Gata3 drives development of RORγt+ group 3 innate lymphoid cells.
Nicolas Serafini, Roel G J Klein Wolterink, Naoko Satoh-Takayama, Wei Xu, Christian A. J. Vosshenrich, Rudi W Hendriks, James P Di Santo

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Group 3 innate lymphoid cells (ILC3) include IL-22–producing NKp46+ cells and IL-17A/IL-22–producing CD4+ lymphoid tissue inducerlike cells that express RORγt and are implicated in protective immunity at mucosal surfaces. Whereas the transcription factor Gata3 is essential for T cell and ILC2 development from hematopoietic stem cells (HSCs) and for IL-5 and IL-13 production by T cells and ILC2, the role for Gata3 in the generation or function of other ILC subsets is not known. We found that abundant GATA-3 protein is expressed in mucosa–associated ILC3 subsets with levels intermediate between mature B cells and ILC2. Chimeric mice generated with Gata3-deficient fetal liver hematopoietic precursors lack all intestinal RORγt+ ILC3 subsets, and these mice show defective production of IL-22 early after infection with the intestinal pathogen *Citrobacter rodentium*, leading to impaired survival. Further analyses demonstrated that ILC3 development requires cell–intrinsic Gata3 expression in fetal liver hematopoietic precursors. Our results demonstrate that Gata3 plays a generalized role in ILC lineage determination and is critical for the development of gut RORγt+ ILC3 subsets that maintain mucosal barrier homeostasis. These results further extend the paradigm of Gata3–dependent regulation of diversified innate ILC and adaptive T cell subsets.
NKp46+ and CD4+ in ILC lineage specification. cell–derived intestinal ILC3. These results suggest a broader the development and function of fetal liver hematopoietic port, we provide evidence that a limited role in bone marrow NK cell development (Samson et al., 2013; Hoyler et al., 2012; Klein Wolterink et al., 2013). Although several of the molecular pathways that generate diverse ILC subsets have been identified, the signals that regulate the earliest stages of ILC lineage development are less well understood. It has been suggested that all ILCs develop from a common ILC precursor based on the common dependence of all known ILC groups for inhibitor of DNA binding 2 (Id2) expression (Yokota et al., 1999; Moro et al., 2010; Satoh-Takayama et al., 2010). In a current model (Vosshenrich and Di Santo, 2013), Id2 expression serves to titrate E protein levels in hematopoietic precursors (including common lymphoid precursors [CLPs]) as these have been shown to have potential to give rise to ILC1, ILC2, and ILC3 subsets (Walker et al., 2013), thereby repressing B and T cell potential in favor of ILC potential. The transcription factors that regulate Id2 are not known, but their deficiency would be expected to impact on the subsequent development of several (or all) ILC groups.

The zinc finger transcription factor Gata3 is required at the earliest stages of T cell development to facilitate T cell specification and at later stages to promote differentiation to the T112 fate (Ansel et al., 2006; Rothenberg, 2012). Similarly, Gata3 is required for generation of ILC2 from lymphoid precursors and to maintain effector functions in fully differentiated ILC2 (Liang et al., 2012; Hoyler et al., 2012; Furusawa et al., 2013; Klein Wolterink et al., 2013). Although Gata3 plays a limited role in bone marrow NK cell development (Samson et al., 2003), Gata3 is essential for the development of thymic NK cells (Vosshenrich et al., 2006) and has been reported as redundant for ILC3 function (Hoyler et al., 2012). In this report, we provide evidence that Gata3 plays a critical role in the development and function of fetal liver hematopoietic cell–derived intestinal ILC3. These results suggest a broader role for Gata3 in ILC lineage specification.

RESULTS AND DISCUSSION

GATA–3 protein is expressed in diverse gut ILC3 subsets

We first analyzed GATA–3 protein expression in CD4+, NKp46+ and CD4–NKp46– ILC3 subsets (Fig. 1, A–C; and Fig. S1). As RORγt+ ILCs are enriched in mucosal sites, we focused our attention on ILC3 present in the lamina propria of the SI and large intestine (LI) and in the Peyer’s patches (PP). ILC3s were identified as CD3+ cells that co-expressed CD90.2 (Thy1.2), CD127 (IL-7Rα), and RORγt as previously described (Satoh-Takayama et al., 2008; Sawa et al., 2010). Intestinal ILC3s are the most abundant ILC group in the SI and PP, and they clearly expressed GATA–3 at levels exceeding those found in B cells, although at reduced levels (roughly fivefold) compared with intestinal ILC2 (Fig. 1 B). Interestingly, GATA–3 was not homogeneously expressed in the gut: ILC3 in the LI expressed about twofold higher levels of GATA–3 compared with ILC3 in the SI or PP (Fig. 1 B). GATA–3 levels were similar within intestinal ILC3 subsets that differentially expressed NKp46 and/or CD4 (Fig. 1 C). The fact that all intestinal ILC3 subsets were GATA–3+ raise the possibility that GATA–3 could play a role in ILC3 differentiation, as has recently been shown for ILC2 (Furusawa et al., 2013; Hoyler et al., 2012; Klein Wolterink et al., 2013; Mjöberg et al., 2012).

Gata3 expression required for ILC3 subset development in vivo

Previous studies demonstrated that deletion of Gata3 leads to lethality during mouse embryogenesis (Pandolfi et al., 1995; Ting et al., 1996). To elucidate the in vivo requirement for Gata3 in ILC3 development, we analyzed mice engrafted with Gata3-deficient (Gata3−/−) hematopoietic precursor cells from rare E12.5–13.5 embryos that could be rescued by pharmacological treatment with β-adrenergic agonists (Kaufman et al., 2003). Rag2−/−Il2rg−/− mice were recipients for the adoptive transfer as these hosts lack endogenous ILC (Moro et al., 2010; Neill et al., 2010; Price et al., 2010). As such, ILC present in these chimeric mice are donor derived (Klein Wolterink et al., 2013). Gata3+/+ and Gata3−/− hematopoietic precursors engrafted to a similar extent in Rag2−/−Il2rg−/− mice, leading to robust B, NK cell, and myeloid cell reconstitution as previously described (Samson et al., 2003; Vosshenrich et al., 2006; García-Ojeda et al., 2013).

We could identify CD127−RORγt+ ILC3 in the SI and LI of Gata3+/+ chimeras that expressed GATA–3 protein levels similar to that observed in ILC3 from control C57BL/6 mice (Figs. 1, D and E). In the Gata3−/− chimeras, total numbers of CD127+ ILC expressing RORγt were dramatically reduced and the remaining RORγt+ ILC3 lacked GATA–3 expression and were depleted in NKp46+ and CD4+ cells (Fig. 1, D–F). Moreover, these residual Gata3−/− ILC3 were unable to normally produce IL–22 after ex vivo IL–23 stimulation (Fig. 1 G). Collectively, these results clearly demonstrate that Gata3 is essential for normal generation of intestinal ILC3 subsets in fetal liver hematopoietic chimeras.

Cell-intrinsic Gata3 is required for ILC3 development

To exclude the possibility that cell–extrinsic effects caused by Gata3-deficiency in non-ILC lineages underlie the observed defects in ILC3 development, we generated and analyzed BM chimeras generated using mixtures (90%/10%) of CD45.2+ Gata3−/− and CD45.1+ wild type C57BL/6 hematopoietic precursors, respectively into CD45.1+ Rag2−/−Il2rg−/− hosts. Recipient mice injected with the same mixtures of CD45.2+ Gata3−/− and CD45.1+ Gata3+/+ precursors served as controls. We previously reported that these mixed Gata3 chimeras...
GATA-3 is required for IL-22–dependent innate responses to C. rodentium

We next investigated the importance of Gata3 for ILC3 function in the protection against infection by C. rodentium. In this model, the control of bacterial infection requires IL-23 signaling that promotes a sequential wave of IL-22 production, first by ILC and later by T cells that results in the clearance of C. rodentium (Zheng et al., 2008; Basu et al., 2012). RORγt+ ILC3 subsets are important producers of IL-22 in the intestinal

and Gata3−/− chimeras. Bars correspond to the mean ± SEM of the values obtained (3 independent experiments with n = 6 mice analyzed for each genotype). *, P < 0.05; ***, P < 0.001. (B) SI lamina propria cells were stimulated for 4 h with IL-23 and IL-22 expression in ILC3 (CD3−CD127−CD90.2−) was assessed by intracellular cytokine staining and flow cytometry. Bar graph represents the percentage (mean ± SEM; n = 4 for each genotype) of IL-22+ cells. Representative results from two independent experiments. *, P < 0.05.

reconstituted to a similar extent with normal B, myeloid and NK cell development from both Gata3+/− and Gata3+/+ precursors at the expected frequencies (Klein Wolterink et al., 2013).

Both sets of mixed chimeras developed phenotypically mature NKp46−, CD4+, and CD4−NKp46− (here referred to as double negative [DN]) RORγt+ ILC3 subsets in the gut as well as the spleen (Figs. 2 A). However, the origin of these ILC3 subsets differed dramatically in these two sets of mice. In mixed chimeras generated with CD45.2+ Gata3+/−/CD45.1+ Gata3−/− precursors, RORγt+ ILC3 derived from both donors, whereas these cells were almost exclusively derived from CD45.1+ B6 (Gata3+/−) precursors in CD45.2+ Gata3+/−/CD45.1+ Gata3−/− chimeras (Fig. 2, B and D). The generation of all ILC3 subsets (NKp46+, CD4+, or DN) was affected by the absence of GATA–3 in mixed chimeras, resulting in a predominance of CD45.1+ WT cells in Gata3−/− mixed chimeras (Fig. 2, E–G). These results demonstrate that Gata3 is required in a cell-intrinsic fashion for ILC3 development.
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**Figure 2.** Cell-intrinsic role for Gata3 in ILC3 development. Mixed chimeras were generated and analyzed as indicated in the Materials and methods. (A and B) ILC3 (CD3−CD127+CD90.2+) in SI lamina propria were analyzed for CD45 allotypes using flow cytometry. Relative percentage of gated populations is indicated. Representative results from two independent experiments. (C) Absolute numbers of SI ILC3 were determined in Gata3+/+ and Gata3−/− mixed chimeras. Bars correspond to the mean ± SEM of the values obtained with five Gata3+/+ and four Gata3−/− mixed chimeras (two independent experiments). *, P < 0.05. (D) Ratio of absolute numbers of CD45.2+ (Gata3+/+ or Gata3−/−) to CD45.1+ (B6) ILC3 in SI. Each bar corresponds to the mean ± SEM of the values obtained with five Gata3+/+ and four Gata3−/− mixed chimeras (two independent experiments). ***, P < 0.001. (E) Representative FACS analysis of ILC3 subsets in SI of Gata3+/+ and Gata3−/− mixed chimeras. ILC3 subsets were subsequently analyzed for expression of CD45 allotypes. (F) Absolute numbers of the indicated SI ILC3 subsets were determined in Gata3+/+ and Gata3−/− mixed chimeras. Bars correspond to mean ± SEM of the values obtained with five Gata3+/+ and four Gata3−/− mixed chimeras (two independent experiments). *, P < 0.05. (G) Ratio of the absolute numbers of CD45.2+ (Gata3+/+ or Gata3−/−) and CD45.1+ (B6) SI ILC3 subsets in mixed chimeras. Bars correspond to the mean ± SEM of the values obtained with five Gata3+/+ and four Gata3−/− mixed chimeras (two independent experiments). ***, P < 0.001.

tract, and genetic deficiencies in ILC3 development or antibody-mediated depletion of ILC render mice susceptible to *C. rodentium* dissemination and lethality (Satoh-Takayama et al., 2008; Cella et al., 2009; Qiu et al., 2012; Sonnenberg et al., 2011b). As *C. rodentium* induces IL-22–producing CD4+ T cells starting from day 8 after infection (Basu et al., 2012), we focused our attention on the early phase of *C. rodentium* infection to assess the innate immune response in Gata3+/+ and Gata3−/− chimeric mice. This early protection against *C. rodentium* is present in mice lacking adaptive immunity (Rag2−/− mice) but not in mice lacking innate and adaptive lymphocytes (Rag2−/−Il2rg−/− mice; Zheng et al., 2008; Satoh-Takayama et al., 2008).

Mice were infected with bioluminescent *C. rodentium* to noninvasively monitor bacterial growth and dissemination (Wiles et al., 2006). Infected Gata3−/− chimeric mice rapidly lost body weight, developed pathological symptoms (diarrhea and rectal bleeding) as indicated by the global clinical score and succumbed to infection (Fig. 3, A–C). Whole-body
in vivo imaging revealed that Gata3−/− mice had higher C. rodentium loads, notably in LI, whereas bacterial growth was controlled in Gata3+/+ chimeras (Fig. 3, D and E). Intestinal IL-22 expression regulates antimicrobial peptides expression by epithelial cells that maintain barrier function (reviewed in Sonnenberg et al., 2011a). IL-22 expression was clearly reduced in lamina propria cells of infected Gata3−/− chimeras compared with their Gata3+/+ counterparts, and as a result, intestinal epithelial cell expression of the antimicrobial peptide RegIIIγ was reduced in absence of Gata3 (Fig. 3 F). The enhanced susceptibility of Gata3−/− chimeras to C. rodentium infection was associated with the loss of intestinal ILC3 (Fig. 3, G and H) and their capacity to produce IL-22 (Fig. 3, I and J). Collectively, these results demonstrate that Gata3 is required for innate immune responses that protect against C. rodentium infection.

**GATA-3 required for normal development of RORγt+ cells in the fetal liver**

To gain insights into the stage at which Gata3 controls ILC3 development, we analyzed RORγt+ fetal liver hematopoietic...
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cells from Gata3+/+, Gata3+/−, and the rare Gata3−/− embryos (ED12.5) that could be obtained after pharmacological rescue in utero (Kaufman et al., 2003). Previous studies have shown that CD135+ common lymphoid progenitors (CLPs) shed their B then T cell potential concomitantly with acquisition of the integrin α4β7 (Yoshida et al., 2001; Walker et al., 2013). Within the subset of fetal liver Lin− α4β7+ cells, a subset expressing Rorc transcripts and RORγt protein can give rise to CD4+ ILC3 cells in vitro (Sawa et al., 2010; Possot et al., 2011; Cherrier et al., 2012). In contrast, NKp46+ RORγt+ ILC3s derive from distinct α4β7− RORγt− fetal liver precursors (Sawa et al., 2010). Using CD135 (Flk2/Flt3) and α4β7, we identified these different RORγt+ subsets within fetal liver Lin−CD117+CD127+ cells (Fig. 4, A and B). α4β7−RORγt+ cells included both CD135+ and CD135− subsets with a distinct population of cells expressing higher levels of CD127 in Gata3-deficient mice in vitro. In contrast, this CD127hi subset of α4β7+RORγt+ cells was essentially absent from Gata3-deficient fetal liver cells, although RORγt+ cells with lower levels of CD127 were still present (Fig. 4, A and C). A small subset of CD135+α4β7− cells expresses RORγt, and we found that these cells also require Gata3−/− to develop (Fig. 4, B and D). This population corresponds to the previously described NKp46+ ILC3 precursor (Sawa et al., 2010), and its Gata3−/− dependency could explain the NKp46+ ILC3 deficiency in our Gata3−/− chimera (Sawa et al., 2012). Interestingly, GATA-3 protein levels varied within α4β7+ cells with lowest levels in RORγt− cells and progressively higher levels as cells acquire RORγt and increase CD127 expression (Fig. 4 E). These results suggest that GATA-3 is not essential for RORγt expression in the ILC3 subset that emerges from α4β7− fetal liver cells, but is required for normal homeostasis of CD127hi RORγt+ ILC3; the latter subset has been previously shown to include CD4+ LTi cells that populate the intestine and promote lymphoid tissue organogenesis (Mebius et al., 1996; Sawa et al., 2011; Cherrier et al., 2012).

Concluding remarks

In this report, we show that the transcription factor Gata3 is essential for the differentiation of ILC3 that express RORγt and can produce IL-17 and/or IL-22 (Spits and Di Santo, 2011; Spits et al., 2013). Gata3 is required in a cell-intrinsic fashion for ILC3 development from fetal liver hematopoietic precursors and is critical to promote innate immune responses in the gut that protect against intestinal pathogens. Conditional Gata3 ablation in HSC from adult mice results in defects in ILC2 development (Furusawa et al., 2013); whether ILC3 differentiation is affected in this context will require further study. Previous studies suggested that Gata3 was redundant for the homeostasis of Id2-expressing intestinal ILC3 as the frequency of RORγt+ ILC3 was unchanged when Gata3 was deleted in Id2+ cells (Hoyler et al., 2012). Our results indicate that the one essential role for Gata3 in ILC3 development (and by analogy in ILC2 development) may occur during the emergence of putative ILC precursors from CLP. Considering the important role for Gata3 in the development of both ILC2 and ILC3, a common GATA-3−/− progenitor shared between group 2 and group 3 ILCs may exist. Alternatively, Gata3 may have an equivalent role in supporting the development, maintenance, or differentiation potential of distinct ILC2 and ILC3 progenitors. The absence of several RORγt+ ILC3 subsets in Gata3−/− fetal liver cells demonstrates the critical role for this transcription factor in the earliest stages of ILC development (Fig. 4 F).

Does Gata3 play a role as a generic promoter of ILC development? Whereas ILC2 (Hoyler et al., 2012; Liang et al., 2012; Klein Wolterink et al., 2013) and now ILC3 (this study) require Gata3 for their development, previous works demonstrated that Gata3 was not required for normal homeostasis of BM or splenic NK cells, although Gata3 conditioned liver and thymic NK cell development (Samson et al., 2003; Vossenruch et al., 2006). As such, Gata3-dependent and -independent pathways of NK cell development are possible, in contrast with ILC2 and ILC3. A human ILC1 subset that strongly produces IFN-γ but lacks classical NK cell markers and is not cytotoxic has recently been described that may represent an innate version of CD4+ Tfh1 cells (Bernink et al., 2013). Although a mouse equivalent of this non-NK ILC1 has not been identified, it seems that ILC1 subset complexity is already substantial. Concerning the possible Gata3-dependent transcriptional targets, genes involved in the development of multiple ILC subsets (IL-7–dependent pathways, Id2) may be involved. The reduction in CD127hi ILC3 fetal liver cells that we observed in the absence of Gata3 is consistent with this hypothesis. Further work will be required to understand how Gata3 promotes the differentiation of distinct ILC subsets.

Figure 4. Characterization of RORγt+ cells in Gata3−/−deficient fetal liver cells. (A) Lymphohematopoietic precursors (CD3−CD19−GR-1−CD11c− Ter119−CD45.2+CD117+CD127+) in E12.5 fetal liver cells of Gata3+/+, Gata3+/−, and Gata3−/− mice were analyzed by flow cytometry. CD117+CD127+ fetal liver cells were gated for CD135 and α4β7 expression before analysis of CD127 and RORγt expression. RORγt versus CD127 expression on α4β7+ cells gated on CD135+ (R2) red box) or CD135− (R3; blue box). Representative results from three independent experiments. (B) Expression of RORγt (green box) was analyzed in CD135+α4β7+ cells (R1; black box) in Gata3+/+, Gata3+/−, and Gata3−/− embryos. Representative results from three independent experiments. (C and D) Bar graph shows the quantification for each precursor subset. Each bar corresponds to the mean ± SEM of the values obtained from Gata3+/+, Gata3+/−, and Gata3−/− embryos (n = 7, 10, and 4, respectively). *, P < 0.05. (E) Representative histograms show intracellular expression of GATA-3 in ILC precursors (gray area for CD135+ α4β7− cells and black line for the others subsets) as indicated in the plots from E12.5 fetal liver. Representative results from three independent experiments. (F) Distinct roles for GATA-3 in ILC3 subset development. CLP generates ILC subsets under the influence of diverse transcription factors including RORγt, RORα, Notch, and GATA-3 as shown.
Because *Gata3* is essential for T cell development (Rothenberg, 2012), it was logical to assume that *Gata3* would activate transcriptional targets involved in T cell specification and commitment. However, despite 20 yr of research, the *Gata3* targets that specifically promote T cell fate remain unknown. With our new results, an alternative role for *Gata3* function can be proposed, one in which *Gata3* is equally essential for both T cell and ILC development. This dual effect of *Gata3* could be achieved through repression of alternative (non-T/non-ILC) potentials in uncommitted lymphoid precursors. Recent results have shown that *Gata3* functions in this way to repress a latent B cell potential in early lymphoid progenitors in the BM and thymus (Banerjee et al., 2013; García-Ojeda et al., 2013). In this way, *Gata3* would globally (and equally) promote ILC and T cell fates from uncommitted precursors in primary lymphoid tissues.

**MATERIALS AND METHODS**

**Generation of chimeric mice.** Rag2<sup>−/−</sup> and Rag2<sup>−/−</sup>Il2rg<sup>−/−</sup> mice on the CD45.1<sup>+</sup> or CD45.2<sup>+</sup> C57BL/6 background and *Gata3*-lacZ mice (Hendriks et al., 1999) were maintained at the animal facilities of the Institut Pasteur. C57BL/6 mice were obtained from Harlan. Chimeric mice were generated as previously described (Samson et al., 2003; Vossenrich et al., 2006; García-Ojeda et al., 2013) using 5 Gy irradiated recipients and E12.5–13.5 fetal liver cells from timed pregnant dams treated with l-phenylephrine (100 µg/ml), isoproterenol (100 µg/ml), and acorbic acid (2 mg/ml; Sigma-Aldrich; Kaufman et al., 2003). This rescue technique did allow for recovery of viable E12.5–13.5 *Gata3<sup>−/−</sup>* embryos but not at expected Mendelian ratios (only 8% were viable in contrast to the expected 25%). All mice were housed under specific pathogen-free condition at the Institut Pasteur, provided with food and water ad libitum, and analyzed 10–15 wk after transplantation. Experimental animal protocols were performed in accordance with guidelines of the Animal Care Use Committee at the Institut Pasteur and were approved by the French Research Ministry (project #2013-0033).

**Cell isolation and FACS analysis.** Fetal liver cells and lamina propria mental animal protocols were performed in accordance with guidelines of the Institut Pasteur, Institut National de la Santé et de la Recherche Médicale, UNCC (Equipe Labellisée Ligue Contre le Cancer), and Agence National pour la Recherche (Program ‘Blanc’ Gut, ILC). The authors declare no financial conflict of interest.

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Figure S1. Representative FACS gating scheme for ILC2 and ILC3 analysis in the SI.

Table S1. Antibodies used for FACS analysis

| Antibody | Clone   | Manufacturer |
|----------|---------|--------------|
| CD3      | 145-211 | BD           |
| NK.1     | PK136   | eBioscience  |
| GATA-3   | TWAJ    | eBioscience  |
| RORγt    | AFKJS-9 | eBioscience  |
| CD127    | A7R34   | eBioscience  |
| Nkp46    | 29A1-4  | eBioscience  |
| CD4      | RM4-5   | eBioscience  |
| CD19     | ebio1D3 | eBioscience  |
| Sca-1    | D7      | eBioscience  |
| CD25     | PC61.5  | eBioscience  |
| CD45.1   | A20     | eBioscience  |
| CD45.2   | 104     | eBioscience  |
| CD135    | A2F10.1 | eBioscience  |
| α4β7     | DATK32  | eBioscience  |
| CD117    | 2B8     | eBioscience  |
| CD11c    | H3L3    | eBioscience  |
| Te-r119  | TER119  | eBioscience  |
| Gr-1     | RB6 8C5 | eBioscience  |
| CD45.2   | 104     | eBioscience  |
| CD90.2   | 53-2.1  | eBioscience  |
### Table S2. Primers used for quantitative PCR

| Gene name | Forward primers          | Reverse primers          |
|-----------|--------------------------|--------------------------|
| Gapdh     | 5'-AGGTCGTCGTGAACGGAATTGTG-3' | 5'-TGTAGACCATGTAGTTGAAGTCA-3' |
| IL22      | 5'-TGAGGTCTCGTCACTCCAGCA-3'   | 5'-AGCCGGAGCCTCGTTGTTA-3' |
| Reg3g     | 5'-CCGTGCTATGCTCTATG-3'     | 5'-GCACAGACACAGATGCTCTG-3' |