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Functional differences between human NKp44\(^{-}\) and NKp44\(^{+}\) RORC\(^{+}\) innate lymphoid cells

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Abstract

Human RORC+ lymphoid tissue inducer cells are part of a rapidly expanding family of innate lymphoid cells (ILCs) that participate in innate and adaptive immune responses as well as in lymphoid tissue (re)modeling. The assessment of a potential role for innate lymphocyte-derived cytokines in human homeostasis and disease is hampered by a poor characterization of RORC+ innate cell subsets and a lack of knowledge on the distribution of these cells in adults. Here we show that functionally distinct subsets of human RORC+ innate lymphoid cells are enriched for secretion of IL-17a or IL-22. Both subsets have an activated phenotype and can be distinguished based on the presence or absence of the natural cytotoxicity receptor NKp44. NKp44+ IL-22 producing cells are present in tonsils while NKp44− IL-17a producing cells are present in fetal developing lymph nodes. Development of human intestinal NKp44+ ILCs is a programmed event that is independent of bacterial colonization and these cells colonize the fetal intestine during the first trimester. In the adult intestine, NKp44+ ILCs are the main ILC subset producing IL-22. NKp44− ILCs remain present throughout adulthood in peripheral non-inflamed lymph nodes as resting, non-cytokine producing cells. However, upon stimulation lymph node ILCs can swiftly initiate cytokine transcription suggesting that secondary human lymphoid organs may function as a reservoir for innate lymphoid cells capable of participating in inflammatory responses.
Introduction

There is an increasing awareness that early innate response involve several types of RORC\(^+\) and RORC\(^-\) lymphoid-like cells that combine aspects of innate and adaptive immunity including the production of cytokines traditionally associated with adaptive immune cells. These innate cells are collectively referred to as innate lymphocytes (ILCs) and are on the one hand important in early immunity to pathogenic bacteria and helminthes as well as tissue integrity after infection, while these cells on the other hand can be part of pathology during experimental colitis and are specifically expanding in Crohn’s disease patients and allergic rhinosinusitis patients.\(^1\)-\(^7\)

The best studied population of RORC\(^+\) ILCs are lymphoid tissue inducer cells (LTi cells) that are present in secondary lymphoid organs and whose prime function is to control fetal development of lymph nodes and Peyer’s patches in mouse and man.\(^8\),\(^9\) Even though lymphoid organogenesis occurs in utero, cells that phenotypically resemble LTi cells have been found in adult mice.\(^10\),\(^11\) Similar to fetal LTi cells, adult cells express molecules involved in LN development such as lymphotoxina1b2, (LT) and TNF-\(\alpha\) and depend on expression of Rorgt and Id2 for their development.\(^11\)-\(^14\) Although it remains to be determined to what extent adult LTi cells are similar to their fetal counterparts in terms of the ability to induce lymphoid organs, adult LTi cells were shown to have additional functions in the support of adaptive immune responses by facilitating memory T cell generation in the spleen.\(^15\),\(^16\) In humans, ILCs that resemble the mouse LTi cells are present in developing fetal lymph nodes.\(^8\) In adult mice and humans, RORC\(^+\) ILCs are found in secondary lymphoid organs, in the skin and in the intestines. In mice, RORC\(^+\) ILCs are essential for the first wave of defense against attaching and effacing intestinal pathogens like *Citrobacter rodentium*.\(^4\),\(^17\) IL-22 produced by ILCs activates the epithelium via the IL-22 receptor to produce antimicrobial products.\(^4\),\(^17\),\(^18\) In humans, several mucosal ILC subsets that produce IL-22 were described. We have previously identified a population of CD56\(^+\)RORC\(^+\) ILCs in the tonsil that constitutively produce IL-22.\(^8\) At the same time, a population of NKp44\(^+\)RORC\(^+\) ILCs were described in tonsils, Peyer’s patches and small intestines and named NK22.\(^17\) Clonal analysis of tonsil-derived RORC\(^+\) ILCs has since shown that CD56\(^+\)RORC\(^+\) ILCs and NKp44+ NK22 cells are the same population of ILCs.\(^19\)

NKp44 belongs to a family of activating receptors found on human NK cells. These receptors are collectively termed Natural Cytotoxicity Receptors (NCRs) and next to NKp44 include NKp30 and NKp46.\(^20\) All three are Ig-like transmembrane receptors that convey activating signals to NK cells. NKp46 and NKp30 are expressed constitutively, while expression of NKp44 is induced upon NK cell activation. NKp46 is also expressed on mouse NK cells, as well as on mouse ILCs in the intestines. NKp30 and NKp44 are not expressed in Mus. Musculus.\(^20\),\(^21\)

Besides production of IL-22, RORC\(^+\) ILCs in mice and man have been reported to produce IL-17a. In man, RORC\(^+\) ILCs in fetal lymph nodes\(^8\) and inflamed intestines\(^22\) contain IL-17a transcripts and in mice, stimulated splenic RORC\(^+\) ILCs and RORC\(^+\) ILCs from the small intestines were shown to produce IL-17a.\(^23\),\(^24\)
In summary, RORC$^+$ ILCs from tonsils and fetal lymph nodes differ strikingly in cytokine production: tonsil ILCs produce IL-22 while fetal lymph node ILCs contain only transcripts for IL-17a.\textsuperscript{8} Whether in vivo IL-17 and IL-22 are produced by the same population of cells or by different ILC populations is still subject to debate.\textsuperscript{25,26} Clarifying the cellular sources of these functionally distinct cytokines will increase our understanding of ILC biology and activation. In this report we determined the cellular source of ILC-derived IL-17a and IL-22 and show that these cytokines are preferentially transcribed by distinct subsets of ILCs located in peripheral or mucosal lymphoid organs respectively.

**Methods**

**Human tissues**
The use of all human tissues was approved by the Medical Ethical Commission of the Erasmus University Medical Center Rotterdam, and use was contingent on informed consent. Fetal tissues were obtained from elective abortions and gestational age was determined by ultrasonic measurement of the diameter of the skull or the femur and ranged from 7 to 22 weeks gestation. Tonsils were obtained from routine pediatric tonsillectomies. Adult hepatic and inguinal lymph nodes were collected post-mortem during multi-organ donation procedures. Adult small intestine, ileum, was collected as residual material after intestinal surgery for colon carcinoma. Healthy ileum was obtained from a clear distance from the tumour. Patients undergoing radiotherapy or chemotherapy were excluded. Informed consent was obtained from all patients, according to the Medical Ethical Commission of the Academic Medical Center, Amsterdam, the Netherlands.

**Cell preparation**
Fetal lymph nodes were dissected from the mesentery using dissecting microscopes, and cell suspensions were prepared by digestion with 0.5 mg/ml collagenase type IV (Sigma, St. Louis, MO) in PBS for 30 min at 37°C, while stirring continuously, and subsequently filtered through a 70 mm nylon mesh. Tonsils and adult lymph nodes were cut into small pieces and cell suspensions were prepared by disrupting the tissue with a GentleMacs (Miltenyi Biotech) in the presence of 0.5 mg/ml collagenase type IV (Sigma, St. Louis, MO). Mononuclear cells were isolated from ficoll gradients. Tonsils were further enriched for ILCs by labeling with CD117 microbeads (Miltenyi Biotech) and positive selection using MidiMacs (Miltenyi Biotech).

Adult intestinal ILCs were isolated as previously described.\textsuperscript{7} Ileum was incubated with HBSS (Gibco) containing DTT (154 $\mu$g/mL), 0.1% $\beta$-mercaptoethanol and 5mM EDTA at 37°C to eliminate mucus and epithelial cells. Thereafter mucosa was cut into small pieces and digested for 30 minutes at 37°C with Liberase TM (125 $\mu$g/mL) and DNaseI (200$\mu$g/mL) (Roche). Cell suspensions were filtered through a 70-$\mu$m nylon mesh and lamina propria mononuclear cells (LPMC) were isolated by Ficoll-Paque PLUS (GE, Healthcare).
Flow cytometry
The following antibodies were used: CD117-PercP.Cy5.5, NKp44-AlexaFluor647, NKp46-AlexaFluor647, NKp30-Pe (Biolegend, San Diego, CA); CD127-APC-eFluor780, CD45-PeCy7, RORgt-Pe (eBioscience, San Diego, CA); CD56-Pacific Blue, CD69-Pe, CD19-PeDY590, CD3-PeDY590, CD14-PeDY590 and CD34-PeDY590 (Exbio, Praha, CZ). Flow cytometry was performed on a BD LSRII and cell sorting on a BD ARIA (Becton Dickinson). Analysis were performed using FlowJo software (Tree Star Inc., Stanford, CA).

Cell culture
Sorted ILC subsets were cultured overnight in the presence of IL-7 (Peprotech) and SCF (R&D Systems) (both at 10 ng/ml) in the presence or absence of PMA (50 ng/ml; Sigma) and Ionomycin (100 ng/ml; Sigma) or for 3 days with IL-7, SCF and either IL-23 or IL-1b. Cells were cultured in 200ml DMEM supplemented with 10% FCS (Hyclone). IL-17a and IL-22 production was measured using the DuoSet ELISA development kit (R&D systems). ELISAs were performed according to the manufacturers’ instructions.

PCR
From fetal samples, adult lymph nodes and tonsil, RNA was extracted using the RNA-XS kit (Machery Nagel) followed by reverse-transcription with random hexamer primers. For quantitative PCR, a Neviti Thermal Cycler (Applied Biosystems) and DyNAmo Flash SYBR Green qPCR kit (Finnzymes) were used, with the addition of MgCl2 to a final concentration of 4 mM. All reactions were done in duplicate and are normalized to the expression of GAPDH (glyceraldehyde phosphate dehydrogenase). Relative expression was calculated by the cycling threshold (CT) method as $2^{-\Delta\Delta CT}$.

Primers used were:

- **GAPDH (Accession: NG_007073.2)**: FW GTC GGA GTC AAC GGA TT; Rev AAG CTT CCC GTT CTC AG
- **IL22 (Accession: NM_020525.4)**: FW CCC ATC AGC TCC CAC TGC; Rev GGC ACC ACC TCC TGC ATA TA
- **IL17A (Accession: NM_002190.2)**: FW GAA GGC AGG AAT CAC AAT C; Rev GCC TCC CAG ATC ACA GA

For cDNA synthesis of the adult ileum samples, the high-capacity cDNA archive kit (Applied Biosystems) was used. PCR was performed using the SYBR Green I master mix (Roche) for LightCycler 480 Instrument II (Roche).

Quantification of expression levels was performed with LinRegPCR software. All reactions were performed in duplicate were normalized using 18S rRNA expression levels and expressed in arbitrary units.

Specific primers were as follows:

- **18S rRNA FW**: AAT CTG GAG CTG GCC TTT CA; Rev CTG GAA GAT CTG CAG CCT TT
Statistical analysis
Samples were analyzed by Mann-Whitney U tests in SPSS PASW 17.0.2. P values < 0.05 were considered significant.

Results

Differential NCR expression on tonsil- and fetal LN-derived ILCs
We hypothesized that expression of Natural Cytotoxicity Receptors could be used to distinguish ILC subpopulations biased towards production of either IL-17a or IL-22. To test this we first compared the ex-vivo expression of NKp30, NKp44 and NKp46 on freshly isolated human ILCs from fetal lymph nodes versus tonsils. The following phenotypic definition was used for ILCs: lineage (CD3; CD19; CD14; CD34) negative cells expressing intermediate levels of CD45 and high levels of both CD127 (IL7Ra) and CD117 (c-Kit). Cells within this gate were uniformly RORC positive (Figure 1a). In fetal lymph nodes, the majority of RORC+ ILCs lacked expression of NKp46 (Figure 1b). Approximately half of the cells expressed NKp30 and a very small fraction of these NKp30+ ILCs co-expressed NKp44 (Figure 1b). In contrast, the majority of tonsil-derived RORC+ ILCs expressed NKp44 as well as NKp30. In addition, a substantial fraction of tonsil RORC+ ILCs expressed NKp46 (Figure 1b). The biggest differences in NCR expression between fetal lymph node and tonsils were observed for NKp44 and upon enumeration the percentage of NKp44-expressing RORC+ ILCs was indeed significantly increased in tonsils compared to fetal lymph nodes (Figure 1c). These data show that the relative distribution of NCR-positive versus NCR-negative ILCs is different between tonsils and fetal lymph nodes and follows the pattern described for IL-22.8

Next, we assessed the proportion of CD56 expressing ILCs in fetal lymph nodes and tonsils. The percentage of CD56+RORC+ ILCs was low in fetal lymph nodes, but was increased in tonsils where on average half of the RORC+ ILCs expressed CD56 (Figure 2a). This implies that CD56 expression follows a pattern similar but not identical to NKp44, and indeed in tonsils only half of the NKp44+ ILC population expressed CD56 (Figure 2b). In summary, NKp44, and not CD56, is the most prominent cell surface marker differentiating between RORC+ ILCs from fetal lymph nodes and adult tonsils.
Figure 1 | NCR expression on ILCs from fetal LN and tonsil. a. Lineage-negative cells in fetal lymph nodes, fetal spleen and tonsil labeled for CD117 and CD127 are RORC positive. Shaded histogram indicates isotype control staining (representative example of 3 independent experiments). b. Flow cytometric analysis of NKp30 (P = 0.07), NKp44 (P = 0.00) and NKp46 (P = 0.03) expression on ILCs and fetal lymph nodes and tonsil c. Percentage of NKp30, NKp44 and NKp46 expressing RORC+ ILCs in fetal lymph nodes and tonsil (n > 5; Average +/- SD).
Figure 2 | CD56 expression on ILCs from fetal LN and tonsil. a. Percentage of CD56 expressing RORC+ ILCs in fetal lymph nodes and tonsil (n >5; Av +/- SD, P = 0.007) b. Flow cytometric analysis of CD56 and NKp44 expression on RORC+ ILCs in fetal lymph nodes and tonsil (representative example of 5 independent experiments).

NKp44 expression allows identification of IL-17 and IL-22 biased ILCs

On NK cells, NKp44 is only expressed upon activation. In addition, production of IL-17a in T cells is restricted to activated or memory cells. This led us to hypothesize that ILCs which contain transcripts for either IL17A or IL22 might also be cells with an activated phenotype. To test this hypothesis, we analyzed the expression of surface proteins known to be regulated during cellular activation on RORC+ ILCs from fetal lymph nodes and tonsils. The early activation marker CD69 was expressed on part of RORC+ ILCs, and the combination of CD69 with NKp44 revealed discrete ILC subpopulations (Figure 3a). In fetal lymph nodes, where the majority of cells lack expression of NKp44, CD69 divided the ILC population into a CD69− and a CD69+ population. In tonsils, NKp44+ ILCs were most abundant, and all NKp44+ cells co-expressed CD69. In addition, a small population of CD69−NKp44− cells was present (Figure 3a).

We next set out to determine the presence of IL22 and IL17A transcripts in these ILC subpopulations. To this end, the NKp44− ILCs were sorted from fetal lymph nodes and separated in CD69− and CD69+ populations. From tonsils, NKp44+ ILCs were purified and divided in CD69− and CD69+ fractions. Transcripts for IL17A and IL22 were determined without ex-vivo stimulation. Within the fetal lymph nodes, IL17A transcripts were enriched within the CD69+NKp44− population (Figure 3b, top right). IL22 transcripts were very low to absent in the fetal lymph nodes (Figure 3b, top left). In tonsil RORC+ ILCs, IL22 transcripts were easily detectable within the CD69+NKp44+ population as expected but were much lower in the NKp44− population (Figure 3b, bottom left). Transcripts for IL17A were undetectable in tonsil ILCs (Figure 3b, bottom right).
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Figure 3 | Differential cytokine production by NKp44+ and NKp44− ILCs. a. Flow cytometric analysis of CD69 and NKp44 expression on RORC+ ILCs from fetal LN and tonsil (representative example of 3 independent experiments). b. Expression of IL22 and IL17A mRNA in sorted ILC populations from tonsils and fetal LN (Representative of 2 individual experiments with 3–5 donors per experiment). c. IL-22 protein production by NKp44− and NKp44+ ILCs from tonsils stimulated overnight with PMA + ionomycin (n = 3).
Figure 4 | Human NKp44+ ILCs are developmentally programmed. a. Flow cytometric analysis of ILCs from fetal intestines of indicated ages (weeks gestation) (representative examples of at least 3 independent experiments per time point). b. Percentage of ILCs expressing NKp44 in the fetal small intestine during 1st trimester (<12 wks) or 2nd trimester (>12wks) (n >6; Average +/- SD; P=0.003). c. Flow cytometric analysis of ILCs in fetal small intestines and mesentery of the same donor at 12 weeks gestation (representative example of 3 independent experiments). d. Expression of IL22 transcripts in NKp44+ ILCs from fetal intestine compared to NK cells from fetal lymph node (5 independent samples per condition, Average +/- SD; P=0.009). e. Flow cytometric analysis of NKp44 expression on ILCs from adult intestine. Filled histogram shows isotype control staining (representative example of 5 independent experiments). f. Expression of IL22 transcripts in NKp44+ and NKp44- ILCs from adult intestine (n = 7, Average +/- SD; P=0.005).
In order to assess whether the divergent cytokine patterns observed directly ex-vivo are maintained after in-vitro stimulation we isolated tonsil NKp44+ and NKp44− ILCs and stimulated these overnight with PMA and ionomycin. Similar to freshly isolated ILCs, overnight stimulation induces IL-22 secretion from NKp44+ ILCs, but not NKp44− ILCs (Figure 3c), confirming the cytokine bias seen directly ex-vivo. The IL22 induction in NKp44+ ILCs by PMA/ionomycin stimulation was observed in all donors analyzed, but did however show a high degree of variability.

These findings imply that tonsil-derived NKp44 positive ILCs preferentially transcribe IL-22, while IL-17 is preferentially transcribed by fetal lymph node-derived NKp44+CD69+ ILCs, enriched within the ILCs that lack expression of NKp44, but do express CD69.

**Human mucosal NKp44+ ILCs are developmentally programmed**

In the mouse, NKp46+ ILCs develop in the absence of microbiota, and appear in the intestines after birth. Since fetal human intestines are not yet colonized by bacteria or exposed to ingested antigens, this allowed us to assess the development of human fetal NKp44+ ILCs in the absence of external stimuli. We analyzed ILCs in first and second trimester fetal small intestines and determined their expression of CD69 and NKp44. First trimester small intestinal-derived ILCs (7 wks gestation) did not express CD69 or NKp44 and resembled putative LTi cells (Figure 4a). CD69+NKp44+ ILCs appeared during late first trimester, between weeks 7 and 10 of gestation and with increasing age replaced the LTi-like cells. From week 12 onwards, the majority of ILCs in the small intestines were expressing both CD69 and NKp44 (Figure 4b). This was specific for the fetal small intestines and was not found in paired mesentery samples containing developing lymph nodes (Figure 4c). Since our analysis of NKp44+ ILCs from tonsils had shown IL22 transcription in these cells, we also probed fetal intestine-derived NKp44+ ILCs for IL22 transcripts. We consistently found low levels of IL22 transcripts in NKp44+ ILCs from second trimester fetal small intestines (Figure 4d). It was technically impossible to purify sufficient NKp44− ILCs from fetal intestines as a comparison. Therefore, CD56+CD127+ NK cells sorted from fetal lymph nodes were used as a negative control. These data show that human NKp44+ ILCs develop in-utero in the absence of microbial colonization and can be found in the small intestine.

To be able to compare intestinal NKp44+ and NKp44− ILCs we next isolated these cells from non-affected adult ilial mucosa acquired during resection procedures for colon cancer. In the adult human intestine, the majority of ILCs express NKp44 (Figure 4e). In line with our data from tonsil-derived ILCs, intestinal NKp44+ ILCs preferentially transcribe IL22, while NKp44− ILCs only contain very low levels of IL22 transcripts (Figure 4f).

**Resting ILCs are present in adult non-inflamed human lymph nodes**

The presence of IL-17 transcribing ILCs in fetal human lymph nodes raised the question whether these cells might also be found in adult lymph nodes. Therefore we determined the presence of RORC+ ILCs in adult peripheral non-inflamed lymph nodes. Lymph nodes were collected during multi-organ donation procedures and were liver-draining hepatic lymph nodes unless stated otherwise. Donor age ranged from 24 – 68 years. In adult lymph nodes a population
of Lineage^- CD45^- CD117^+ CD127^+ ILCs was found that uniformly expressed RORC (Figure 5a). Based on expression of NCRs, adult LN-derived RORC^+ ILCs resembled ILCs from fetal lymph nodes rather than from tonsils in that they were mostly negative for NKp46 and NKp44 and only a part of the cells expressed CD56 and NKp30 (Figure 5a and 5b). There was no difference in the percentage of NKp30 or NKp44 expressing ILCs between fetal and adult LN, while slightly more adult ILCs expressed NKp46 (Figure 5b). These data show that NKp30 is the only NCR that is consistently expressed on approximately half of all ILCs, regardless of whether they were isolated from fetal LN, adult LN or tonsil.

Upon staining for CD69, the presence of CD69^+ and CD69^- ILCs became apparent, very much alike the fetal LN-derived ILCs. This phenotype was not restricted to hepatic lymph nodes as a similar distribution of NCR was seen in adult inguinal nodes (Figure 5c). To determine cytokine production by the ILCs from adult lymph nodes, total NKp44^- ILCs were purified and analyzed for IL22 and IL17A transcripts directly ex-vivo. Transcript levels for these cytokines were compared to the levels found in NKp44^- and NKp44^+ ILCs from tonsil. Strikingly, adult lymph node ILCs lacked detectable IL22 or IL17A transcripts (Figure 5d). These data suggest that, in contrast to fetal lymph node-derived ILCs, adult non-inflamed lymph node-derived ILCs are not actively transcribing detectable levels of IL17A in-vivo.

To test whether these peripheral ILCs were biased towards the production of either IL17A or IL22 upon activation, we stimulated adult lymph node ILCs overnight with PMA and ionomycin (Figure 6). After overnight stimulation we could detect low levels of both IL17A and IL22 transcripts in adult ILCs. Induction of IL-17 was specific for adult lymph node ILCs as tonsil-derived ILCs did not contain IL17A transcripts after stimulation (Figure 6a). However, the levels of IL17A transcripts were much lower than those found in freshly isolated fetal LN-derived CD69^+ ILCs. Even more so, the IL22 transcripts found in adult ILCs after overnight stimulation were very low in comparison to the levels found in either stimulated or unstimulated tonsil ILCs. These findings indicate that throughout adulthood human lymph nodes contain a resting ILC population that is characterized by the absence of NKp44 and the absence of active transcription of IL17A or IL22.

Finally, IL-17a and IL-22 protein levels produced by adult lymph node-derived NKp44^- ILCs stimulated with physiological stimuli were determined by ELISA. Unfortunately, the scarcity of adult human tissue precluded the analysis of sufficient donors to draw statistical conclusions. This notwithstanding, in two independent donors 3 day culture in the presence of either IL-23 or IL-1β did induce detectable levels of IL-22 protein (Figure 6c). These culture conditions did not induce IL-17a secretion to levels detectable by our ELISA (detection limit = 31 pg/ml)(data not shown). This suggests that even though low level transcription of IL17A can be initiated, no detectable protein is secreted. The reason for this is presently unknown. These data suggest that resting adult lymph node-derived ILC retain the capacity to secrete IL-22 upon in vitro stimulation with IL-23 or IL-1β. Further work is needed to substantiate these findings.
Figure 5 | NKp44$^-$ ILCs in adult non-inflamed lymph nodes. a. Flow cytometric analysis of ILCs from adult hepatic lymph nodes for expression of RORC, NKp44, NKp30, NKp46 and CD56 (representative example of 3 independent experiments). b. Flow cytometric analysis of CD69 and NKp44 expression on ILCs from adult hepatic and inguinal lymph nodes (representative example of at least 3 independent experiments). c. Percentage of NKp30, NKp44 and NKp46 expressing RORC$^+$ ILCs in fetal lymph nodes, adult lymph nodes and tonsil (representative example of at least 3 independent experiments) d. PCR analysis for IL17a and e. IL22 transcripts of sorted ILCs from adult hepatic lymph nodes compared to NKp44$^-$ and NKp44$^+$ ILCs from tonsil (Adult LN vs NKp44$^-$ $P = 0.02$; adult LN vs NKp44$^+$ $P = 0.02$; $n = 4$).
Figure 6 | Stimulated adult CD69^NKp44^- ILCs produce IL-22. a. IL17A transcripts in NKp44^- ILCs from adult hepatic lymph nodes and in NKp44^+ ILCs from tonsils stimulated overnight with PMA + ionomycin as well as in freshly isolated fetal LN-derived CD69^+ ILCs (n = 3) b. IL22 transcripts NKp44^- ILCs from adult hepatic lymph nodes and in NKp44^+ ILCs from tonsils stimulated overnight with PMA + ionomycin (n = 3) c. IL-22 protein production by CD69^-NKp44^- ILCs from adult hepatic lymph nodes after 3 day culture with IL-23 or IL-1β (n = 2).

Discussion

RORC^+ ILCs are increasingly recognized as important mediators of early innate immunological defenses against mucosal pathogens and as essential for safeguarding tissue integrity during infections. Both effects are mediated by ILC-derived cytokines, and especially IL-22 and IL-17a have been studied in this respect. In mice, IL-22 secreting ILCs mediate the innate response to *Citrobacter rodentium* and IL-22 is an important mediator of epithelial homeostasis. Conversely, IL-17a producing ILCs are pathogenic in a T cell-independent mouse model of intestinal inflammation. Most importantly, the balance between IL-22 and IL-17a secreting ILCs was shown to be skewed towards IL-17a in patients with Crohn’s disease, suggesting that ILC-derived cytokines might be involved in human disease.
The systematic analysis of ILC subsets in humans and the detection of any changes in subset distribution as a result of disease are hampered by the poor characterization of functionally distinct human ILCs. In this study we show that expression of the NCR NKp44 is a good predictor for ILCs that are actively transcribing IL-22, and that these cells are mainly found in mucosal tissues. In contrast, our data suggest that throughout adulthood, non-inflamed lymph-nodes may function as a reservoir of resting, RORC+ non-cytokine secreting ILCs that lack NKp44 expression, yet retain the capacity to secrete IL-22 after appropriate cytokine activation in vitro.

Production of IL-17a by T cells is normally tightly controlled to avoid unwanted or excessive inflammation and the fact that freshly isolated CD69+NKp44− ILCs in non-inflamed lymph nodes lack IL17A transcripts suggests that similar levels of restraint are operational for ILCs. Unraveling the exact signals that can either induce or inhibit ILC activation is needed to understand regulation and control of innate IL-17 secretion.

IL-17a has been associated with several human diseases and ILC-derived IL-17a has been reported in experimental models of colitis. In addition, an increase in IL-17 producing ILCs has now also been found in the intestines of some Crohn’s disease patients. The IL-17 producing ILCs in Crohn’s disease patients were mainly found within the CD56− ILC fraction, while the CD56+ ILCs were more prominent producers of IL-22. Our current data would predict that a dissection based on NKp44 expression, rather than expression of CD56, could further enhance the exact enumeration of IL-22 vs. IL-17a producing ILCs in humans.

The biological functions of IL17a produced by fetal LN-derived ILCs remain enigmatic. Development of lymphoid organs has many similarities to a controlled inflammation and the inflammation-related cytokine IL-17a would fit that concept. However, IL-17a is unlikely to have an essential function during organogenesis as IL-17Rα deficient mice display no gross abnormalities in LN development (KH and TC, unpublished observations), suggesting that IL-17a serves another yet to be determined function.

In-vivo, distinct subsets of RORC+ ILCs seem biased towards either IL17A (CD69+NKp44− ILCs) or IL22 (CD69+NKp44+ ILCs) transcription. It is not clear whether these subsets belong to different ILC lineages, or whether they represent different activation or differentiation states of cells within a single lineage. In mice, conflicting data exists on the relationship between NKp46+ and NKp46− ILCs. Genetic approaches indicated that these two cell types belong to separate lineages and do not have a precursor-progeny relationship. Conversely, transfer of purified populations of ILCs showed that NKp46− cells could give rise to NKp46+ ILCs in-vivo. In humans, these relationships are even less clear. After in-vitro culture, freshly isolated NKp44− fetal LN-derived ILCs acquired NKp30, NKp44 and NKp46. In-line with this, the adult-lymph node-derived ILCs also upregulate NKp44 when cultured (KH and TC, unpublished). Whether the observed IL-22 production by lymph node ILCs is functionally linked to this expression of NKp44 is currently under investigation. Our current results indicate that in ex-vivo isolated ILCs, NKp44 predicts for IL-22 production whereas in mice NKp46 is a marker for IL-22 producing ILCs, again adding to the complexity of comparing data gathered in human and mouse studies.
NKp44⁺ ILCs are preferentially found in mucosal tissues like tonsil and the intestines (this report and 17). Within this mucosal environment NKp44⁺ ILCs constitutively produce IL-22 that, based on mouse models, acts on intestinal epithelial cells and conditions these cells to cope with the hostile environment to which they are exposed.⁴,⁵,³³

Here we show that the appearance of ILCs in the human intestine is developmentally programmed and NKp44⁺ ILCs are present from early second trimester. In mice NKp46⁺ ILCs is also a programmed event independent of microflora, yet these cells only appear after birth.²⁵,²⁹ The observed differences between mouse and man in this respect might be due to the longer pregnancy in humans. NKp44⁺ ILCs in the developing human intestine initiate low level IL22 transcription during second trimester pregnancy. However, these IL22 levels are much lower than those found in NKp44⁺ ILCs from pediatric tonsils or adult intestines. Current it is unknown whether this difference reflects a role for microbial colonization of the intestines in inducing a postnatal increase in IL-22 levels. This would be different from the observations done in mice, where microbial colonization was not essential for IL-22 induction but actually induces a decrease in intestinal IL-22 postnatal.²³,²⁵,²⁹ Again, an alternative and perhaps more likely explanation is that due to the longer gestation time in humans compared to mice, the low levels of IL22 transcription found during the second trimester will steadily increase throughout the third trimester, reaching levels comparable to postnatal ILCs just before birth. Even though the intestines are culture sterile, they are by no means devoid of potential immune stimuli such as TLR ligands and cytokines and these could still be a factor in ILC development and activation.³¹,³²

NKp44⁻ ILCs reside within peripheral lymph nodes throughout life but in the absence of activating signals do not transcribe detectable levels of IL17A or IL22. However, upon stimulation NKp44⁻ ILCs can produce at least IL-22, and also initiate low level IL17A transcription. This raises the hypothesis that secondary lymphoid organs are a reservoir for ILCs that can participate in inflammatory responses in an antigen independent manner. Detailed analysis of human lymph node biopsies from inflammatory diseases or the study of relevant animal models is needed to determine the contribution of LN-derived ILCs to systemic immune responses.

Acknowledgements
We want to thank the staff of the CASA clinics in Leiden and Rotterdam for collection of fetal tissues and Dr. Jaap Kwekkeboom of the Department of Gastroenterology & Hepatology, Erasmus University Medical Center Rotterdam for coordinating the acquisition of adult lymph nodes. Reina Mebius (VU Medical Center Amsterdam), Mark Coles (University of York), Janneke Samsom and Rogier Reijmers (Erasmus University Medical Center) are thanked for critical reading of the manuscript. KH was supported by an ErasmusMC grant from the Erasmus University Medical Center. TC was supported by Innovational Research Incentives Scheme Vidi grant #91710377 from the Netherlands Organization for Scientific Research (Zon-MW).
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