Gut Microbiota and the Paradox of Cancer Immunotherapy

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<td>As Published</td>
<td><a href="http://dx.doi.org/10.3389/fimmu.2014.00157">http://dx.doi.org/10.3389/fimmu.2014.00157</a></td>
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<tr>
<td>Publisher</td>
<td>Frontiers Research Foundation</td>
</tr>
<tr>
<td>Version</td>
<td>Final published version</td>
</tr>
<tr>
<td>Accessed</td>
<td>Fri Mar 31 21:18:50 EDT 2017</td>
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<tr>
<td>Citable Link</td>
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The neoplastic process is characterized by overwhelming complexity. Cancer is comprised of a genetically unstable population of cells that proliferate at an extraordinarily high rate. Millions of cancer deaths each year make it obvious that the battle against cancer is asymmetric, with humankind often being the weaker element (1). To date, cancer research efforts directly confront malignancy by targeting properties of individual cancer cells. In 2000, Hanahan and Weinberg described that most of the research on origins and treatment of cancer had just contributed toward "adding further layers of complexity to a scientific literature that is already complex almost beyond measure" (2). In the same landmark paper, however, the authors were optimistic enough to predict groundwork upcoming advances in the conceptual rather than the technical level (2). They were proven right. One such advancement was the increased awareness for the importance of the tumor microenvironment in the etiopathogenesis of neoplasia (3, 4). We now know that initially transformed cells are much less autonomous in their growth than previously thought (5, 6). Among the microenvironment elements, immune cells and factors have emerged as fundamental players (4–6).

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INTRODUCTION

It is recently shown that beneficial environmental microbes stimulate integrated immune and neuroendocrine factors throughout the body, consequently modulating regulatory T-lymphocyte phenotypes, maintaining systemic immune balance, and determining the fate of preneoplastic lesions toward regression while sustaining whole body good health. Stimulated by a gut microbiota-centric systemic homeostasis hypothesis, we set out to explore the influence of the gut microbiome to explain the paradoxical roles of regulatory T-lymphocytes in cancer development and growth. This paradigm shift places cancer prevention and treatment into a new broader context of holobiont engineering to cultivate a tumor-suppressive macroenvironment.

Keywords: tumor macroenvironment, regulatory T-cells, cancer immunotherapy, inflammation and cancer, probiotic bacteria

REG homeostasis and good health

FOX3P+ CD4+ CD25+ /high TREG are dominant cellular elements of the professional suppressor arm of the immune system and are important for orchestrating the control of peripheral immunological tolerance (18). The transcription factor FOXP3 is a fundamental regulator of TREG function in rodents and humans, and so far the most reliable phenotypic indicator of their identity. Recent studies on human TREG subpopulations, however, revealed that low but discernible levels of FOXP3 expression could be detected in non-suppressive TREG or even in activated effector T-cells. It is probable that this finding reflects the inherent plasticity of TREG FOXP3+ cells co-expressing effector T-cell phenotypic markers or cytokines may be in stages of a progressive, epigenetically regulated, phenotypical, and functional shift process (14, 16, 19–22), ultimately favorable for healthful recovery of the host after environmental challenges. The role of TREG is central in preserving immune system homeostasis for health and the balance of beneficial inflammatory responses during infections while minimizing collateral tissue damage. In cancer, however, roles of TREG are traditionally considered to be negative (14–23).

TREG gather near tumors and favor cancer survival

A large body of data suggest that TREG gather near tumors and suppress the anti-tumor inflammatory response, thus favoring cancer
cell survival. To this end, tumor-associated $T_{\text{REG}}$ are thought as a major impediment of anti-tumor vaccines (13–16, 23). Clinical and experimental data suggest that tumor-associated $T_{\text{REG}}$ recognize both self and neoantigens expressed by tumor cells, counteracting antigen-specific effector T-cell responses. Consequently, immunotherapy strategies based on the vaccination with tumor-associated antigens fail to evoke an effective response against cancer cells due to the activation and expansion of tumor antigen-specific $T_{\text{REG}}$ (14–16). This potential interplay of $T_{\text{REG}}$ within tumors has been reviewed in detail elsewhere (12–16), and has led to the proposal of several anti-$T_{\text{REG}}$ regimes for cancer immunotherapy. These regimens aim to deplete $T_{\text{REG}}$, inhibit their suppressive function, prevent their homing into tumor sites, or block their differentiation/proliferation (12–16).

Several of these $T_{\text{REG}}$-targeting modalities have already been tested in the clinic, with mixed results (13, 16). Blocking $T_{\text{REG}}$ function by depleting the cytotoxic T-lymphocyte-associated antigen 4 (CTLA-4) appears promising (24), due to the depletion of $T_{\text{REG}}$ from tumor tissues (25, 26). However, a similar regimen could lead to an opposite effect with the accumulation of $T_{\text{REG}}$ and CD8$^{+}$ T-cells in tumors (27, 28). A phase III study of melanoma patients using a gp100 peptide vaccine with interleukin (IL)-2 administration led to equally promising results with discovery of $T_{\text{REG}}$ expansion in responding patients (29).

**GUT MICROBIOTA INDUCE POTENT $T_{\text{REG}}$ WITH SYSTEMIC ANTI-NEOPLASTIC PROPERTIES**

As the results of these trials are anticipated, the literature reveals contradictory evidence. Indeed, the studies associating high densities of tumor-associated cells expressing $T_{\text{REG}}$ markers including FOXP3 with a poor prognosis in several types of human cancers are now challenged by similar studies on the very same types of cancer showing the opposite outcome (30–34). The different CD8$^{+}$:$T_{\text{REG}}$ ratios and the presence of FOXP3$^{+}$ cell subsets of undetermined identity in the tumor microenvironment have been proposed as probable explanations (16). Indeed, data from animal models show under certain conditions of microbial priming that $T_{\text{REG}}$ not only protect but also alter the tumor microenvironment to induce remission of already established intestinal, mammmary, and prostate cancers (35–41). The hypothesis that the composition of the different subsets of FOXP3$^{+}$ cells, which may include effector Foxp3$^{+}$ cells, is intriguing (16). Indeed, it was previously shown that IFN-$\gamma$ levels were increased during $T_{\text{REG}}$-mediated tumor regression in mice (37). Further, feeding of probiotic microbes to mice induces systemic oxytocin secretion that shifts immunity toward IFN-$\gamma$ and CD25 for improved wound healing capacity and systemic good health (42). A question subsequently arising is whether gut microbiota may be engineered to harness an anti-neoplastic FOXP3$^{+}$ cell milieu (5, 10, 41).

**GUT-CENTRIC HYPOTHESIS: PRIOR EXPOSURES TO MICROBES EXPLAIN BENEFICIAL ROLES OF $T_{\text{REG}}$**

Stimulated by a gut-centric homeostasis hypothesis, we set out to explore and explain the paradoxical roles of $T_{\text{REG}}$ in cancer using several different mouse models of cancer and adoptive cell transfer methodologies (10). We found that $T_{\text{REG}}$ may suppress, promote, or have no effect in carcinogenesis depending upon their timing and prior exposure to gut bacterial antigens and presence of IL-10 (35–39, 41, 43, 44). Under some conditions, adoptive transfer of $T_{\text{REG}}$ rapidly led to apoptosis of emerging tumor cells (37, 45). Using as a model organism an opportunistic pathogen, *Helicobacter hepaticus*, commonly residing in the lower bowel of mice, we have shown in Rag2-deficient mice (otherwise lacking lymphocytes) that gut microbiota modulate inflammatory bowel disease and inflammation-associated colon cancer, a cancer process inhibited by properly functioning IL-10-dependent $T_{\text{REG}}$ (35, 36). Subsequently, by introducing *H. hepaticus* into the large bowel flora of mice lacking the APC tumor suppressor gene ($Apc^{Min/+}$), we found that intestinal polyposis was greatly enhanced by bacteria and subsequently suppressed by immune-competent $T_{\text{REG}}$. Furthermore, adenomas of infected $Apc^{Min/+}$ mice progressed into adenocarcinoma, a transition atypical of polyps of aged-matched uninfected controls (38, 41). Interestingly, $Apc^{Min/+}$ mice having *H. hepaticus* in their gut flora were prone to develop cancer in tissues distant from intestine, such as prostate and the mammary glands (40, 41, 43, 46, 47). *H. hepaticus*-induced tumorigenic events were inhibited by supplementation with $T_{\text{REG}}$ from immune-competent wild type donor mice.

A potent treatment to counteract these local and systemic *H. hepaticus*-induced tumorigenic events was supplementation with $T_{\text{REG}}$ in an IL-10-dependent manner (10, 36, 38–40, 44, 46, 48). Purified $T_{\text{REG}}$ exhibited greatest anti-cancer potency when taken from donor mice previously colonized with *H. hepaticus*. By contrast, $T_{\text{REG}}$ taken from donor mice without prior *H. hepaticus* exposure were ineffective, and in some cases actually enhanced tumorigenesis (10). Based on these results, we theorize that the tumor microenvironment is subject to systemic inflammatory events arising from environmental exposures in the gastrointestinal tract (Figure 1). This microbe-inducible pro-inflammatory condition contributes to tumor trophic signaling. Interestingly, bacterial antigen triggered IL-10-dependent activities in the GI-tract impart sustained protection from the aforementioned events, resulting in immune cell recruitment, including $T_{\text{REG}}$, which, by being more potent in their anti-inflammatory roles, work locally and systemically to suppress sepsis, myeloid precursor mobilization, and inflammatory signaling important in extra-intestinal cancer evolution (10, 43). These systemic events comprise the tumor microenvironment.

The roles of intestinal microflora in promoting cancer development within the bowel have been well established (35, 49–52). Linking gut microbial flora and local and systemic effects that promote (38) or suppress (45) tumors throughout the body, expands this paradigm in a challenging manner. Recent findings show that gut flora imbalances considerably undermine the response to both immune (53, 54) and non-immune chemotherapeutic regimens, such as cisplatin and oxaliplatin (53).

**A WEAKENED $T_{\text{REG}}$ FEEDBACK LOOP UNIFIES AUTOIMMUNE DISEASES AND CANCER**

These gut microbe-centric findings in mice are consistent with the “hygiene hypothesis,” according to which insufficient microbial exposures earlier in life predispose to allergies, autoimmunity disorders, and uncontrollable inflammation-associated pathologies later in life. We have shown that the basic principles of this
Gut bacteria modulate the tumor macroenvironment

**FIGURE 1** Gut bacteria–host crosstalk is continuous and reciprocal in the cancer macroenvironment. Beneficial microbes trigger IL-10-mediated GI-tract immune and neuronal networks that lower systemic inflammatory tone and up-regulate hypothalamic–hypophyseal targets, including oxytocin, constituting a gut–systemic immunity-endocrine-axis. In this way, microbiota stimulate CD4+ lymphocytes including regulatory T cells (T$_{REG}$) that suppress, promote, or have no effect in carcinogenesis depending upon their timing and prior exposure to gut bacterial antigens and presence of interleukin (IL)-10. This places neoplastic development and growth into a new broader context of the holobiont (comprised of the mammalian host plus resident microbes) and the cancer macroenvironment, highlighting microbes that may be engineered for sustained good health.

BEFICAL SYSTEMIC EFFECTS OF GUT MICROBES ARE TRANSPANTABLE VIA FOXP3$^+$ T$_{REG}$ INTO NAÏVE HOSTS

Adoptive cell transfer models offer mechanistic insight as these beneficial effects were isolated to bacteria-primed T$_{REG}$ (42, 47, 57–59). In fact, healthful phenotypes were entirely reproducible in naïve recipient mice by the adoptive transfer of highly purified T$_{REG}$ derived from probiotic-fed cell donors (42, 57, 59). These results suggest gut microbes-induced crosstalk with the host in a continuous and reciprocal manner. The fate of preneoplastic and neoplastic lesions arising in epithelia throughout the body depends upon this macroenvironment at the whole organism level. Consequently, the tumor macroenvironment is defined as the "holobiont," i.e., the mammalian organism plus the microbial symbionts it bears. The T$_{REG}$ population is a central player of the tumor macroenvironment connecting gut bacteria with reproductive fitness, youthful phenotypes, and anti-neoplastic properties.

MICROBIAL ENGINEERING OFFERS NEW STRATEGIES FOR PUBLIC HEALTH

Taken together, microbial engineering strategies using food-grade bacteria highlight alternative directions in cancer immunotherapy. Modulating beneficial T$_{REG}$ via diet is a biologically safe and efficient approach, originating from genetic programs that have been shaped during the millions of years of co-evolution of mammals with their gut bacteria symbionts. These attributes remain largely inactive in individuals with a modern lifestyle, Westernized dietary habits, and stringent hygiene practices. Awakening these latent T$_{REG}$-mediated capabilities may provide an alternative avenue to reduce cancer risk at a population level for public health. The perspectives presented here should be considered as an alternative paradigm – not only for fighting cancer – but also for promoting overall good health and longevity.
AUTHOR CONTRIBUTIONS
Theofilos Poutahidis, Markus Kleine新股eld, and Susan E. Erdman wrote the paper.

ACKNOWLEDGMENTS
This work was supported by National Institutes of Health grants P30-ES002109 (pilot project award to Susan E. Erdman), U01 CA164337 (to Susan E. Erdman), and RO1CA108854 (to Susan E. Erdman).

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Frontiers in Immunology | Tumor Immunity
April 2014 | Volume 5 | Article 157 | 4

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.


This article was submitted to Tumor Immunity, a section of the journal Frontiers in Immunology.

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