Mesenchymal Cells Regulate Retinoic Acid Receptor-Dependent Cortical Thymic Epithelial Cell Homeostasis

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The vitamin A metabolite and transcriptional modulator retinoic acid (RA) is recognized as an important regulator of epithelial cell homeostasis in several tissues. Despite the known importance of the epithelial compartment of the thymus in T cell development and selection, the potential role of RA in the regulation of thymic cortical and medullary epithelial cell homeostasis has yet to be addressed. In this study, using fetal thymus organ cultures, we demonstrate that endogenous RA signaling promotes thymic epithelial cell (TEC) cell-cycle exit and restricts TEC cellularity preferentially in the cortical TEC compartment. Combined gene expression, biochemical, and functional analyses identified mesenchymal cells as the major source of RA in the embryonic thymus. In reaggregate culture experiments, thymic mesenchyme was required for RA-dependent regulation of TEC expansion, highlighting the importance of mesenchyme-derived RA in modulating TEC turnover. The RA-generating potential of mesenchymal cells was selectively maintained within a discrete Ly51<sup>+</sup>gp38<sup>+</sup> subset of Ly51<sup>+</sup> mesenchyme in the adult thymus, suggesting a continual role for mesenchymal cell-derived RA in postnatal TEC homeostasis. These findings identify RA signaling as a novel mechanism by which thymic mesenchyme influences TEC development. The Journal of Immunology, 2012, 188: 4801–4809.
retinol to retinal is mediated by alcohol dehydrogenases, whereas retinal is converted to RA by retinaldehyde dehydrogenases. Two enzyme families, the cytosolic alcohol dehydrogenases and the microsomal retinol dehydrogenases (RDHs), have been implicated in the conversion of retinol to retinal, of which RDH10 has been shown to play a nonredundant role in priming of RA synthesis during embryonic development (26). The oxidation of retinal to RA is carried out by three retinaldehyde dehydrogenases (RALDH1, RALDH2, and RALDH3; encoded by the genes Aldh1a1, Aldh1a2, and Aldh1a3, respectively), mutations in two of which (Aldh1a2 and Aldh1a3) result in early embryonic (Aldh1a2) or neonatal (Aldh1a3) lethal phenotypes (for review, see Ref. 27). RA is a major physiological regulator of epithelial cell homeostasis in multiple organs such as the lung (28), kidney (29), pancreas (30), gut (31), and skin (32). Regarding thymus development, mesenchyme-derived RDH10- and RALDH2-dependent RA signaling in the pharyngeal arch endoderm, a region that gives rise to TEC progenitors, is a critical prerequisite to the initial formation of the thymus (26, 33, 34). The potential ability of RA to interfere with later stages of thymus development has been suggested based on hypoplastic and ectopic thymus phenotypes generated in embryos treated with teratogenic doses of exogenous retinoids (35). Notably, there is also evidence of continualRAR signaling in the postnatal thymus (36), and the broad spectrum of immune abnormalities observed in vitamin A-deficient animals includes a marked atrophy of the thymus (37), indicating that RA signaling events may play additional roles in thymus ontogeny. In this study, we demonstrate that mesenchymal cells represent a major source of RA in both the embryonic and adult thymus. In functional experiments involving fetal thymus organ cultures (FTOCs), we show that mesenchymal cell-derived RA plays an important role in regulating TEC numbers predominantly within the cTEC compartment, thereby highlighting a novel mechanism by which thymic mesenchyme influences the development of TEC.

Materials and Methods

Animals

C57BL/6 mice were bred and maintained at the Biomedical Centre Animal Facility (Lund University, Lund, Sweden), unless otherwise stated. BALB/c and C57BL/6 Rag–1−/− mice were housed in the Biomedical Services Unit at the University of Birmingham (Birmingham, U.K.). Day of vaginal plug detection was designated as day 0 of gestation. All animal procedures were approved by the Lund/Malmö animal ethics committee.

Abs and reagents

The following Abs and reagents were used: biotin-Ly51/BP-1 (6C3), FITC or PE-Ki67 (B56), FITC-BrdU (3D4), PE-mouse IgG1, isotype control, bio-rat IgG2a, isotype control, bio-PDGFRb (AP5), bio-PDGFRA (AP58), Alexa 488-CD45 (30-F11), Cell sorting.

FTOC and reaggregate thymus culture

FTOCs were established as previously described (38). Briefly, thymic lobes were dissected from mouse embryos at embryonic day (E15) gestational stage and placed at the air–medium interface on top of a 0.8-µm isopore membrane filter (Millipore, Billerica, MA) resting on an Artigrap gelatin sponge (Medipour, Weymouth, Dorset, U.K.). The filter and sponge were submerged in DMEM-10 (High-glucose Glutamax-supplemented DMEM, 10 mM HEPES, 100 U ml−1 penicillin, 100 µg ml−1 streptomycin, 50 µM 2-ME, 0.1 mM MEM Non-Essential Amino Acids Solution [all from Invitrogen], and 10% FCS [Sigma-Aldrich]) and incubated in 7–10% CO2 at 37°C. Medium containing freshly prepared dilution of RA, LE540, or carrier DMSO (0.5%) was supplied to the cultures at 2- to 3-d intervals. Cell numbers were determined using a Bürker chamber or with CountBright Absolute Counting Beads (Invitrogen).

Reaggregate thymus organ cultures (RTOCs) were performed as previously described (39). Briefly, FACS-sorted E15 mesenchymal, TEC, and thymocyte populations (for gating strategy, see Supplemental Fig. 2) were combined at a 1.0:2.4:1.4 ratio and reaggregated by depositing cells on the surface of 0.8-µm Nucleopore filters (Whatman; Maidstone, Kent, U.K.) under organ culture conditions as described above. Initial TEC numbers used to establish mesenchyme-containing and mesenchyme-deprived RTOCs were 1.3 × 105 and 1.74 × 105, respectively.

Cell isolation

Isolated embryonic thymus lobes and FTOC/RTOC cultures were digested with 0.5% trypsin-EDETA (Invitrogen) at 37°C for 30 min and single-cell suspensions used in the allele assay or directly stained with Abs for analysis and cell sorting.

To isolate stromal cells from postnatal thymuses, organs were cut into tissue pieces and digested enzymatically with collagenase IV (Roche Diagnostics, Basel, Switzerland) and DNase I (50 Kunitz U ml−1; Sigma-Aldrich) in R-5 medium (t-glutamine–supplemented RPMI 1640, 1 mM sodium pyruvate, 50 µg ml−1 gentamicin [all from Invitrogen], 100 U ml−1 penicillin, 100 µg ml−1 streptomycin, 10 mM HEPES, and 5% FCS) at 37°C for 35 min using an orbital shaker (350 rpm). Enzymatic treatment was repeated for an additional 20–25 min followed by incubation with 5 mM EDTA on ice for 5–10 min. Remaining tissue fragments were mechanically dispersed by careful pipetting. Cell suspensions obtained after each digestion were pooled in ice-cold PBS containing 2% FBS and 2 mM EDTA to prevent aggregate formation. Stromal cells were enriched by immunomagnetic depletion of CD45+ cells by MACS (Miltenyi Biotec, Bergish Gladbach, Germany) according to the manufacturer’s protocol and used in the allele assay or directly stained with Abs for analysis and cell sorting.

Measurement of aldehyde dehydrogenase activity

Aldehyde dehydrogenase (ALDH) activity was measured using the ALDEFLUOR Kit (StemCell Technologies, Vancouver, BC, Canada) according to the manufacturer’s instructions. Briefly, cells were suspended in ALDEFLUOR assay buffer containing activated aldefluor reagent (Bodipy-aminomocetadylde; final concentration 1.5 µM) with/without inclusion of the ALDH competitive inhibitor 4-diethylamino-benzaldehyde (DEAB; final concentration 75 µM) and incubated at 37°C for 30–40 min. Remaining cell aggregates were broken up by sonication and stained with FITC-conjugated anti-BrdU Ab (FITC BrdU Flow Kit; BD Biosciences) labeled with surface Abs to CD45 and EpCAM, followed by staining with FlowJo software (Tree Star, Ashland, OR). Sorting was performed on an FACSaria (BD Biosciences) using FITC channel for the detection of aldefluor signal.

Flow cytometry and cell sorting

Flow cytometry was performed according to standard procedures. Dead cells (identifiable as propidium iodide+ or using the LIVE/DEAD Violet Fixable Dead Cell Staining Kit [Invitrogen]) and cell aggregates (identified on forward light scatter-A versus forward light scatter-W scatter plots) were excluded from all analyses. Data acquisition was performed on FACSaria, LSRII, or LSRFortessa (BD Biosciences, Franklin Lakes, NJ) and analyzed using FlowJo software (Tree Star, Ashland, OR). Sorting was performed on an FACSaria (BD Biosciences). For analysis of BrdU incorporation, day 7 FTOCs were pulsed with BrdU (10 µM; BD Biosciences) for 5 h. Lobes were trypsinized as above and single-cell suspensions labeled with surface Abs to CD45 and EpCAM, followed by staining with FITC-conjugated anti-BrdU Ab (FITC BrdU Flow Kit; BD Biosciences) according to the manufacturer’s protocol. For analysis of Ki67 expression, surface-labeled FTOC cell suspensions were then permeabilized with the Foxp3 Staining Buffer Set (eBioscience) according to the manufacturer’s protocol, and stained with PE-conjugated anti-Ki67 Ab (BD Biosciences).
The F9-RARE-lacZ reporter cell line (40) was maintained on gelatin-coated surfaces in DMEM/F-12 medium (Invitrogen) containing 100 μg/ml penicillin, 100 μg/ml streptomycin, 10% FCS, and 0.8 mg/ml G418 or in DMEM-10.

For incubation with E15 thymic populations, reporter cells (5 × 10⁶ cells/well) were plated onto gelatin-coated, round-bottom, 96-well plates in DMEM/F-12 in 2% FCS 24 h prior to the assay. FACS-sorted cell populations were suspended in DMEM/F-12 and added to the wells (5 × 10⁵ cells/well) together with 25 nM retinol. LacZ induction was measured 22 h later with the β-Glo Assay System (Promega, Madison, WI) according to the manufacturer's protocol. Chemiluminescence was quantified in white luminometer 96-well plates (Nunc; Thermo Fisher Scientific) with a Glo-Max 96 luminescence (Promega). Thymic subset-induced β-galactosidase (β-Gal) activity was calculated by subtracting the activity in cultures incubated with retinol alone.

For incubation with 2-wk-old mesenchymal populations, reporter cells (3 × 10⁶ cells/well) were plated onto gelatin-coated, flat-bottom, half-area, 96-well plates in DMEM-10 24 h prior to the assay. FACS-sorted cell populations were suspended in DMEM and added to the wells (10⁵ cells/well) together with 25 nM retinol, followed by measurement of LacZ induction 19 h later as described above.

RNA isolation and quantitative RT-PCR

Total RNA was extracted using RNeasy Micro Kit (Qiagen) and reverse transcribed with SuperScript III (Invitrogen) according to the manufacturer's instructions. First-strand cDNA synthesis was primed with a 1:1 mixture of oligo(dT) and random oligonucleotide hexamers (both from Invitrogen). Quantitative RT-PCR (qRT-PCR) reactions (20 μl volume) were set up using Maxima SYBR Green qPCR Master Mix (Fermentas) and carried out in a Bio-Rad MyQ Thermal Cycler (Bio-Rad) with the following cycling conditions: 50°C hold for 2 min, 95°C hold for 10 min, and then 45 cycles of 95°C for 10 s and 60°C for 30 s. Samples were assayed in duplicates. Gene expression was calculated using the comparative ΔΔCt method and normalized to β-actin or GAPDH. Product specificity was evaluated by melting curve analysis and further confirmed by electrophoresis on agarose gels.

Primer sequences are as follows: β-actin forward, 5'-GAGAGGGGAATCGTGCAGTACA-3' and reverse, 5'-GTTCTATAGATGAGCCACAGGAT-3' ; Gapdh forward, 5'-TGTGTCGTAGTGATCCTCTGA-3' and reverse, 5'-CCTCTCTACACCTCTCTGTGA-3' ; βS (PonB1) forward, 5'-ACTCAGCACCACCCAGACG-3' and reverse, 5'-GTTGAGCAGAAAGCGCAAAGC-3' ; claudin 3 forward, 5'-ACACACCTGCTAACAGGACGAC-3' and reverse, 5'-CAGGCCCCAGTACAAACCCAGC-3' ; claudin 4 forward, 5'-GACTACACGTCCTGGAATCTCC-3' and reverse, 5'-GTCTTGTGCCGTGTACGTTGTC-3' ; cathepsin F forward, 5'-GGGAGGCGGTGC-3' and reverse, 5'-AGTGAAGGCCTCCCAACGCTCT-3' ; delta-like 4 forward, 5'-AGGTGCCTCCTGCTTCAC-3' and reverse, 5'-GGCTCCTCTGTACGAGAC-3' ; FGF7 forward, 5'-CTGCCTTGATGCTCTATCAG-3' and reverse, 5'-AAGTGGACCCGCAGTATCG-3' ; FGF8 forward, 5'-GGCAGAGGAGGAGAGGAGA-3' and reverse, 5'-GGCAGAGGAGGAGAGGAGA-3' ; Fgf10 forward, 5'-TGTGAGAAACGCAGTACAG-3' and reverse, 5'-GATTTCCCTCTTCTGTGACTG-3' ; Igf1 forward, 5'-GGTTGAGTCTCTCAGTCTGCTG-3' and reverse, 5'-ATGACAGTCCGAGCAACAC-3' ; Igf2 forward, 5'-TCTCATTGAGCCGCTTCAAGC-3' and reverse, 5'-TATTGAGAAGTCTGGCCACGCCG-3' ; II7 forward, 5'-CGTGCAATCTATTGTTCGTC-3' and reverse, 5'-CGGAGAATTTCCTACATCTAC-3' ; claudin 3 forward, 5'-GGAGACCCCTTGGAGGATCAG-3' and reverse, 5'-GGAAGACCCCTTGGAGGATCAG-3' ; claudin 4 forward, 5'-GGAGAGGAGAAGAGGAGA-3' and reverse, 5'-GGAGAGGAGAAGAGGAGA-3' ; cathepsin F forward, 5'-AGGTGGACCCGCAGTATCG-3' and reverse, 5'-AAGTGGACCCGCAGTATCG-3' ; delta-like 4 forward, 5'-AAGTGGACCCGCAGTATCG-3' and reverse, 5'-AAGTGGACCCGCAGTATCG-3' ; FGF7 forward, 5'-AAGTGGACCCGCAGTATCG-3' and reverse, 5'-AAGTGGACCCGCAGTATCG-3' ; FGF8 forward, 5'-AAGTGGACCCGCAGTATCG-3' and reverse, 5'-AAGTGGACCCGCAGTATCG-3' ; claudin 3 forward, 5'-GGAGACCCCTTGGAGGATCAG-3' and reverse, 5'-GGAAGACCCCTTGGAGGATCAG-3' ; claudin 4 forward, 5'-GGAGAGGAGAAGAGGAGA-3' and reverse, 5'-GGAGAGGAGAAGAGGAGA-3' ; cathepsin F forward, 5'-AGGTGGACCCGCAGTATCG-3' and reverse, 5'-AAGTGGACCCGCAGTATCG-3' ; delta-like 4 forward, 5'-AAGTGGACCCGCAGTATCG-3' and reverse, 5'-AAGTGGACCCGCAGTATCG-3' ; cathepsin F forward, 5'-AGGTGGACCCGCAGTATCG-3' and reverse, 5'-AAGTGGACCCGCAGTATCG-3'.

**Statistical analysis**

Statistical analyses were performed using unpaired two-tailed Student t test except for Fig. 1E and Supplemental Fig. 1, in which one-way ANOVA with Bonferroni's multiple comparison test was used: *p < 0.05, **p < 0.01, ***p < 0.001.

**Results**

**RA signaling regulates TEC proliferation in FTOC**

To investigate the potential role of RA signaling during thymus development, we studied the effects of the pan-RAR antagonist LE540 (41) on embryonic thymus growth in FTOC. To this aim, E15 thymus lobes were cultured in the presence/absence of LE540 and TEC, mesenchyme, and thymocyte numbers were assessed 7 to 8 d later by flow cytometry. RA antagonist treatment resulted in the generation of markedly larger organs (Fig. 1A), revealing that thymus growth in FTOC is subject to negative regulation by ongoing RA signaling. At the cellular level, blockade of RA signaling caused an increase in TEC numbers and an accompanying rise in total thymocyte cellularity, whereas the mesenchymal compartment remained unaffected (Fig. 1B). To determine whether the elevated number of TEC in LE540-treated
FTOC may be due to enhanced TEC expansion, Ki67 staining and short-term BrdU incorporation studies were performed. LE540 induced a dose-dependent increase in TEC numbers and TEC proliferation rate compared with control FTOC (Fig. 1C, Supplemental Fig. 1), suggesting that RA signaling restricts TEC cellularity by inhibiting TEC proliferation. TEC proliferation was also enhanced in LE540-treated Rag-1<sup>−/−</sup> FTOC, indicating that this effect was independent of DP and SP thymocytes, although changes in total TEC number were less dramatic (Fig. 1D). Consistent with these findings addition of exogenous RA to FTOC led to a dose-dependent reduction in TEC numbers and TEC proliferation rates (Fig. 1E), without affecting cell viability (data not shown). Together, these results identify RA signaling as a novel pathway that negatively controls TEC expansion and organ size during embryonic thymus development in vitro.

**RA signaling acts preferentially to regulate cTEC homeostasis**

To determine which TEC populations were affected by inhibiting RA signaling in FTOC, the phenotype of TEC in 7-d FTOC was assessed by flow cytometry (Fig. 2A). LE540 treatment increased the total number of CD80<sup>+</sup> TEC (Fig. 2A) that are thought to comprise mature and immature cTEC and mTEC progenitors (14), but did not affect CD80<sup>+</sup>UEA<sup>hi</sup> mature mTEC numbers (42). To further define the CD80<sup>−</sup> cells that expanded in the absence of RA signaling, CD80<sup>−</sup> TEC were sorted from LE540-treated and control FTOC and assessed for expression of a panel of genes differentially expressed in cTEC and mTEC lineages by QRT-PCR (Fig. 2B). CD80<sup>−</sup> TEC that were isolated from LE540-treated cultures expressed significantly higher levels of genes associated with the cTEC lineage including βSt, Dil4, and Prrs16 (43–46) and lower levels of the mTEC-associated genes such as cathepsin S, claudin 3, claudin 4, and Ccl21a (4, 7, 47, 48), indicating that RA signaling preferentially regulates cTEC differentiation/proliferation. Consistent with these findings, the proportion and total number of CD80<sup>−</sup> cells expressing high levels of the cTEC maturation marker CD205 (DEC205) increased significantly in LE540-treated cultures (Fig. 2C). Together, these results suggest that RA primarily regulates cTEC homeostasis in FTOC.

**Mesenchymal cells are the major source of RA in the embryonic thymus**

The impact of the RAR antagonist on the expansion and phenotype of TEC in FTOC suggested ongoing vitamin A metabolism and RA production in the cultured organs. To determine which populations in the embryonic thymus are capable of generating RA, TEC, thymocytes, and mesenchymal cells were sorted from E15 thymuses (Supplemental Fig. 2) and analyzed for expression of RALDH1–3 (Aldh1a1, -2, and -3), which catalyze the last rate-limiting step during RA synthesis (49) by real-time PCR (Fig. 3A). TEC were sorted into CD205<sup>+</sup>CD40<sup>−</sup> cTEC and CD205<sup>−</sup>CD40<sup>+</sup> mTEC, which represent the major TEC compartments at this stage of thymus ontogeny (7). Importantly, Aldh1a2, the presence of which most strongly correlates with RA generation in vivo (27), was highly and selectively expressed by CD45<sup>+</sup>EpcAM<sup>+</sup> mesenchymal cells, whereas Aldh1a1 and -3 were mainly produced by cTEC and at much lower levels (note the different y-axis scales of the graphs in Fig. 3A). To further evaluate the RA-generating potential of thymic cell populations, ALDH activity in mesenchyme, TEC, and thymocytes was assessed by flow cytometry using the fluorescent ALDH substrate Bodipy-aminocoumaraldehyde (commercially called aldefluor) (50). Consistent with their expression of Aldh1a2, mesenchymal cells, but not TEC or thymocytes, showed prominent aldefluor staining (Fig. 3B, 3C). This staining was specifically reflecting ALDH-mediated enzymatic activity because it was blocked by the specific ALDH inhibitor DEAB (51) (Fig. 3B, 3C). To directly assess the RA-generating capacity of mesenchymal cells, TEC, and thymocytes, each population was sorted from E15 thymuses and incubated together with the RA-reporter cell line F9-RARE-lacZ (40), which express β-Gal under control of an RA-sensitive promoter. Consistent with the data above, mesenchymal cells but not TEC or thymocytes induced RA-dependent β-Gal activity in the reporter cells (Fig. 3D). Together, these data demonstrate that mesenchymal cells are a major source of RA in the embryonic thymus.

**Mesenchymal cells regulate RAR-dependent TEC expansion in RTOCs**

To determine whether mesenchymal cells mediated the RA-dependent regulation of TEC proliferation in FTOCs, TEC and thymocytes were sorted from E15 thymuses and used to establish reaggregate cultures in the presence or absence of E15 mesenchymal cells.
Mesenchymal cells continue to generate RA in the adult thymus.

To assess whether adult mesenchymal cells are capable of metabolizing vitamin A and thus could potentially modulate TEC growth in the adult thymus, ALDH activity in adult thymic mesenchyme was assessed by flow cytometry using the aldefluor assay (for gating strategy, see Fig. 5A). Thymic endothelial cells, defined as CD31<sup>+</sup>CD45<sup>–</sup>EpCAM<sup>–</sup> cells, did not possess ALDH activity (Fig. 5B). Two major mesenchymal subsets were identified based on expression of Ly51 and gp38 (podoplanin): Ly51<sup>hi</sup>gp38<sup>+</sup> and Ly51<sup>int</sup>gp38<sup>+</sup> cells in the adult thymus. Next, FACS-purified gp38<sup>+</sup> mesenchymal cells in the adult thymus were analyzed for ALDH activity in adult thymic mesenchyme minus background (Fig. 5D), and β-Gal activity was measured in cell lysates 22 h later. Results are mean (SD) from three biological replicates using cells sorted from seven mice per replicate. ***p < 0.001.

FIGURE 3. Mesenchymal cells generate RA in the embryonic thymus. (A) TEC, thymocytes (CD45<sup>+</sup>), and mesenchymal populations were sorted from E15 thymuses and used to establish reaggregate cultures (RTOCs) with/without E15 mesenchymal cells (for gating strategy, see Supplemental Fig. 2). RTOCs were analyzed after 8 to 9 d of culture in the presence/absence of LE540 (8 μM). Representative FACS profiles of CD45 versus EpCAM staining in indicated RTOCs. Numbers show percentage of cells in the live cell gate. (B) Fractional abundance (upper panel) and total number (lower panel) of TEC in indicated RTOCs. (C) Total number of CD80<sup>+</sup> and CD80<sup>–</sup> TECs in indicated RTOCs. (D) Total number of CD80<sup>+</sup>CD205<sup>+</sup> and CD80<sup>–</sup>CD205<sup>+</sup> TECs in indicated RTOCs. (B–D) Results are the mean (SD) of three (mesenchyme-containing RTOC) and four (mesenchyme-deprived RTOC) biological replicates per condition from two experiments. *p < 0.05, **p < 0.01, ***p < 0.001.

FIGURE 4. Mesenchymal cells regulate RAR-dependent TEC expansion in RTOCs. (A–D) TEC and thymocytes were sorted from E15 thymuses and used to establish reaggregate cultures (RTOCs) with/without E15 mesenchymal cells (for gating strategy, see Supplemental Fig. 2). RTOCs were cultured for 8 to 9 d of culture in the presence/absence of LE540 (8 μM). (A) Representative FACS profiles of CD45 versus EpCAM staining in indicated RTOCs. Numbers show percentage of cells in the live cell gate. (B) Fractional abundance (upper panel) and total number (lower panel) of TEC in indicated RTOCs. (C) Total number of CD80<sup>+</sup> and CD80<sup>–</sup> TECs in indicated RTOCs. (D) Total number of CD80<sup>+</sup>CD205<sup>+</sup> and CD80<sup>–</sup>CD205<sup>+</sup> TECs in indicated RTOCs. (B–D) Results are the mean (SD) of three (mesenchyme-containing RTOC) and four (mesenchyme-deprived RTOC) biological replicates per condition from two experiments. *p < 0.05, **p < 0.01, ***p < 0.001.
fraction induced RAR-dependent β-Gal activity in the RA reporter cell line F9-RARE-lacZ (Fig. 5E). Together, these data demonstrate that RA-producing mesenchymal cells persist in the adult thymus, suggesting continual involvement of mesenchymal cell-derived RA in postnatal TEC homeostasis.

Comparative analysis of aldefluor+ and aldefluor− Ly51intgp38+ thymic mesenchymal cells. Finally, we determined whether Ly51intgp38+ mesenchymal cells that displayed ALDH activity (aldefluor+ cells) and Ly51intgp38− mesenchymal cells that did not have ALDH activity (aldefluor− cells) differed in their expression of known mesenchymal markers and mesenchyme-derived soluble mediators. Aldefluor+ and aldefluor− Ly51intgp38+ mesenchymal cells expressed similar levels of PDGFRβ and LTβR, whereas aldefluor+Ly51gp38+ mesenchymal cells expressed higher levels of PDGFRα and lower levels of ICAM-1 and VCAM-1 (Fig. 6A). Gene-expression analysis demonstrated that aldefluor+ and aldefluor− Ly51intgp38+ mesenchyme subsets expressed similar levels of FGF-10, IGF-1, stem cell factor, and IL-7 mRNA, whereas aldefluor+ mesenchyme expressed significantly more FGF-7 and IGF-2 and significantly less CCL19 and CCL21a transcripts than aldefluor− mesenchyme (Fig. 6B).

Discussion

The establishment and maintenance of organized cortical and medullary epithelial microenvironments play an essential role in the development and selection of a self-tolerant T cell pool. The control of TEC growth for optimal T cell development is a non–cell-autonomous process that has been linked to numerous factors including IGFs and FGFs, with the latter implicated as both positive and negative regulators (18, 19, 52). In this study, we identify mesenchymal cell-derived RA as a novel negative regulator of TEC proliferation in FTOCs that acts preferentially on the cortical TEC compartment. We also demonstrate that a subset of mesenchymal cells maintains RA-generating activity in the adult thymus.

FIGURE 5. Mesenchymal cells continue to generate RA in the adult thymus. (A–C) ALDH activity of mesenchymal and endothelial cells in 7–10-wk-old adult thymus was assessed by the aldefluor assay. (A and B, upper panel) Gating strategy used to identify CD31+ endothelial and Ly51+gp38+ and Ly51−gp38+ mesenchymal populations in adult thymus digests. (B) Representative histograms of aldefluor signal (lower panel) in the absence (black line) or presence (gray filled) of DEAB. (C) Median fluorescence intensity of aldefluor signal in ALDH− Ly51+ gp38− and Ly51− gp38+ mesenchymal populations. Results are the mean (SD) from three biological replicates using pooled cells from two to three thymuses/replicate and are from one representative experiment of two performed. (D) gp38+ and gp38− PDGFRβ mesenchymal populations were sorted from 2-wk-old thymus and expression of Aldh1a1, -2, and -3 was determined by real-time PCR. Results are the mean (SD) of three biological replicates using cells sorted from eight mice/replicate. (E) FACS-sorted gp38+ and gp38− PDGFRβ+ mesenchymal populations were sorted from 2-wk-old thymuses and incubated with the RA-reporter cell line F9-RARE-lacZ in the presence/absence of 1 μM LE540, and β-Gal activity was measured in cell lysates 19 h later. Results are mean (SD) from three biological replicates using cells sorted from seven to eight mice per replicate. ***p < 0.001. n.a., Not analyzed.

FIGURE 6. Comparative analysis of aldefluor+ and aldefluor− Ly51intgp38+ thymic mesenchymal cells. (A) Phenotypic characterization of aldefluor+ (ALDH+) and aldefluor− (ALDH−) Ly51intgp38+ mesenchyme in 7–10-wk-old thymus. Representative FACS plots from three to five biological replicates using pooled cells from two to eight mice/replicate from two (PDGFRβ, LTβR) or three (PDGFRα, ICAM-1, and VCAM-1) independent experiments. (B) Aldefluor+ and aldefluor− Ly51intgp38+ mesenchymal populations were sorted from 7–8-wk-old thymuses for analysis of gene expression by real-time PCR. Results are the mean (SD) of 3 biological replicates using cells sorted from 10 mice/replicate. *p < 0.05, **p < 0.01.
thymus, suggesting a potential role for mesenchymal-derived RA in regulating TEC homeostasis in the adult. These results add RA to the list of mesenchymal cell-derived signals that regulate TEC homeostasis and highlight a role for thymic mesenchyme as both positive and negative regulators of TEC growth.

Notably, RAR antagonism had a dramatic effect on TEC composition in day 7 FTOC. The RAR antagonist appeared not to affect CD80⁺ TEC numbers but significantly enhanced the number and proportion of CD80⁻ cells expressing high levels of the cTEC marker CD205. Furthermore, CD80⁻ TECs, which contain both immature mTEC and cTEC (14), showed increased levels of cTEC and decreased levels of mTEC-specific gene transcripts in RAR antagonist-treated cultures. Although the precise stages in cTEC development that are influenced by RA are unclear, fully mature MHC class IIhigh mature cTECs are largely absent from the fetal stages of thymus development analyzed in this study (7), suggesting that RA signaling may act preferentially to limit the size of the cTEC compartment by promoting cell-cycle exit of committed cTEC progenitors. We cannot, however, rule out that in addition to inhibiting cell proliferation, RA signaling may also affect fate decision events in common cTEC/mTEC progenitors.

Our observation that the RAR antagonist promoted TEC expansion in Rag1⁻/⁻ FTOC as well as preliminary FTOC experiments using CD3εTg26 thymuses, which have a developmental block in the earliest T cell precursors, indicate that thy-mocytes are not required for RA-dependent regulation of TEC proliferation. One possibility is that RA functions directly on TECs to regulate their proliferation, as previously observed in primary and transformed epithelial cell lines from the skin (53), intestine (54), cervix (55), and mammary gland (56, 57). Indeed, RA has been shown to downregulate FGF binding protein production (58) and inhibit bone morphogenetic protein signaling (59, 60), a pathway central to FGF-7–induced TEC proliferation (19). In addition, RA can influence the expression of IGF binding proteins (61) and has been shown to inhibit expression of del-taNpf3, a P63 transcription factor family member that is required for maintaining the proliferative potential of TEC precursors (62, 63) in nasopharyngeal epithelial cells (64). An alternative possibility is that RA indirectly regulates TEC proliferation by modulating growth-promoting signaling pathways. For example, RA regulates FGF-7 expression (65) and inhibits FGF-10 transcription (66). Notably, we have found that mesenchymal expression of FGF-7 and FGF-10 is not altered in RAR antagonist-treated day 7 FTOC (K.M. Sitnik, unpublished observations), indicating that transcriptional regulation of these factors is not involved in RA regulation of TEC growth. The exact mechanism(s) by which RA regulates TEC homeostasis awaits further studies.

Our observation that a subset of mesenchymal cells maintains the ability to generate RA after birth suggests that RA signals may help to regulate TEC homeostasis in the adult. Consistent with this possibility, endogenous RA signaling in the postnatal thymus has been demonstrated using RA-reporter mice (36, 67). Based on the presence of Aldh1a1 expression in TECs and the detection of aldefluor⁺ cells in developing lymph nodes (68, 69), raising the interesting possibility that aldefluor⁺ and aldefluor⁻ subsets of Ly5¹intgp38⁺ mesenchyme represent progressive developmental stages with a lower and higher maturation status, respectively.

In summary, we have identified mesenchymal cell-derived RA as a novel regulator of TEC homeostasis and identify a subset of RA-producing mesenchymal cells in the adult thymus. Future studies using genetic deletion of the RA-generating and signaling pathways in mesenchymal cells and TEC, respectively, should help further delineate the role of this pathway in the in vivo setting.

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