Orchestration and Prognostic Significance of Immune Checkpoints in the Microenvironment of Primary and Metastatic Renal Cell Cancer

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Abstract

Purpose: Clear cell renal cell carcinoma (ccRCC) has shown durable responses to checkpoint blockade therapies. However, important gaps persist in the understanding of its immune microenvironment. This study aims to investigate the expression and prognostic significance of immune checkpoints in primary and metastatic ccRCC, in relation with mature dendritic cells (DC) and T-cell densities.

Experimental Design: We investigated the infiltration and the localization of CD8+ T cells and mature DC, and the expression of immune checkpoints (PD-1, LAG-3, PD-L1, and PD-L2) in relation with prognosis, in 135 primary ccRCC tumors and 51 ccRCC lung metastases. RNA expression data for 496 primary ccRCC tumors were used as confirmatory cohort.

Results: We identify two groups of tumors with extensive CD8+ T-cell infiltrates. One group, characterized by high expression of immune checkpoints in the absence of fully functional mature DC, is associated with increased risk of disease progression. The second group, characterized by low expression of immune checkpoints and localization of mature DC in peritumoral immune aggregates (tertiary lymphoid structures), is associated with good prognosis.

Conclusions: The expression of the immune checkpoints and the localization of DC in the tumor microenvironment modulate the clinical impact of CD8+ T cells in ccRCC. Clin Cancer Res; 21(13); 3031–40. ©2015 AACR.
Immune checkpoints on infiltrating T cells are key regulators of immune escape in cancer. In primary ccRCC, several studies have shown that the expression of the inhibitory receptor PD-1 on the immune cells (15, 16) or its ligand PD-L1 on tumor cells (17–19) is associated with a poor clinical outcome. Interestingly, antibodies that block the PD-1 axis have yielded a 20% to 30% response rate in metastatic ccRCC (20, 21) that seems to be related to the expression of PD-L1 by the tumor cells (20, 22). Another inhibitory molecule that has gained recent attention is the lymphocyte activation gene-3 (LAG-3), which is coexpressed with PD-1 on CD8+ tumor-infiltrating lymphocytes in melanoma (23), and together with PD-1 synergistically regulates T-cell function (24). We expected immune checkpoints high ccRCC patients to have a worse prognosis than the immune checkpoint low.

In these newly described scenarios in which CD8+ T-cell infiltration correlates with poor prognosis, it is important to define the combination of immune-based biomarkers that will predict patients’ prognosis and further guide immunotherapeutic approaches. This study aims to investigate the expression and prognostic significance of immune checkpoint receptors and paired ligands on primary and metastatic ccRCC in relation with TLS-DC and T-cell densities.

Materials and Methods
Patients
A cohort of 135 primary ccRCC human tumors and another of 51 ccRCC lung metastases were collected. The primary cases derived from specimens of radical nephrectomy operated between 1999 and 2003 at the hospital Necker-Enfants Malades (Paris, France). The ccRCC lung metastases cohort resected at the Hotel Dieu hospital (Paris, France) or Hôpital Européen Georges Pompidou (HEGP, Paris, France) between 1992 and 2010 was already described in ref. (14). This research was conducted according to the recommendations outlined in the Helsinki declaration and approved by the medical ethics boards of all participating institutions, and with the agreement of the Ile-de-France II ethics committee (no. 2012-0612). The demographic characteristics of the cohorts are depicted in Supplementary Table S1 (14).

In addition, expression data for 496 primary ccRCC samples with complete follow-up were downloaded from The Cancer Genome Atlas (TCGA) study, using version 2 of the normalized RNA sequencing data. Corresponding clinical data (updated on 2013-04-06) were downloaded from (25).

Clinic and pathologic features
The original histologic diagnosis was confirmed on archival hematoxylin and eosin–stained slides, and histopathologic features such as histologic subtype (26), tumor size, regional lymph node invasion, distant metastases at surgery, Fuhrman nuclear grade (27), and sarcomatoid features were collected. All tumors were pathologically staged according to the TNM (tumor–node–metastasis) classification (28). The duration of follow-up was calculated from the date of the surgery (nephrectomy or metastasectomy) to the date of cancer progression, last follow-up or death.

Immunohistochemical and immunofluorescence staining
Serial 5-μm formalin-fixed paraffin-embedded (FFPE) tissue sections from primary and metastatic ccRCC were stained using autostainerPlus Link 48 (Dako). Antigen retrieval and deparaffinization were carried out on a PT-Link (Dako) using the EnVision FLEX Target Retrieval Solutions (Dako). The antibodies used in this study for IHC and immunofluorescence (IF) are listed in Supplementary Table S2. IF-stained slides were scanned after secondary antibody incubation and mounting. For the IHC staining, peroxidase activity was detected using 3-amino-9-ethylcarbazole substrate or Novared and alkaline phosphatase using alkaline phosphatase substrate III (Vector Laboratories).

Tests of the specificity and sensitivity of PD-1, PD-L1, PD-L2 and LAG-3 monoclonal antibodies for IHC experiments were performed using generated FFPE cell pellets from transfected 300.19 cells (for PD-1, PD-L1, and PD-L2; ref. 29) and CHO cells (for LAG-3), whereas parental untransfected cells served as negative controls (Supplementary Fig. S1). Costim Pharmaceuticals. Multiple organs (n = 32), human TMA (FDA999a, US Biomax), and malignant cancer tissues (n = 10) from different oncology indications were also tested using the above mentioned protocols. Normal human FFPE tonsil sections for PD-1, LAG-3, PD-L2, and normal placenta for PD-L1 were used as positive controls (Supplementary Fig. S1).

Immunohistochemical quantification
Stained slides were scanned with a Nanozoomer (Hamamatsu) and analyzed with Calipix software (Tribvn). For quantification purposes, tissues were divided into Invasive Margin (IM) and Tumor Center (TC) as previously described (30), and the density of positive cells was calculated in the whole tumor region (IM and TC). Because of the small size (or absence) of TC region in the majority of the metastases, the analysis on this cohort was done not discriminating between the two regions. The percentages of tumor cells stained positive for PD-L1 and PD-L2 were quantified by two independent reviewers (A. Lupo and N.A. Giraldo) without prior knowledge of patient outcome, and the tumors above 5% tumor cell expression were considered as positive in accordance with studies in other types of cancer (20, 31).

Statistical analysis
Comparisons among the demographic and pathologic features, immune marker densities, and PD-L1 and PD-L2 expressions were
evaluated by using $\chi^2$, Fisher exact, and Wilcoxon rank-sum tests. Association of variables to prognosis was assessed using the Kaplan–Meier method, univariate and multivariate Cox regression analyses. To segregate patients in two groups based on numerical variables (cell density or gene expression), Log-rank $P$ values of each possible cutoff were computed. The cutoff that minimized the $P$ value of a log-rank test for DFS was retained, and the corresponding $P$ value was corrected using the method published by Altman and colleagues (32). These cutoffs were later used to segregate patients into two groups, and their associated Kaplan–Meier curves are displayed throughout the figures. To further confirm and validate the prognosis association of the cell densities, we determined the median and third quartile cutoff and calculated the corresponding univariate Cox-regression $P$ values (Supplementary Table S3). Only those variables univariately associated with prognosis were included in the multivariate Cox regression analysis. The duration of follow-up was calculated from the date of nephrectomy or metastasectomy to the date of death or last follow-up.

Results

Tumor infiltration by CD8$^+$ T lymphocytes and expression of Th1-associated genes correlate with poor prognosis in ccRCC

The density of CD8$^+$ T cells in the IM of the primary tumors was heterogeneous in the cohort of 135 primary ccRCC. On the basis of the Optimal $P$ value cutoff for DFS (OPv; 630 cells/mm$^2$) we found that the CD8$^{\text{High}}$ ($n = 41/135$, 30%) group had a shorter disease-free survival (DFS, $P = 0.0001$, Fig. 1A) and OS ($P = 0.001$, Fig. 1A). The density of CD8$^+$ T cells in the TC had no prognostic impact (Supplementary Table S4). The density of CD8$^+$ T cells in the IM correlated with the Fuhrman grade (Supplementary Fig. S2), but not with any other pathologic variables, including TNM (data not shown).

An independent cohort of lung metastases of ccRCC, in which the negative impact of high densities of CD8$^+$ T cells on OS had been previously described using semiquantitative counting techniques (14), was reanalyzed using a quantitative approach on 51 cases. The OPv for CD8$^+$ T cells density was 490 cells/mm$^2$, and the CD8$^{\text{High}}$ ($n = 14/51$, 27%) group displayed a shorter OS ($P = 0.001$, Fig. 1B). This result confirms our previous observations (14).

From TCGA public database of 496 primary ccRCC, we analyzed the expression of 844 immune-related genes, from which we extracted data concerning seven genes expressed in a Th1- and CD8$^+$ T-cell–oriented response according to Galon and colleagues (30). We found that the expression of most of the genes associated with this cell signature correlated with poor prognosis: CD3z $P = 0.04$, TBX21 $P = 0.03$, IFI19 $P = 0.01$, GZMB $P = 4.4 \times 10^{-5}$, and IFNG $P = 3.17 \times 10^{-7}$ that displayed the lowest $P$ value (Fig. 1C). On the basis of the OPv for IFNG, patients that had high quantities of intratumoral mRNA for this gene displayed a shorter OS ($P = 0.006$, Fig. 1D).

Simultaneous expression of immune checkpoints in primary and metastatic ccRCC identifies patients with poor clinical outcome

Primary tumors. To investigate the impact of immune checkpoint molecules on the negative prognostic impact of the CD8$^{\text{High}}$ group, we analyzed the protein expression of PD-1, LAG-3, PD-L1, and PD-L2 molecules in this group of tumors (we could analyze 40/41 tumors) and a randomly matched group of the same size ($n = 40/41$) coming from the CD8$^{\text{Low}}$.

Figure 1.

CD8$^+$ T cells and CD8/Th1 gene signature are associated with poor prognosis in ccRCC. OS and DFS according to the presence of a high or low density of CD8$^+$ T cells in the IM of primary ccRCC (A) and ccRCC lung metastases (B). The $P$ values by univariate Cox regression analysis are displayed, $P = 0.05$ dotted black line, HR $>$1.0 gray columns (C). OS according to IFNG gene expression in primary ccRCC (D).
On the basis of the OPv cutoff, 15 tumors of 80 were considered as PD-L1^High in the IM and they displayed a shorter DFS (P = 0.0005, Fig. 2A) and OS (P = 0.03, Fig. 2A). The density of PD-1^+ cells in the TC was not significantly associated with prognosis (Supplementary Table S4). The Fuhrman grade was lower with the PD-1^+ cell density in the IM (Supplementary Fig. S2).

Of the 80 patients, 9 were considered as LAG-3^High (subdivided by the OPv cutoff) in the IM and they displayed a shorter DFS (P = 0.07, Fig. 2A). The density of LAG-3^+ cells in the TC was not significantly associated with patients DFS or OS (Supplementary Table S4). Representative pictures of the IHC staining of highly and poorly PD-1– and LAG-3–infiltrated lesions are shown in Supplementary Fig. S3A and S3B, respectively.

On the basis of the 5% cutoff generally used in clinical trials with anti-checkpoint antibodies (20), 22 of 80 (27%) and 27 of 80 (34%) patients were PD-L1^+ and PD-L2^+; respectively (Supplementary Fig. S3C and S3D); among them, 9 tumors were double positive. Patients with PD-L1^+ tumors had a shorter OS than those with less than 5% positive tumor cells (P = 0.02, Fig. 2A); a trend toward shorter DFS was also found (P = 0.06, Fig. 2A). Univariately, patients with PD-L1^+ tumors were 2.9 times more likely to die in the 5 years post-nephrectomy than patients with less than 5% PD-L1^+ tumor cells [OS risk ratio, 2.87; 95% confidence interval (CI), 1.2–7.1; P = 0.02, Supplementary Table S4]. Patients with PD-L2^+ tumors displayed a shorter OS compared with those with less than 5% positive tumor cells (P = 0.005, Fig. 2A), but no impact on the DFS was found (P = 0.13, Fig. 2A). Univariately, patients with PD-L2^+ tumors were 3.4 times more likely to die than those with negative tumor cells (risk ratio, 3.4; 95% CI, 1.4–8.5; P = 0.005, Supplementary Table S4).

Patients with tumors exhibiting both high densities of PD-L1^+ lymphocytes in the IM and PD-L1^+ and/or PD-L2^+ tumor cells (n = 11) had the worst prognosis, as assessed by DFS and OS (DFS, P = 1.3 × 10^{-6}; OS, P = 0.005; Fig. 2B). Patients that met these criteria had 6.1 times more risk to progress after resection than patients who did not (risk ratio, 6.08; 95% CI, 2.4–15.0; P < 0.001, Supplementary Table S4). Strikingly, 91% of the patients having a PD1^High infiltrate and tumor cells expressing PD-L1 and/or PD-L2 progressed in the subsequent 5 years of surgery versus 36% in the negative group (complete 5-years follow-up n = 70. Fisher exact test P = 0.001, Fig. 2C). In the TCGA public datasets of 496 primary ccRCC, the gene expression of PD-L1 (PDCD1), LAG-3, and PD-L2 (PDCD1LG) was associated with shorter OS (P = 0.03, P = 0.0001, and P = 0.0003, respectively) whereas PD-L1 (CD274) was not (P = 0.67; Fig. 2D).

It has been reported that IFNγ can induce PD-L1 expression on tumor cells (27). We found a significant positive correlation between the gene expression of IFNG with PD-L1 (R = 0.13,
Figure 3.
Expression of immune checkpoints correlates with CD8+ T cells infiltration in primary ccRCC. Dot plot of the gene expression of PD-L1 (red dots) and PD-L2 (blue dots; y-axis) against IFNG (x-axis; A). Dot plot of the Log10 cell density and gene expression of PD-1 (red dots) and LAG-3 (blue dots; y-axis) against CD8 (x-axis; B). Dot plot of the Log10 cell density and gene expression of PD-1 (y-axis) against LAG-3 (x-axis; C). Pearson r value and the number of samples for each correlation are displayed. IF staining on 1 paraffin-embedded ccRCC showing the colocalization of CD8 (green), PD-1 (red), and LAG-3 (white) proteins in lymphocytes (D); nuclei are stained with DAPI.

Metastases. Metastatic ccRCC has been one cancer in which antibodies inhibiting the PD-1 axis have induced remarkable tumor regression in some patients (20), highlighting the necessity to define prognostic and predictive immune-based biomarkers in this disease. Of the 51 patients with ccRCC lung metastasis, 13 were considered as PD-1high, and the latter displayed a shorter OS ($P = 0.008$, Fig. 4A). Seven of 51 were considered as LAG-3high, and again they displayed a shorter OS ($P = 0.048$, Fig. 4A).

On the basis of a 5% cutoff, 5 of 51 (10%), and 15 of 51 (29%) metastases were PD-L1+ or PD-L2+, respectively; of them, 3 were double positive. Whereas patients with PD-L1+ metastases did not have a significantly worse clinical outcome ($P = 0.12$, Fig. 4A), the expression of PD-L2 on tumor cells was associated with a shorter OS ($P = 0.03$, Fig. 4A). Univariate patients with PD-L2+ metastasis were 2.2 times more likely to die compared with patients with PD-L2- ones (risk ratio, 2.17; 95% CI, 1.03–4.35; $P = 0.04$, Supplementary Table S4).

Patients with high densities of PD-1+ lymphocytes and PD-L1+ and/or PD-L2+ tumor cells in their ccRCC lung metastases ($n = 12$) had the worst prognosis as assessed by OS ($P = 0.003$, Fig. 4B). The patients that met these criteria had 3.1 times more risk to die after metastasectomy than patients who did not (risk ratio, 3.1; 95% CI, 1.28–6.66; $P = 0.003$, Supplementary Table S4). Strikingly, 100% of the patients having a PD1High infiltrate and metastases simultaneously expressing one or both of its ligands (PD-L1 or PD-L2) died in the subsequent 5 years after surgery versus 57% in the negative group (Fisher tests, $P$ value = 0.004, Fig. 4C).
Opposite correlations of TLS-DC and NTLS-DC with prognosis and their association with immune checkpoints

It has been shown that TLS-DC orchestrate intratumoral CD8+ cytotoxic T cells and Th1 responses in NSCLC (3, 4). In the primary ccRCC cohort (n = 135), DC-Lamp+ cells were detected within TLS (TLS-DC) in the IM. They coexisted CD83 and high amounts of MHC Class II, and were localized in the vicinity of PNAd+ high endothelial venules (HEV; Fig. 5A) as described in other tumor types (3). There was a trend where high densities of TLS-DC were associated with longer DFS (OPv = 0.09), but not with OS (Supplementary Table S4). TLS-DC densities in the TC were not associated with prognosis. Interestingly, high densities of TLS-DC (based on the OPv cutoff) in the IM identified a group of patients with good prognosis among the CD8High group for both DFS (P = 0.001, Fig. 5A) and OS (P = 0.03, Fig. 5A).

However, in contrast with NSCLC where most of the DC-Lamp+ cells are localized within TLS (4), in ccRCC a large percentage (79% ± 20%) of DC-Lamp+ cells with DC morphology was found isolated and outside TLS (NTLS-DC, Fig. 5B). They colocalized with CD34+ blood vessels, but not with PNAd+ HEV, expressed low amounts of MHC class II and were CD83 negative (Fig. 5B). The majority of NTLS-DC was localized in the IM (71±14%) and their high densities (based on the OPv cut-off) were associated with poor clinical outcome in primary ccRCC patients (DFS P = 0.006, OS P = 5.1×10-7, Fig. 5B).

The opposite influence of TLS-DC and NTLS-DC on prognosis prompted us to explore their relationships with the expression of PD-1 and its ligands in the CD8High group of patients. A negative correlation was found between the densities of TLS-DC and PD-1+ cells (r = −0.23, P = 0.04, Fig. 5C). Tumors containing PD-L1+ and/or PD-L2+ tumor cells exhibited less TLS-DC (P = 0.014; Supplementary Fig. S4), but similar densities of CD8+ T cells (P = 0.96). In contrast, the density of NTLS-DC was associated with the tumor expression of PD-L1 (OR, 6.54; 95% CI, 1.23–45.45; P = 0.012) and PD-L2 (OR, 2.7; 95% CI, 1.2–18.1; P = 0.04). Most of the patients that were PD-1High and PD-L1+ and/or L2+ (8 of 11) were also CD8High and TLS-DCLow in primary ccRCC (OR, 15.02; 95% CI, 1.66–72.7; P = 0.004), and the presence of one or both patterns correlated with shorter DFS (P < 0.0001) and OS (P = 0.001, Fig. 5D).

Identification of a group of patients with worst prognosis in primary and metastatic ccRCC

To define the independent prognostic significance of the previously mentioned immune profiles (CD8High and TLS-DCLow or PD-1High and PD-L1+ and/or L2+), we included them in a multivariate Cox regression analysis with the other significant prognostic clinical variables (TNM and Furhman grade). The strongest independent poor prognostic factors in primary ccRCC for DFS were to have a CD8High and TLS-DCLow (P = 0.001, Table 1) or PD-1High and PD-L1+ and/or PD-L2+ (P = 0.03, Table 1) immune profile. For the metastatic cohort, we found that the strongest independent worst prognostic variable for OS was being CD8High (P = 0.004, Table 1) or having a tumor with PD-1High and PD-L1+ and/or PD-L2+ immune profile (P = 0.02, Table 1).

Discussion

Compared with other neoplasia, the immune microenvironment in ccRCC has not yet been studied in detail. However, it is of paramount importance to understand its regulation in view of the paradoxical correlation of CD8+ T-cell infiltration with poor prognosis (13, 14) and the recent advances of immunotherapy with anti-checkpoint antibodies (anti PD-1 and anti PD-L1; refs. 20, 21).

cCRCC has been described as a proinflammatory neoplasia where tumor cells produce several cytokines (such as VEGF, IL6 and TGFβ; refs. 33–35) that may lead to the recruitment and
activation of polyclonal CD8$^+$ T cells (36–39). Our data suggest that these recruited CD8$^+$ T cells could only be locally educated when high densities of TLS-DC are present, and in only in these cases their density correlates with favorable prognosis. ccRCC is the first tumor type where a large proportion of DC-Lamp$^+$ cells outside TLS structures have been observed (NTLS-DC). Interestingly, we found that these cells do not express activation and costimulatory markers, and they are probably recruited directly from the blood into the tumor stroma—contrary to the usual path that DC-Lamp$^+$ cells follow in other type of tumors (5, 40).

Accordingly, several studies have shown that the ccRCC microenvironment can induce a dysfunctional DC maturation, a down-regulation of costimulatory molecules and tolerogenicity (34, 41, 42), whereas DC in the TLS are likely to be protected from these effects (43). Altogether, our results suggest that the particular proinflammatory milieu initiated by tumor cells induces the recruitment of CD8$^+$ T cells that—due to the low number of fully functional mature DC present in specialized T-cell–priming sites, or the presence of DC with suppressive phenotype—are not able to mount an effective antitumor immune response, but rather express exhaustion/inhibition molecules. This work reinforces the concept that T-cell exhaustion/inhibition (44) plays an important role in ccRCC pathogenesis. It has been described that the density of PD-1$^+$ cells (15, 16) and the tumor expression of PD-L1 (17–19) in primary ccRCC are associated with a poor clinical outcome. In this study, we confirm

Figure 5.
Characteristics of TLS-DC and NTLS-DC and their relationships with prognosis and immune checkpoints. IHC photomicrographs of DC-Lamp(Red)/CD3(Blue) illustrating the presence of mature DC in TLS (A, white arrows) or outside TLS (B, black arrows); DC-Lamp(Red)/PNAd(Blue) and DC-Lamp(Red)/CD34 (Blue) illustrating TLS-DC near HEV (A) and NTLS-DC near endothelial cells (B) in primary ccRCC. IF staining showing the colocalization of CD3 (green), DC-Lamp (red) with HLA-DR or CD83 (white) expression in TLS-DC (A), but not in NTLS-DC (B); nuclei are stained with DAPI. OS and DFS according to the presence of a high- or low-density TLS-DC in the CD8High group (A, bottom) or NTLS-DC in the entire cohort (B, bottom). Dot plot of the PD-1$^+$ against TLS-DC$^+$ cell densities (blue dots; C); Pearson $r$ value is displayed. OS and DFS according to the presence of a CD8High and TLS-DCLow and/or PD-1High and PD-L1 and/or L2$^+$ immune profiles (D).
these findings and extend them to ccRCC lung metastases. This information is highly relevant because metastatic ccRCC-treated patients have shown one of the highest objective durable response rates to PD-1 blockade (approximately 30%; ref. 20) and many efforts are being dedicated to define therapeutic tools in this pathology. Furthermore, we describe for the first time the prognostic significance of PD-L2. This molecule seems to be expressed in a higher proportion of tumors than PD-L1, and up to 30% of them might express it solely according to our results. This might be of clinical relevance because—although in two different nonrandomized cohorts—the anti–PD-L1 treatment alone seems to have a lower response rate than the anti–PD-1 (12% and 27%, respectively; refs. 20, 21). Furthermore, there are PD-L1-negative tumors that respond to anti–PD-1 treatment (22), suggesting that indeed there are other molecules beside PD-L1 implicated in the PD-1 inhibition axis of ccRCC. Few publications have reported PD-L2 mRNA or protein expression in other tumors, including primary mediastinal large B-cell lymphoma (29), NSCLC (45), ovarian (46), and esophageal (47), where it has shown a limited impact of patients’ prognosis.

To our knowledge, this is the first report on the poor prognostic impact associated with high densities of LAG-3+ cells in human tumors. Furthermore, we provide clear evidence that the expression of PD-1 and LAG-3 is highly correlated in ccRCC. Some studies on mouse models have shown a synergistic effect of the inhibition of both pathways in boosting antitumor immune response (24). Therefore, our data support the rationale of dual blockade of these molecules in ccRCC.

Although recent works have emphasized that PD-L1 is preferentially upregulated by IFNγ (31, 48), whereas PD-L2 is regulated by IL4 (49), the weak association of PD-L1 mRNA with IFNG might suggest an important role for posttranscriptional regulation of PD-L1 expression in ccRCC as for other aggressive tumors (50). Furthermore, it is highly suggestive that IFNγ can also induce PD-L2 upregulation in tumors, as in immune cells (51), and supports the rationale to use therapeutic antibodies targeting this ligand. Taken together, our results suggest that the expression of these molecules is related with a chronic inflammatory and highly suppressive process that is unselectively recruiting CD8+ and NTLS-DC cells from the circulation, and overall is associated with a poor prognosis.

Another characteristic of ccRCC is the lack of prognostic significance of the immune cells in the TC. Although CD8+, PD-1+, LAG-3+, and NTLS-DC densities in the IM of the primary tumors were associated with poor prognosis, they had no prognostic significance when present in the TC. In colorectal carcinoma, both regions are important to define the best immune score, which correlates with patient’s longer survival (30). Whether this dichotomy between ccRCC and colorectal carcinoma reflects different tumor tissue organization or relates to other factors of the tumor microenvironment remains to be clarified.

Recent unsupervised gene clustering of stage IV primary ccRCC showed that tumors with high inflammatory immune infiltrate (approximately 15%) also have a high expression of PDCD1 (PD-1) and its ligands, and correlate with the worst prognosis (52). Indeed, this inflammatory/proangiogenic profile (probably originated from the ccRCC tumor cells) found in ccRCC primary tumors and in ccRCC lung metastases (14), is not found in colorectal carcinoma lung metastases (14). Highly supporting that it may contribute to local immunosuppression process, the absence of fully mature DC, and high expression of immune checkpoints (53).

In summary, we identify a subset of primary and metastatic ccRCC patients characterized by (i) an extensive CD8+ T-cell infiltrate, (ii) expression of immune checkpoints, and (iii) the absence of fully functional DC, which is associated with poor clinical outcome. Our results highlight novel independent prognostic factors in ccRCC based on the comonquantification of densities of DC, CD8+, PD-1+, and LAG-3+ lymphocytes in addition to PD-L1/PD-L2 expression by tumor cells. These immune profiles should guide the selection of suitable patients to receive immunotherapies and need to be further validated in larger and independent cohorts. Because this choice depends on both the extent of CD8+ T-cell infiltration and the maturation and localization of DC, it invites revision of the idea that intratumoral CD8+ T cells are always associated with favorable prognosis in human tumors.

Disclosures of Potential Conflicts of Interest

Y. Vano reports receiving other research grants from Novartis and is a consultant/advisory board member for Novartis and Pfizer. G.J. Freeman has ownership interest (including patents) in Amplimmune, Boehringer-Ingelheim, Bristol-Myers Squibb, EMD Serono, Merck, Novartis, and Roche and is a consultant/advisory board member for Novartis and Roche. S.M. Oudard reports receiving speakers bureau honoraria from and is a consultant/advisory board member for Costim. W.-H. Fridman is a consultant/advisory board member for Janssen, Novartis, and Roche, and is a consultant/advisory board member for Costim. No potential conflicts of interest were disclosed by the other authors.

Authors’ Contributions

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Table 1. Multivariate Cox regression analysis for DFS and OS of the pathologic and immune variables in primary and metastatic ccRCC

<table>
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<th>Variable</th>
<th>Multivariate Cox regression analysis DFS</th>
<th>Multivariate Cox regression analysis OS</th>
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<td>Primary ccRCC</td>
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<td>CD8+ (TILs-DC)</td>
<td>3.19 (1.42–3.85)</td>
<td>1.57 (0.45–1.82)</td>
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<td>PD-L1 or L2 5%–100% + PD-I (yes vs. no)</td>
<td>1.88 (1.56–2.89)</td>
<td>2.22 (0.80–1.66)</td>
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<td>Fuhrman grade</td>
<td>1.90 (0.99–2.00)</td>
<td>2.68 (0.93–2.16)</td>
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<td>TNM stage (I–IV)</td>
<td>1.59 (0.18–2.35)</td>
<td>2.74 (1.01–3.05)</td>
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<td>Metastatic ccRCC</td>
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<td>CD8 group (high vs. low)</td>
<td>2.86 (1.21–3.10)</td>
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<td>PD-L1 or L2 5%–100% + PD-I (yes vs. no)</td>
<td>1.41 (1.19–2.48)</td>
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<td>Lymph node invasion (yes vs. no)</td>
<td>0.72 (0.35–1.42)</td>
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