Characteristics and Clinical Impacts of the Immune Environments in Colorectal and Renal Cell Carcinoma Lung Metastases: Influence of Tumor Origin

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Abstract

**Purpose:** If immune cells are involved in tumor surveillance and have a prognostic impact in most primary tumors, little is known about their significance in metastases. Because patients' survival is heterogeneous, even at metastatic stages, we hypothesized that immune cells may be involved in the control of metastases. We therefore characterized the tumor immune microenvironment and its prognostic value in colorectal and renal cell carcinoma (RCC) metastases, and compared it to primary tumors.

**Experimental Design:** We analyzed by immunohistochemistry (n = 192) and qPCR (n = 32) the immune environments of colorectal carcinoma and RCC lung metastases.

**Results:** Metastases from colorectal carcinoma and RCC have different immune infiltrates. Higher densities of DC-LAMP 

+ mature dendritic cells (P < 0.0001) and lower densities of NKp46 

+ NK cells (P < 0.0001) were observed in colorectal carcinoma as compared to RCC metastases, whereas densities of T cells were similar. High densities of CD8 

+ T cells cytotoxic orientation or of mature dendritic cells correlated with improved survival in RCC (P = 0.008) and shorter OS in RCC (P < 0.0001). High NK-cell densities were associated with improved survival in RCC (P = 0.002) but not in colorectal carcinoma. Densities of immune cells correlated significantly from primary to relapsing metastases for the same patient. A Th1 orientation was found in colorectal carcinoma metastases, whereas a heterogeneous immune gene expression was found in RCC metastases.

**Conclusions:** Our results show a major prognostic value of the immune pattern (CD8+/DC-LAMP+ cell densities) in colorectal carcinoma and RCC, reproducible from primary to metastatic tumors, although with opposite clinical impacts, and highlight the role of the tumor cell in shaping its immune environment. *Clin Cancer Res; 19(15): 1–13. ©2013 AACR.*
Translational Relevance

This article demonstrates for the first time, in a large cohort of patients with lung metastasis from 2 different primary tumors, colorectal and renal cell carcinoma, that densities of CD8+ T cells and DC-LAMP+ mature dendritic cells ("immune pattern"), evaluated in paraffin sections, were independent prognostic factors of patients' survival, and stronger prognosticators than currently evaluated clinical and pathological parameters. Furthermore, tumor immune environment is reproduced throughout cancer disease, from primary tumor to relapsing metastasis. This finding is the first important step for further extensive studies on the role of the tumor cells in shaping their own immune environment and the patients' outcome.

escape local and systemic immune control (19) and consequently invade and metastasize in distant organs. This hypothesis would predict that the immune microenvironment in metastatic sites should be poor and have no impact on clinical outcome. Only a limited number of studies have reported the presence of immune cells in metastatic lesions. They showed that high densities of CD8+ T cells were associated with longer survival in colorectal carcinoma (20) and ovarian cancer (21), and potential response to chemotherapy in liver metastases from colorectal carcinoma (22). Another question, which remains largely unanswered, concerns the respective roles of the malignant cells and the seeding organ in shaping the immune microenvironment.

We therefore analyzed the immune environment of colorectal carcinoma and RCC metastases seeded in a same organ, the lung, compared coincident and relapsing metastases in the lung, and the primary tumor from the same patients, and determined their clinical impacts. We report that tumor cells induce a characteristic and reproducible immune pattern in the primary and metastatic tumors, supporting the hypothesis that the malignant cells, rather than the host organ, shape their microenvironment. We found that a high infiltration by DC-LAMP+ mature dendritic cells and CD8+ T cells is a major predictor of good survival in lung metastases from colorectal carcinoma, whereas it is associated with poor survival in lung metastases from RCC. This shows that the immune microenvironment pattern remains a major prognostic factor even in advanced cancer stages, but with different consequences depending on the origin of the primary tumor. Altogether our results suggest a strong influence of the tumor origin on the immune environment characteristics and clinical impact.

Patients and Methods

Patients

We constituted a retrospective and unselected cohort of 140 patients with colorectal carcinoma lung metastasis operated at Hôtel-Dieu hospital between 2000 and 2010 and 52 patients with RCC lung metastasis, operated at Hôtel-Dieu or Laennec/Hôpital Européen Georges Pompidou hospitals between 1992 and 2010. In the RCC series, 51 of 52 patients were treated with radical nephrectomy and 1 with partial nephrectomy. None of the patients had signs of local recurrence of primary tumor. We also analyzed 25 colorectal carcinoma and 24 RCC primary tumors from the same patients, operated at Saint-Antoine, Cochin, or Necker-Enfants Malades hospitals between 1987 and 2008. In addition, 14 coincident and 12 recurrent colorectal carcinoma lung metastases from the same patients were studied. Altogether, 218 lung metastases from 192 patients were analyzed.

Among these 192 patients, 32 frozen samples of lung metastases were available for patients with colorectal carcinoma (n = 19) or RCC (n = 13).

Baseline characteristics of these patients are summarized in Supplementary Tables S1 and S2.

All experiments were conducted with the agreement of the Ile de France II ethics committee (no. 2012-0612).

Immunohistochemistry

For each tumor, 2 observers (R. Remark and D. Damotte, A. Lupo, A. Cazes, L. Gibault, or V. Verkarre, expert pathologists) selected the tumor section containing the highest density of immune cells on hematoxylin and eosin stained slides. Serial 5-μm formalin-fixed and paraffin-embedded tissue sections were stained with autostainer Link 48 (Dako). Tissue sections were incubated with primary antibodies [CD3 polyclonal antibody (Dako), CD8 (SP16, Spring Bioscience), CD20 (L26, Dako), DC-LAMP (1010.01, Dendritics), granzyme B (11F1, Novocastra), NKp46 (195314, R&D Systems), or PNAd (MECA-79, BD Pharmingen)] followed by secondary antibodies coupled with biotin or alkaline phosphatase. Biotinylated antibodies were coupled with streptavidin-peroxidase and peroxidase activity was revealed using 3-amino-9-ethylcarbazole substrate (Vector Laboratories). Alkaline phosphatase activity was revealed using alkaline phosphatase substrate III (Vector Laboratories).

The density of DC-LAMP+ cells was manually counted on the entire section as previously described (23). CD3+, CD8+, granzyme B+, and NKp46+ cells were counted in the center of the tumor and in the invasive margin of the tumor with the convergence to the mean method (24). For each slide, 40 to 100 high-power fields (1.37–3.43 mm²) were examined on each tumor zone. Both immunostaining and scoring were evaluated by 3 independent observers blinded to clinical data (R. Remark, L. Crozet, and A. Lupo, expert pathologist).

Gene expression analyses

RNA from the frozen tissues of 32 lung metastases was extracted with the RNeasy Mini Kit (Qiagen) according to the manufacturer's instructions and controlled for quantity and quality on an Agilent 2100 Bioanalyzer (Agilent Technologies). Then, reverse transcription PCR was conducted with the High-Capacity cDNA Reverse
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Transcription kit (Applied Biosystem). Finally, the quantitative gene expression analysis of selected targets was conducted in duplicates with the TaqMan Human Immune Array on an Applied Biosystems 7900HT Fast Real-Time PCR System. Expression levels of genes were determined using threshold cycle (Ct) values normalized to actin B (ΔCt) and were represented using the Genesis program.

Statistical analyses

We used the Mann–Whitney test to compare the densities of infiltrating immune cells in the different tumors and ΔCt, and the Wilcoxon matched pairs test to compare the density of infiltrating immune cells in different tumors from the same patient. Because all gene expression comparisons were preplanned and the 51 genes clustered according to their immune functions before analysis, the P values were not corrected by Bonferroni or similar methods. Correlations were evaluated by the Spearman test. Overall survival (OS) curves were estimated by Kaplan–Meier method and differences between the groups of patients were calculated using the log-rank test. The start of follow-up for OS was the time of lung surgery.

Figure 1. Prognostic value of the densities of CD8⁺ T cells, DC-LAMP⁺ mature dendritic cells, and NKp46⁺ NK cells in lung metastases from colorectal carcinoma. Kaplan–Meier curves for the duration of OS according to a separated (A, B) and combined (C) analysis of CD8⁺ and DC-LAMP⁺ densities in colorectal carcinoma lung metastases. D, Kaplan–Meier curves for the duration of OS according to the densities of NKp46⁺ cells in colorectal carcinoma lung metastases (n = 84). The numbers of at risk patients according to a separated and combined analysis of CD8⁺ and DC-LAMP⁺ densities and NKp46⁺ cells densities were given. Statistical comparison was conducted by the log-rank test and all OS log-rank P values were corrected using the formula proposed by Altman and colleagues.

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metastasis diagnosis to surgery (RCC), disease-free interval (RCC), alkaline phosphatase, hemoglobin, neutrophils, and platelets levels (RCC). The lower limit of normal was used for hemoglobin (cutoff values: men \(= 13 \text{ g/dL} \) and women \(= 12 \text{ g/dL} \)) and the upper limit (ULN) was used for alkaline phosphatase (cutoff value: 80 \(\text{U/L} \)), neutrophils (cutoff value: \(7500/\text{mm}^3\)), and platelets (cutoff value: \(400,000/\text{mm}^3\)). With respect to immune cell densities and number of metastases, the "minimum \(P\) value" approach was used to determine the cutoff for the best separation of patients referring to their OS outcome (outcome-oriented approach). Because the \(P\) values obtained might be overestimated, OS log-rank \(P\) values were corrected using the formula proposed by Altman and colleagues (25) and using 10-fold cross-validations as recommended by Faraggi and colleagues (26). The confidence interval was important around the optimal \(P\) value (Supplementary Table S3). We have also ensured that the significance established at the optimal cutoff remained valid at the quartiles (data-oriented approach). A \(P\) value less than 0.05 was considered statistically significant. Independent parameters

**Figure 1. (Continued)** E, expression of genes related to immune cell populations, \(T_{H_1}/T_{H_2}\) orientations, inflammation, angiogenesis, immuno-suppression, cytotoxicity, chemokines/chemokine receptors according to the densities of CD8\(^+\) and DC-LAMP\(^+\) cells (high/high vs. low/low) in lung metastases from colorectal carcinoma. Expression levels of genes were determined using threshold cycle (\(\Delta\text{Ct}\)) values normalized to \(\beta\text{actin B (ACTB)}\). We used Mann–Whitney test to identify genes with significantly different levels of expression among patient groups (high vs. low CD8\(^+\)/DC-LAMP\(^+\) densities). 

\(^*\); \(P < 0.05\) for individual gene expression.
identified at univariate analysis as possibly influencing outcome ($P < 0.1$) were introduced in a multivariate Cox proportional hazards regression model. All analyses were conducted with Prism 5 (GraphPad), Statview (Abacus Systems), and the R (http://www.r-project.org/).

**Results**

**The densities of immune cells correlate with OS in lung metastases from colorectal carcinoma**

Because densities of CD8$^+$ T cells and DC-LAMP$^+$ mature dendritic cells in primary tumors correlate with survival (1), we counted these cells in lung metastases from 140 colorectal carcinoma patients. We also quantified NKp46$^+$ NK cells as a marker of innate immune response. High densities of infiltrating CD8$^+$ T cells (Fig. 1A) and mature dendritic cells (Fig. 1B) were associated with prolonged OS ($P = 0.039$ and 0.001, respectively). Combination of these 2 immune parameters allowed to identify patients with better outcome (CD8$^+$high/DC-LAMP$^+$high; Fig. 1C, $P = 0.008$). NKp46$^+$ cell density did not predict clinical outcome ($P = 0.12$; Fig. 1D). Significance was established at the optimal cutoff, but remained valid at quartiles including the median (Supplementary Table S3). The quantification of CD8$^+$ T cells separately in the center of the tumor and the invasive margin yielded similar results (Supplementary Fig. S1). Univariate analysis of other clinical and pathological parameters is reported in Table 1. At multivariate analysis (Table 1), immune pattern (CD8$^+$ /DC-LAMP$^+$ densities) of metastases was the strongest independent predictor of survival.

As reported in colorectal carcinoma primary tumors (3), gene expression analyses revealed that a strong CD8$^+$ and DC-LAMP$^+$ cell infiltration was associated with a higher

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**Table 1. Univariate and multivariate Cox proportional hazards analyses for OS according to clinical parameters and immune cell densities in colorectal carcinoma and RCC lung metastases**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Colorectal carcinoma lung metastases</th>
<th>RCC lung metastases</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
<td>Univariate analyses</td>
<td>Multivariate analyses</td>
</tr>
<tr>
<td></td>
<td>HR 95% CI $P$ value</td>
<td>HR 95% CI $P$ value</td>
</tr>
<tr>
<td>Stage$^6$ (stage 3 + 4 vs. stage 1 + 2)</td>
<td>1.68 (0.88–3.20) 0.116</td>
<td>Not included in the multivariate analysis</td>
</tr>
<tr>
<td>Presence of extrathoracic metastases (yes vs. no)</td>
<td>1.56 (0.88–2.75) 0.128</td>
<td>Not included in the multivariate analysis</td>
</tr>
<tr>
<td>Completeness of resection (R1 vs. R0)</td>
<td>2.49 (0.77–8.05) 0.129</td>
<td>Not included in the multivariate analysis</td>
</tr>
<tr>
<td>CEA level (&gt;5 ng/mL vs. ≤5 ng/mL)</td>
<td>1.55 (0.86–2.82) 0.148</td>
<td>Not included in the multivariate analysis</td>
</tr>
<tr>
<td>NK cells (high vs. low)</td>
<td>0.58 (0.28–1.16) 0.123</td>
<td>Not included in the multivariate analysis</td>
</tr>
<tr>
<td>Thoracic lymph node invasion (yes vs. no)</td>
<td>1.49 (0.60–3.66) 0.503</td>
<td>Not included in the multivariate analysis</td>
</tr>
<tr>
<td>Number of metastases (≤2 vs. &gt;2)</td>
<td>1.84 (1.03–3.28) 0.0405</td>
<td>2.17 (1.20–3.93) 0.011</td>
</tr>
<tr>
<td>Immune pattern (high/mix/low)</td>
<td>0.54 (0.39–0.76) 0.0002</td>
<td>0.54 (0.39–0.75) 0.0003</td>
</tr>
<tr>
<td>Immune pattern (high/mix/low)</td>
<td>2.68 (1.58–4.57) 0.00028</td>
<td>2.70 (1.37–5.29) 0.0039</td>
</tr>
</tbody>
</table>

NOTE: To be able to conduct regression with a categorical variable, they were coded before entered into the Cox model. Parameters with significant impact on survival appear in bold.

$^6$The stage was determined by pathologic examination at the time of diagnosis. None of the variables violated the proportional hazards assumption.
expression of genes linked to Th1 orientation, cytotoxicity, and lymphoid chemokines/chemokine receptors in lung metastases (Fig. 1e). Expressions of clusters of genes associated with Th2 orientation, inflammation, angiogenesis, or immunosuppression were not correlated with the CD8+/DC-LAMP+ densities. However, individual gene expression of VEGF was inversely correlated with CD8+/DC-LAMP+ infiltration, as reported in primary colorectal carcinoma.
whereas that of IL17 and CTLA4 were positively correlated (Fig. 1e). The in situ immune pattern is reproduced from primary tumors to metastases in colorectal carcinoma

To investigate whether the in situ immune pattern varies during the course of the metastatic disease for a given patient, we analyzed coincident colorectal carcinoma lung metastases occurring in the other lung side (n = 14) operated 1 to 9 months after the initial metastatic surgery, and/or relapsing metastasis occurring 14 to 52 months after surgical removal of the lung metastasis (n = 12; Fig. 2A). Densities of CD8+ (Fig. 2B), DC-LAMP+ (Fig. 2C), and NKp46+ (Fig. 2D) cells were not significantly different between 2 coincident metastatic sites or between the first lung metastasis and its relapse. We found correlations in the densities of immune cells between coincident and relapsing metastases (Fig. 2B–D).

To address the question of the relationship between immune cell densities in the primary tumor and metastasis, we compared immune infiltrates of primary tumors and lung metastases from the same individuals (n = 25; Fig. 2E). Primary colorectal carcinoma differed from lung metastases by significantly higher density of CD8+ T cells (P < 0.05; Fig. 2F), but the density of each cell type was positively correlated between the primary and the metastatic tumors (Fig. 2F–H for CD8+, DC-LAMP+, and NKp46+ cells, respectively). We had access to a small number (n = 5) of matched hepatic metastases and the correlation was also found between primary colorectal carcinoma, lung, and liver metastases (data not shown).

The densities of immune cells correlate with OS in lung metastases from RCC

We have also analyzed a cohort of 52 RCC lung metastases. Patients with high densities of infiltrating CD8+ T cells (3, 27) whereas that of IL17 and CTLA4 were positively correlated (Fig. 1e).

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clinical oncology and RCC lung metastases.

Because CD8$^{+}$, DC-LAMP$^{+}$, and NKP46$^{+}$ cell densities in lung metastases have different clinical impacts in colorectal carcinoma and RCC, we compared their microenvironments. Histologic analyses revealed profound differences between colorectal carcinoma and RCC lung metastases. We found glands, often necrotic, in an abundant and collagenous stroma surrounded by a high density of tertiary lymphoid structures (TLS) in colorectal carcinoma metastases (Fig. 5A). In contrast, in RCC metastases, tumor cell nests were separated by a thin stroma with few and scattered TLS (Fig. 5A). TLS contained a B-cell follicle, a T-cell zone, and PNA$^{+}$ high-endothelial venules (Fig. 5B).

We found similar densities of CD3$^{+}$ and CD8$^{+}$ T cells in the whole tumor zone (Fig. 5C). Mature dendritic cells, located in the T-cell area of TLS, were found at higher density in colorectal carcinoma than in RCC ($P < 0.0001$; Fig. 5B and C), in accordance with the higher number of TLS in colorectal carcinoma lung metastases. The colorectal carcinoma metastases contained significantly lower densities of NK cells as compared to RCC metastases ($P < 0.0001$; Fig. 5B and C). No significant differences in the densities of CD8$^{+}$, DC-LAMP$^{+}$, and NKP46$^{+}$ cells were observed in tumors from colorectal carcinoma or RCC patients having received or not preoperative treatment (chemotherapy, IL-2/IFN, or association of bevacizumab and chemotherapy; Fig. S3 and Supplementary Tables S1 and S2 for treatment details).

Although expression of genes linked to adaptive immune populations was not significantly different between both types of metastatic tumors, we found a lower expression of CD68 gene in colorectal carcinoma lung metastases.
A similar TH1 orientation was found in colorectal carcinoma and RCC metastases, but a stronger expression of genes linked to TH2 was detected in RCC lung metastases. Genes linked to acute inflammation were upregulated in colorectal carcinoma lung metastases and genes linked to chronic inflammation, angiogenesis, or immunosuppression were upregulated in RCC lung metastases. A higher expression of cytotoxicity-related genes in RCC metastases was observed, in accordance with their higher NK-cell content. Chemokines and receptors genes prone to attract TH1, T regulatory, and dendritic cells were more expressed in colorectal carcinoma metastases, whereas RCC lung metastases were characterized by the expression of inflammatory chemokines and chemokine receptors genes.

**Discussion**

The objective of our study was to characterize the immune microenvironment of metastatic lesions and its clinical impact. If several clinical parameters have been reported to be associated with survival in metastatic patients, none has obtained general agreement (17, 28), justifying the search of new nonclinical prognostic markers. We report here a major prognostic value of the immune pattern (densities of mature dendritic cells and CD8<sup>+</sup> T cells) in metastases from colorectal carcinoma and RCC, although with opposite impact on OS. In our cohorts of oligometastatic surgically treated patients, the strongest prognosticator was the immune pattern, that is CD8<sup>+</sup> and DC-LAMP<sup>+</sup> cell density combination, as reported for many primary tumors (1–13, 23, 27, 29–31). NK cells density had also a prognostic value in RCC. It seems that the immune pattern is a powerful prognostic factor and a potentially important parameter for metastatic patients' management. Because of the incomplete data collection (especially for laboratory values which were difficult to collect in a retrospective analysis), conclusions remain difficult to draw on the prognostic value of the Memorial Sloan-Kettering Cancer Center (32) and Heng and colleagues (33) prognostic factor models. Our previous studies showed the highly clinical impact of the CD8<sup>+</sup> cell densities in primary colorectal carcinoma up to stage III, that is without distant metastases at the time of diagnosis (2). In this study, the impact of the immune pattern on OS was lower in primary tumors \( (P = 0.15 \text{ and } 0.01 \text{ for } \text{CD8}^+ \text{ and } \text{DC-LAMP}^+ \text{ cells, respectively; data not shown}) \) than in lung metastases from colorectal carcinoma \( (P = 0.039 \text{ and } 0.001 \text{ for } \text{CD8}^+ \text{ and } \text{DC-LAMP}^+ \text{ cells, respectively; data not shown}) \).
Clinical significance of CD8$^+$ T cells density seems to be contrasted, according to primary tumor's origin. Although we found similar densities of CD8$^+$ T cells in both colorectal carcinoma and RCC metastases, the prognostic value of these cells was different. Similar conflicting observations about the prognostic role of immune infiltrate have been reported in primary colorectal carcinoma and RCC (2, 4, 15, 27) and one could hypothesize that the seeding organ (colon or kidney) may explain this variability in the outcome. Because it remains valid in the lung metastases, our data support the idea that the kind of primary tumor is essential in determining the prognostic value of the host immune infiltrate at metastatic level. This is in accordance with the fact that primary RCC seems as an exception to the well-documented general findings that Th1/CD8 immune cell infiltrate and high density of mature dendritic cells correlate with favorable prognosis in the majority of solid tumors (1). The differential clinical impacts of the T cells might be due to their site of activation. Indeed, we have previously reported that TLS in early stages of non–small cell lung cancer may act as potential structures of antitumor T-cell generation (23, 34). We found more TLS, reflected by higher densities of mature dendritic cells and higher expression of CCL19 gene, a chemokine expressed in TLS (34), in colorectal carcinoma than in RCC metastases. Because TLS are scarce in RCC lung metastases and numerous in lung metastases from colorectal carcinoma, one may postulate that the T cells present in the former have not been educated in tumor-adjacent TLS (35) and reflect rather a chronic inflammatory reaction which is known to be deleterious for the host (36). Indeed, gene expression analyses revealed significant differences between lung metastases from colorectal carcinoma and RCC, which share a Th1 profile, but the latter exhibit also a Th2, inflammatory, and immune-suppressive pattern. The high expression of VEGF, IL-6, and M-CSF genes in RCC may also inhibit the differentiation of dendritic cells and induce monocyte differentiation to macrophages (37–39), which could initiate an impaired T-cell response in RCC, resulting in poor prognosis. Interestingly, VEGF gene expression was positively correlated with high CD8$^+$ and DC-LAMP$^+$ infiltration in RCC lung metastases and with low CD8$^+$ and DC-LAMP$^+$ infiltration in colorectal carcinoma lung metastases. Because it has been suggested that VEGF may induce non-coordinated immune responses (27), affect cytotoxic Th1 adaptive immune responses (39, 40) and contribute to the progression of malignant disease, the correlation between CD8$^+/DC$-LAMP$^+$ densities and VEGF expression could be one explanation among others to explain the negative impact associated with this immune signature. Moreover, staining] showing the organization of tumors. Original magnification: $\times$ 40 and $\times$ 200. TLS, tertiary lymphoid structure; T, tumor; S, stroma. B, location and organization of CD20$^+$ B-cell follicles (red) surrounded by high-endothelial venules (blue), DC-LAMP expressing mature dendritic cells (red, black arrows), CD3$^+$ T cells (red), CD8$^+$ T cells (red), and NKp46$^+$ NK cells (red) in colorectal carcinoma (left) and RCC (right) lung metastases. Original magnification: $\times$ 200 and $\times$ 400.
upregulation of IL6 and STAT3 genes in the CD8\textsuperscript{high}/DC-LAMP\textsuperscript{high} group could reflect the inflammatory milieu of the RCC microenvironment (41, 42). It could also explain the reasons that immunotherapies, which modify the acute/chronic inflammatory microenvironment, are often reported to have some efficacy in metastatic renal cell carcinoma (43).

The Von Hippel Lindau phenotype, often found in RCC, may also be involved in the shaping of peculiar tumor microenvironments, through induction of hypoxia, production of VEGF, induction of regulatory immune circuits (44–47), and increased sensitivity of tumor cells to NK-cell lysis (48). It may also influence differently the stroma characteristics, the vascularization, or the collagen content which could also impact on the migration, organization, and functionality of intratumor immune cells (49). Together, these data may explain the negative clinical impact of the adaptive immune pattern at the primary and advanced stages of RCC.

We found that colorectal carcinoma and RCC have a correlated pattern of DC-LAMP\textsuperscript{+}, CD8\textsuperscript{+}, and NKp46\textsuperscript{+} cells, from primary tumor to relapsing metastasis, which could reflect, either a potential "imprinting" of the immune microenvironment by the tumor cells or the possibility that the immune contexture in the primary tumor, results in "educated" immune cells that are recalled in the metastatic sites.

In conclusion, our findings highlight the fact that during all steps of cancer development, reciprocal interactions occur between immune and cancer cell and are critical for patients’ survival. The immune signature seems to be a phenotypic

Figure 5. (Continued) C, quantification of CD3\textsuperscript{+}, CD8\textsuperscript{+}, DC-LAMP\textsuperscript{+}, and NKp46\textsuperscript{+} cells in lung metastases from colorectal (colorectal carcinoma-LM, \(n = 140\)) and renal cell carcinoma (RCC-LM, \(n = 52\)). Whiskers length represents 10 to 90 percentile. ns, not significant; *** \(P < 0.0001\) (Mann–Whitney test).

D, heat map of the expression levels of genes according to the origin of lung metastases (colorectal carcinoma and RCC) represented using the Genesis program. LM, lung metastasis; ns, not significant; *, \(P < 0.05\) (Mann–Whitney test).
marker for the disease and is remarkably reproduced between primary and metastatic sites in the same patient. The immune contexture affects OS in lung metastases from colorectal carcinoma and RCC, and the analysis of the immune pattern might be useful to guide therapeutics (50).

Disclosure of Potential Conflicts of Interest

S. Ouardard has honoraria from speakers bureau of Sanofi, Roche, Novartis, BMS, Takeda, and Jansen. No potential conflicts of interest were disclosed by the other authors.

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Conception and design: R. Remark, J.-F. Régnard, C. Sautès-Fridman, W.H. Fridman, D. Damotte
Development of methodology: R. Remark, M.-C. Dieu-Nosjean, D. Damotte
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): R. Remark, M. Alfiano, A. Lupu, M. Riquet, H. Ouakrim, J. Goc, A. CASEZ, J.F. Flejou, I. GIBAUD, J.-F. Régnard, O.N. Pages, S. Ouardard, D. Damotte
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): R. Remark, M. Alfiano, I. CRENER, M.-C. Dieu-Nosjean, S. Ouardard, W.H. Fridman, D. Damotte
Writing, review, and/or revision of the manuscript: R. Remark, M. Alfiano, I. CRENER, M.-C. Dieu-Nosjean, J. Goc, S. Ouardard, C. Sautès-Fridman, W.H. Fridman, D. Damotte

Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): R. Remark, L. Crozet, A. CASEZ, L. Gibault, V. Verkarre, B. Mlecnik, C. Sautès-Fridman, W.H. Fridman, D. Damotte
Study supervision: W.H. Fridman, D. Damotte

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