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CD164 identifies CD4+ T cells highly expressing genes associated with malignancy in Sézary syndrome: the Sézary signature genes, FCRL3, Tox, and miR-214

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Abstract

Sézary syndrome (SS), a leukemic variant of cutaneous T-cell lymphoma (CTCL), is associated with a significantly shorter life expectancy compared to skin-restricted mycosis fungoides. Early diagnosis of SS is, therefore, key to achieving enhanced therapeutic responses. However, the lack of a biomarker(s) highly specific for malignant CD4$^+$ T cells in SS patients has been a serious obstacle in making an early diagnosis. We recently demonstrated the high expression of CD164 on CD4$^+$ T cells from Sézary syndrome patients with a wide range of circulating tumor burdens. To further characterize CD164 as a potential biomarker for malignant CD4$^+$ T cells, CD164$^+$ and CD164$^-$CD4$^+$ T cells isolated from patients with high-circulating tumor burden, B2 stage, and medium/ low tumor burden, B1–B0 stage, were assessed for the expression of genes reported to differentiate SS from normal controls, and associated with malignancy and poor prognosis. The expression of Sézary signature genes: T plastin, GATA-3, along with FCRL3, Tox, and miR-214, was significantly higher, whereas STAT-4 was lower, in CD164$^+$ compared with CD164$^-$CD4$^+$ T cells. While Tox was highly expressed in both B2 and B1–B0 patients, the expression of Sézary signature genes, FCRL3, and miR214 was associated predominantly with advanced B2 disease. High expression of CD164 mRNA and protein was also detected in skin from CTCL patients. CD164 was co-expressed with KIR3DL2 on circulating CD4$^+$ T cells from high tumor burden SS patients, further providing strong support for CD164 as a disease relevant surface biomarker.

Introduction

Cutaneous T-cell lymphoma (CTCL) is a malignancy of skin-trafficking CD4$^+$ T cells most commonly manifested as mycosis fungoides (MF) and Sézary syndrome (SS). Whereas mycosis fungoides are primarily an indolent disease restricted to the skin, with the presence of patches or plaques, Sezary syndrome represents a leukemic variant with erythroderma, circulating malignant CD4$^+$ T cells and a significantly shorter life expectancy. Early diagnosis of SS is, therefore, key to achieving enhanced therapeutic responses [23]. The lack of a biomarker(s) highly specific for malignant CD4$^+$ T cells in SS patients has been a serious obstacle in making an early diagnosis and in evaluating the extent of the disease, thereby prompting continuous attempts to find a CTCL specific marker.

Currently, it is accepted that malignant CD4$^+$ T cells in Sézary syndrome are a single TCRVβ clonal population with central memory phenotype, high expression of CCR4, and lack of CD26 [7, 12, 39, 44]. At the transcriptional level, the expression of GATA-3, Twist 1, and Tox is increased, while the expression of STAT-4 is decreased in patients' CD4$^+$ T cells compared to healthy controls [13, 18, 21, 38, 41]. In addition, the intracellular protein T plastin was found in CD4$^+$ T cells from SS patients but not in normal controls [21]. GATA-3, T plastin, STAT-4, and CD26 were named ''Sézary signature'' genes, and differences between patients' and healthy individuals' in their expression in CD4$^+$ T cells have aided in diagnosis of Sézary syndrome [33]. Recently, small, non-coding RNA molecules, microRNAs (miR-) were found to have potential diagnostic value in CTCL. Overexpression of several microRNAs, including miR-214 and miR-21, made it possible to distinguish CTCL and SS patients with a poor prognosis from benign disorders [3, 32]. The identification and isolation of malignant cells expressing the aforementioned genes critically depend on finding a cell-surface marker unique to malignant cells in CTCL. The presence of such

biomarker(s) will aid in diagnosis and monitoring of the disease as well as in designing effective treatments targeting malignant cells and sparing of normal immunocompetent cells. Several surface molecules, namely, NKp46, syndycan 4 (SD-4), ganglioside GD3 (CD60), mucin 1 (Muc 1), and CD158k/KIR3DL2, have been found to be highly expressed on CD4^{+} T cells from some SS patients compared with healthy controls [5, 9, 19, 36, 37]. SD-4, CD60, and Muc-1 molecules are also upregulated on activated normal CD4^{+} T cells [1, 8, 27]. Prior to its detection on CD4^{+} T cells from SS patients, KIR3DL2, a killer immunoglobulin-like receptor was mainly associated with a population of CD8^{+} T cells and NK cells in healthy controls. The report by Poszepszynska-Guine et al. which demonstrated high expression of KIR3DL2 on CD4^{+} T cells representing the malignant clonal cell population, provided an opportunity to utilize KIR3DL2 in diagnosis of SS [36].

Our studies focus on finding cell-surface marker (-s) unique to CTCL patients with varying tumor burdens in the circulation. We recently reported high expression of CD164 and FCRL3 on CD4^{+} T cells in Sézary syndrome patients [43]. CD164 is a sialomucin adhesion receptor that was originally demonstrated on a population of CD34^{+} hematopoietic progenitor cells, but recently has been shown in some human cancer cells, where it has been implicated to play a role in the development as well as metastasis of cancer [16, 26, 42]. Fc-receptor-like 3 (FCRL3) expression, originally associated with naturally occurring human T regulatory cells, was found by our group to correlate with SS progression [31, 43]. The expression of CD164 on CD4^{+} T cells correlated positively with a wide range of circulating tumor burdens, whereas FCRL3 expression was noted mainly in high tumor burden patients. The potential for CD164 to serve as a marker for malignant CD4^{+} T cells was underscored by the following findings: CD164 acquisition correlated with loss of CD26 expression and it was co-expressed with a dominant TCRVβ; CD164^{+}CD4^{+} T cells demonstrated the morphology of Sézary cells and were diminished or no longer detectable in patients who experienced clinical remission.

In the present studies, we further addressed the specificity of CD164 as a marker of malignant cells. We used the level of expression of Sézary signature genes, along with FCRL3, Tox, miR-214, and miR-21 expression as an indication of malignancy in populations of CD164+- and CD164--circulating CD4+ T cells. The results demonstrate that the malignancy genes are predominantly associated with CD164+CD4+ T cells and that CD164 is also expressed in skin-residing CD4[1] T cells of CTCL patients. In addition, our results show the expression of both, CD164 and KIR3DL2 on CD4+ T cells in 82 % of SS patients. These results provide support for CD164 as a cell-surface biomarker for CD4+ T cells with a malignant phenotype in CTCL.

Materials and methods

Patients

Patients were diagnosed on the basis of clinical, histopathologic, and immunohistologic criteria as previously defined [30]. Patients with erythroderma and circulating malignant T cells were diagnosed as B0, B1, or B2, according to criteria defined by Olsen et al.; all B2 patients were stage IVA1, and B0–B1 patients were stage III A–B [34]. Mycosis fungoides patients, with clinically and histologically defined skin lesions of patches, plaques, tumors, or erythroderma, but without blood involvement were diagnosed as stages IA through IIIA. Specimens were obtained from CTCL patients seen at the Cutaneous T-Cell Lymphoma Clinic and psoriasis patients seen at Psoriasis Clinic of the University of Pennsylvania. Atopic Dermatitis patients were seen in the Division of Dermatology in the Department of Medicine at the Washington University School of Medicine. Healthy control skin samples were obtained as residual healthy marginal skin from patients undergoing routine dermatologic surgery at the Department of Dermatology, University of Pennsylvania Health System.

All samples were collected in accordance with protocols approved by the University of Pennsylvania and Washington University Institutional Review Board, and studies were conducted according to the Declaration of Helsinki Principles.

Flow cytometry

To exclude the effect of treatment on the expression of different genes, peripheral blood mononuclear cells (PBMC) isolated from patients with no prior treatments were used in the studies. The cells were stained with fluorochrome-conjugated antibodies allowing the identification of live CD164$^+$ and CD164$^-$CD4$^+$/CD3$^+$ T cells. Antibodies were purchased from BD Biosciences (San Jose, CA), and the Live/Dead Fixable Aqua Dead Cell Stain Kit was purchased from Invitrogen (Grand Island, NY). Stained PBMC were sorted using BD FACS Aria II cell sorter.

To assess the expression of CD158k/KIR3DL2 (clone MOG1-M-K322-13E4c, provided by Innate Pharma), 100ll of patient's blood sample was incubated with antibodies against CD3, CD4, CD26, and KIR3DL2 in room temperature (RT) for 45 min. To assess the co-expression of CD164 and KIR3DL2, patient's PBMC ($1x10^6$) were stained with anti-CD164 antibody plus antibodies indicated above followed by 45 min incubation in RT. In addition, KIR3DL2 expression on patients' CD4$^+$ T cells was tested using antibody DX31. DX31 antibody was the gift of Dr. Lewis Lanier, UCSF and was purified from the hybridoma by the UCSF Hybridoma Core Facility. PBMC were stained with biotinylated antibody DX31 and with antiCD3, CD4, and CD26 for 30 min at 4 C followed by 15 min incubation at 4 C with Streptavidin-APC. Both antibodies against KIR3DL2 generated similar results.

Skin lymphocytes were isolated using a modified method described by Kim et al. [22]. Skin biopsies were stored in 0.08 % trypsin, overnight at 4C followed by 2 h incubation in a 37C/5 %CO_2 incubator with 0.125 mg/ml Libertase TL (Roche). Isolated cells were stained with fluorochrome-conjugated antibodies to identify CD3/CD4 T cells expressing CD164. Cells were analyzed on an

LSRII flow cytometer (Becton Dickenson, San Jose, CA) at the Flow Cytometry and Cell Sorting Core, Abramson Cancer Center, University of Pennsylvania. FlowJo software was used to analyze data (Tree Star, Ashland, OR). RNA isolation and quantitative real-time PCR

To assess the expression of T plastin, Gata-3, STAT-4, FCRL3, and Tox on sorted CD164$^+$/CD164$^-$ CD4$^+$ T cells, total RNA was extracted from sorted and normal CD4^1 T cells using the Qiagen RNeasy Mini Kit (Qiagen) according to the manufacturers' instructions. For skin samples, total RNA was extracted from formalin-fixed paraffin embedded (FFPE) samples and normal tissue using the Qiagen RNeasy FFPE Kit and Fibrous Tissue Kit (Qiagen) following the manufacturers' instructions. Single-stranded cDNA was synthesized by reverse transcription of 40 nanograms of RNA from CD164$^+$/CD164$^-$CD4$^+$ T cells and skin biopsies using the High Capacity RNA to cDNA Kit (Applied Biosystems) for further analysis. QRT-PCR was performed using Taqman gene expression assays (Applied Biosystems) with Taqman Gene Expression Master Mix (Applied Biosystems) according to the manufacturers' instructions. Expression levels were normalized to b-actin and analyzed using the DDCT method.

To evaluate expression of miR-214 and miR-21 in CD4$^+$ T cells and skin biopsies, 10 nanograms of total RNA was reverse transcribed to cDNA using the Taqman microRNA Reverse Transcription Kit (Applied Biosystems) following their custom RT and preamplification protocols. QRT-PCR was performed with Taqman microRNA primers (Applied Biosystems) according to the manufacturers' instructions. Samples always were run in triplicate on the Applied Biosystem 7500 Ral Time PCR System. Expression levels were normalized to U6 snRNA and analyzed using the DDCT method.

Results

The expression of Sézary signature genes, FCRL3, Tox, and miR-214 is mainly associated with circulating CD164$^+$CD4$^+$ T cells in Sézary syndrome patients Sézary

We assessed the expression of Sézary signature genes in sorted CD164$^+$/CD164$^-$ CD4$^+$ T cells. In addition, we evaluated expression of FCRL3 and Tox (Fig. 1). [31, 43]. Tox, a nuclear factor critically involved in CD4$^+$ development in the thymus but downregulated on normal peripheral CD4$^+$ T cells, was demonstrated in CD4$^+$ T cells from CTCL patients and its high expression correlated with increased mortality [2, 6, 11, 29].

Patients' PBMC were sorted into CD164$^+$CD4$^+$ and CD164$^-$CD4$^+$ T cells, and the expression of Sézary signature genes as well as FCRL3 and Tox was assessed by quantitative real-time PCR (qRT-PCR). In patients defined as B2; stage IVA1, experiencing advanced disease and C50 % of CD26$^-$ CD4$^+$ T cells highly expressing CD164, the population of CD164$^+$CD4$^+$ T cells demonstrated a significant increase in mRNA expression of T plastin (1.4 fold), GATA-3 (1.3 fold), but 6.3 fold decrease in STAT-4 mRNA expression compared with CD164$^-$CD4$^+$ T cells. Similarly, FCRL3 and Tox mRNA expression was significantly higher in CD164$^+$CD4$^+$ T cells from B2 patients compared with CD164$^-$CD4$^+$ T cells (1.9 and 1.5 fold higher, respectively) (Fig. 1, upper panel). In patients with low tumor burden, B1–B0; stages III B–A, and B50 % CD26$^-$ CD164$^+$CD4$^+$ T cells, CD164$^+$CD4$^+$ T cells demonstrated a 4.4 fold higher expression of T plastin and 1.8 fold lower expression of STAT-4 compared with CD164$^-$CD4$^+$ T cells (Fig. 1 lower panel). However, the differences between these two populations lacked statistical significance due to the variability between patients. An overall expression of T plastin in B1–B0 patients was several folds lower, whereas STAT-4 expression was higher compared with levels in B2 patients. The levels of GATA-3 expression in both CD164$^+$ and CD164$^-$CD4$^+$ T cells were comparable to those in healthy controls. B1–B0 patients also demonstrated

low levels of FCRL3 expression. Although a 2.2-fold increase in FCRL3 expression was observed in CD164$^+$ compared with CD164$^-$CD4$^+$ T cells, it was not significant. Interestingly, the expression of Tox was significantly increased (2.9 fold) in CD164$^+$CD4$^+$ T cells compared with CD164$^-$CD4$^+$ T cells from B1 to B0, patients pointing to the potential association between CD164 and Tox expression in patients with a low-circulating burden of malignant cells (Fig. 1, lower panel).

CD164 expression is increased in skin from CTCL patients

To establish CD164 expression in skin-residing malignant cells, skin biopsies from patients diagnosed with SS, MF, atopic dermatitis (AD), psoriasis (PS), and healthy marginal skin from patients undergoing routine dermatologic surgery (HC) were assessed for CD164 mRNA expression. As shown in Fig. 2, the expression of CD164 mRNA in skin from SS and MF patients was significantly several fold increased (19.5 fold and 12.2 fold, respectively) compared with its level in skin from AD patients or control skin (left panel). A 5.3-fold increase in CD164 mRNA was noted in skin from psoriasis patients. T plastin mRNA was also increased in skin lesions of CTCL patients, as previously reported by other authors (data not shown) [25].

To determine if CD164 protein is expressed in skin CD4$^+$ T cells, lymphocytes were isolated from skin biopsies of SS patients and healthy controls using the modified method described by Kim et al. [22]. Cells were stained with fluorochrome-conjugated antibodies and analyzed by flow cytometry to identify CD4$^+$ T cells expressing CD164. As shown in Fig. 3a, 33.7 % of the CD4$^+$ T cells from the skin of patients expressed CD164 compared with 9.7 % CD4$^+$ T cells from normal skin. In Fig. 3b, a flow cytometry histogram shows CD164 expression on CD4$^+$ T cells of a representative SS patient and control.

MiR-214 expression is significantly upregulated in circulating CD164⁺CD4⁺ T cells

It has been reported that miR-214 and miR-21 are overexpressed in CD4⁺ T cells of SS patients with a poor prognosis [32]. We first determined that miR-214 was expressed in circulating CD4⁺ T cells of 89 % of patients, whereas miR-21 (data not shown) was detected only in 17 % of patients. This result prompted us to focus on miR214. MiR-214 expression was highly upregulated in CD4⁺ T cells from B2 patients, but only marginally upregulated in B1–B0 patients (Fig. 4a, b). Next, we determined the expression of miR-214 in sorted CD164⁺ and CD164⁻CD4⁺ T cells from B2 patients. As shown in Fig. 4c, miR-214 expression was significantly, 1.8 fold, upregulated in CD164⁺CD4⁺ T cells compared with CD164⁻CD4⁺ T cells.

   In contrast to circulating CD4⁺ T cells, miR-21 but not miR-214 expression was demonstrated in skin biopsies from both SS and MF, suggesting that the skin environment may promote the expression of different microRNAs (data not shown).

CD164 and KIR3DL2 are co-expressed on CD4⁺ T cells from SS patients

Since KIR3DL2 was demonstrated as a reliable cell-surface marker for Sézary cells, we examined the association between KIR3DL2 and CD164 expression on CD4⁺ T cells from SS patients [28, 36]. As shown in Fig. 5, CD164 and KIR3DL2 are expressed on patients' CD4⁺ T cells and the level of expression correlates with the severity of disease. In B2 patients (Fig. 5a), with an average of 68.7 % of CD4⁺ T cells lacking CD26 expression, KIR3DL2 expression was demonstrated on 32.7 % of CD4⁺ T cells, whereas CD164 was present on 47.7 % of CD4⁺ T cells. Only 4 out of 31 B2 patients (13 %) showed no or B2 % of KIR3DL2 expression on their CD4⁺ T cells that were positive for CD164. In contrast, five out of ten B1–B0 patients (Fig. 5b) showed no expression of KIR3DL2. In the remaining five patients, KIR3DL2 expression on CD4⁺ T cells varied from 4.2 to 50.6 %. On

average, 30.2 % of CD4$^+$ T cells from B1 to B0 patients showed no expression of CD26, 25 % of CD4$^+$ T cells expressed CD164, but only 9.5 % expressed KIR3DL2. Our results indicate that KIR3DL2 expression is mainly evident in patients with advanced B2 disease. Importantly, in patients expressing both molecules, CD164 and KIR3DL2 were predominantly co-expressed on the same CD4$^+$ T cells (Fig. 5c).

Vβ

Discussion

In our previous report, we showed that CD164 was coexpressed with a single dominant TCRVβ on CD26$^-$CD4$^+$ T cells and its expression correlated positively with a wide range of circulating tumor burdens in SS patients [43]. Our results were subsequently supported by studies of Guenova et al. confirming that CD164 is expressed on clonal malignant CD4$^+$ T cells [14]. Based on this data, we have postulated that CD164 may serve as a positive cell-surface marker that distinguishes between normal and malignant CD4$^+$ T cells in SS patients, particularly among patients, whose TCRVβ could not be defined by antibodies. Our current studies were designed to further examine the malignant status of CD164$^+$CD4$^+$ T cells by assessing the expression of genes reported to differentiate SS patients from healthy individuals and by examining the pattern of expression of CD164 and KIR3DL2 on patients' CD4$^+$ T cells.

We show that predominantly CD164$^+$CD4$^+$ T cells express genes associated with the Sézary signature phenotype. In accordance with this phenotype, the expression of T-plastin and the Th2-associated transcription factor GATA-3 is significantly higher in CD164$^+$CD4$^+$ T cells compared with CD164$^-$CD4$^+$ T cells. As expected, the expression of STAT-4 is significantly lower in CD164$^+$ compared to CD164$^-$CD4$^+$ T cells. Furthermore, the expression of FCRL3, Tox, and miR-214 is also higher in CD164$^+$CD4$^+$ T cells in comparison with CD164$^-$CD4$^+$ T cells. We demonstrate the presence

of CD164 mRNA and protein in skin-residing CD4$^+$ T cells from SS patients. Levels of CD164 mRNA are significantly increased in skin lesions from SS and MF, compared to AD, PS, and normal skin. Interestingly, low levels of CD164 expression were demonstrated in skin biopsies from patients with psoriasis, however, significantly lower, compared with SS or MF patients (3.6 fold, p= 0.006 and 2.4 fold, p= 0.02, respectively). Considering that CD164 is expressed in skinresiding CD4$^+$ T cells, this result is different from pattern of CD164 expression in circulating CD4$^+$ T cells, where CD164 expression is restricted to Sézary syndrome, a leukemic variant of CTCL but not MF, atopic dermatitis, or psoriasis patients [14, 43]. The presence of CD164 expression in skin of psoriatic patients is suggestive of some common pathways operational in the skin manifestations of these diseases, but this remains to be established.

Our results also suggest the likely existence of an association between T plastin and CD164 in patients' skinresiding CD4$^+$ T cells, similar to circulating malignant CD4$^+$ T cells, as mRNAs for both CD164 and T plastin are present in skin lesions from SS and MF patients.

Our data show that B1–B0 patients do not demonstrate a fully developed malignant status identified by the presence of Sézary signature phenotype, high expression of FCRL3, and miR-214 that is apparent in B2 patients. In B1–B0 patients, T plastin, FCRL3, and miR-214 are expressed in some patients, predominantly in CD164$^+$ CD4$^+$ T cells. However, the levels are low, and the differences between CD164$^+$ and CD164$^-$ populations are not significant due to high variability in expression of these genes between the patients. Similarly, STAT-4 and Gata-3 expression in CD164$^+$CD4$^+$ T cells is not significantly different from that in CD164$^-$CD4$^+$ T cells. It is noticeable that overall, levels of STAT-4 expression in B1–B0 patients are higher than those in B2 patients, whereas Gata-3 expression is comparable to the levels observed in normal controls. However, Tox, which is highly expressed in B2 patients, is also highly expressed in B1–B0 patients, and its expression is significantly higher (2.9 fold) in CD164$^+$CD4$^+$ T cells compared with CD164$^-$CD4$^+$ T cells. Our

results point to an important observation; the significant expression of Tox predominantly in CD164$^+$CD4$^+$ T cells from B1 to B0 patients strongly suggests that Tox may be one of the early transcription factors associated with malignant transformation in CD164$^+$CD4$^+$ T cells in SS patients. Its high expression in CD4$^+$ T cells and in the skin from SS patients, in conjunction with the expression of CD164 and other clinical data, may aid in specific diagnosis of SS [11].

Our data demonstrate that CD164$^+$CD4$^+$ T cells are the population that predominantly expresses genes linked with malignancy and poor prognosis. However, particularly in B2 patients, CD164$^-$CD4$^+$ T cells also express the Sézary signature phenotype as well as FCRL3, Tox, and miR-214, but at significantly lower levels compared to CD164$^+$CD4$^+$ T cells. The level of gene expression in the CD164population appears to depend upon circulating tumor burden; the highest expression is found in patients with the highest percentage of circulating CD4$^+$ T cells bearing a single TCRVβ. The study of Guenova et al. [15] showed that in the presence of malignant cells, benign CD4$^+$ T cells from SS patients acquire a Th2 biased phenotype, including elevated GATA-3 expression that could be reversed by separating malignant and benign CD4$^+$ T cells. This study implies that the phenotype of CD164$^-$CD4$^+$ T cells in patients is influenced by the presence of pathogenic CD164$^+$CD4$^+$ T cells and factor(s) released by these cells. A high percentage of malignant cells may correspond to a high concentration of factor(s) influencing the phenotype of benign cells. This may explain the highly reduced STAT-4 expression in CD164$^-$CD4$^+$ T cells from B2 patients compared with close to normal expression of STAT-4 in CD164$^-$CD4$^+$ T cells from B1 patients. It is also possible that some of CD164$^-$CD4$^+$ T cells are normal T cells activated by malignant cells, and as such, they may express various molecules, including T plastin or miR214, that have been shown to be upregulated in activated T cells [4, 20]. Whether the expression of malignancy associated genes in CD164$^-$CD4$^+$ T cells results from the direct effect of factor(s) triggering malignant transformation or results from factor(s) released by CD164$^+$CD4$^+$ malignant T cells, remains to be established.

In support of our results indicating CD164 as an important marker for malignant cells in CTCL, elevated CD164 expression has been associated with several human cancers, including prostate, ovarian, colon, and breast carcinoma. It has also been identified as a new marker for acute lymphoblastic leukemia [10, 16, 17, 24, 40].

In summary, our results show that CD164 is expressed predominantly on CD4$^+$ T cells expressing genes linked to malignancy and poor prognosis in Sézary syndrome patients. A well-defined Sézary signature phenotype and the expression of FCRL-3, Tox, and miR-214 are significantly associated with CD164$^+$ rather than with CD164$^-$CD4$^+$ T cells. The high expression of miR-214 in CD164$^+$CD4$^+$ T cells deserves further study as miR-214 contributes to cancer formation and progression by affecting several signaling pathways and is controlled by transcription factor Twist 1, reported to be highly expressed in SS patients' CD4$^+$ T cells [35, 45]. Our results also show that CD164 is co-expressed with KIR3DL2 on CD4$^+$ T cells from a majority of SS patients with advanced B2 disease. Assessing the expression of both markers can be useful in the diagnosis of Sézary syndrome and monitoring of the disease, particularly in patients, whose TCRVβ cannot be defined by the existing panel of antibodies. However, as our data show, B1−B0 patients do not consistently express KIR3DL2; therefore, the increased expression of CD164, along with the expression of Tox, could be the first indication of malignant transformation.

Our studies represent one of the first attempts to use a surface biomarker, such as CD164, to isolate malignant cells and characterize their phenotype in detail. Given the heterogeneous nature of the disease and variability among patients, potentially more markers will be discovered allowing for the precise identification of the phenotype of malignant cells, facilitating earlier diagnosis and the monitoring of disease progression, but may also provide a means for discovering new therapeutic targets.

Acknowledgments

Conflict of interest Dr. Helene Sicard is employed by Innate Pharma, Marseille, France. The authors state no conflict of interest.

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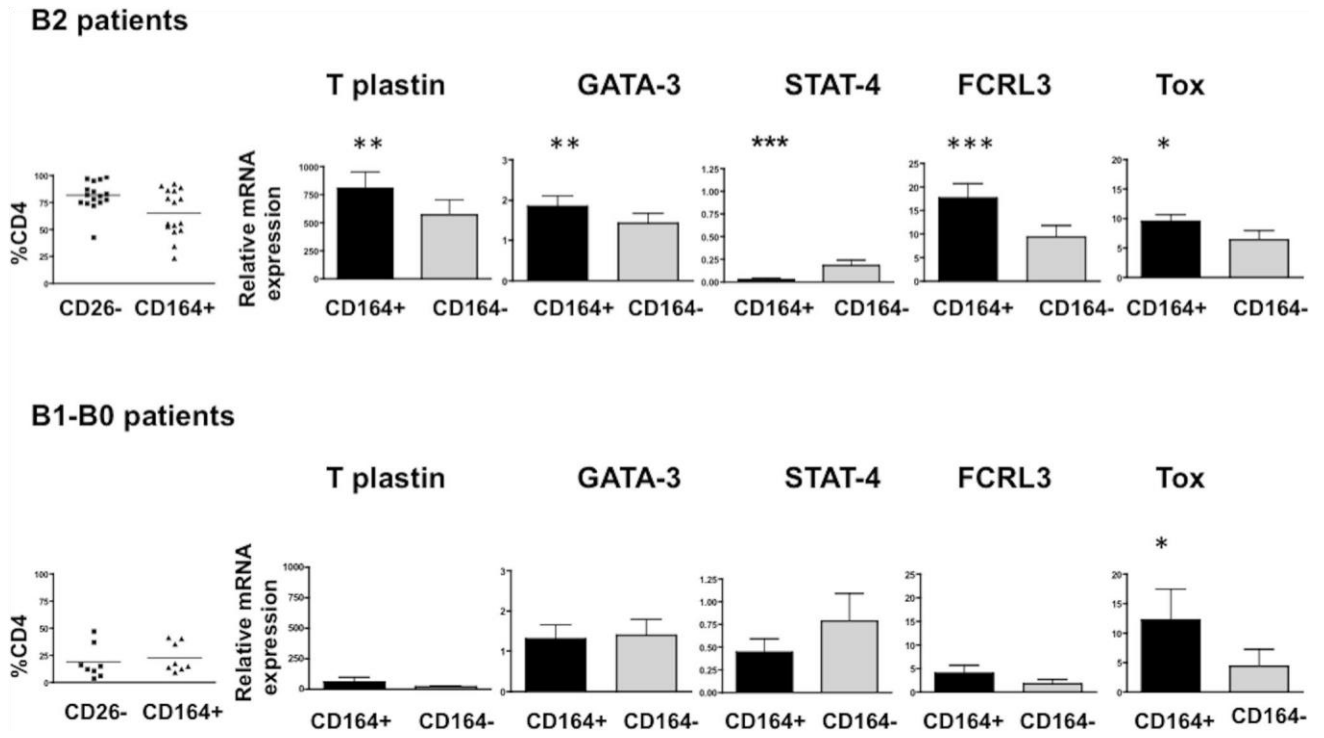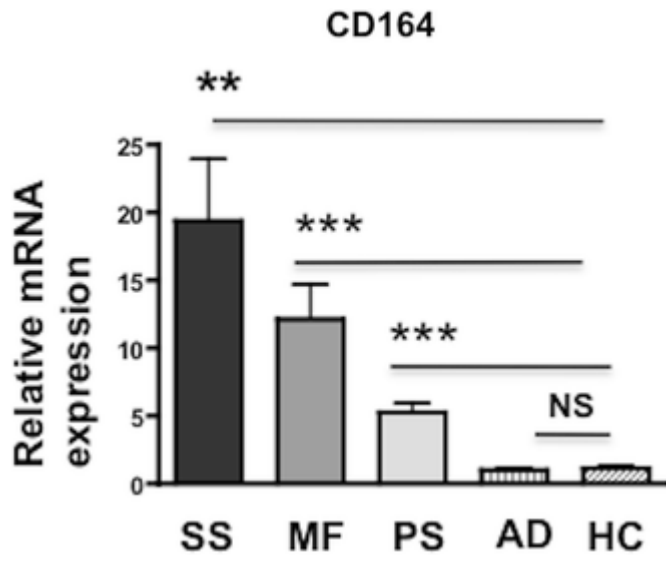
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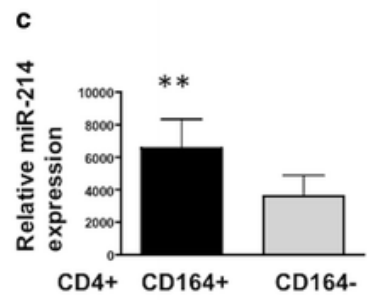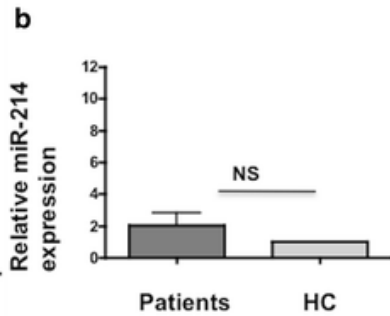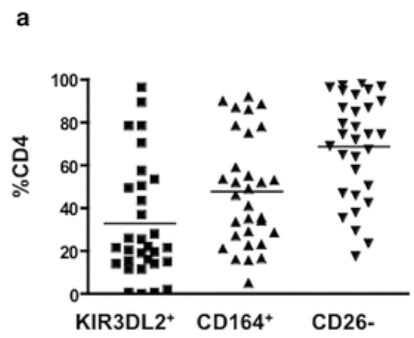
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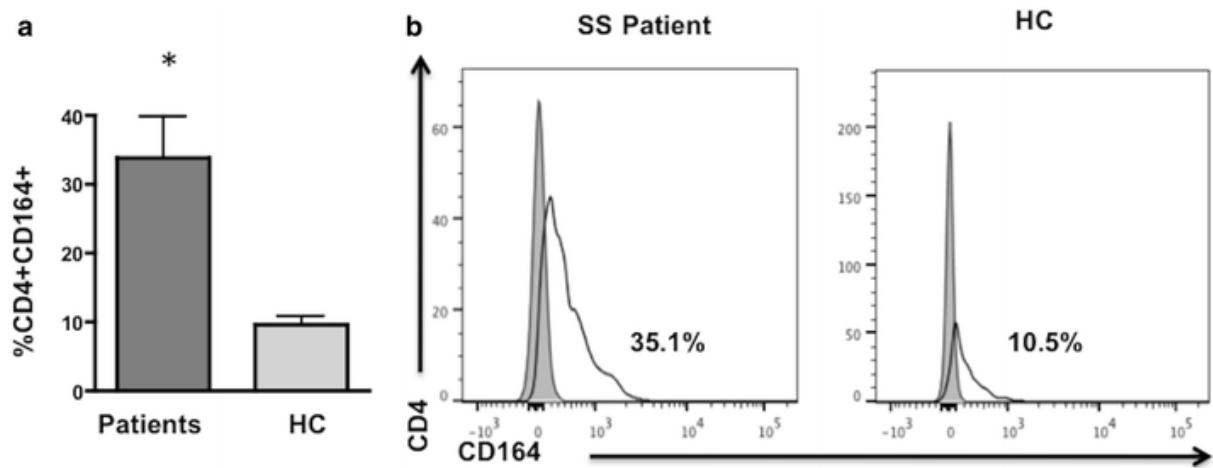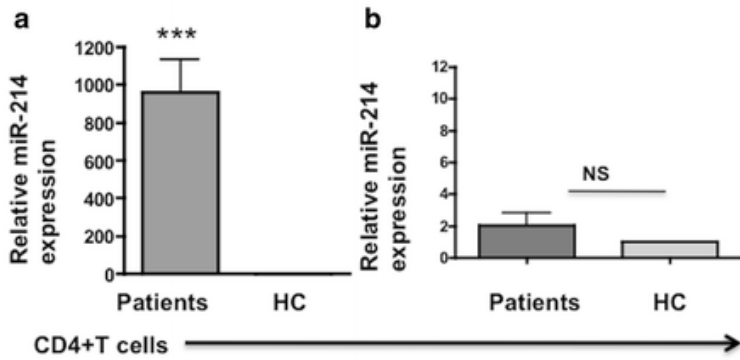
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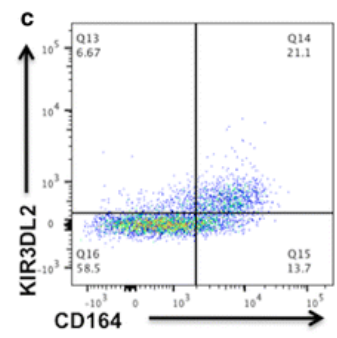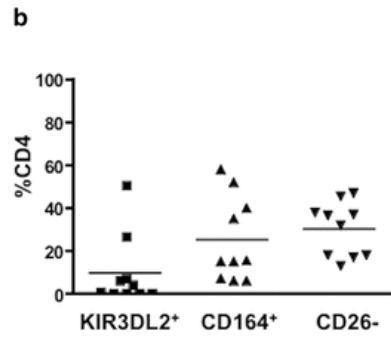
Figure 4

Figure 5

Figure legends

Fig. 1

CD164$^+$CD4$^+$ T cells from Sézary syndrome patients are the predominant population expressing the Sézary signature phenotype and significantly upregulated expression of FCRL3 and Tox. PBMC from high tumor burden SS patients diagnosed as B2, upper panel (with ≥50 % of CD26$^-$ CD164$^+$CD4$^+$ T cells, $n = 15$, *left graph*), and PBMC from medium-to-low tumor burden patients diagnosed as B1–B0, lower panel (with ≤50 % CD26$^-$ CD164$^+$CD4$^+$ T cells, $n = 9$, *left graph*), were sorted into CD164$^+$/CD164$^-$CD4$^+$ T cells. Each population was assessed for the expression of mRNA for T plastin, GATA-3, STAT-4, FCRL3, and Tox by qRT-PCR. CD4$^+$ T cells isolated from PBMC of healthy donors ($n = 9$, pooled) were used as controls. *Graphs* show relative expression of given mRNA in CD164$^+$ and in CD164$^-$CD4$^+$ T cells. *Error bars* represent mean ± SEM. The nonparametric Wilcoxon signed-rank test was used to assess differences between groups. *P* values ***<0.0005; **<0.005; *<0.05

Fig. 2

CD164 mRNA is expressed in skin from Sézary syndrome and mycosis fungoides patients. Skin samples from seven Sézary syndrome patients (SS), nine mycosis fungoides patients (MF), four atopic dermatitis patients (AD), three psoriasis patients (PS), and nine healthy controls (HC) were examined for the expression of the genes by qRT-PCR. Fold difference for CD164 was calculated versus expression levels in skin from healthy controls. *Error bars* represent mean ± SEM. Unpaired *t* test used to assess differences. *P* values ***<0.0005; **<0.005; *<0.05

Fig. 3

CD164 is expressed on the cell surface of skin-resident CD4$^+$ T cells from Sézary syndrome patients. **a** Percentage of CD164$^+$CD4$^+$ T cells isolated from skin of 5 Sézary syndrome patients (SS) and 11 healthy controls (HC) analyzed by flow cytometry. *Error bars* represent mean ± SEM. *P* value *<0.05. **b** Representative histogram illustrating CD164 expression on CD4$^+$ T cells isolated from skin of SS patient (*left panel*) and healthy control (*right panel*)

Fig. 4

MicroRNA-214 is mainly expressed in CD164$^+$CD4$^+$ T cells from Sézary syndrome patients. CD4$^+$ T cells from B2 patients (**a**, *n* = 17) and from B1 to B0 patients (**b**, *n* = 8) were assessed for the expression of miR-214 by qRT-PCR. The expression of miR-214 was subsequently assessed in sorted CD164$^+$/CD164$^-$CD4$^+$ T cells from B2 patients (**c**, *n* = 15). *Error bars* represent mean ± SEM. *P* values **<0.005

Fig. 5

CD164 and KIR3DL2 are co-expressed on CD4$^+$ T cells from Sézary syndrome patients. PBMC from patients diagnosed as B2 (**a**, *n* = 31) and B1–B0 (**b**, *n* = 10) were gated on CD3$^+$/CD4$^+$ T cells and analyzed for the expression of KIR3DL2, CD164, and CD26 by flow cytometry. *Graphs* show percentage of CD4$^+$ T cells from each patient expressing these molecules. **c** CD164 and KIR3DL2 are co-expressed on CD4$^+$ T cells from SS patient diagnosed with advanced B2 disease. *Error bars* represent mean ± SEM