1) and cytotoxic T-lymphocyte antigen 4 (CTLA-4). These inhibitory ligands are normally upregulated in activated immune effector cells such as T cells, B cells, and NK T cells as part of a safety mechanism that controls the intensity of the immune response and as part of inflammation resolution. Activation of PD-1 and CTLA-4 by their ligands (PD-L1, PD-L2, and B7-1 [D80], B7-1 [CD86], respectively) directly inhibits TCR and BCR signaling. This activation also inhibits T cell cytotoxic function, regulates their cell cycle, and inhibits their activation as CTLA4 competes with CD28 (costimulatory) binding. PD-L1 and PD-L2 are differentially expressed, with PD-L1 constitutively expressed by immune cells including T cells, B cells, macrophages, DCs, nonhematopoietic cells, and cancer cells. In contrast, PD-L2 expression is limited to antigen-presenting cells (APCs). Its expression is induced in monocytes and macrophages by CSF1, IL-4, and INF-γ (Loke and Allison, 2003). Both PD-L1 and L2 are regulated in TAMs and myeloid-derived suppressor cells (See below—MDSC) (Belai et al., 2014; Duraiswamy et al., 2013). Recently, Noman et al. showed that MDSCs and TAMs in hypoxic tumor regions upregulate the expression of PD-L1 as a consequence of HIF-1α signaling (Noman et al., 2014). Hypoxia acting via hypoxia inducible factor 1- α (HIF-1α) also induces T cell suppression by TAMS although the mechanism is unknown (Doedens et al., 2010). It has also been shown that monocytes from blood of glioblastoma patients express higher amounts of PD-L1 compared to healthy donors and that glioblastoma-cell-conditioned medium can upregulate PD-L1 expression in monocytes from healthy donors (Bloch et al., 2013). Similarly, monocytes from patients with hepatocellular carcinoma express PD-L1 that contributes to human tumor xenograft growth in vivo, while the blocking of PD-L1 reverses this effect (Kuang et al., 2009). The identification of B7-1

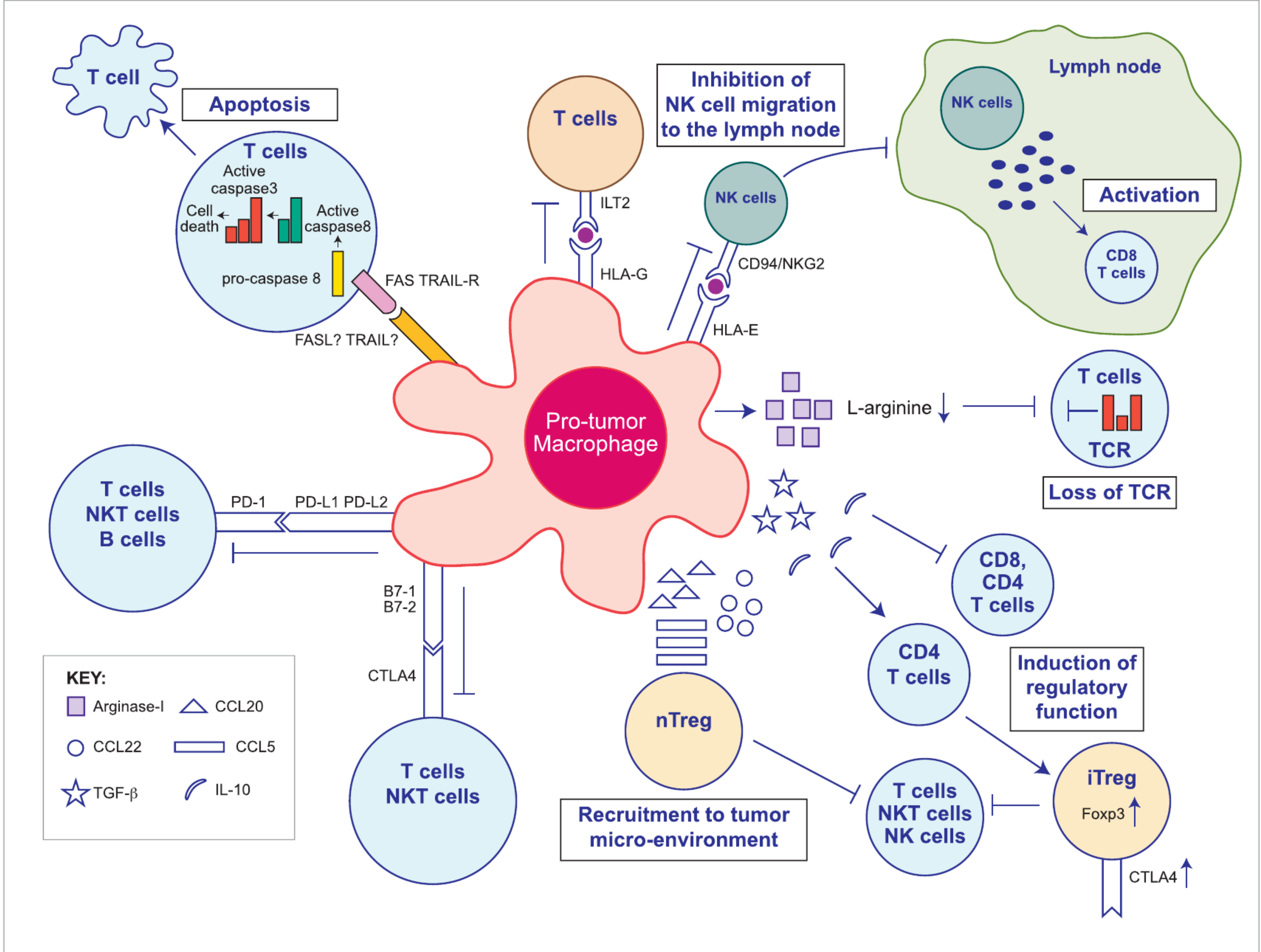


**Figure 2. Protumor Macrophage Mechanisms of Effector Cells Inhibition**

TAMs express an array of effector molecules that inhibit the antitumor immune responses; this includes cell surface receptors, cytokines, chemokines, and enzymes. Inhibition of immune responses by direct cell-to cell-contact is based on the interaction of TAMs receptors ligands with their counterpart death and/or inhibitory receptors expressed by the target immune effector cells. TAMs express the ligand receptors for PD-1 and CTLA-4 that upon activation suppress cytotoxic functions of T cell, NK T cells and NK cells. TAMs also express the ligand for the death receptors FAS and TRAIL that triggers caspase-dependent cell death (apoptosis) in target cells. TAMs also express the nonclassical HLA-G that inhibits T cell function through interaction with the costimulatory signal of T cells ILT2 and HLA-E that inhibit NK cells through CD94 (also known as NKG2). TAMs secrete the cytokines IL-10 and TGF-β that inhibit T cells effector functions and induce regulatory functions and chemokines CCL5, CCL20, and CCL22 that recruit nTreg cells. TAMs secrete Arginase I that inhibit TCR ζ chain re-expression in activated T cells by the depletion of L-arginine.

(CD80) as an additional inhibitory receptor for PD-L1 suggested the possibility of reverse signaling. Indeed, the culture of bone-marrow-derived DCs with anti PD-L1 antibody inhibits their activation, induces IL-10 expression, and suppresses cocultured $CD4^+$ T cell activation (Kuipers et al., 2006). However, it is challenging to determine the specific impact of TAM PD-1 ligand expression on effector cells inhibition in vivo since numerous cells in the tumor microenvironment express PD-L1 (Greaves and Gribben, 2013). Thus it is yet to be discovered whether the signals from PD-1 and PD-1 ligands contribute to TAMs immunosuppressive phenotype in vivo.

The CTLA-4 ligands B7-1 and B7-2 are differentially expressed by APCs. B7-2 is constitutively expressed in low amounts and it is upregulated during activation, whereas B7-1 is expressed only upon APC activation. B7-1 and B7-2 are also the ligands of the T cell costimulatory CD28; however, they bind with higher affinity to the inhibitory receptor CTLA-4. This differential affinity suggests direct competition for the ligand binding as a mechanism to induce suppression (Greenwald et al., 2002). TAM expression of B7-1 and B7-2 was shown to be dependent on their activation phenotype; both molecules are expressed by proinflammatory macrophages and are downregulated by anti-inflammatory macrophages (Ding et al., 1993; Flores Villanueva et al., 1994; Kennedy et al., 2013). However, the specific inhibitory effect mediated by TAMs in vivo is still unknown and as with PD1 ligands, CTLA-4 ligands are expressed on some human tumors and other immune cells (Greaves and Gribben, 2013; Tamura et al., 2005; Tirapu et al., 2006). Finally, evidence from studies on the DC-T cell immunological synapse suggests that interaction of CTLA-4 with B7 ligands not only signals for the

inhibition of T cells but also induces a DCs inhibitory phenotype (Butte et al., 2007; Mellor et al., 2004). Additional investigation is needed to determine whether such reverse signaling in TAMs is associated with a proinflammatory to anti-inflammatory switch.

B7-H4 is a relatively new member of the B7 superfamily that was implicated with suppression of T cells activation and is expressed on TAMs. The coreceptor for B7-H4 is currently unknown. In human ovarian cancer, TAMs expressing B7-H4 suppress the activation of antigen-specific T cells. Moreover, the inhibition of B7-H4 restores the stimulating function of TAMs and contributes to tumor regression (Kryczek et al., 2006). In addition, the expression of B7-H4 on TAMs was found to correlate with clinical stage of lung carcinoma and gastric cancer (Chen et al., 2012; Matsunaga et al., 2011).

TAMs also secrete an array of cytokines, chemokines, and enzymes that can suppress $CD4^+$ and $CD8^+$ T cells effector function directly or indirectly by recruitment of natural regulatory T (nTreg) cells to the tumor microenvironment, as well as by inducing the $CD4^+$ regulatory fraction (iTreg) cells and sustaining their survival. Chemokine receptors CCR4, CCR5, CCR6, and CCR10 expressed by nTreg cells are involved in their migration into the tumor microenvironment (Adeegbe and Nishikawa, 2013). Curiel at al. demonstrated that CCL22 secreted by TAMs recruits $CCR4^+$ nTreg cells to human ovarian carcinoma tumors and foster tumor growth (Curiel et al., 2004). In colorectal cancer, CCL20 secreted by TAMs recruit $CCR6^+$ nTreg cells (Liu et al., 2011). In addition, CCL3, CCL4, and CCL5 expressing myeloid-MDSC from a melanoma mouse model recruited nTreg cells through CCR5 signaling. TAMs in this mouse model expressed some of the CCR5 ligands (Schlecker et al., 2012). In addition, CCL5 is expressed by TAMs in other mouse tumor models (Biswas et al., 2006; Liou et al., 2013). The induction of iTreg cells in the tumor microenvironment is a complex process that is not completely understood. Nevertheless, TGF-$\beta$ and IL-10 induce regulatory functions by the upregulation of the pivotal regulatory transcription factor, Foxp3, in $CD4^+$ T cells (Adeegbe and Nishikawa, 2013). TAMs have been found to express IL-10 and TGF-$\beta$ in different pathological scenarios including human and mouse cancers (Pollard, 2004). Macrophages in the intestinal immune system were shown to induce iTreg cells by the secretion of IL-10 and TGF-$\beta$ (Denning et al., 2007). Savage and coworkers investigated the ability of human macrophages to induce regulatory T cells and showed that IL-10 expressing anti-inflammatory macrophages but not proinflammatory macrophages are responsible for induction of iTreg cells (Savage et al., 2008). In addition, TAMs isolated from human renal cell carcinoma induce the expression of CTLA4 and Foxp3 in $CD4^+$ T cells (Daurkin et al., 2011). TGF-$\beta$ and IL-10 are also involved in direct modulation of T cells functions. TGF-$\beta$ inhibits cytotoxic T lymphocyte, Th1, and Th2 $CD4^+$ T cells (Oh and Li, 2013), whereas IL-10 inhibits Th1 and Th2 $CD4^+$ T cell helper functions (Ng et al., 2013).

TAMs can also suppress T cell activity by the depletion of L-arginine in the tumor microenvironment. Nitric-oxide synthase (NOS) and arginase I (ARGI) are L-arginine processing enzymes that were shown to be differentially secreted by macrophages as a function of their activation state (proinflammatory and anti-inflammatory, respectively) (Biswas and Mantovani, 2010). TAMs secrete ARGI into the microenvironment in different human cancers and mouse cancer models (Doedens et al., 2010; Sharda et al., 2011). ARGI metabolizes L-arginine to urea and L-ornithine, hence depleting it from the tumor microenvironment. L-arginine is necessary for T cells function, and its depletion inhibits the re-expression of the CD3 $\zeta$ chain after internalization caused by antigen stimulation and TCR signaling (Rodriguez et al., 2003, 2004). In fact, the expression of ARGI is considered to be the hallmark of anti-inflammatory macrophages, so-called M2 macrophages (see below), in mice and a marker of many TAM populations (Sica and Mantovani, 2012).

In addition to bona fide macrophages, there is extensive literature on a group of cells collectively called myeloid-derived suppressor cells (MDSCs) that accumulate in the spleen and tumors during malignant progression. These cells in ex vivo CTL assays can suppress T cell responses (Gabrilovich et al., 2012). Furthermore, in vivo MDSCs block DC maturation at the invasive edge of tumors (Gabrilovich et al., 2012). In mice, MDSCs are defined as being $CD11b^+$ and $Gr1^+$. These markers define both monocytic and granulocytic cells (both Ly6C and Ly6G antigens are recognized by the anti-GR1 antibody). The consensus view is that MDSCs consist of a mixed population (Gabrilovich et al., 2012). The majority of MDSCs being $Ly6G^+$ immature granulocytes will not be further discussed in this review, and they have been well reviewed recently (Gabrilovich et al., 2012). The minority population is $Ly6C^+$ $Ly6G^-$, suggesting they are monocytic in origin and thus have been termed monocytic MDSCs (M-MDSCs). These M-MDSCs have greater immunosuppressive potency than the granulocytic ones and are further defined as $F4/80^+$ a marker also found on inflammatory monocytes (Gabrilovich and Nagaraj, 2009; Gabrilovich et al., 2012). It has long been recognized that monocytes can be immunosuppressive, but it is unclear in cancer whether such cells accumulate in excessive numbers as a transient to mature macrophages or even granulocytes or whether M-MDSCs represent a monocyte-derived terminal cell type. These cells are $MHC^{lo}$ and costimulatory molecule low or negative suggesting they do not directly induce anti-T cell activity. Instead, they highly express TGF-$\beta$ and ARG1, which contribute to nonspecific immune suppression (Gabrilovich and Nagaraj, 2009; Gabrilovich et al., 2012; Yang et al., 2008). Despite the obvious distinction between monocytic and granulocytic subtypes, the usual lack of discrimination between these groups in experiments and the lack of unique markers on M-MDSCs precluding specific ablation of these cells makes the specific in vivo function M-MDSCs in immunosuppression hard to define. Consequently, they will not be further discussed here, and there are excellent reviews defining their functions and classification elsewhere (Gabrilovich and Nagaraj, 2009; Gabrilovich et al., 2012; Montero et al., 2012). These studies with M-MDSCs also calls into question the cell type that can present antigens to the incoming T cells in tumors and thus cause recognition of tumors at early stages. Krummel and colleagues developed a system to detect OVA antigen presentation in the PyMT mouse model and using this model defined an APC that was $Cd11c^+$ $F4/80^+$ in the tumor margin that could be either a TAM or DC, but not an M-MDSC. However, this antigen presentation by this TAM/DC population to T cells while present was abortive (Engelhardt et al., 2012). In fact, these DC-like cells and $CD8^+$ T cells appear to be "trapped" in the tumor margin, even in xenograft models in the face of

chemotherapy, suggesting an immunosuppressive mechanism (Boissonnas et al., 2013; Engelhardt et al., 2012).

Altogether, TAM expression of cell surface receptors, secreted cytokines, chemokines, and enzymes suggest they have an important role in recruitment and activation of Treg cells and the suppression of effector cells in the tumor microenvironment (Figure 2). Nevertheless, the dominant mechanisms in vivo even in simple xenograft mouse models are unknown. This failure is not surprising given that the exact myeloid cell type(s) that engages the acquired immune system is ill-defined and because most experiments use homogeneous, transplanted tumor models that are inherently immunogenic due to upregulation of latent retroviruses and other epigenetic changes caused by cell culture. A better definition of these immunosuppressive mechanisms needs complex evolving autochthonous and thus "self" models in which immune response can be tracked as the tumor evolves. These models will allow specific definition of antigen presentation and the means whereby cells of the monocyte and/or macrophage lineage suppresses this response.

## Macrophages at the Metastatic Site

Once tumor cells escape from the primary site, they passage through the lymphatic and/or circulatory system and ultimately a few establish at distant sites to give metastases. These sites vary according to cancer; for example, in the breast they primarily go to bone then lung and brain. It is essential to understand this process because 95% of deaths from solid tumors in the developed world are due to metastasis. Monocytes and/or macrophages are essential metastasis promoters acting both to prepare sites and also to promote the extravasation, survival, and persistent growth of metastatic cells (Joyce and Pollard, 2009; Qian et al., 2009). Even before tumor cells arrive, the frequency and site specificity of metastatic growth can be influenced by primary tumors through the formation of sites that enhance homing of circulating tumor cells known as premetastatic niches (Psaila and Lyden, 2009). These niches are populated by $Cd11b^{+}$ $VEGFR1^{+}$ myeloid cells whose recruitment is promoted by Lysyl Oxidase and S110A and whose ablation inhibits the formation of these sites (Psaila and Lyden, 2009). Several other factors have been shown to be important for premetastatic niche formation, most recently, tumor derived exosomes that program the myeloid cells to be protumoral and proangiogenic through activation of the receptor tyrosine kinase MET (Peinado et al., 2012). Exosomes derived from different melanoma strains can also redirect metastatic cell target tropisms from one tissue to another (Peinado et al., 2011). The formation of the niche is also dependent on platelets that presumably deposit fibrin in the target tissues that attract myeloid cells. Consequently, premetastatic niche formation is blocked by anticoagulants (Gil-Bernabé et al., 2012).

Studies of lung metastasis show that upon their arrival at the target site, tumor cells together with associated platelets recruited via their expression of tissue factor form microclots and arrest in the target tissue vessels (Gil-Bernabé et al., 2012). This arrest enables CCL2 synthesized by the tumor cells to generate a chemoattractive gradient that recruits Ly6C monocytes through their expression of the CCL2 receptor, CCR2 (Cortez-Retamozo et al., 2012; Qian et al., 2011). In addition, clotting upregulates VECM1 on endothelial cells that promote myeloid cell attachment and thus their recruitment (Ferjančič et al., 2013). These recruited monocytes enhance extravasation of tumor cells in part by expression of VEGF, which cause vascular permeability. Consistent with this is that inhibition of CCR2 signaling blocks tumor cell extravasation and inhibits metastasis (Qian et al., 2011). These recruited monocytes differentiate into $CCR2^{+}$, $VEGFR1^{+}$ $Ly6C^{-}$ $F4/80^{+}$ metastasis-associated macrophages (MAMs) (Figure 3). Ablation of this MAM population using genetic and chemical means inhibits metastatic seeding and persistent growth, the latter effect being evident even after the metastases have been established (Qian et al., 2009, 2011). Mechanistically, this is via the maintenance of CSF1 signaling in macrophages and through the enhancement of tumor cell survival (Qian et al., 2009) via engagement of VCAM1 expressed upon the tumor cells that generates an AKT mediated antiapoptotic signal (Chen et al., 2011). Myeloid cells also promote mesenchymal-to-epithelial transition (MET) and tumor growth by inhibiting TGF-$\beta$ signaling in these epithelial metastatic cells (Gao et al., 2012).

Many cancers also metastasize to the bone such as breast and prostate. In this process, another cell from the mononuclear phagocytic lineage, the osteoclast, plays an important role. This cell is lineage regulated by CSF1 followed by differentiation and proliferation in response to RANK ligand that lead to the multinuclear functional osteoclast. These cells are often activated by metastatic cells to degrade bone and release growth factors resulting in a vicious cycle. Because this process is dependent on a different cell type to classical macrophages it will not be reviewed further here, but readers are referred to recent reviews that discuss the process and therapeutic opportunities (Camacho and Pienta, 2014; Esposito and Kang, 2014; Mundy, 2002).

## Macrophages as Therapeutic Targets

Macrophages are exceptionally diverse in their functions reflecting the different origins, local environment, and responses to challenges (Wynn et al., 2013). Consideration of macrophage function in immunity let to the proposal of two classes of macrophages: (1) the activated macrophages responding to IFN-$\gamma$, TNF-$\alpha$, and Toll-like receptor 4 (TLR4) activation capable of killing pathogens through mechanisms such as iNOS, and (2) alternatively activated macrophages responding to IL-4 and IL-13 involved in antiparasitic immunity and in asthma (Gordon, 2003). The original in vitro characterizations were extended to in vivo models by Mills and coworkers who called these states M1 (activated) and M2 (alternatively activated) (Mills, 2012). These descriptions were captured to suggest that TAMs could be either tumor killing (M1) or tumor promoting (M2) (Sica et al., 2008). However, although these extreme forms of polarization are seductive, the already described multiple phenotypes of TAMs activity engaged in different biological functions in the tumor suggested such definitions are limiting and probably do not exist in the complex tumor microenvironment (Qian and Pollard, 2010). In fact, different macrophages associated with diverse phenotypes and particular to different tumor types argues for a plethora of different populations. Furthermore, in most large-scale transcriptome analysis, macrophages have a mixed phenotype expressing both M1 and M2 markers (Qian and Pollard, 2010). In addition, there have been no definitive experiments where unique ablation of macrophages designated as

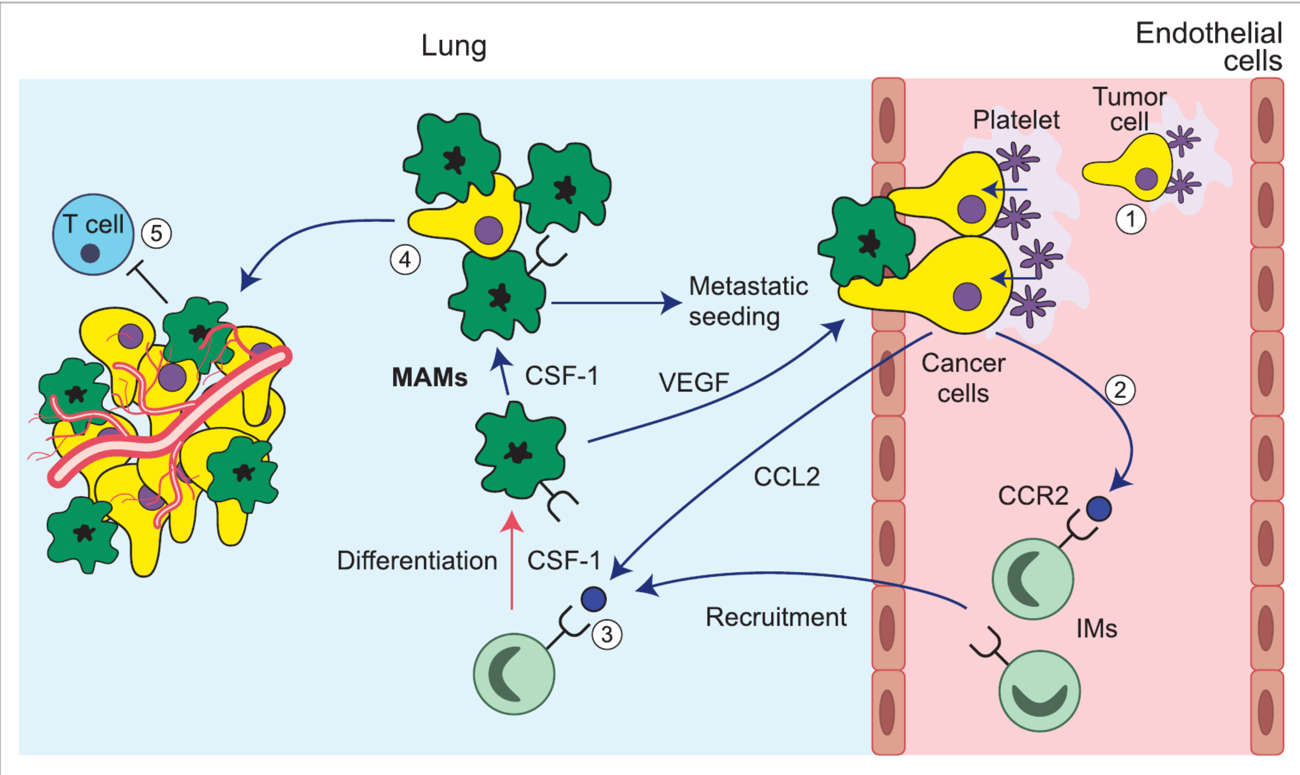


**Figure 3. Macrophages Promote Metastasis**
Arrest of tumor cells in the vasculature of target organs through the formation of microclots (1) results in CCL2-mediated recruitment of CCR2-expressing circulating inflammatory monocytes (2). These monocytes differentiate into metastasis-associated macrophages (MAMs) that mediate tumor cell extravasation via VEGF that increases vascular permeability (3). MAMS under the influence of CSF-1 further promote tumor cell survival (4) and persistent growth associated by angiogenesis and might also prevent T cell cytotoxicity (5).

M1 or M2 has been achieved and thus their role in tumor promotion is unknown. In contrast, ablation of specific subpopulations such as TIE2$^{+}$ or MAMs can be demonstrated to affect specific activities such as angiogenesis or metastatic seeding. We have always proposed that subpopulations should be defined by biology rather than enforcing preexisting nomenclature upon function (Qian and Pollard, 2010). Thus despite ongoing discussion on nomenclature, the clinical challenge remains to block macrophage trophic phenotypes together with their immunosuppressive behaviors and enhance their activation and antitumoral activities. Several recent studies suggest that such an approach is feasible and therapeutic (Coussens et al., 2013; De Palma and Lewis, 2013). The major strategy so far is based upon genetic experiments whereby inhibition of CSF1 signaling in PYMT models inhibits tumor progression and metastasis (Lin et al., 2001) and uses anti-CSF1 receptor-neutralizing antibodies or small-molecule inhibitors to interfere with this pathway (Coussens et al., 2013). Strikingly inhibition of CSF1R in glioblastoma mouse models results in a dramatic reduction in tumor volume and long-term survival of the mice. This CSF1R inhibition did not kill the TAMs but caused them to repolarize to a state regulated by GM-CSF that has been suggested to be antitumoral (Quail and Joyce, 2013). Similar results can be seen in cervical and breast cancer models (Strachan et al., 2013). Small-molecule inhibitors to CSF1R also have been shown to deplete some populations of TAMs and in established tumors to dramatically enhance responses to chemotherapy. This effect is at least in part due to the removal of macrophage-mediated immunosuppression during the tumor recovery period (DeNardo et al., 2011; Mitchem et al., 2013). These effects seem not to be restricted to chemotherapy because TIE$^{+}$ positive TAMs limit the efficacy of antivascular reagents, and their ablation strongly increases the therapeutic efficacy of these agents (Priceman et al., 2010; Welford et al., 2011). In other models, M-MDSCs modulate the efficacy of antivascular therapies (Shojaei et al., 2007). Furthermore, low-dose irradiation of tumors programs macrophages to an activated state that orchestrate T cell immunotherapy (Klug et al., 2013). Macrophages also enhance the therapeutic efficacy of monoclonal antibodies (De Palma and Lewis, 2013). In addition, the chemotherapeutic agent Trabectedin directly kills monocytes and/or macrophages and has therapeutic efficacy against tumors in mouse models (Germano et al., 2013). Similarly, amphotericin B enhances macrophage-mediated inhibition of glioma tumor-initiating cells (Sarkar et al., 2014). Most importantly a recent clinical trial reports objective clinical responses in diffuse-type giant cell tumors that overexpress CSF1 by using a neutralizing antibody to the CSF1R in a single-molecule approach, and this response is characterized by an increase in the CD8$^{+}$/CD4$^{+}$ T cell ratio (Ries et al., 2014). This dramatic result together with the other examples given

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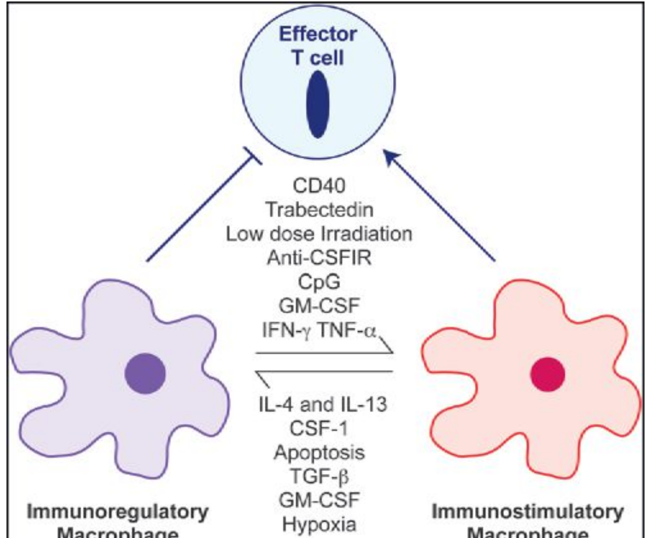


**Figure 4. Reprogramming Macrophages to Be Antitumoral**
Macrophages in the tumor in general are immunoregulatory and suppress immune responses to tumor-derived antigens. However, in some circumstances particularly with appropriate therapeutic interventions, macrophages can be antitumoral by direct tumor cell killing, the removal of vital support such as inhibition of angiogenesis or by the activation of T cells. This differential polarization is under the control of many stimuli (as shown) that alters the differentiated state of the macrophages. Some factors such as GM-CSF act in protumoral or antitumoral fashion dependent on context (Pyonteck et al., 2013; Su et al., 2014). Therapeutic interventions can repolarize these cells to become immunostimulatory macrophages that on their own can cause tumor regression or that enhance the activity of chemovascular, antivascular, or immunotherapies. References to these polarizing agents can be found in (De Palma and Lewis, 2013; Sica and Mantovani, 2012).

above strongly support targeting the destruction or redifferentiation of macrophages as an important part of combinatorial therapies in human cancer patients.

## Perspectives

We have argued previously that TAMs recapitulate the roles of macrophages in tissue development and repair that is coupled with suppression of immune responses to the tissue damage caused by invading epithelial structures (Pollard, 2004). Gene profiling of TAMs supports this hypothesis while at the same time defines many subpopulations with different protumoral functions (Qian and Pollard, 2010). The preclinical experimental data described above suggest that targeting TAMs either by ablation or repolarization can be beneficial in cancer therapy. This is an attractive approach because these diploid normal cells do not have the enhanced mutation rates of tumor cells that inevitably lead to drug resistance. Indeed, several clinical trials are underway targeting CSF1R signaling as a means of removing macrophage protumoral support, and the most recent of these studies reports clinical efficacy (Ries et al., 2014). However, these pan-macrophage therapeutic approaches will have systemic toxicities as they target all macrophages. As we move forward, the realization of diverse origins of macrophages with recruited ones being different from resident ones (Wynn et al., 2013) suggest that more sophisticated therapies that only target TAMs or MAMs might be possible (Modi et al., 2012). Importantly, a definition of macrophage subpopulations in different human cancers and in different subtypes of cancer in a particular tissue is needed to advance these options. Another exciting therapeutic approach is to enhance chemotherapy or immunotherapy by removing the immunosuppressive activities of macrophages. In this arena, preclinical data (Figure 4) indicate several strategies that can be combined to improve the already encouraging antitumoral clinical results obtained by inhibiting regulatory T cell mechanisms through the use of neutralizing anti-PD1, -PD-L1, or -CTLA4 antibodies (Page et al., 2014). Further definition of the regulation of immunoregulatory mechanisms in macrophages should allow the development of a whole new range of therapeutics.

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# Development, Differentiation, and Diversity of Innate Lymphoid Cells

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**Recent years have witnessed the discovery of an unprecedented complexity in innate lymphocyte lineages, now collectively referred to as innate lymphoid cells (ILCs). ILCs are preferentially located at barrier surfaces and are important for protection against pathogens and for the maintenance of organ homeostasis. Inappropriate activation of ILCs has been linked to the pathogenesis of inflammatory and autoimmune disorders. Recent evidence suggests that ILCs can be grouped into two separate lineages, cytotoxic ILCs represented by conventional natural killer (cNK) cells and cytokine-producing helper-like ILCs (i.e., ILC1s, ILC2s, ILC3s). We will focus here on current work in humans and mice that has identified core transcriptional circuitry required for the commitment of lymphoid progenitors to the ILC lineage. The striking similarities in transcriptional control of ILC and T cell lineages reveal important insights into the evolution of transcriptional programs required to protect multicellular organisms against infections and to fortify barrier surfaces.**

## Introduction

The last years have witnessed an unprecedented change in our understanding of innate lymphocyte lineages. It was previously believed that innate lymphocytes were represented by a single lymphoid lineage, namely natural killer (NK) cells, that, in many aspects, resembles cytotoxic T cells. However, it has become apparent that additional innate lymphocyte subsets exist that use transcriptional programs and display functions distinct from conventional NK (cNK) cells. All innate lymphocytes including cNK cells are now referred to as ILCs. In addition to cNK cells, three additional groups of ILCs are now being discriminated, ILC1s, ILC2s, and ILC3s. Strikingly, the transcriptional and effector programs of the various ILC populations resemble those of T helper subsets, suggesting that the underlying transcriptional circuitry is evolutionarily more ancient than previously appreciated (Tanriver and Diefenbach, 2014). Here, we will discuss our current view of developmental and transcriptional programs common to all ILC lineages and those required for specification of distinct ILC populations. These recent data provide a framework for our current view of two principal ILC lineages, cytotoxic or killer ILCs (i.e., cNK cells) and helper-like ILCs (i.e., ILC1s, ILC2s, ILC3s) (Figure 1). We will put a focus on recent progress in dissecting the ILC1 lineage and on common transcriptional programs controlling ILC specification.

## Identification of ILC1s: More Than Just NK Cells?

ILC1s have only recently been better characterized and are now classified as an ILC group distinct of cNK cells that expresses and requires the transcription factor T-bet for lineage specification (Bernink et al., 2013; Daussy et al., 2014; Fuchs et al., 2013; Klose et al., 2014) (Figure 1; Tables 1, 2, and 3). The identification of bona fide ILC1s in mice was obscured by the fact that ILC1s were found to express NK cell receptors such as natural killer cell p46-related protein (NKp46) and NK1.1, which have served as an operative definition of NK cells. Early on, Di Santo and colleagues noticed that thymic NK cells in mice have a distinct phenotype; they are less cytotoxic but secrete more interferon-$\gamma$ (IFN-$\gamma$) than splenic NK cells do (Table 2) (Vosshenrich et al., 2006). They proposed that the dichotomy between splenic NK cells and thymic NK cells in mice might parallel the division of CD56$^{lo}$ and CD56$^{hi}$ NK cell subsets in human blood (Caligiuri, 2008) (Table 1). Recent data from organ-resident "NK cells" indicated that the population of NKp46$^{+}$NK1.1$^{+}$ cells might in fact be heterogeneous and composed of various ILC lineages (Daussy et al., 2014; Fuchs et al., 2013; Gordon et al., 2012; Klose et al., 2014; Vosshenrich et al., 2006). Indeed, liver-resident NKp46$^{+}$NK1.1$^{+}$ cells can be separated into a VLA2 (CD49b)$^{+}$ population expressing the T-box transcription factors Eomes and T-bet and into a VLA2$^{-}$TRAIL$^{+}$IL-7R$\alpha^{lo}$ population that expressed T-bet, but not Eomes (Daussy et al., 2014; Gordon et al., 2012; Peng et al., 2013; Takeda et al., 2001). VLA2$^{+}$TRAIL$^{-}$ cells likely represent cNK cells in that they are cytotoxic, require Eomes for development, and express class I major histocompatibility complex (MHC)-specific inhibitory receptors (i.e., Ly49 receptors, NKG2A). VLA2$^{-}$TRAIL$^{+}$NKp46$^{+}$NK1.1$^{+}$ cells did not express Eomes but strictly required T-bet for their development (Gordon et al., 2012). It has been controversial whether VLA2$^{-}$ TRAIL$^{+}$ cells constitute immature cNK cells (Gordon et al., 2012; Takeda et al., 2005) or a distinct ILC lineage (Daussy et al., 2014; Peng et al., 2013; Sojka et al., 2014). In the intestine,

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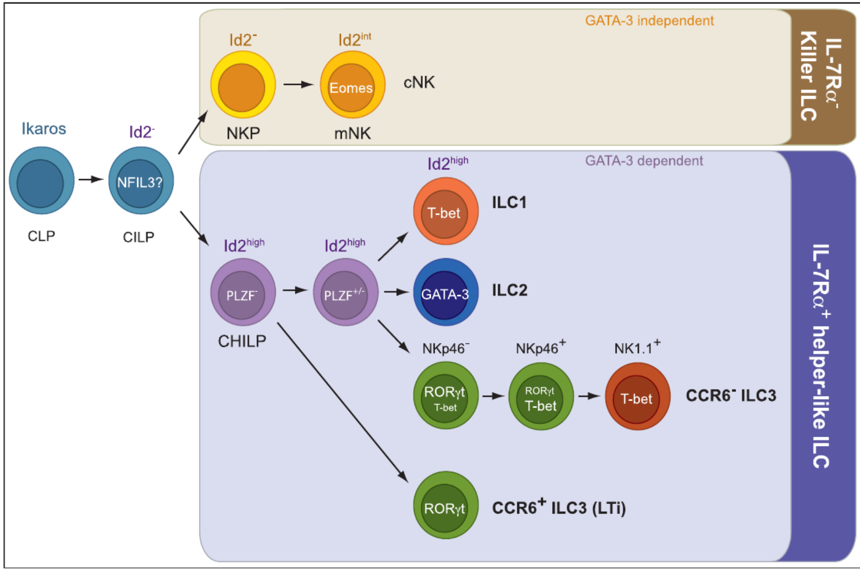


**Figure 1. Refined Lineage Map for the Development of ILC Lineages**
All lymphoid lineages are the progeny of the CLP. After the branchpoint with the B and T lineages, an ILC-restricted progenitor might exist (CILP). Downstream of the CILP, two main ILC lineages can be discriminated—killer ILCs and helper-like ILCs. Killer ILCs are represented by cNK cells and helper-like ILCs are composed of the various cytokine-producing ILC subsets (i.e., ILC1s, ILC2s, ILC3s). Whereas helper-like ILCs express IL-7Rα and require GATA-3 for differentiation, killer ILCs do not express IL-7Rα and are normally represented in GATA-3-deficient mice. All helper-like ILCs (but not killer ILCs) differentiate from the $Id2^+$ CHILP. A $PLZF^+$ CHILP population has been identified that has more restricted differentiation potential. Whether $PLZF^-$ CHILP are the precursors of $PLZF^+$ CHILP remains to be experimentally addressed. CLP, common lymphoid progenitor; CILP, common ILC progenitor; CHILP, common helper-like ILC progenitor; NKP, cNK-restricted progenitor.

distinction between the various subsets of $NKp46^+NK1.1^+$ cells was even more complex because $NKp46^+$ ILC3s were recognized as well (Cella et al., 2009; Cupedo et al., 2009; Luci et al., 2009; Sanos et al., 2009; Satoh-Takayama et al., 2008). Within the intraepithelial space of the intestine, an ILC1 subset was identified that was phenotypically distinct from cNK cells and required T-bet and nuclear factor, interleukin-3 (IL-3) regulated (NFIL3, also known as E4BP4) for differentiation (Tables 2 and 3) (Fuchs et al., 2013). Genetic reporter systems for lineage-defining transcription factors allowed to identify intestinal ILC1s as an ILC lineage separate from cNK cells (expressing an *Eomes* reporter) and NKp46-expressing ILC3s (expressing a *Rorc* reporter). Intestinal ILC1s produced copious amounts of IFN-γ in response to IL-12 and provided innate protection against the intracellular parasite *Toxoplasma gondii* (Klose et al., 2014).

## Identification of ILC2s

IL-25, IL-33, and thymic stromal lymphopoietin (TSLP), all of which are epithelial cell-derived cytokines, regulate type 2 innate immune responses against helminths and pathophysiology of airway allergens (Koyasu and Moro, 2012). The existence of lineage-negative innate immune cells producing type 2 cytokines was first reported by Fort et al. demonstrating that IL-25 administration induced production of IL-5 and IL-13 in *Rag2*$^{-/-}$ mice that lack all B and T cells (Fort et al., 2001). It was later shown that a non-B non-T c-$Kit^+$ FcεR$1^-$ (non-mast cell) population, which appears during the initial stages of helminth infection, is capable of producing IL-4, IL-5, and IL-13 in response to IL-25 (Fallon et al., 2006; Humphreys et al., 2008; Hurst et al., 2002; Voehringer et al., 2006). The identity of such innate effector cells had been obscure until 2010 when natural helper cells (Moro et al., 2010) and nuocytes (Neill et al., 2010), which are now known as ILC2s, were identified. ILC2s, which produce large amounts of IL-5 and IL-13 in response to IL-25 or IL-33, were identified in mesenteric fat-associated lymphoid clusters (FALC) in naive mice as natural helper cells (Moro et al., 2010) and in mesenteric lymph nodes of mice administered with IL-25 or IL-33 as nuocytes (Neill et al., 2010). ILC2s were later shown to be present in other tissues such as lung, intestinal lamina propria, bone marrow, liver, and skin (Furusawa et al., 2013; Halim et al., 2012a; Hoyler et al., 2012; Kabata et al., 2013; McHedlidze et al., 2013; Roediger et al., 2013; Salimi et al., 2013). In addition to type 2 cytokines, ILC2s produce amphiregulin and support the recovery of epithelial barrier integrity after tissue damage (Monticelli et al., 2011). Recent studies have identified a role of ILC2s in the initiation of type 2 adaptive immune responses through class II MHC and cytokine-mediated activation of T helper 2 (Th2) cells (Halim et al., 2014; Oliphant et al., 2014). Another type 2 innate cell population, $MPP^{type2}$ induced by IL-25 administration was also reported in 2010 (Saenz et al., 2010). $MPP^{type2}$ cells, however, differ from ILC2s in that they express neither IL-7 receptor (IL-7R) nor IL-33R and possess the potential to differentiate into myeloid cells (Saenz et al., 2013; Saenz et al., 2010). IL-5 and IL-13 produced by ILC2s are critical for innate protection against helminth and nematode infections (Koyasu et al., 2010).

## ILC3s: Lymphoid Tissue-Inducer Cells and More

The first ILC subset to be characterized were retinoic acid-related orphan receptor γ t (RORγt)-expressing ILC3 in human tonsils (Cella et al., 2009; Cupedo et al., 2009) and the lamina propria of the intestine (in both human and mice) (Cella et al., 2009; Cupedo et al., 2009; Luci et al., 2009; Sanos et al., 2009; Satoh-Takayama et al., 2008), a subpopulation of which expressed cell surface markers also found on NK cells (e.g., NKp46, NKG2D, NKp44, or CD56). Intestinal ILC3s require RORγt for lineage specification and, consequently, mice genetically lacking RORγt have no ILC3s (Table 3). A fetal liver-derived innate lymphocyte subset, termed lymphoid tissue (LTi) inducer cells, has been identified in humans and mice that also depends on RORγt for development (Adachi et al., 1997; Cupedo et al., 2009; Kurebayashi et al., 2000; Mebius et al., 1997; Sun et al., 2000). It is now believed that LTi cells constitute a subpopulation of ILC3s (Cupedo et al., 2009). While