Myeloid-Derived Suppressor Cells Predict Survival of Patients with Advanced Melanoma: Comparison with Regulatory T Cells and NY-ESO-1- or Melan-A–Specific T Cells

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Abstract

Purpose: To analyze the prognostic relevance and relative impact of circulating myeloid-derived suppressor cells (MDSC) and regulatory T cells (Treg) compared with functional tumor antigen–specific T cells in patients with melanoma with distant metastasis.

Experimental Design: The percentage of CD14+CD11b+HLA-DR−/low MDSCs, CD4+CD25+FoxP3+ Tregs, and the presence of NY-ESO-1- or Melan-A–specific T cells was analyzed in 94 patients and validated in an additional cohort of 39 patients by flow cytometry. Univariate survival differences were calculated according to Kaplan–Meier and log-rank tests. Multivariate analyses were performed using Cox regression models.

Results: NY-ESO-1–specific T cells, the M-category, and the frequency of MDSCs were associated with survival. The absence of NY-ESO-1–specific T cells and the M-category M1c independently increased the risk of death. In a second Cox model not considering results on antigen-specific T cells, a frequency of >11% MDSCs showed independent impact. Its association with survival was confirmed in the additional patient cohort. Median survival of patients with a lower frequency of MDSCs was 13 months versus 8 months for others (P < 0.001, combined cohorts). We observed a strong correlation between high levels of MDSCs and the absence of melanoma antigen–specific T cells implying a causal and clinically relevant interaction. No prognostic impact was observed for Tregs.

Conclusions: Circulating CD14+CD11b+HLA-DR−/low MDSCs have a negative impact on survival and inversely correlate with the presence of functional antigen–specific T cells in patients with advanced melanoma. Our findings provide a rationale to investigate MDSC-depleting strategies in the therapeutic setting especially in combination with vaccination or T-cell transfer approaches.

Introduction

The prognosis of patients with melanoma with unresectable distant metastasis is poor, with a median survival time of 9 months (1). Lactate dehydrogenase (LDH) is the only well-established blood biomarker, and has been part of the AJCC staging system since 2001 (2). We have previously demonstrated that circulating functional T cells targeting certain melanoma-associated antigens have strong prognostic impact in patients with melanoma (3). Whether other circulating immune cells such as regulatory T cells or myeloid-derived suppressor cells also have prognostic impact has so far only been analyzed in small cohorts of patients with melanoma (4–7). In addition to prognostic information, which may influence therapeutic decisions, immune system–based biomarkers might serve as predictive markers for response to immunotherapies.
Translational Relevance

The level of myeloid-derived suppressor cells (MDSC) in the peripheral blood is strongly associated with survival of patients with melanoma with distant metastasis. After further validation, the MDSC level may represent a candidate to serve as a prognostic factor for stratification/classification purposes and for patient counseling. The correlation between high levels of MDSCs and the absence of melanoma antigen–specific T cells emphasizes their key role in the adaptive immune system. Our observations provide a rationale to investigate a potential predictive function of the MDSC levels about outcome of immunotherapies and to investigate MDSC-depleting strategies in the therapeutic setting, especially in combination with vaccination or T-cell transfer approaches.

Patients and Methods

Patients

Cryopreserved peripheral blood mononuclear cells (PBMC) were accessed from the Department of Medical Oncology and Immunotherapy (Siena, Italy) and the Departments of Dermatology (Essen and Tübingen, Germany). PBMCs had been immediately isolated from fresh blood by Ficoll/hypaque density gradient centrifugation and cryopreserved until usage. Inclusion criteria were presence of unresectable distant melanoma metastasis at the time of blood draw and available follow-up data after blood draw. If the number of available PBMCs allowed the full spectrum of analyses or if results of the analysis of NY-ESO-1 or Melan-A–responsive T cells was already known (n = 48) from the already published related project (3) patients were allocated to cohort 1. In samples with a low cell number, the analysis was limited to the ex vivo analysis of Tregs and MDSCs (cohort 2). All patients gave their written informed consent for biobanking. This study was approved by the Ethics Committee, University of Tübingen (approvals 425/2012BO2 and 524/2012BO2).

Analysis of immune cell subsets

All analyses were performed centrally by 2 investigators (A. Martens and H. Zelba). PBMCs were thawed using a step 2 procedure by incubation for 1 to 2 minutes in a 37°C water bath, followed by addition of equal amounts of 4°C cold RPMI 1640 (Life Technologies GmbH), before and after incubation for 5 minutes at room temperature. After thawing, different populations of immune cells were evaluated immediately using multicolor flow cytometry. For analysis of MDSCs and Tregs, Fc receptors were initially blocked with Gamunex (human immunoglobulin; Bayer), and dead cells were labeled for exclusion with ethidium monoazide (EMA; Invitrogen).

MDSCs were characterized by the CD14+CD11b+HLA-DR−/flow phenotype (6, 7, 18, 19, 32). PBMCs were stained with CD3/PerCP, CD4/PerCP, CD8/PerCP, HLA-DR/PerCP-Cy5.5, CD11b/APC-Cy7 (BD Biosciences), and CD14/Per-Cy7 (BioLegend). The percentage of MDSCs was calculated as the relation between CD14+CD11b+HLA-DR−/flow cells and all viable PBMCs.

Tregs, which were characterized by the CD25+FoxP3+ phenotype (33), were stained with CD25/PE, CD4/PerCP, and CD8/APC-H7 (BD Biosciences). After fixation and permeabilization with Human FoxP3 buffer (BD Biosciences), cells were surface stained with CD3/Pacific Orange (Invitrogen) and intracellularly stained with FoxP3/Alexa647 (BD Biosciences). The percentage of Tregs was calculated as the relation between CD25+FoxP3+ cells and all CD4+ cells.

NY-ESO-1- and Melan-A–specific T-cell responses were detected as described previously (3). Briefly, cells were stimulated with protein-spanning overlapping peptides (1 μg/mL; PepMix; IPT Peptide Technologies). After culture for 12 days, T cells were restimulated at a ratio of 1:2 with autologous, fluorescent-labeled PBMCs (5 μmol/L CFSE;
Invitrogen; replaced after February 2012 by 10 μmol/L Cell Proliferation Dye eFluor 450; eBioscience) either unpulsed (negative control) or presenting one of the antigens in the presence of Golgi-Plug (1 μL/mL; BD Biosciences) for 12 hours. Alternatively, if cell numbers were limited, T-cell cultures were restimulated by addition of peptides alone. After blocking with Gamunex and labeling with EMA cells were fixed and permeabilized with CytoFix/CytoPerm (BD Biosciences) and stained with the following antibodies: CD3/Qdot655, CD4/Pacific Orange (both Invitrogen), CD8/APC-H7, IL-4/APC, IFN-γ/PE-Cy7 (all BD Biosciences), TNF/PE (Miltenyi Biotec), IL-10/Pacific Blue, IL-17/PerCP-Cy5.5 (both eBioscience), and IL-2/Alexa700 (BioLegend). After February 2012, subsequent analyses were performed with an optimized panel that was identical except for the following positions: CD3/eFluor605 (eBioscience), CD4/PerCP (BD Biosciences), TNF/FITC (BioLegend), IL-10/PE (eBioscience). Antigen-specific T cells were defined as being present if the following criteria were met for at least 1 of the 6 analyzed cytokines. The cytokine-producing cell population had to be clearly distinguishable from nonproducing cells and the ratio between the peptide-pulsed and -unpulsed samples had to be greater than 2. Samples were measured immediately using an LSR II and FACSDiva software (both BD Biosciences). Data were analyzed using FlowJo software (Tree Star Inc.).

Figure 1.

Kaplan–Meier survival curves of nonresectable stage IV patients according to the frequency of circulating CD14+CD11b+HLA-DR−/low MDSCs (A), CD4+CD25+FoxP3+ Tregs (B), the presence of NY-ESO-1–specific T cells (C), and according to the M-category (D).
presented. Multivariable Cox proportional hazard analyses were used to determine the independent effects of prognostic factors. Patients with missing data in variables analyzed in the given Cox regression model were excluded. Models were established using backward and forward stepwise procedures. Remaining nonsignificant factors were assessed for potential confounding effects. Changes in the estimates of factors in a model by more than 5% were taken as indicative for confounding. Results of the Cox model were described by means of HRs together with 95% CIs, and P values were based on the Wald test. Associations between presence of antigen-specific T cells and frequencies of MDSCs were calculated by the $\chi^2$ and Fisher exact tests.

Throughout the analysis, $P$ values less than 0.05 were considered statistically significant. All analyses were carried out using SPSS Version 21 (IBM SPSS).

### Results

#### Patients

For the most detailed investigations, 94 patients were included with enough PBMCs available for the full spectrum of analyses including the detection of NY-ESO-1- and Melan-A–specific T cells (cohort 1). The MST was 10 months. Median follow-up was 15 months for patients who were alive at the last follow-up, and 8 months for patients who died. Of 93 patients with known M-category, 67 were assigned to the M-category M1c (72%) and 13 (14%) each to M1a and M1b. Median age was 56 years with an interquartile range of 48 to 69 years, and 63.8% were male. NY-ESO-1- or Melan-A–specific T cells were detectable in 52.1% and 39.4% of patients, respectively. The median percentage of MDSCs and Tregs was 11.3% and 6.7%, respectively.

#### Survival analysis

Kaplan–Meier analysis of 94 patients (Table 1) showed that the presence of functional NY-ESO-1–specific T cells ($P < 0.001$), a low frequency of MDSCs ($P = 0.011$), and the M categories M1a/M1b ($P = 0.012$) were associated with prolonged survival. No differences in disease outcome were observed according to the frequency of Tregs ($P = 0.64$) and similarly according to the frequency of MDSCs (59.9% for $\leq 11\%$ MDSCs vs. 30.4% for $>11\%$ MDSCs). The largest

### Table 1. Patient characteristics and analysis of overall survival in cohort 1

<table>
<thead>
<tr>
<th>Prognostic factor</th>
<th>n</th>
<th>%</th>
<th>% Dead</th>
<th>1-year survival rate (95% CI) (%)</th>
<th>2-year survival rate (95% CI) (%)</th>
<th>$P^a$</th>
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<tbody>
<tr>
<td>All patients</td>
<td>94</td>
<td>100</td>
<td>76.6</td>
<td>45.4 (35.0–55.9)</td>
<td>23.3 (13.7–32.8)</td>
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<tr>
<td>Gender</td>
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<td></td>
</tr>
<tr>
<td>Male</td>
<td>60</td>
<td>63.8</td>
<td>78.3</td>
<td>42.6 (29.7–55.5)</td>
<td>22.9 (11.0–34.7)</td>
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</tr>
<tr>
<td>Female</td>
<td>34</td>
<td>36.2</td>
<td>73.5</td>
<td>50.7 (33.3–68.1)</td>
<td>23.4 (7.5–39.3)</td>
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</tr>
<tr>
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<td></td>
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<td>0.274</td>
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<tr>
<td>$\leq 55$ y</td>
<td>46</td>
<td>48.9</td>
<td>78.3</td>
<td>39.4 (24.8–53.9)</td>
<td>18.8 (6.0–31.5)</td>
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<tr>
<td>$&gt;55$ y</td>
<td>48</td>
<td>51.1</td>
<td>75.0</td>
<td>51.3 (36.6–66.0)</td>
<td>27.7 (13.8–41.6)</td>
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<td></td>
<td></td>
<td>0.012</td>
</tr>
<tr>
<td>M1a or M1b</td>
<td>26</td>
<td>28.0</td>
<td>65.4</td>
<td>62.8 (43.4–82.2)</td>
<td>43.5 (22.8–64.2)</td>
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</tr>
<tr>
<td>M1c</td>
<td>67</td>
<td>72.0</td>
<td>82.1</td>
<td>38.0 (26.0–50.0)</td>
<td>13.7 (4.1–23.3)</td>
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<td>NY-ESO-1–specific T cells</td>
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<td>Present</td>
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<td>52.1</td>
<td>65.3</td>
<td>60.4 (46.1–74.7)</td>
<td>32.8 (17.8–47.8)</td>
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<td>Absent</td>
<td>45</td>
<td>47.9</td>
<td>88.9</td>
<td>29.5 (15.8–43.1)</td>
<td>13.6 (2.9–24.4)</td>
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<tr>
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<td></td>
<td>0.101</td>
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<tr>
<td>Present</td>
<td>37</td>
<td>39.4</td>
<td>73.0</td>
<td>55.9 (39.7–72.1)</td>
<td>32.6 (16.2–49.1)</td>
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<tr>
<td>Absent</td>
<td>57</td>
<td>60.6</td>
<td>78.9</td>
<td>38.2 (24.8–51.5)</td>
<td>16.9 (5.9–27.9)</td>
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<td>$\leq 7%$</td>
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<td>54.8</td>
<td>80.4</td>
<td>43.8 (28.7–59.0)</td>
<td>17.7 (5.2–30.2)</td>
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</tr>
<tr>
<td>$&gt;7%$</td>
<td>38</td>
<td>45.2</td>
<td>78.9</td>
<td>43.8 (27.8–59.8)</td>
<td>26.5 (12.0–41.0)</td>
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</tr>
<tr>
<td>MDSCs</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.011</td>
</tr>
<tr>
<td>$\leq 11%$</td>
<td>48</td>
<td>51.1</td>
<td>79.2</td>
<td>30.4 (16.4–44.3)</td>
<td>15.8 (3.0–28.6)</td>
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</tr>
<tr>
<td>$&gt;11%$</td>
<td>46</td>
<td>48.9</td>
<td>73.9</td>
<td>59.9 (45.6–74.3)</td>
<td>30.0 (15.9–44.0)</td>
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</table>

$^aP$ values are results of log-rank tests excluding cases with missing values.
differences in long-term outcome were seen with the presence or absence of NY-ESO-1–specific T cells corresponding to 17% vs. 3.4% survival at 5 years.

The M-category represented the most powerful predictor of survival with an increased risk of death for M1c patients (HR = 2.2; \(P = 0.006\)) according to multivariable Cox proportional hazards analysis. In addition, the absence of NY-ESO-1–specific T cells independently worsened the prognosis (HR = 1.7; \(P = 0.041\)). The frequency of MDSCs did not add independent prognostic information in this model (Table 2, model 1).

Next, we performed Cox proportional hazards analysis without consideration of NY-ESO-1- and Melan-A–specific T cells (Table 2, model 2). In this second model, a high level of MDSCs was independently associated with impaired overall survival (HR = 1.7; \(P = 0.029\)) in addition to the predictive function of the M-category (HR = 1.9; \(P = 0.019\) for M1c).

The association between specific T cells and MDSCs

NY-ESO-1–specific T cells were more frequently observed in patients with low frequencies of MDSCs compared with those with high frequencies of MDSCs (65.2% vs. 39.6%; \(P = 0.015\)) and similar albeit not significant results (50.0% vs. 31.3%; \(P = 0.092\)) were observed for Melan-A–specific T cells (Fig. 3A). The same trend was observed when CD4\(^+\) and CD8\(^+\) T cells were analyzed separately (Fig. 3B). In the subgroup of

### Table 2. Cox models for disease-specific death

<table>
<thead>
<tr>
<th>Prognostic factor</th>
<th>Model 1</th>
<th></th>
<th>Model 2</th>
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<td></td>
<td>N(a)</td>
<td>% Dead</td>
<td>HR (95% CI)</td>
<td>(P)</td>
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<td>M-category</td>
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</tr>
<tr>
<td>M1a or M1b</td>
<td>26</td>
<td>65.4%</td>
<td>1</td>
<td>0.006</td>
</tr>
<tr>
<td>M1c</td>
<td>67</td>
<td>82.1%</td>
<td>2.2</td>
<td>(1.3–4.0)</td>
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<tr>
<td>NY-ESO-1–specific T cells</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Present</td>
<td>48</td>
<td>66.7%</td>
<td>1</td>
<td>0.041</td>
</tr>
<tr>
<td>Absent</td>
<td>45</td>
<td>88.9%</td>
<td>1.7</td>
<td>(1.02–2.8)</td>
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<tr>
<td>Melan-A–specific T cells</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Present</td>
<td>38</td>
<td>73.7%</td>
<td>1</td>
<td>0.067</td>
</tr>
<tr>
<td>Absent</td>
<td>55</td>
<td>80.0%</td>
<td>1.6</td>
<td>(0.97–2.8)</td>
</tr>
<tr>
<td>MDSCs (\leq 11%)</td>
<td>45</td>
<td>75.6%</td>
<td>1</td>
<td>0.199</td>
</tr>
<tr>
<td>MDSCs &gt;11%</td>
<td>48</td>
<td>79.2%</td>
<td>1.4</td>
<td>(0.84–1.3)</td>
</tr>
</tbody>
</table>

NOTE: Significant findings in the final models are shown in bold. Model 1 was adjusted for the confounding effects of Melan-A–specific T cells and CD14\(^+\)CD11b\(^-\)HLA-DR\(^低\) MDSCs and no confounding or significant interactions were detected in model 2.

\(a\)One patient had an unknown M-category and was excluded.
entire population (cies of MDSCs, neither in patients of cohort 1 nor in the presence of IFN-γ-releasing T cells, the differences in the detection rate according the MDSCs frequencies were more evident in CD8+ T cells than CD4+ T cells, if patients are analyzed for the presence of IFN-γ-releasing NY-ESO-1- or Melan-A–specific T cells (C).

If IFN-γ–releasing T cells, the differences in the detection rate according the MDSCs frequencies were more evident in CD8+ T cells than CD4+ T cells (Fig. 3C). No association was found between the M category and the frequencies of MDSCs, neither in patients of cohort 1 nor in the entire population (P = 1.000 and 0.565, respectively).

Discussion

The strongest associations with favorable survival of patients with advanced melanoma in this study were the presence of NY-ESO-specific T cells (P < 0.001) and a low frequency of MDSCs with the CD14+CD11b+HLA-DRhigh phenotype (P = 0.011). In addition, the prognostic relevance of the M category was likewise evident in our patients but less significant compared with the 2 immune cell subsets in univariate analysis (P = 0.012). The presence of NY-ESO-1-specific T cells predicted favorable survival independent of the M category and was the strongest factor to indicate the chance for long-term survival, as we already reported before (3). The frequency of MDSCs did not add independent prognostic information according to Cox regression analysis if analyzed in addition to NY-ESO-1–specific T cells. In contrast, the MDSCs blood level predicted survival independently of the AJCC M category in patients with distant metastasis if NY-ESO-1 and Melan-A–specific T cells were not considered. We found a high degree of correlation between high levels of MDSCs and the absence of functional antigen-specific T cells, suggesting a causal interaction between these immune cell subsets.

It was shown before that MDSCs are responsible for induction of antigen-specific T-cell tolerance (12, 35–37), but the present study is the first to demonstrate directly the triple-correlation between MDSCs, antigen-specific T cells, and clinical outcome.

There are 2 possible interpretations of the inverse correlation between MDSCs and the detection of antigen-specific T cells observed in our study. The first interpretation is that differences in the detection rate of antigen-specific T cells in our assays reflect true in vivo differences in the frequency of preexisting specific memory T cells. In this case, the assumed interaction between MDSCs and the detection of specific T cells takes place in vivo. The second possibility is that MDSCs, which are present during the expansion period of our assay impact the proliferation of antigen-specific T cells in vitro depending on the MDSC frequency. If present at high concentrations, MDSCs would exert their suppressive effects on T cells during the expansion period making it less likely that T cells proliferate to detectable levels. We did not obtain conclusive results in additional MDSC-depletion experiments to investigate the impact of MDSCs in the expansion phase of our assay to detect antigen-specific T cells in 10 patients with available PBMCs (data not shown).

Studies supporting both possibilities can be found in the literature, and an in vivo correlation was demonstrated in different mouse models (36, 38–40). However, coculture experiments show that MDSCs can effectively suppress not only CD3+ T-cell proliferation in general (22, 41) but also CD4+ and CD8+ T cells (6, 17) and can affect the quality of antigen presenting DCs in vitro (37). Clarification in future studies is clearly required, because MDSCs might influence the results of broadly used in vitro assays analyzing specific T-cell responses after restimulation.

The prognostic impact of MDSCs was not restricted to patients with limited stage IV disease, because this study was driven by 72% of patients with visceral metastases other than lung, and/or with elevated LDH. The association of a high frequency of these cells with poor patient survival as shown in our study supports the hypothesis that MDSCs have a clinically relevant immunosuppressive function, at least in malignant melanoma (32). There are other recent studies that are in line with our findings. Filipazzi and colleagues analyzed patients with stage II/III melanoma with no evidence of disease and found a trend for better disease-free survival in patients with low amounts of CD14+ MDSCs, which are present during the expansion period of our assay impact the proliferation of antigen-specific T cells.
CD11b^+ HLA-DR^-/low MDSCs compared with those with a high frequency of these cells ($P = 0.08$), but their patient cohort ($n = 33$) was very small (21). A negative impact of this particular MDSCs population on survival was also observed in a completely different setting by Walter and colleagues, who reported a strong association with outcome after multipeptide vaccination and survival in patients with renal cell cancer (19).

Generally, we did not observe substantial differences in the frequencies of Tregs or MDSCs according to prior therapies (Supplementary Table S2). In 2 patients who received systemic IL-2–based therapies within 4 weeks before blood draw for this study, unusually high frequencies of Tregs were observed. An increase of Tregs after IL-2 has been described before (42, 43). Therefore, we cannot rule out that the high levels were related to the treatment. Nevertheless, the lack of association between Tregs and survival remained basically unchanged if these patients were not considered in univariate analysis ($P = 0.509$). There was no pretreatment with fludarabine or cyclophosphamide and no other meaningful differences were observed in the frequencies of Tregs or MDSCs for other systemic treatments comparing patients treated within 4 weeks before blood draw to the others. Moreover, no differences were observed between 99 pretreated patients irrespective of the kind of therapy compared with those 34 without any prior systemic therapy. Based on these data, the impact of prior treatments in general, as well as the timing of blood draw seems to be limited about treatment-induced changes in frequency of these immune-cell subsets. Nevertheless, the treatment-related short-term effects need to be analyzed in subsequent studies.

Our findings highlight the role of MDSCs to serve as a prognostic marker, whereas the applicability of the detection of antigen-specific T cells to serve as a prognostic marker is limited. This is because the frequency of tumor antigen-reactive memory T cells in vivo is too low to be detected directly ex vivo by intracellular cytokine staining. Therefore, an initial in vitro stimulation period is applied to ensure expansion of memory T cells to a measurable extent. This requires the availability of fully equipped laboratories able to perform T-cell culturing and more sophisticated flow cytometry. A large number of PBMCs is also required and the minimum amount of blood draw is 25 mL to ensure sufficient cells to perform the analysis of antigen-specific T cells. The complex protocol requirements and data analysis require the involvement of specially trained and experienced personal but nevertheless a high degree of interobserver variability has to be assumed. Compared with the detection of NY-ESO-1–specific T cells, the analysis of MDSCs alone was less powerful to predict survival of patients with melanoma with distant metastases. Nevertheless, prognosis prediction was considerably improved by the analysis of MDSCs compared with the classification based on the M-category alone. Moreover, the analysis of MDSCs can be performed ex vivo without the need for in vitro presensitization and in contrast to the detection of antigen-specific T cells, only PBMCs corresponding to 5 mL peripheral blood are needed. Therefore, the feasibility of analyzing the frequency of MDSCs in clinical practice can be assumed.

The threshold of the MDSCs frequency was established based on the median value measured among all cohort 1 patients (11.3%), but was adapted to the next integral number (11%) to allow reasonable clinical usage and further validation.

The high clinical relevance of specific T-cell immunity is again highlighted by our study and further provides a rationale to pursue vaccination and T-cell transfer strategies targeting NY-ESO-1, at least in melanoma. Our findings also provide a rationale to investigate MDSC-depleting strategies in the therapeutic setting especially in the frame of specific immunotherapies, such as anticancer vaccination or adoptive T-cell transfer. Another strategy in addition to their depletion might be to block the suppressive effects of MDSCs. This can be achieved by inhibition of the cyclooxygenase-2 (COX-2)/prostaglandin E2 pathway (39, 41, 44, 45) or after application of phosphodiesterase inhibitors (40).

In contrast to MDSCs, the level of circulating Tregs was not associated with prognosis in our patients. This finding is in contrast to an initial report by Baumsartner and colleagues (3), who analyzed 14 patients with melanoma. No prognostic relevance has been reported in patients with head and neck cancer (46), but poor survival was described in patients who had high levels of circulating Tregs in ovarian (47) and renal cell cancer (48). Schwartzzenburg and colleagues even observed higher blood levels of Tregs in patients with clinical response after high-dose IL-2/vaccine treatment compared with those with progressive disease (49). Summarizing the prognostic role of circulating Tregs, in contrast to other malignancies, there is no compelling clinical evidence either in the literature, or based on our own data reported here, to suggest an important unfavorable prognostic impact of their cell frequencies in the peripheral blood of patients with melanoma.

In conclusion, circulating CD14^+ CD11b^+ HLA-DR^-/low MDSCs have strong prognostic impact in patients with melanoma with distant metastasis and are inversely correlated with the presence of functional antigen-specific T cells. A frequency greater than 11% was independently associated with poor survival and was as important as the M-category in predicting outcome according to Cox regression analysis. The role of MDSCs to serve as a prognostic marker in stage IV melanoma needs to be confirmed in independent studies. Our findings warrant further investigation of MDSCs-depleting strategies in the therapeutic setting especially in combination with vaccination or T-cell transfer approaches.

Disclosure of Potential Conflicts of Interest

M. Maio is a consultant/advisory board member for BMS and Roche. D. Schadendorf has received speakers bureau honoraria from Amgen, BMS, GSK, Novartis, and Roche. D. Schadendorf is a consultant/advisory board member for Roche, GSK, BMS, Novartis, and Amgen. No potential conflicts of interest were disclosed by the other authors.
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