The prognostic value of FoxP3+ tumor-infiltrating lymphocytes in cancer:

A critical review of the literature

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Running title: Prognostic significance of FoxP3+ T cells in human carcinoma

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Funding: British Columbia Cancer Foundation, Canadian Institutes of Health Research, and National Science and Engineering Research Council of Canada.
Statement of Translational Relevance

Although FoxP3+ T cells are conventionally thought to suppress tumor immunity, this idea has been challenged by recent studies showing that, in some patient cohorts, tumor-infiltrating FoxP3+ T cells are associated with favorable prognosis. To investigate this apparent discrepancy, we performed a comprehensive review of the literature concerning the prognostic significance of tumor-infiltrating FoxP3+ T cells in human cancer. We conclude that FoxP3 is inadequate as a single functional or prognostic marker. Moreover, the prognostic significance of FoxP3+ T cells can vary according to tumor site. Thus, the original view that FoxP3+ T cells invariably suppress tumor immunity is oversimplified. We require better understanding of the functional subtypes of FoxP3+ T cells, and their biological properties in different tumor microenvironments, if we wish to rationally modulate their behavior to enhance tumor immunity.
Abstract

CD8+ tumor-infiltrating lymphocytes (TIL) are associated with survival in a variety of cancers. A second subpopulation of TIL – defined by FoxP3 expression – has been reported to inhibit tumor immunity, resulting in decreased patient survival. Based on this premise, several groups are attempting to deplete FoxP3+ T cells to enhance tumor immunity. However, recent studies have challenged this paradigm by showing that FoxP3+ T cells exhibit heterogeneous phenotypes and, in some cohorts, are associated with favorable prognosis. These discrepant results could arise from differences in study methodologies or the biological properties of specific cancer types. Here we conduct the first systematic review of the prognostic significance of FoxP3+ T cells across non-lymphoid cancers (58 studies from 16 cancers). We assessed antibody specificity; cell scoring strategy; multivariate modeling; use of single versus multiple markers; and tumor site. Two factors proved important. First, when FoxP3 was combined with one additional marker, double positive T cells were generally associated with poor prognosis. Second, tumor site had a major influence. FoxP3+ T cells were associated with poor prognosis in hepatocellular cancer and generally good prognosis in colorectal cancer, while other cancer types were inconsistent or understudied. We conclude that FoxP3+ T cells have heterogeneous properties that can be discerned by the use of additional markers. Furthermore, the net biological effects of FoxP3+ T cells appear to depend on tumor site, perhaps reflecting microenvironmental differences. Thus, depletion of FoxP3+ T cells might enhance tumor immunity in some patient groups but be detrimental in others.
Introduction

Many studies across a wide variety of human cancers have demonstrated a clear association between the presence of tumor infiltrating lymphocytes (TIL) and patient survival (1-4). To further understand this phenomenon, additional immune markers have been used to subdivide CD3+ T cells into functional subsets, with special emphasis on cytotoxic (e.g., CD8+, nucleolysin TIA-1 isoform p40 (TIA-1)+) and regulatory (e.g., CD4+, IL-2 receptor subunit alpha (CD25)+, FoxP3+) phenotypes (3, 5). Whereas TIL expressing cytotoxic markers are generally associated with favorable prognosis, TIL expressing regulatory markers (referred to as Tregs) were initially reported to correlate with poor prognosis (5). This fit with the general notion that Tregs suppress adaptive immune responses and lead many groups to pursue strategies to deplete Tregs from cancer patients as a means to enhance tumor immunity (6-8).

In the past decade, much effort has been devoted to finding molecular markers that uniquely define Tregs. Initially, these cells were characterized as CD4+ and CD25^{high}(9). Further investigation revealed that Tregs express and functionally depend on the transcription factor forkhead box protein P3 (FoxP3) (10). Indeed, humans and mice that lack an intact $\text{FOXP3}$ gene suffer a severe autoimmune syndrome known as immune dysregulation/ polyendocrinopathy/ enteropathy/ X-linked syndrome (IPEX) in humans or the Scurfy phenotype in mice (10, 11). Given its essential role in Treg development and function, FoxP3 became a popular single marker for Treg studies in cancer. Intriguingly, studies of the prognostic value of FoxP3+ T cells have lead to highly discrepant findings. In some studies, tumor-
infiltrating FoxP3+ T cells have been associated with poor prognosis, consistent
with the initial hypothesis that FoxP3+ Tregs inhibit anti-tumor immunity. In
contrast, other studies have found that FoxP3+ T cells are associated with a
favorable prognosis.

How can these widely discrepant prognostic claims be explained? On the one
hand, they could reflect technical differences between studies, including the specific
FoxP3 antibody used, scoring strategy, and statistical methods. Alternatively, the
differing claims could reflect biological factors. For example, it is conceivable that
FoxP3+ T cells exhibit conventional regulatory (i.e., inhibitory) properties in some
contexts but not others. Alternatively, FoxP3+ T cells may be consistently regulatory
in nature but appear as favorable prognostic markers in some cancers due to their
association with tumor-infiltrating CD8+ T cells or other effectors(12, 13). Others
have suggested that, in colorectal and gastric cancers, FoxP3+ T cells may inhibit
tumor-promoting inflammatory responses to microbes, which could explain their
association with favorable outcomes in these and similar contexts(14). Finally,
emerging evidence indicates that FoxP3 expression encompasses a heterogeneous
population of cells that contain both regulatory T cells, which produce cytokines
such as transforming growth factor beta-1 and interleukin 10, and non-regulatory T
cells, which may express interferon gamma and interleukin 17 (15-19) (reviewed
in(20)). Given these various possibilities, it seems reasonable to question whether
depletion of Tregs based on FoxP3 expression is likely to be beneficial or
detrimental to cancer patients.
To investigate this controversy, we performed a comprehensive and critical review of the literature concerning tumor-infiltrating FoxP3+ T cells and prognosis in human cancer. Articles for review were identified during a PubMed search using the terms “FoxP3” and “cancer” and vetted by title and abstract by an author (RJD). Several selection criteria were applied. First, we excluded studies of lymphoid cancers, because the immunological nature of these malignancies makes it difficult to assess whether FoxP3+ T cells are acting directly on tumor cells or indirectly on anti-tumor effector lymphocytes. Second, we excluded studies that only correlated FoxP3+ T cells with late-stage disease as opposed to patient survival. Third, we included only those studies that measured FoxP3 expression by immunohistochemistry (IHC) or immunofluorescence to ensure that the intratumoral location of FoxP3+ cells was known. Finally, we reviewed a given data set only once, excluding secondary or tertiary studies that referred to a previously published data set.

In the end, we reviewed 58 studies encompassing 16 different cancer types (Table 1), including bladder(19), breast(21-28), cervical(29, 30), colorectal(12, 31-39), endometrial(40-42), gastric(14, 43-46), head and neck(47), hepatocellular(48-52), lung(53, 54), melanoma(55-58), mesothelial(59), oral(4, 60-63), ovarian(2, 3, 13, 64-67), pancreatic(68), renal(69, 70), and vulvar cancers(71) (Supplementary Table 1). The reported prognostic value of FoxP3+ T cells in these 58 studies ranged from poor (n=23) to neutral (n=23) to good (n=12). To better understand why the prognostic value of FoxP3+ T cells varies so widely, we assessed each study for technical factors (including the specific FoxP3 antibody used, scoring strategy, and
the use of multivariate modeling) and biological factors (including the use of additional markers to define Tregs, and the tumor site studied).

Antibody specificity

Different FoxP3 antibodies can yield different staining patterns, indicating that some antibodies may have suboptimal sensitivity or specificity (72, 73). While 18 of the 58 reviewed studies failed to state which specific FoxP3 antibody was used, within the remaining 40 studies a total of 11 different FoxP3 antibodies were used (Table 1). The most commonly used antibody was a monoclonal designated 236A/E7. In the 23 studies that used 236A/E7, the prognostic significance of FoxP3+ T cells ranged from poor (n=10) to neutral (n=8) to good (n=5). Given that a single FoxP3 antibody can yield prognostic results this disparate, it appears that FoxP3 prognostic variability is not solely attributable to antibody selection.

Cell scoring strategy

We investigated four aspects of the scoring strategies used to categorize tumors as positive or negative for FoxP3+ T cells: cutoff points, intratumoral location, use of tissue microarrays versus whole sections, and computerized versus manual counting (Table 1). Although there is no standard cutoff point for TIL studies, 32/58 of the reviewed studies used the median number of FoxP3+ T cells as the cutoff point. Within these 32, the distribution between poor, neutral, and good prognostic claims was 16, 11, and 5 studies, respectively. The remaining studies used a variety of scoring strategies, including the presence versus absence of
FoxP3+ T cells, the mean number of FoxP3+ T cells, or other criteria. A fairly even distribution between poor, neutral or good prognostic claims were observed regardless of the cutoff point used (Table 1). Thus, differing scoring strategies do not account for the variable claims of FoxP3 prognostic significance.

TIL can reside in tumor epithelium, stroma or both, and this may influence their prognostic significance. Among the 58 reviewed studies, 15 did not discriminate between the epithelial or stromal location of FoxP3+ T cells and instead provided a general count; 19 counted only FoxP3+ T cells in the epithelium; and 24 counted FoxP3+ T cells from both epithelial and stromal compartments independently (Table 1). Regardless of the location of enumerated FoxP3+ T cells, a fairly even distribution was seen between poor, neutral and good prognostic claims.

We next examined the use of tumor tissue microarrays (TMAs) versus whole sections (Table 1). TMAs were used in 18 of the 58 studies and prognostic claims ranged from poor (n=7) to neutral (n=6) to good (n=5). A similar range of prognostic claims was seen with studies using whole tissue sections. Regarding cell counting, 38 studies used manual counting by one or more investigators, 6 studies used a computer based quantification method, and 14 studies did not state the counting method (Table 1). Studies that utilized manual counting showed an unbiased spread between poor (n=16), neutral (n=14) and good (n=8) prognostic claims, regardless of the number of investigators who performed cell counting. Definitive conclusions could not be drawn regarding the use of computerized counting, as only six studies used such methods, three of which involved colorectal cancer (see below).
Multivariate correction for stage or grade of disease

In principle, the density of FoxP3+ T cells could reflect the stage and/or grade of disease, which could influence prognosis. Of the 45 studies that correlated FoxP3+ T cells to stage and/or grade, 25 found a significant association between FoxP3+ T cells and the stage and/or grade of disease, with 11 reporting a P-value of ≤0.001 (Supplementary Table 1). A potential confounding effect is that the quantity of TIL can influence nodal staging, especially in colorectal cancer (74). Nonetheless, these studies support the possibility that FoxP3+ T cells could simply serve as a marker of more advanced disease.

This issue was addressed in 42 studies by use of multivariate models that included stage, grade and other clinicopathologic features (Table 1). Among these studies, the prognostic significance of FoxP3+ T cells ranged from poor (n=20) to neutral (n=11) to good (n=11). Notably, in four studies, FoxP3+ T cells were a significant univariate prognostic indicator only to be removed during multivariate analysis. Of the 16 studies that did not use multivariate analysis, the potentially confounding effects of stage and grade were mitigated in most by the fact that (a) FoxP3+ T cells showed no prognostic significance even in univariate analysis, or (b) only specific stages or grades of disease were included in the study. In summary, even though FoxP3+ T cells are frequently associated with the stage and/or grade of disease, we found that this factor was well controlled in most studies and does not account for the variability of FoxP3 prognostication.
**Multivariate correction for other TIL subsets**

FoxP3+ T cells are usually found together with other TIL subsets, which can make it difficult to discern their independent prognostic effect. While multivariate analysis can solve this problem, it requires that all TIL subtypes significant in univariate analysis be included in the multivariate model. In the eight studies that included all TIL subsets in multivariate analysis, the prognostic value of FoxP3+ T cells ranged from poor (n=2) to neutral (n=3) to good (n=3) (Table 1). Thus, although the number of studies is low, it appears that the prognostic significance of FoxP3+ T cells is not solely attributable to the presence of other TIL subpopulations.

Several studies made prognostic claims based on the ratio of FoxP3+ T cells to other lymphocyte subsets, including CD3+/FoxP3+ (n=2), CD4+/CD25+FoxP3+ (n=1), CD68+/FoxP3+ (n=2), CD8+/FoxP3+ or FoxP3+/CD8+ (n=18), CD8+/CCR4+FoxP3+ (n=1), FoxP3+/CD4+ (n=2), FoxP3+/CD3+/CD45RO+ (n=1), and Granzyme-B+/FoxP3+ (n=1) (Supplementary Table 1). Among these 28 studies, prognostic claims for FoxP3+ TIL ranged from poor (n=12) to neutral (n=11) to good (n=5). Thus, the use of lymphocyte ratios has been inconsistently applied and yielded inconsistent prognostic claims.

**Clinical significance and publication bias**

We next evaluated whether the magnitude of the prognostic effect was similar for studies claiming good versus poor prognosis. Of the 58 studies, 32 reported multivariate hazard ratios for overall survival. A funnel plot revealed no significant difference between the magnitude of hazard ratios for studies claiming
poor versus good prognosis (Figure 1). Furthermore, there was no evidence of
publication bias, as the studies were evenly distributed throughout the plot.

Use of multiple markers to define FoxP3+ T cells

Although FoxP3 was originally thought to uniquely define conventional CD4+
Tregs(75), more recent studies indicate that, in some circumstances, FoxP3 can also
be expressed by effector T cells(16, 18). We assessed whether studies that
subdivided FoxP3+ T cells using a second marker yield more consistent prognostic
results. Of the 58 reviewed studies, 50 used FoxP3 as a sole marker, which resulted
in variable prognostic claims ranging from poor (n=19) to neutral (n=19) to good
(n=12) (Table 1). The remaining eight studies measured at least one marker in
addition to FoxP3, including CD4, CD8, CD25, and C-C chemokine receptor 4 (CCR4).
Four of these eight studies showed that FoxP3+ T cells that co-expressed a second
marker were associated with poor prognosis. The remaining four claimed that the
identified subset did not have any prognostic significance. Of note, none of the eight
studies claimed an association with good prognosis.

Based on the above, we investigated more closely which markers were used
in addition to FoxP3. Shah et al. utilized two-color IHC to identify both CD4+FoxP3+
and CD8+FoxP3+ T cells in cervical cancer. Intriguingly, they found CD8+FoxP3+ T
cells at a mean number of 3.32 per high-power field and CD4+FoxP3+ T cells at a
mean number of 11.45 per high-power field(30). Thus, had they used FoxP3 as a
single marker, only ~75% of the cells they measured would have been CD4+ T cells,
which underscores the fact that not all FoxP3+ T cells are conventional Tregs. In
another study, Watanabe et al. used co-expression of CCR4 to delineate a subset of FoxP3-expressing T cells in oral cancer (62). An average of 58% of FoxP3+ cells were found to co-express CCR4. Whereas total FoxP3+ T cells had no prognostic value (similar to 3 other studies of oral cancer (60, 61, 63)), CCR4+FoxP3+ T cells showed a highly significant association with survival. These studies highlight the importance of using additional markers to account for the heterogeneity of FoxP3+ T cells.

Tumor site and subtype

It is conceivable that the biological and prognostic effect of FoxP3+ T cells depends on microenvironmental context, in which case tumor site and histological/molecular subtype may be important factors. Indeed, when tumor site was taken into consideration, we found clear prognostic associations in some cases. For example, the five studies of hepatocellular cancer unanimously concluded that FoxP3+ T cells are associated with a poor prognosis (Table 1). Conversely, 4/10 studies investigating colorectal cancer concluded that FoxP3+ T cells correlated with a good prognosis, while the remaining six studies found no prognostic association. In considering colorectal cancer, Ladoire et. al. recently hypothesized that the favorable prognostic effect of FoxP3+ T cells may reflect their ability to suppress tumor-promoting inflammatory responses to gut microbes (76).

In contrast to the above examples, the prognostic significance of FoxP3+ T cells remains controversial in several other cancers. In breast cancer, the reported prognostic effect of FoxP3+ T cells ranges from poor (n=5) to neutral (n=1) to good (n=2). Although ovarian cancer was one of the first tumor sites in which CD4+ Tregs
were associated with poor prognosis (5), subsequent studies utilizing FoxP3 as a marker are split between poor (n=1), neutral (n=4) and good (n=2) prognostic claims. Similarly, studies looking at gastric cancers show an equal split between poor (n=2), neutral (n=1), and good (n=2) prognostic claims. For the remaining ten tumor sites, the number of published studies is insufficient to make definitive conclusions about the prognostic significance of FoxP3+ T cells.

In addition to tissue of origin, tumors can be classified based on their molecular features, as discussed recently by Ogino et al. (77). Hence, it is conceivable that the variability of FoxP3+ T cell prognostication could be attributable to the inherent molecular heterogeneity within tumor types. In support of this idea, the prognostic value of FoxP3+ T cells is stronger in mismatch repair proficient colorectal cancer compared to mismatch repair deficient colorectal cancer (31). Similarly, FoxP3+ T cells are prognostically significant in estrogen receptor (ER)+ but not ER- breast cancer (22, 27). In uveal melanoma, FoxP3+ T cells provide prognostic significance in cyclooxygenase-2 positive cases (58). Although few in number, these studies suggest that the molecular subtype of tumors may influences the prognostic value of FoxP3 T cells.

Conclusions

Having critically reviewed the literature concerning the prognostic value of FoxP3+ T cells, we can make several recommendations for future studies. 1) We recommend that prognostic marker studies follow a standard reporting structure such as the REMARK criteria (78). 2) In many cancers, FoxP3+ T cells are highly...
correlated with the stage and grade of disease, therefore it is important to correct
for these and other appropriate clinicopathological factors. 3) FoxP3+ T cells are
invariably found together with other lymphocytes, therefore all TIL subsets with
prognostic value should be included in multivariate models. 4) The use of multiple
markers to identify functional subsets of FoxP3+ T cells can lead to greater clarity
about their prognostic value. 5) The prognostic value of FoxP3+ T cells appears to
depend significantly on tumor site and possibly molecular subtype, suggesting that
the biological properties of FoxP3+ T cells are influenced by the tumor
microenvironment in which they reside. Overall, this study provides a cautionary
note for the concept of depleting FoxP3+ cells from cancer patients as a means to
enhance tumor immunity. Our findings suggest that this strategy may be beneficial
for some tumor sites (e.g., liver) but detrimental to others (e.g. colorectal).
Improved understanding of the different FoxP3+ T cell subsets in human cancer will
likely enable the development of more precise and effective immunotherapies.

Figure Legends

**Figure 1:** Analysis of clinical significance and publication bias. The figure shows a
funnel plot of log transformed hazard ratios versus standard error for the reviewed
studies. Each symbol represents one study: ▼ poor prognostic claim, ▲ good
prognostic claim, and □ neutral prognostic claim. Bars represent 95% confidence
intervals.
1 References


delineation and differentiation dynamics of human CD4+ T cells expressing the
A unique subset of CD4+CD25highFoxp3+ T cells secreting interleukin-10 and
transforming growth factor-beta1 mediates suppression in the tumor
Expression of Helios, an Ikaros transcription factor family member, differentiates
thymic-derived from peripherally induced Foxp3+ T regulatory cells. J Immunol
2010;184: 3433-41.
2010;125: S272-83.
number of tumor-infiltrating FOXP3-positive cells during primary systemic
chemotherapy correlates with favorable anti-tumor response in patients with breast
22. Bates GJ, Fox SB, Han C, Leek RD, Garcia JF, Harris AL, et al. Quantification of
regulatory T cells enables the identification of high-risk breast cancer patients and
predictive value of HLA class I tumor cell expression and presence of intratumoral
Tregs for chemotherapy in patients with early breast cancer. Clin Cancer Res
Pathologic complete response to neoadjuvant chemotherapy of breast carcinoma is
associated with the disappearance of tumor-infiltrating foxp3+ regulatory T cells.
of Foxp3 expression in tumor cells predicts better survival in HER2-overexpressing
breast cancer patients treated with neoadjuvant chemotherapy. Breast Cancer Res
and FOXP3(+) regulatory T cell infiltration in relation to breast cancer survival and
evaluation of the clinical significance of FOXP3+ infiltrating cells in human breast
of regulatory T cells is correlated with hypoxia-induced CXCR4 expression, and is
associated with poor prognosis in basal-like breast cancers. Breast Cancer Res
2011;13: R47.
Human leukocyte antigen class I, MHC class I chain-related molecule A, and


68. Hiraoka N, Onozato K, Kosuge T, Hirohashi S. Prevalence of FOXP3+
regulatory T cells increases during the progression of pancreatic ductal
of peritumoral regulatory T cells and its correlation with intratumoral
cyclooxygenase-2 expression in clear cell renal cell carcinoma. BJU Int 2009;103:
399-405.
70. Siddiqui SA, Frigola X, Bonne-Annee S, Mercader M, Kuntz SM, Krambeck AE,
et al. Tumor-infiltrating Foxp3-CD4+CD25+ T cells predict poor survival in renal cell
Status of cellular immunity lacks prognostic significance in vulvar squamous
carcinoma. Gynecol Oncol 2012.
72. Tran DQ, Ramsey H, Shevach EM. Induction of FOXP3 expression in naive
human CD4+FOXP3 T cells by T-cell receptor stimulation is transforming growth
factor-beta dependent but does not confer a regulatory phenotype. Blood 2007;110:
2983-90.
73. Woo YL, Sterling J, Crawford R, van der Burg SH, Coleman N, Stanley M.
FOXP3 immunohistochemistry on formalin-fixed paraffin-embedded tissue: poor
Lymphocytic reaction to colorectal cancer is associated with longer survival,
independent of lymph node count, microsatellite instability, and CpG island
regulatory T cells in human tumor and autoimmune disease. Cancer Res 2009;69:
3995-4000.
76. Ladoire S, Martin F, Ghiringhelli F. Prognostic role of FOXP3+ regulatory T
cells infiltrating human carcinomas: the paradox of colorectal cancer. Cancer
77. Ogino S, Galon J, Fuchs CS, Dranoff G. Cancer immunology--analysis of host
78. McShane LM, Altman DG, Sauerbrei W, Taube SE, Gion M, Clark GM.
REporting recommendations for tumor MARKer prognostic studies (REMARK).
Breast Cancer Res Treat 2006;100: 229-35.
Table 1: Study characteristics

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Ron J deLeeuw, Sara E Kost, Juzer A Kakal, et al.

Clin Cancer Res Published OnlineFirst April 17, 2012.

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doi:10.1158/1078-0432.CCR-11-3216

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