Identification of Adipose Tissue Dendritic Cells Correlated With Obesity-Associated Insulin-Resistance and Inducing Th17 Responses in Mice and Patients

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Obesity has become a major worldwide health problem. It is associated with an increased risk in developing of type 2 diabetes, hypertension, and nonalcoholic fatty liver disease (NAFLD), which reduces life expectancy and leads to huge economic and social consequences (1). Obesity is characterized by low-grade chronic inflammation, as evidenced by an increased systemic concentration of proinflammatory molecules such as interleukin (IL)-6 (2). Thus, cytokine production can be deregulated in obesity, contributing substantially to insulin resistance (3).

In both humans and rodents, macrophage accumulation in adipose tissue (AT) in obese conditions correlates with insulin resistance (4–7). These macrophages might be a source of proinflammatory cytokines such as tumor necrosis factor-α and IL-6 that inhibit insulin action in adipocytes and provide a potential link between inflammation and insulin resistance (4,5). A recent study reported that a specific subset of F4/80+ macrophages is recruited into AT in diet-induced obesity in mice. These macrophages express a low level of CD11c (CD11clow) and produce a high level of proinflammatory cytokines involved in the development of insulin resistance (8). Depletion of CD11c+ cells by conditional ablation based on transgenic expression of the diphtheria toxin receptor under the control of CD11c promoter normalized insulin sensitivity in obese and insulin-resistant animals (9). Such an approach probably depletes dendritic cells (DCs) since CD11c is considered to be a specific marker of mouse DCs (10). However, few data are available concerning either DCs in AT or their potential role in the inflammatory process associated with obesity and insulin resistance (11,12).

DCs are key participants in innate and adaptive immune responses (13). The prevalent model of DC migration is a unidirectional pathway whereby precursor DCs arise from bone marrow progenitors, reach the blood, and traffic into secondary lymphoid organs and peripheral tissues where they contribute to the front line of defense against pathogens (14). DCs are a heterogeneous population of cells including the conventional/myeloid DCs (cDCs) and the plasmacytoid DCs (pDCs), which were originally isolated from the spleen but which are found in almost all tissues in a steady state (15,16). Recently, a novel DC population called inflammatory DCs (inf-DCs) was described to be generated from inflammatory monocytes while absent in a steady state and to be related to infection or inflammation (17,18). Furthermore, DCs are well recognized for their role in the priming and differentiation of naive CD4+ T cells. Upon antigenic stimulation, naive CD4+ T cells become effector T helper Th1, Th2, or Th17 cells, or even regulatory T cells (Tregs) depending on their cytokine microenvironment (19–21).

Recent studies have reported that T cells are also regulated in AT and might contribute to obesity-induced inflammation (22). In AT of lean mice, the major T-cell population corresponds to Tregs (23). Under high-fat diet (HFD), the number of AT Tregs decreases, whereas Th1 cells increase following the recruitment of inflammatory macrophages into AT (24). Moreover, it was suggested that AT T cells exhibited specific rearrangements in T-cell receptor, suggesting the presence in AT of DCs that presents antigens and induces T-cell polarization. Thus, our aim was...
to identify and characterize DCs in AT and to study their potential role in AT T-cell polarization in lean and obese mice and patients.

Here, we defined human CD11c<sup>hi</sup>CD1c<sup>+</sup> DCs and mouse CD11c<sup>hi</sup>Flt<sup>−/−</sup>DCs as inflammatory DCs in AT during obesity-associated insulin resistance, and we showed their potential capacity to induce Th17 cell responses.

**RESEARCH DESIGN AND METHODS**

**Study population.** For flow cytometric analysis, subcutaneous AT was obtained from healthy women undergoing elective procedures for fat removal for aesthetic purposes (n = 24 individuals, age = 44.6 ± 2.5 years, BMI = 28.3 ± 1.2 kg/m²). This protocol was approved by the Institutional Research Board of INSERM and the Toulouse University Hospital. For gene expression, morbidly obese patients (n = 20) undergoing bariatric surgery were recruited through the Department of Digestive Surgery and Liver Transplantation (Nîmes hospital) as described previously (25–27). Before surgery, fasting blood samples were obtained to measure glucose, insulin, and HbA1c. Insulin resistance was calculated using the homeostatic model assessment (HOMA-IR) index. Abdominal subcutaneous AT was obtained during surgery. Control subcutaneous AT was obtained from four lean subjects (2 females and 2 males; age = 42.2 ± 1.7 years, BMI = 21.1 ± 0.7 kg/m²) undergoing liposuction for cosmetic purposes. Information about the cohort was obtained from all subjects for this study, which was set up in accordance with French legislation regarding Ethics and Human Research (Huriert-Serusat). The Comité Consultatif de Protection des Personnes dans la Recherche Biomédicale de Nice approved the study (07/04/2003, N° 03.017).

**Animals.** Wild-type C57BL/6 male mice (7–10 weeks of age) from Janvier (Le Genest-St-Ise, France) had free access to water and were fed an HFD containing 45% fat (D12451; Research Diet) for 15 weeks. As expected, these mice exhibited increased weight. Obese db/db mice 8 weeks old were purchased from Janvier (Le Genest-St-Ise, France). Both obese models displayed marked insulin resistance as evaluated by a higher fasting glucose level (db/db: 275 ± 37 mg/dL vs. 100 ± 17 mg/dL, P = 0.0081; HFD: 187 ± 12 mg/dL, normal diet [ND]: 133 ± 6 mg/dL, P = 0.0137; five mice per group) and area under the curve (AUC) of the glucose tolerance test compared with the db/+ and lean mice (ND) (db/db: AUC 24,342 ± 3,345 vs. db/+: 10,976 ± 1,900, P = 0.0067; HFD: AUC 22,313 ± 1,551 vs. ND: AUC 13,381 ± 2,830, P = 0.0126; five mice per group), respectively. C57BL6 recombinase-activating gene deficient (Rag1<sup>−/−</sup>) mice and ovalbumine (OVA)-specific T-cell receptor (OT2) mice were obtained from Charles River Laboratories. The guidelines of laboratory animal care were followed, and the local Ethical Committee approved the animal experiments.

**Preparation of the stromal vascular fraction from adipose tissue.** In mouse studies, white epididymal AT pads were removed, immediately cut into small pieces, and rinsed in a buffer containing 120 mM NaCl, 4 mM KCl, 1.8 mM KH<sub>2</sub>PO<sub>4</sub>, 1 mM MgSO<sub>4</sub>, 750 μM CaCl<sub>2</sub>, 10 mM NaI, 0.05 M Hepes, and 30 mM EDTA (pH 7.4). Incubates were washed with PBS at 37°C for 30 min in 15 mL of the above buffer supplemented with 1% BSA, 280 μM glucose, and 15 mg of type-I collagenase (Worthington Biochemical Corporation). Adipocytes were then collected by filtration and flotation. The stromal vascular fraction (SVF) was collected by centrifugation for 15 min at 200g. In human studies, AT was immediately processed after removal and digested using collagenase (250 units/mL in PBS×1, 2% BSA [pH 7.4]) for 30 min under constant agitation. After centrifugation (300g, 10 min), the pellet containing the SVF was resuspended in erythrocyte lysis buffer (155 mM NaCl, 5.7 mM K<sub>2</sub>PO<sub>4</sub>, 0.1 mM EDTA) for 10 min. Finally and after successive filtration through 100-, 70-, and 40-μm sieves, the cells were resuspended in PBS plus 2% FCS. The SVF was analyzed by flow cytometry or used to separate the different cellular fractions. Cells were stained as described previously (28).

**Antibodies and flow cytometric analysis.** Rat antibodies mouse-CD3 (17A2), -CD4 (H129.19), -CD8 (53.67), -CD11b (M1/70), -CD11c (HL3), -CD45, -CD62L (M1-14), -CD86 (GL1), -CD103 (M209), -Iad (25D), -IL-4 (BVDV-2462), -IL-10 (JES5-10E4), -IL-17 (TCl1-18H10.1), -interferon (IFN)-γ (XM12.1) were purchased from BD Biosciences. Mouse antibodies against human CD4 (SK3) and CD45RA (H100) were purchased from BD Biosciences.

**RESULTS**

**Homing of naive T cells into adipose tissue.** AT consists of adipocytes but also stromal and vascular cells including vascular endothelial and immune cells. We first analyzed the T-cell populations present in the SVF from epididymal AT of lean C57BL/6 mice. Flow cytometric analysis of T cells for CD4, CD8, and CD45 expression revealed three CD3<sup>+</sup> populations: CD4<sup>+</sup>CD8<sup>+</sup>, CD4<sup>+</sup>CD8<sup>+</sup>, and CD4<sup>+</sup>CD8<sup>−</sup>CD<sup>8</sup><sup>−</sup> cells. The majority of these T cells had a memory phenotype (CD4<sup>+</sup>CD62L<sup>−</sup>) (83.3 ± 4.5%), and only 8% were naive T cells (CD4<sup>+</sup>CD62L<sup>+</sup>). As expected (Fig. 1A), the majority of CD4<sup>+</sup> T cells from the spleen were naive cells (CD4<sup>+</sup>CD62L<sup>+</sup>). These results prompted us to determine the homing and activation status of naive T cells in AT.

To achieve this, adoptive transfer of naive OVA-specific CD4<sup>+</sup> T cells (from OT2 mice) into mice depleted in T and B cells (Rag1<sup>−/−</sup> mice) and immunized with OVA was performed (Fig. 1B). After one week, the majority of transferred CD4<sup>+</sup> naive T cells were activated (CD4<sup>+</sup>CD62L<sup>−</sup>) in AT (Fig. 1C) and in mesenteric lymph nodes used as a positive control. Whether activation of these cells occurred directly in AT or in the lymphoid organs before their migration into the AT remains to be determined. These activated T cells differentiated into Th1 and Th17 cells according to the relative intracytoplasmic expression level of IFN-γ and IL-17 in both AT and mesenteric lymph nodes (Fig. 1D). In contrast, these cells did not express either IL-4 or IL-10 (Fig. 1D). Taken together, these results suggest the presence of active antigen-presenting cells in AT.

**Phenotypic characterization of adipose tissue DCs.** In mice, two major DC subsets have been described to activate T cells: the CD11c<sup>low</sup>B220<sup>−</sup> pDCs and the CD11c<sup>high</sup>B220<sup>−</sup>DCs that include cDCs and other DC populations including CD4<sup>+</sup> and CD8<sup>+</sup> DC as described previously (15). To characterize the DCs from AT, we first evaluated the cell surface expression level of the CD11c anti-
and B220 markers in the CD45+ cells from SVF of AT and spleen of lean mice by flow cytometric analysis (Fig. 2A and B). Although two main DC subsets were present in the spleen, only the CD11c\textsuperscript{high}B220\textsuperscript{neg} DCs were detected in SVF of lean mice AT (Fig. 2B). The frequency and absolute number of this population increased with age in AT (Fig. 2B and C) as expected (29), and these cells were able to induce T-cell proliferation in a mixed lymphocyte reaction (MLR) (data not shown), indicating that they are functional. We then investigated whether obesity affected the AT DCs content. After 15 weeks of a 45% HFD, mice displayed obesity and intolerance to glucose (see RESEARCH DESIGN AND METHODS). The SVF of AT from these insulin-resistant obese mice exhibited a marked increase in the level of CD11c\textsuperscript{high}B220\textsuperscript{neg} DCs (Fig. 2D and E). To further characterize these CD11c\textsuperscript{high}B220\textsuperscript{neg} DCs, we evaluated the expression of the F4/80 marker, which is widely used as a marker of macrophages. FACS analysis revealed that the SVF of lean mice did not contain double positive F4/80\textsuperscript{pos}CD11c\textsuperscript{pos} DCs (Fig. 2F). HFD challenge led to an increase in CD11c\textsuperscript{high}F4/80\textsuperscript{pos} cells but also to the emergence of an atypical cell population CD11c\textsuperscript{high}F4/80\textsuperscript{low} that might be equivalent to the one already described (8) (Fig. 2F). Similar cell subsets were also observed in the AT of obese diabetic, leptin receptor-deficient db/db, and leptin-deficient ob/ob mice (Fig. 2F).

Ex vivo–purified AT CD11c\textsuperscript{pos} cells from lean and obese mice were used to further characterize these cells. The ability to induce proliferation of allogeneic CD4\textsuperscript{pos} T cells in a MLR is one of the defining features of DCs. The two sorted AT CD11c\textsuperscript{pos} populations (F4/80\textsuperscript{pos} and F4/80\textsuperscript{neg}) displayed a typical dendritic morphology (Fig. 3A) and typical dendritic activity since they induced the proliferation of naive CD4\textsuperscript{pos} T cells from BALB/c mice, in a MLR (data not shown). This result suggested that these two types of DCs play an important role in inflammation associated with obesity.

We next examined the expression of a set of DC markers described previously by flow cytometric analyses. As shown in Fig. 3B, all CD11c\textsuperscript{pos} cells expressed major histocompatibility complex I-A molecules and the CD86 costimulatory molecule. Recently, CD103 and CX3CR1, in combination with CD11c, have been reported to define two DC populations. The CD103\textsuperscript{pos} DCs induce the differentiation of
FIG. 2. Characterization of DCs in AT from lean and obese mice. Epididymal fat pads as well as spleen were isolated from young (6 weeks old), old (1 year old), ND, HFD, ob/ob, and db/db mice, and the SVF was stained for CD45, CD11c, and B220. Cells were gated on CD45+ cells as indicated (A). B: Flow cytometric analysis of CD11c and B220 on the SVF CD45+ cells from epididymal fat tissue of young (6 weeks old) and old (1 year old) mice. C: The numbers of CD11c+ cells were calculated from FACS data and the SVF cell counts and expressed per gram of epididymal fat tissue. D: Flow cytometric analysis of CD11c and B220 on the SVF CD45+ cells from epididymal fat tissue of ND and HFD mice. E: The number of CD11c+ cells was calculated from FACS data and the SVF cell counts and expressed per gram of epididymal fat tissue. F: Flow cytometric analysis of CD11c and F4/80 on B220 on the SVF CD45+ cells from epididymal fat tissue of ND, HFD, db/db, and ob/ob mice. A representative result of 5 independent experiments with 5 mice per group and with similar results is shown. *P < 0.05. SSC-A, side scatter-air; FSC-A, forward scatter-air.
Foxp3+CD4+ Treg cells (30), and CX3CR1+ DCs were identified as cells that preferentially support the differentiation of Th17/Th1 cells (31) in the gut. In AT, the majority of DCs were CD103+ and CX3CR1 in lean mice and the atypical CD11c\textsuperscript{high}F4/80\textsuperscript{low} DCs were CD103\textsuperscript{−} and CX3CR1\textsuperscript{+} in obese mice (Fig. 3B). This CD11c\textsuperscript{high}F4/80\textsuperscript{low} population was also present in the AT from lean mice with an equivalent phenotype but at a very low frequency (<1%) (Fig. 3A) and absolute number (4,000 ± 200 cells/g of fat in lean mice vs. 350,000 ± 10,000 cells/g of fat in obese mice).

Besides, in AT, we showed the presence of a DC population expressing CD4+, the role of which remains to be determined in obesity.

Finally, CD11c\textsuperscript{high}F4/80\textsuperscript{neg} and CD11c\textsuperscript{high}F4/80\textsuperscript{low} cells sorted from AT were also capable of processing the antigen BODIPY fluorochrome-conjugated OVA (OVA-DQ green) since cell fluorescence was detected (Fig. 3C). Taken together, CD11c\textsuperscript{high}F4/80\textsuperscript{neg} cells and CD11c\textsuperscript{high}F4/80\textsuperscript{low} cells from AT of lean and obese mice present the characteristic features of DCs.

**FIG. 3.** Identification of atypical CD11c\textsuperscript{high}F4/80\textsuperscript{low} DCs. A: Sorted cell populations based on the expression of CD11c and F4/80 on B220 on the SVP CD45+ cells from epididymal fat tissue of ND and HFD mice, as indicated, were cytocentrifuged and stained with May-Grünwald-Giemsa. B: Phenotypic analysis by flow cytometry of AT DCs gated on CD45+ cells, from lean C57BL/6 and HFD mice, was performed by triple immunofluorescent staining after gating of different cell populations as indicated in A. C: Sorted cell populations were incubated with OVA-DQ, and 2 h later the cells were analyzed for the uptake and processing of DQ by flow cytometry. OVA-DQ fluoresced green when processed in acidified lysosomes. A representative result of 3 independent experiments with 5 mice per group and with similar results is shown.
CD11c<sup>high</sup>F4/80<sup>low</sup>CX3CR1<sup>pos</sup> DCs induce Th17 differentiation. Before evaluating the role of these DCs in T-cell differentiation, we characterized the nature of the CD4<sup>+</sup> T cells present in AT of lean, HFD, and db/db mice. Intracytoplasmic cytokine expression analysis showed the presence of more IFN-γ-secreting Th1 cells than IL-17-secreting Th17 cells in lean mice AT (Fig. 4A). In obese HFD and db/db mice, we observed a switch from a Th1 toward a Th17 response (Fig. 4A). This result prompted us to determine the role of each DC subset in the induction of CD4<sup>+</sup> T cells.

To analyze the influence of the different DC subsets on the priming and differentiation of naive OVA-specific T cells (from OT2 mice) in vitro, two rounds of 5 days of stimulation of T cells were performed with CD11c<sup>high</sup>F4/80<sup>neg</sup> and CD11c<sup>high</sup>F4/80<sup>low</sup> DCs sorted from AT of lean and obese mice. As shown in Fig. 4B, ex vivo–purified CD11c<sup>high</sup>F4/80<sup>low</sup> DCs from obese mice induced exclusively the differentiation of Th17 cells that produced high levels of IL-17 (Fig. 4B, R2). In contrast, the sorted CD11c<sup>high</sup>F4/80<sup>neg</sup> DCs primed both Th1 and Th17 cells, which produced low levels of IFN-γ and IL-17, respectively (Fig. 4B, R3). In lean mice, sorted CD11c<sup>high</sup>F4/80<sup>low</sup> DCs induced only the differentiation of Th1 cells (Fig. 4C, R3). In contrast, CD11c<sup>high</sup>F4/80<sup>low</sup> induced only a weak Th17 response (Fig. 4C, R2). However, we did not detect IL-4 or IL-10 in our cocultures (data not shown). Taken together, these results indicate that the induction of Th17 cells in obesity is mainly a result of the emergence and expansion of CD11c<sup>high</sup>F4/80<sup>low</sup> DCs.

Characterization of DC and T-cell phenotype in the subcutaneous AT of human patients. We then extended our study to humans and analyzed the DCs present in the subcutaneous AT from lean, overweight, and obese patients.
FACS analyses were performed on freshly isolated SVF from human subcutaneous AT of healthy individuals using human dendritic markers including CD1c, CD11c, and CD83. Positive cell subsets were identified in SVF of human AT and the number of CD1c+, CD11c"CD141", and CD83" cells was found to be positively associated with BMI (Fig. 5A-C). We then determined the expression level of IL-17 in T cells as a function of obesity. To do this, the gene expression level of IL-17 was evaluated in CD3" cells purified from SVF of freshly harvested AT that was depleted in CD34" progenitor and capillary endothelial cells and CD14" monocytes/macrophages. The expression of IL-17 in AT was strongly increased in overweight and obese patients compared with lean subjects (Fig. 5D). The intracellular expression of IL-17 evaluated by flow cytometric analysis was also found in CD4" T cells in AT of obese patients (Fig. 5E). Finally, the capacity of CD1c+ DCs from obese patients to drive Th17 differentiation was tested in vitro in an allogeneic MLR. As shown in Fig. 5F, CD1c+ DCs sorted from obese patients were able to induce Th17 cell differentiation in vitro.

**Elevated CD1c expression in subcutaneous AT correlated with HOMA-IR in morbidly obese patients.**

To determine the link between the accumulation of DCs and insulin resistance, we next evaluated the gene expression of Glut4, CD11c, and CD83 in AT from morbidly obese patients without (obese, n = 10, BMI = 42.8 ± 3 kg/m²) or with type 2 diabetes (n = 10; BMI = 46.8 ± 2 kg/m²; not significant vs. obese patients) compared with AT from four lean subjects (BMI = 21.1 ± 0.7 kg/m²). All diabetic patients were mainly women (diabetic: 9 women and 1 man; obese patients: 10 women; not significant), insulin resistant as evaluated by the HOMA-IR (diabetic patients = 1.4 ± 2.6; obese patients = 2.1 ± 0.2, P < 0.05), and had an elevated level of HbA1c (diabetic patients = 8.1 ± 0.7%, obese patients = 5.4 ± 0.1, P < 0.05), fasting glucose (diabetic patients = 10 ± 1.2 mmol/L; obese patients = 5 ± 0.1 mmol/L, P < 0.05), and insulin (diabetic patients = 26.1 ± 4.7 mmol/L; obese patients = 9.6 ± 1.1 μmol/L, P < 0.05). Glut4 mRNA expression was strongly decreased in the AT of diabetic obese patients compared with obese patients and with lean control patients (Fig. 6A). Moreover, Glut4 expression negatively correlated with HOMA-IR (Fig. 6B). In contrast, when compared with lean subjects, CD1c and CD83 gene expression increased progressively with obesity and then with diabetes (Fig. 6A). In AT, CD1c expression correlated negatively with Glut4 expression (rs = −0.613, P = 0.001) and positively with HOMA-IR (Fig. 6B). These results indicate that AT was enriched in activated CD1c+ DCs and that their accumulation directly correlated with insulin resistance.

**DISCUSSION**

AT inflammation is now considered to be a crucial event leading to metabolic syndrome, diabetes, arteriosclerotic cardiovascular, and liver disease. It has also been established that AT is not only involved in energy storage but also functions as an endocrine organ that secretes various bioactive substances referred to as adipokines with pro- or anti-inflammatory properties (32,39). Nevertheless, how inflammation is initiated and maintained in AT is still elusive.

Here, we showed that DCs residing in AT of lean mice may be capable of taking up and presenting antigens to naive CD4" T cells in an antigen-specific manner. Upon antigenic stimulation, naive CD4" T cells become effector T cells with a predominance of Th1 cells over Th17 cells. However, the naive T cells could be either activated directly in lymphoid organs before their migration into the AT or directly in the AT. This point remains to be determined.

Moreover, intracytoplasmic cytokine analysis of CD4" T cells purified from lean mice AT confirmed this observation. In contrast, the AT of insulin-resistant obese and type 2 diabetic mice displayed a switch from a Th1 toward a Th17 responses. Our data are supported by the recent report from Dorsch's group demonstrating the importance of obesity in the expansion of CD4" Th17 cells (34). We have also shown for the first time that the number of Th17 cells increases in AT of overweight and obese patients versus lean subjects. Although an anti-diabetic role for IL-17 has been described (35), emerging studies indicate that obesity selectively promotes the expansion of CD4" Th17 cells in AT, exacerbating autoimmune in murine models of colitis and experimental autoimmune encephalomyelitis (34,35). Taken together, these observations indicate that IL-17 may play an important role in metabolic processes. However, future investigations are necessary to explore this role more in details.

In this study, we identified a potential role of DCs in the regulation of AT inflammation and its potential consequence on insulin resistance in mice and humans. In mice, we reported that insulin-resistant and type 2 diabetic mice display an increase in cDCs (CD11c"F4/80"high cells) but also the emergence of atypical DCs expressing CD11c"F4/80"low markers. Furthermore, the CD11c"F4/80"low cells had all the features of DCs including their morphology, the expression of specific surface markers, and the capacity to process antigens. These atypical DCs also expressed CX3CR1, suggesting their preferential role in the differentiation of Th17 cells, as recently demonstrated in gut (31). Indeed, the CD11c"F4/80"low"CX3CR1" DCs induced Th17 differentiation in AT of obese mice. In lean mice, the CD11c+ DCs also led to differentiation of naive CD4" T cells into Th17 cells but to a very lower extent. However, the majority of CD11c+ DCs in lean AT were CD103", suggesting a role on the induction of fat Foxp3+CD4" Treg cells providing anti-inflammatory signals to block AT inflammation as described previously (30,36) and data not shown.

Our study is the first detailed analysis of human DCs in AT. Human DCs are a heterogeneous cell population that comprises ~1% of circulating peripheral blood mononuclear cells. They can be subdivided into the CD11c"CD303" plasmacytoid DCs and CD11c+ myeloid DCs, which can be further subdivided into two subsets based on differential expression of CD1c and CD141. Moreover, each CD1c+ and CD141+ DC has a unique gene expression profile distinct from monocytes and monocyte-derived DCs predicting distinct functions (37-39). We first observed that the levels of human CD11c"CD141" DCs were the same in overweight/obese and lean patients and that plasmacytoid DCs (CD11c"CD303") were not detected in human AT (data not shown). In contrast, the number of human CD11c"CD141" DCs correlated with the BMI and gene expression of CD11c+ subcutaneous AT, which increased in obese patients and even more so in diabetic patients compared with lean subjects. CD1c expression strongly correlated with HOMA-IR in patients with a high BMI. The accumulation of human CD11c+CD1c+ DCs was associated with an increase in human Th17 cells in AT, suggesting a role of these DCs in the induction of Th17 cells. Indeed, our results show that CD1c+ DCs sorted from obese patients were able to induce Th17 cells in vitro. In
FIG. 5. Characterization of human dendritic cells and the expression level of IL-17 in purified T cells as a function of the BMI. FACS analyses were performed on total SVF (patient age = 44.6 ± 2.5 years, BMI ranging from 19.5 to 38 kg/m², n = 20 to 24). A: Cell number of CD1c⁺ cells per gram of AT (P < 0.05, Spearman r = 0.3826, n = 24). B: Cell number of CD1c⁺ CD11c⁺ cells per gram of AT (P < 0.05, Spearman r = 0.4947, n = 20). C: Cell number of CD83⁺ cells per gram of AT (P < 0.05, Spearman r = 0.3870, n = 21). D: The gene expression level of IL-17 was evaluated by real-time PCR on immunoselected CD3⁺ T cells of the AT SVF of lean (n = 10 to 12), overweight (OW; n = 6 to 7), and obese (Ob; n = 12 to 14) patients. Results are means ± SEM. *P < 0.05. E: Intracellular cytokine analysis for IL-17 on immunoselected CD3⁺ T lymphocytes of the AT SVF of OW (n = 6 to 7) and Ob (n = 12 to 14) patients. F: Allogeneic CD4⁺ T cells purified from blood of healthy donors (n = 3) were cultured for 6 days with sorted CD1c⁺ DCs from the CD19⁺CD14⁺ cells of the SVF of obese patients (n = 3). CD4⁺ T cells were collected, stimulated, and stained for intracellular IL-17 and IFN-γ cytokines. The experiment was repeated three times with similar results. SSC-A, side scatter-aire; AU, arbitrary unit.
In this sense, Hänsel et al. showed recently that dermal CD1c+ DCs from patients with psoriasis were capable of driving a Th17 cell response in vitro (40).

Collectively, our study defines human CD11c+CD1c+ and mouse CD11chighF4/80low DCs as inflammatory DCs in AT in obesity-associated insulin resistance and identifies their potential capacity to induce Th17 cell responses. Finally, understanding the role of IL-17 in metabolic processes and its direct clinical implications is clearly the next challenge for the field.

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