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IL-21 induces IL-22 production in CD4+ T-cells

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Abstract

IL-22 produced by innate lymphoid cells (ILCs) and CD4+ T cells plays an important role in host defense and mucosal homeostasis, thus it is important to investigate the mechanisms that regulate IL-22 production. We investigated the regulation IL-22 production by CD4+ T cells. Here we show that IL-21 triggers IL-22, but not IL-17 production by CD4+ T cells. STAT3, activated by IL-21, controls the epigenetic status of the *il22* promoter and its interaction with the aryl hydrocarbon receptor (AhR). Moreover, IL-21 and AhR signaling in T cells control IL-22 production and the development of dextran sodium sulfate-induced colitis in ILC-deficient mice. Thus, we have identified IL-21 as an inducer of IL-22 production in CD4+ T cells *in vitro* and *in vivo*.

Introduction

IL-22 is a member of the IL-10 family of cytokines; cytokines in this family display homologous secondary structures and 20%-30% amino acid identity¹. IL-22 acts on non-hematopoietic cells in epithelial tissues, which express a functional IL-22 receptor composed of an heterodimer of IL-22R1 and IL-10R2^{2,3}. IL-22 signaling triggers the production of anti-microbial peptides and pro-inflammatory molecules, and it also promotes tissue repair by inducing epithelial cell proliferation and survival^{2,3}. These effects of IL-22 are thought to be responsible for its important role in the control of host defense against bacterial infections, and also in limiting tissue destruction during hepatitis, colitis, graft versus host disease and thymus involution⁴⁻⁹. Conversely, dysregulated IL-22 signaling

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contributes to the pathogenesis of psoriasis, arthritis, inflammatory bowel disease and colon cancer¹⁰⁻¹³.

IL-22 is produced by cells of the innate system, particularly innate lymphoid cells (ILCs), and also by CD4⁺ T cells, CD8⁺ T cells and $\gamma\delta$ T cells^{2, 3}. ILCs expressing the transcription factor ROR γ t are an important source of IL-22 *in vivo*¹⁴. Following activation with IL-23 or IL-1 β , ROR γ t⁺ ILCs produce IL-22 through a mechanism controlled by the ligand-activated transcription factor aryl hydrocarbon receptor (AhR)¹⁵⁻¹⁷. AhR signaling is also critical for the development of ILCs, thus it has been postulated that AhR ligands in the diet or produced by commensal bacteria regulate ILC development and function¹⁵⁻¹⁷. However, commensal bacteria can also promote IL-22 production through AhR-independent mechanisms, for example by inducing the production of IL-1 β and IL-23 by myeloid cells^{18, 19}.

CD4⁺ T cells also produce significant amounts of IL-22. We²⁰ and others²¹⁻²³ have shown that AhR signaling regulates the production of IL-22 by Th17 cells differentiated in the presence of IL-6 and TGF β 1. Indeed, the production of IL-22 by IL-17⁺ CD4⁺ T cells has been shown to limit tissue destruction during experimental acute hepatitis⁷ and inflammatory bowel disease (IBD)^{8, 24}. Although IL-22 expression is usually linked to Th17 cells²⁵, human and murine CD4⁺ T cells that produce high amounts of IL-22 but not IL-17 have also been identified^{13, 25-28}. These CD4⁺ IL-22⁺ IL-17⁻ T cells play a protective role in mucosal antimicrobial host defense^{9, 29}. Thus, considering the significant role of IL-22 produced by CD4⁺ T cells in host defense and mucosal barrier integrity it is important to investigate the mechanisms that regulate IL-22 production in T cells.

In vitro, the activation of naïve CD4⁺ T cells in the presence of cytokines that trigger STAT3 activation, such as IL-6, triggers the production of IL-22 but almost no IL-17¹³. IL-21, a cytokine that belongs to the type I four- α -helical-bundle family of cytokines, can replace IL-6 during the differentiation of Th17 cells^{30, 31}. Thus, in this work we investigated the role of IL-21 in the differentiation of IL-22-producing CD4⁺ T cells. We found that IL-21 induces the differentiation of CD4⁺ T cells that produce IL-22, but not IL-17, by a mechanism that involves the transcription factors STAT3, AhR and ROR γ t. Moreover, AhR and IL-21 signaling control IL-22 production by CD4⁺ T cells that limit mucosal inflammation in ILC-deficient mice. Taken together, these results indicate that IL-21 signaling controls IL-22 production by T cells that limit mucosal inflammation.

Results

IL-21 induces IL-22 expression in CD4⁺ T cells

IL-6 triggers the production of IL-22 by naïve CD4⁺ T cells in the absence of IL-17 production¹³. Based on the ability of IL-21 to replace IL-6 during the differentiation Th17 cells^{30, 31}, we investigated the role of IL-21 in the differentiation of IL-22 producing CD4⁺ T cells. We found that the activation of naïve CD4⁺ T cells with antibodies to CD3 and CD28 in the presence of IL-21 results in the production of IL-22 but not IL-17 (Figs. 1a-b); no significant changes in IFN γ expression were detected. The production of IL-22 induced by activation with IL-21 was comparable to that observed following activation with IL-6

(Supplementary Fig. 1a). Moreover, in agreement with previous reports^{31, 32} we found that exogenous IL-21 also up-regulated its own expression in T cells (Fig. 1c), suggesting that a positive feed forward loop stabilizes IL-22 production in IL-21 stimulated T cells. The up-regulation of *il21* expression was reduced by TGF β 1 blockade, suggesting that it is boosted by trace amounts of TGF β 1 provided either by the medium or the T cells (Supplementary Fig. 1b).

The production of IL-22 by T cells activated in the presence of IL-21 was associated to proliferation, peaking at 3 cell divisions as determined by staining with carboxyfluorescein succinimidyl ester (CFSE)(Fig. 1d). To investigate the stability of IL-22 producing T cells induced with IL-21, naïve CD4⁺ T cells were initially activated in the presence of IL-21, rested, and reactivated in the presence of IL-21, or under Th17 (IL-6 and TGF β 1) or FoxP3 iTreg (TGF β 1) polarizing conditions. The re-stimulation of T cells that have been previously activated in the presence of IL-21 resulted in a significant population of IL-17⁻ IL-22⁺ T cells, similar results were found upon reactivation in the presence of IL-21 (Supplementary Fig. 2c). Re-stimulation under Th17 polarizing conditions resulted in similar numbers of IL-17⁻ IL-22⁺ T cells, however under these experimental conditions we also detected the generation of IL-17 producing T cells (IL-17⁺ IL-22⁺ and IL-17⁺ IL-22⁻ T cells) (Supplementary Fig. 2c). Similar results were obtained following re-activation under FoxP3 iTreg polarizing conditions, probably as a result of the promotion of Th17 cell differentiation by exogenous TGF β 1 acting in combination with T-cell produced IL-21^{30, 31} (Supplementary Fig. 2c). These results suggest that IL-22 producing T cells induced with IL-21 are relatively stable, and that additional Th17 cells can be differentiated from non-polarized T cells in the culture.

Since IL-6 and IL-23 have also been shown to trigger the production of IL-22 by CD4⁺ T cells^{9, 13, 28, 29}, we studied the effects of IL-21 on the expression of IL-6R, IL-23R and IL-21R. T-cell activation in the presence of IL-21 resulted in a significant up-regulation of *il23r* expression, but did not modify the expression of *il6r* or *il21r* (Fig. 1e), suggesting that IL-21 signaling may also modulate the production of IL-22 triggered in CD4⁺ T cells by IL-23. Similar levels of *il21r* and *il23r* expression were observed following T-cell stimulation in the presence of IL-21 or IL-6 (Supplementary Fig. 1d). In accordance with these findings, we found a significant synergism between IL-21 and IL-23 in inducing IL-22 expression in CD4⁺ T cells (Fig. 1f,g). IL-23, however, did not synergize with IL-21 to boost *il21* expression by T cells (Fig. 1h).

IL-1 β boosts IL-22 production by Th17 cells³³, thus we investigated the effects of IL-1 β in the production of IL-22 triggered by IL-21. We found that IL-21 up-regulated *il1r1* expression in T cells, this up-regulation was partially dependent on TGF β 1 signaling (Fig. 1i and Supplementary Fig. 1d). Moreover, IL-1 β synergized with IL-21 in inducing the production of IL-22, but not of IL-17 (Fig. 1j,k). IL-1 β , however, did not boost *il21* expression induced by IL-21 (Fig. 1l). Taken together, these results suggest that IL-21, alone or in combination with IL-23 or IL-1 β , triggers IL-22 production independently of IL-17 in CD4⁺ T cells.

Transcriptional profiling of IL-21-stimulated CD4⁺ T cells

To study the molecular mechanisms mediating the production of IL-22 by CD4⁺ T cells stimulated with IL-21, we analyzed the mRNA expression profile by whole-genome microarrays. We compared the mRNA expression profiles of naïve CD4⁺ T cells activated in the presence of IL-21, IL-6 and TGFβ1 (Th17 cells) or without the addition of exogenous cytokines (Th0 cells). We found 869 genes that were up- or down-regulated at least 1.5 fold in CD4⁺ T cells stimulated in the presence of IL-21 relative to their expression in control Th0 cells (Fig. 2a). Principal-component analysis (PCA) showed that the transcriptional signature of CD4⁺ T cells treated with IL-21 is significantly different from that of Th17 cells differentiated with IL-6 and TGFβ1 (Fig. 2b). Although there was a partial overlap between genes up-regulated in IL-22+ IL-17- T cells and Th17 cells, a direct comparison of their transcriptional profile identified 179 genes with differences in expression. We found significant differences in the expression of key cytokines, chemokines, receptors and transcription factors recently associated with Th17 cells differentiated *in vitro* with TGFβ1 and IL-6³⁴ (Fig. 2c). We focused our attention on transcriptional modules recently identified to control Th17 cell differentiation: a module of “Th17-positive factors” that promote Th17 cell differentiation and a module of “Th17-negative factors” that interferes with this process³⁴. We found that IL-22 producing T cells induced with IL-21 differed from Th17 cells in the expression of genes belonging to these Th17-positive and Th17-negative transcriptional modules (Fig. 2d).

On the basis of the biological function of their products, we selected a representative subset of genes coding for transcription factors such as *ahr*, *rora*, *rorc*, *tbx21*, *socs3*; granzymes A and B (*gzma* and *gzmb*) which have been linked to effector and regulatory T cells³⁵; the IBD linked mucin 1 (*muc1*), known to be a transcriptional target of STAT3³⁶⁻³⁸, and the inhibitors of IL-10 production metallothioneins 1 and 2 (*mt1*, *mt2*)³⁴ and confirmed their differences in expression by qPCR (Fig. 2e). The up-regulation of AhR and RORγt expression was also confirmed at the protein level by western blot (Fig. 2f). However, and in agreement with previous reports on IL-22 producing T cells generated with IL-6²⁸, this up-regulation was promoted by trace amounts of TGFβ1 provided either by the medium or the T cells, because it could be inhibited with TGFβ1-specific blocking antibodies (Supplementary Fig. 2a). Of note, activation of T cells in the presence of IL-21 did not result in a significant up-regulation of *tbx21*, which has been recently linked to the production of IL-22 triggered in CD4⁺ T cells IL-6²⁹. We also failed to detect *foxp3* expression in T cells activated in the presence of IL-21 (Supplementary Fig. 2b).

Finally, we used Ingenuity Pathways Analysis to analyze the genes found to be differentially expressed between Th0 and IL-22+ IL-17- T cells. The resulting model identified important roles for STAT3, RORγt and AhR in the control of IL-22+ IL-17- T cell differentiation triggered by IL-21 (Fig. 2g). In conclusion, these data suggest that IL-21 triggers a transcriptional program in CD4⁺ T cells that differs from the one of Th17 cells and is controlled by STAT3, RORγt and AhR.

STAT3 is required for IL-21 induced IL-22 expression

Based on our transcriptional analysis and the reported activation of STAT3 by IL-21 signaling, we studied the role of STAT3 in the production of IL-22 triggered by IL-21. T-cell activation in the presence of IL-21 led to a significant phosphorylation of STAT3, and also to a significant increase in *stat3* expression (Fig 3a-b). T-cell activation in the presence of IL-6, with or without TGF β 1-blocking antibodies, resulted in similar amounts of STAT3 phosphorylation (Supplementary Fig. 3a).

To investigate the function of STAT3 in the regulation of IL-22 production, we activated wild type (WT) and STAT3-deficient CD4⁺ T cells in the presence of IL-21. The production of IL-22 in response to IL-21 was significantly decreased in STAT3-deficient CD4⁺ T cells (Fig. 3c). Moreover, in agreement with our bioinformatic analysis STAT3 was also required for the up-regulation of *il21*, *ahr* and *rorc* expression in response to IL-21 (Fig. 3d,e).

Of note, we also found that STAT3 mediated the upregulation of *il23r* and *illr1* expression in response to IL-21 (Fig. 3f). However, IL-23 or IL-1 β did not up-regulate *stat3* expression when their effects on CD4⁺ T cells were analyzed alone or in combination with IL-21 (Fig. 3g). Taken together, these data suggest that STAT3 plays a central role in the differentiation of IL-22 producing CD4⁺ T cells in response to IL-21.

ROR γ t and AhR control IL-22 expression induced by IL-21

The up-regulation of *rorc* expression was linked to the induction of IL-22 expression in CD4⁺ T cells triggered by IL-21 (Fig. 2). Based on our studies on the transcriptional effects of IL-21 on CD4⁺ T cells and the reported role of ROR γ t in the control of *il22* expression in Th17 cells and ILCs^{16, 39} we investigated the role of ROR γ t in the production of IL-22 triggered by IL-21. We found that ROR γ t deficiency led to a significant reduction in the production of IL-22 induced by IL-21 in naïve CD4⁺ T cells (Fig. 4a). ROR γ t-deficiency also decreased the expression of *il23r* but not of *illr1*, and abrogated the ability of IL-23 to boost IL-22 production triggered by IL-21 (Fig 4b-c). Conversely, activation of naïve T cells in the presence of IL-23 or IL-1 β alone did not result in a significant upregulation of *rorc* expression, but IL-23 synergized with IL-21 to boost *rorc* expression (Fig. 4d). Thus, similarly to what has been described for Th17 cells and ILCs, ROR γ t controls the production of IL-22 by CD4⁺ T cells treated with IL-21. Moreover, these data suggest that in addition to its effects on the production of IL-22 triggered by IL-21, ROR γ t also controls the ability of IL-23 to synergize with IL-21 and boost IL-22 expression in T cells.

We²⁰ and others²¹⁻²³ found that AhR activation modulates IL-22 production in Th17 cells. Moreover, AhR also participates in the production of IL-22 triggered by IL-6²⁸. Based on these observations and the results of our transcriptional profiling of CD4⁺ T cells activated in the presence of IL-21 (Fig. 2), we investigated the role of AhR in the control of IL-22 production triggered by IL-21. The addition of the AhR agonist 6-formylindolo[3,2-b]carbazole (FICZ) led to a significant increase in the production of IL-22 triggered by IL-21 (Fig. 4e). Conversely, the use of the AhR specific antagonist CH-223191 resulted in a significant reduction in IL-22 production triggered by IL-21 (Fig. 4e). A similar reduction in IL-22 production was detected when we used T cells from AhR-d mice, which carry an *ahr*

allele coding for a mutant AhR with reduced affinity for its ligands⁴⁰ (Fig. 4f). Of note, *ahr* expression levels were not significantly up-regulated in response to T-cell activation in the presence of IL-23 or IL-1 β alone, and IL-23 or IL-1 β did not synergize with IL-21 to up-regulate *ahr* expression (Fig. 4g). These findings suggest that AhR plays a more important role in the regulation of IL-22 production by CD4⁺ T cells activated by IL-21 than in response to IL-23 or IL-1 β .

AhR has been shown to interact with STAT proteins and modulate their activity^{21, 22, 41}. Considering the important role of STAT3 in the production of IL-22 triggered by IL-21, we analyzed whether STAT3 activation in response to IL-21 is modulated by AhR. We found that modulation of AhR signaling with FICZ or CH-223191 had no significant effect in the phosphorylation of STAT3 in T cells in response to IL-21 (Fig. 4h). Similarly, we found no significant differences in STAT3 phosphorylation in response to IL-21 between WT and AhR-d T cells (Supplementary Fig. 3b). Taken together, these data suggest that ROR γ t and AhR control the IL-22 production triggered by IL-21, and these effects do not involve the modulation of STAT3 activation.

STAT3 controls the accessibility of the *il22* promoter

We recently reported that AhR and STAT3 co-operate to regulate *ikzf3* expression in Th17 cells⁴². A bioinformatic analysis of the *il22* promoter revealed 2 putative STAT3 responsive elements (SRE-1 and SRE-2) upstream of the transcription start site and 3 putative binding sites for AhR (xenobiotic response elements, XRE-1, XRE-2 and XRE-3) (Fig. 5a). Thus, to investigate whether STAT3 and AhR interact with these potential binding sites in the *il22* locus we performed chromatin immunoprecipitation (ChIP) assays. We detected a significant interaction of AhR and STAT3 with the *il22* promoter in CD4⁺ T cells activated in the presence of IL-21 (Fig. 5b-c).

We then analyzed the functional effects of the interaction of STAT3 and AhR with its DNA responsive elements using a reporter plasmid carrying the firefly luciferase under the control of the *il22* promoter (*il22*:Luc). Transfection with vectors coding for AhR or constitutively activated STAT3 did not result in a significant induction of luciferase activity (Fig. 5d). However, co-transfection with constructs coding for constitutively activated STAT3 and AhR induced a significant up-regulation of luciferase activity, suggesting a synergistic effect of STAT3 and AhR in the production of IL-22 (Fig. 5d).

c-Maf interacts with AhR to transactivate the *il10* promoter^{35, 43}, but it suppresses *il22* expression induced with IL-6²⁸. Although we detected a small up-regulation of *maf* in response to IL-21 (Supplementary Fig. 4a), we found no significant binding of c-Maf to its potential binding sites in the *il22* promoter (Supplementary Fig. 4b). These data suggest that, similarly to what has been described for IL-22⁺ IL-17⁻ T cells induced with IL-6, c-Maf does not promote *il22* expression in T cells activated in the presence of IL-21²⁸.

Both AhR and ROR γ t have been shown to control IL-22 expression in Th17 cells. Indeed, AhR and ROR γ t physically interact, and in over-expression experiments in EL4 cells it was shown that a constitutively active mutant AhR is recruited to the *il22* locus in a ROR γ t-dependent manner¹⁶. Since we found that ROR γ t-deficient T cells show a significant

decrease in IL-22 production following activation in the presence of IL-21, we investigated whether ROR γ t was needed for the recruitment of endogenous AhR to its target sequences in the *il22* locus. We found that ROR γ t deficiency results in a significant decrease in the recruitment of AhR to the *il22* promoter (Fig. 5e). We also detected a decrease in the acetylation of histones 3 and 4 and the trimethylation of histone 3 at Lys4, concomitant with increased histone trimethylation at Lys9 and Lys 27, supporting our findings on the lack of *il22* expression in the absence of ROR γ t (Supplementary Fig. 4c).

Overexpression of AhR and ROR γ t in CD4⁺ T cells activated under non-polarizing Th0 conditions, however, does not result in IL-22 expression²². The ability of transcription factors to bind regulatory regions on target genes is affected by the structure of the chromatin, which is regulated by several processes including post-translational histone modifications⁴⁴. Thus, we reasoned that the lack of IL-22 expression observed in CD4⁺ T cells overexpressing AhR and ROR γ t²² might reflect the need for epigenetic mechanisms that increase the accessibility to regulatory elements in the *il22* promoter. First, we analyzed the acetylation status of histone H3 and H4 in the *il22* promoter of naive T cells activated in the presence of IL-21. We found a significant increase in the acetylation of histones H3 and H4 in CD4⁺ T cells activated in the presence of IL-21 (Fig 5f), which is usually associated with a relaxed chromatin structure that facilitates the interaction of transcription factors with target sequences. We also found that T-cell activation in the presence of IL-21 results in increased histone 3 trimethylation in Lys4, associated to actively transcribed genes, concomitant with decreased trimethylation in Lys9 and Lys27, which have been associated with the silencing of transcription⁴⁵ (Fig. 5f). Of note, we detected no changes in the methylation status of the *il22* promoter (Supplementary Fig. 4d).

STAT3 binds target sequences in the *il22* promoter and is required for the production of IL-22 triggered by IL-21 (Figs. 3c and 5c). Given the reported role of STAT3 in regulating the epigenetic status of target genes⁴⁶, we investigated the role of STAT3 in regulating the epigenetic status of the *il22* locus using WT and STAT3-deficient T cells activated in the presence of IL-21. We found that the lack of STAT3 recruitment to the *il22* promoter in STAT3-deficient T cells resulted in a significant decrease in H3 and H4 acetylation in STAT3 and AhR binding sites (Figs. 5g-i). We also detected a decrease in histone 3 trimethylation at Lys4 and an increase in trimethylation at Lys9 and Lys27 in STAT3-deficient T cells (Supplementary Fig. 4e). Moreover, the reduced histone acetylation observed in STAT3-deficient T cells was concomitant with a reduced recruitment of AhR to the *il22* promoter (Fig. 5j). Taken together, these results demonstrate that in addition to its effects on the expression of AhR and ROR γ t, STAT3 activated in response to IL-21 controls the accessibility to regulatory elements in the *il22* promoter recognized by AhR and probably additional transcription factors.

IL-21 and AhR control IL-22 expression in vivo

IL-22 maintains the integrity of the colonic epithelium during inflammation^{8, 24}. Dextran sodium sulfate (DSS)-induced colitis is thought to result from the disruption of the epithelial barrier in the colon, resulting in the translocation of commensal bacteria, the activation of innate immunity and up-regulation of IL-23 and IL-6⁴⁷.

IL-22 plays a central role in the control of intestinal inflammation^{2, 3}. Although both ILCs and CD4⁺ T cells produce IL-22 during the course of DSS-induced colitis, ILCs constitute a more abundant source of IL-22 in WT mice (Supplementary Fig. 5). The development of ILCs is regulated by IL-7 signaling through the IL-2 receptor common gamma chain (IL-2RG)⁴⁸. Thus, to focus our studies on the role of IL-22 producing CD4⁺ T cells during gut inflammation, we used mice deficient in both RAG2 and IL-2RG (RAG2/IL2RG mice); these mice lack T cells and also NK cells and ILCs^{3, 17}. To study the role of AhR and IL-21 in the regulation of IL-22 production by T cells *in vivo*, we reconstituted RAG2/IL2RG mice with WT CD4⁺ T cells, IL-21R-deficient (IL-21R KO) T cells or AhR-d T cells. Following confirmation of successful T-cell reconstitution by flow cytometry from blood samples, we induced DSS colitis in the recipient mice and monitored weight change daily. We found a significant worsening of DSS-induced colitis in mice reconstituted with AhR-d or IL-21R-deficient T cells, manifested as increased weight loss (Fig. 6a) and colon shortening (Fig. 6b) suggestive of augmented colon inflammation. Accordingly, IL-21R KO and AhR-d mice showed increased colon inflammation upon blind histological examination (Fig. 6c).

To directly investigate the impact of IL-21 and AhR signaling in T cells on the immune response during DSS-induced colitis, we analyzed cytokine production by excised colon cultures prepared from mice reconstituted with WT, AhR-d or IL-21R-deficient T cells. We found a significant reduction in the production of IL-22 by colon explants isolated from AhR-d or IL-21R deficient mice (Fig. 6d) and a concomitant increase in the levels of the pro-inflammatory cytokines IL-6 and IL-23 (Fig. 6e). The decreased production of IL-22 correlated with a decrease in the frequency of IL-22 producing T cells in AhR-d and IL21R-deficient mice compared to WT (Fig. 6f). Of note, we did not detect significant changes in *il10* expression nor in the frequency of FoxP3⁺ T cells (Fig. 6g). Taken together, these results demonstrate that IL-21 and AhR signaling in T cells limit gut inflammation.

Discussion

IL-22 regulates tissue homeostasis and inflammation at mucosal surfaces^{2, 3}. ILCs have been identified as an important source of IL-22 *in vivo*, but the importance of IL-22 producing T cells and the mechanisms regulating their differentiation and function are largely unknown. Human and murine $\gamma\delta$ T cells, Th1 and Th17 cells produce IL-22^{2, 3}. In addition, IL-22⁺ IL-17⁻ cells named Th22 cells have been described in humans^{26, 27} but it has proven difficult to identify the murine equivalent of this population. CD4⁺ T-cell activation in the presence of IL-6, IL-21 or IL-23 induces IL-22⁺ IL-17⁻ T cells that have been linked to early host defense against *Citrobacter rodentium*^{9, 13, 28, 29, 49}. Activation of Notch signaling has also been shown to induce IL-22 production by CD4⁺ T cells in a STAT3-independent manner⁵⁰. These data suggest that, similarly to what is observed for human Th22 cells, IL-22 can be expressed independently of IL-17 in mouse T cells. However, until specific transcription factors are identified to act as master regulators of IL-22⁺ IL-17⁻ T cells, it cannot be determined whether these cells constitute a separate CD4⁺ T cell lineage or simply represent an activation stage of CD4⁺ T cells.

IL-21 is produced by NKT cells, $\gamma\delta$ T cells, follicular helper T cells, Th17 cells, type 1 regulatory T cells and a recently described subpopulation of mucosal CCR9⁺ Th cells^{43, 51}.

Thus, these cell populations may regulate the production of IL-21 dependent IL-22 by T cells *in vivo*. We found that IL-21 up-regulates *rorc* expression, and also *il1r1* and *il23r* in a ROR γ t-dependent manner. Indeed, IL-21 synergized with IL-1 β and IL-23 to induce IL-22 production by CD4⁺ T cells. These data suggest that by increasing *il1r1* and *il23r* expression, IL-21 decreases the activation threshold for IL-1 β and IL-23-triggered IL-22 production. In addition, IL-6 has also been shown to induce IL-21 production by T cells³². Thus, it is likely that similarly to their reported effects on Th17 cell differentiation⁵², IL-21 acts in combination with IL-23, IL-1 β and IL-6 to stabilize and boost the production of IL-22 by T cells *in vivo*. IL-21 can replace IL-6 during the differentiation of Th17 cells, and IL-21 and IL-6 exhibit redundancy during the differentiation of follicular T helper cells^{30, 31, 51}, however that redundancy is not complete *in vivo*⁵³. Future studies should determine the relative contribution of IL-6 and IL-21, and also IL-1 β and IL-23 during the regulation of IL-22 production by T cells and other cell populations.

Group 3 ILCs comprises an heterogeneous group of cell populations identified as a major source of IL-22 *in vivo*^{2, 14, 24}. Interestingly, AhR and ROR γ t are reported to control IL-22 production by ILCs in response to IL-23, a known activator of STAT3 signaling^{15, 16}. These reports and the data presented in this manuscript highlight the transcriptional similarities existing between CD4 T cells activated in the presence of IL-21 and group 3 ILCs, and suggest that additional transcriptional elements involved in the control of IL-22 expression might be shared by these two sources of IL-22. Of note, it has been recently shown that T-bet controls the production of IL-22 production triggered with IL-6²⁹. In our experiments we did not detect an up-regulation of *tbx21* following T-cell activation in the presence of IL-21. This finding suggests that similarly to the heterogeneity that characterizes the ROR γ t+ IL-22+ cells included in group 3 ILCs, distinct IL-22+ IL-17- CD4+ T cell populations might be induced in response to different environmental, microbial and cytokine stimuli.

Because of the dominant role of ILCs and $\gamma\delta$ T cells in mucosal IL-22 production we used T-cell reconstituted RAG2/IL-2RG mice to study the role of T-cell produced IL-22 in mucosal inflammation. We found that IL-21 and AhR modulate the production of IL-22 by intestinal CD4⁺ T cells *in vivo*. In addition, it has been reported that the protective effects of some AhR dietary ligands in the DSS colitis model are T-cell dependent, suggesting that IL-22 production by T cells plays a physiological role in the modulation of mucosal inflammation⁵⁴. Additional support for this interpretation was recently provided by Basu *et al*, who described sequential waves of IL-22 production by ILCs and T cells responsible for host defense against *Citrobacter rodentium* infection²⁹. Indeed, it is possible that specialized ILCs with antigen-presenting cell activity participate in the induction and regulation of IL-22 producing mucosal T cells *in vivo*⁵⁵. The study of the factors that control IL-22 production by different cell types is likely to identify appropriate targets for the therapeutic modulation of IL-22 production.

A partial protection from DSS-induced colitis has been previously reported in complete, non-tissue specific IL-21 deficient mice⁵⁶. We believe that the differences on the role of IL-21 on DSS-induced colitis (protective in our work versus pathogenic in⁵⁶) might reflect differential effects of IL-21 on ILCs and CD4⁺ T cells and the absence of ILCs in RAG2/IL2RG mice. Alternatively, these different outcomes might result from the use of IL-21

deficient mice in the work of Araki *et al*⁵⁶, instead of the IL-21R KO mice used in our studies.

We found that AhR modulates IL-22 production by IL-22+ IL-17- T cells induced with IL-21, but AhR inhibition does not completely abrogate IL-22 production *in vitro*. Similar results have been recently reported for the role of AhR in the regulation of IL-22 production triggered in CD4+ T cells by IL-6²⁸. Our data, however, suggest that AhR plays a more prominent role in the regulation of IL-22 production *in vivo*. A large proportion of intestinal IL-22+ T cells co-express IL-17, probably as a result of the local abundance of TGFβ1 which in combination with IL-6 and IL-21 favors the differentiation of Th17 cells that may control intestinal inflammation^{8, 57}. Indeed, our experiments using blocking antibodies indicate that TGFβ1 promotes AhR expression in IL-22 producing T cells. Th17 cells differentiated in the presence of TGFβ1 express higher amounts of AhR, and consequently AhR is a stronger regulator of IL-22 expression in Th17 cells than in IL-22+ IL-17- T cells²⁸. Thus, the more prominent effects of AhR in the regulation of IL-22 *in vivo* might reflect the increased role of Th17 cells as a source of intestinal IL-22. It is also possible that local AhR ligands provided by the host, the diet or the commensal flora are more potent inducers of IL-22 expression in intestinal T cells.

We and others have shown that AhR controls IL-22 and IL-10 production by Th17^{20, 22, 23} and Tr1^{35, 43, 58} cells. Considering the importance of IL-10 and IL-22 for the control of mucosal homeostasis and inflammation^{2, 3, 59}, AhR seems to be closely linked to a transcriptional program that limits immunopathology at environmental interfaces by the combined effects of IL-10 on the adaptive and the innate immune response, and the effects of IL-22 on epithelial cells. The regulation of AhR activity by endogenous, microbial, dietary and environmental ligands, provides a molecular mechanisms to adjust the mucosal production of IL-10 and IL-22. Moreover, it provides a potential target for therapeutic intervention.

Methods

Mice

Eight weeks old C57BL/6 and double RAG2- IL-2RG-deficient female mice were purchased from the Jackson Laboratories. AhR-d, IL21R- and RORγt-deficient mice were bred at Harvard Medical School, from breeders provided by the Jackson Laboratories. Mice were kept in a conventional, pathogen-free facility at the Harvard Institutes of Medicine. All mouse handling and *in vivo* experiments were carried out in accordance with guidelines prescribed by the Institutional Animal Care and Use Committee (IACUC) at Harvard Medical School.

T-cell differentiation *in vitro*

Naïve CD4+ T cells were stimulated with plate bound antibodies against CD3 (145-2C11, 2μg/ml) and CD28 (PV-1, 2μg/ml), in the presence of IL-21 (30ng/ml) or IL-21 (30ng/ml) and IL-23 (30ng/ml) to generate Th22 cells; and IL-6 (30ng/ml), TGFβ1 (3ng/ml). Mouse IL-6, IL-21, IL-23 and TGFβ1 were purchased from R&D Systems. In

some experiments we used TGF β 1-blocking antibodies at a final concentration of 10 μ g/ml from R&D (Cat. #AF-101-NA). FICZ was obtained from Enzo Life Sciences (PA, USA) and CH-223191 from EMD Chemicals (NJ, USA). We used an RPMI-based medium to minimize the activation of the cells by tryptophan-derived AhR ligands present in other tissue culture mediums²². RPMI was supplemented with 0.1 mM nonessential amino acids, 1 mM sodium pyruvate, L-glutamine (2 mM), penicillin (100 U/ml), streptomycin (100 U/ml), 10% heat-inactivated FBS (BioWhittaker, Inc.) and 2-mercaptoethanol. To evaluate the stability of IL-22 producing T cells induced with IL-21, in some experiments after an initial phase of activation in the presence of IL-21, T cells were re-stimulated with plate bound antibodies to CD3 and CD28 for 48h in the presence of medium, IL-21, TGF β 1 or TGF β 1 and IL-6.

Cytokine Analysis

Secreted cytokines were measured in supernatants of differentiated CD4⁺ T cells *in vitro* and in supernatants of colon samples *ex vivo* after 48h by ELISA. For intracellular cytokine staining, cells were stimulated for 4h at 37C in culture medium containing PMA (50 ng/ml; Sigma, USA), ionomycin (1 μ g/ml; Sigma) and GolgiStop (1 μ l/ml; BD Biosciences, USA). After staining for the surface markers CD3 and CD4, cells were fixed and permeabilized using Cytofix/Cytoperm and Perm/Wash according to the manufacturer's instruction (BD Biosciences, USA; eBioscience, USA). All antibodies were purchased from Biolegend and eBioscience. Data were acquired on a FACSCalibur (BD Biosciences) and analyzed using the FlowJo software (Tree Star).

qPCR

RNA was extracted with RNAeasy columns (Qiagen, USA). cDNA was prepared using High Capacity cDNA Reverse Transcriptase kit following the manufacturer's instructions (Applied Biosystems, USA) and used as template for real-time PCR. Probes were purchased from Applied Biosystems, and were used on the ViiATM 7 Real-Time PCR System (Applied Biosystems). Expression was normalized to the expression of *gapdh*. The following probe mixtures were used: *il1r* (Mm01226962_m1), *il6r* (Mm00439653_m1), *il21r* (Mm00600319_m1), *il23r* (Mm00519942_m1), *il10* (Mm0043614_m1), *il17* (Mm00439619_m1), *il21* (Mm00517640_m1), *il22* (Mm00444241_m1), *ahr* (Mm01291777_m1), *maf* (Mm02581355_s1), *ror* (Mm01173766_m1), *rorc* (Mm00441144_g1), *stat3* (Mm01219775_m1), *foxp3* (Mm00475156_m1), *socs3*, *mt1* (Mm00496660_g1), *mt2* (Mm00809556_s1), *gzma* (Mm01304452_m1), *gzmb* (Mm00442834_m1), *tbx21* (Mm00450960_m1), *gapdh* (Mm99999915_g1).

Gene expression analysis

Transcriptome analysis was done using Affymetrix microarray MoGene_1_0_st on CD4⁺ T cells stimulated for 48 h in the presence of medium, IL-21 or IL-6 and TGF β 1. Microarray data was analyzed using GeneSpring version 12.5 software package (Agilent, Santa Clara, CA). Samples were normalized using Quantile Normalization Algorithm. Fold change difference between IL-21-treated and untreated naïve CD4⁺ T cells was calculated to observe the differential expression profile of genes. Hierarchical clustering was performed

on genes with fold change ≥ 1.5 using Euclidean distance metric to generate heat-maps. We also performed Principle Component Analysis (PCA) to observe the separation between samples using GeneSpring version 7.3 software package (Agilent, Santa Clara, CA). GEO: microarray data GSE55509.

Western blot analysis

Cells were lysed with RIPA buffer supplemented with protease inhibitor cocktail (Sigma, USA). Total T cell lysates (20 μ g) were resolved on 4–12% Bis-Tris Nupage gels (Invitrogen, USA) and transferred onto PVDF membranes (Millipore). The following primary antibodies were used: Anti-AhR from Enzo Life Sciences (BML-SA210; 1/2000 dilution); anti-ROR γ t from Abcam (Cat. #78007; 1/1000 dilution) and anti-GAPDH from Cell Signaling Technology (Cat. #2111; 1/1000 dilution). Western blot analysis was performed as described⁶⁰ and developed using SuperSignal West Femto Maximum Sensitivity Substrate, as instructed by the manufacturer (Pierce).

Chromatin immunoprecipitation (ChIP)

Cells were cross-linked with 1% paraformaldehyde and lysed with 0.35 ml of lysis buffer (1% SDS, 10 mM EDTA, 50 mM Tris-HCl, pH 8.1) containing 1X protease inhibitor cocktail (Roche Molecular Biochemicals, USA). Chromatin was sheared by sonication and supernatants were collected after centrifugation and diluted in buffer (1% Triton X-100, 2 mM EDTA, 150 mM NaCl, 20 mM Tris-HCl, pH 8.1). Five μ g of antibody was prebound for a minimum of 4 h to protein A and protein G Dynal magnetic beads (Invitrogen, USA) and washed three times with ice-cold PBS plus 5% BSA, and then added to the diluted chromatin and immunoprecipitated overnight. The magnetic bead-chromatin complexes were then washed 3 times in RIPA buffer (50 mM HEPES [pH 7.6], 1 mM EDTA, 0.7% Na deoxycholate, 1% NP-40, 0.5 M LiCl) followed by 2 times with TE buffer. Immunoprecipitated chromatin was then extracted with 1% SDS, 0.1 M NaHCO₃ and heated at 65°C for at least 6 h to reverse the paraformaldehyde cross-linking. DNA fragments were purified with a QIAquick DNA purification Kit (Qiagen, USA) and analyzed using SYBR green real time PCR (Takara Bio Inc., USA). We used the following antibodies for ChIP: anti-pSTAT3 (Cat. #9132, Cell Signaling Technology, Inc., USA), anti-AhR (Cat. #9172, Cell Signaling Technology, Inc., USA), anti-cmaf (Cat. #9172, Cell Signaling Technology, Inc., USA), anti-Acetyl-H3 (Cat. #06-599, Millipore, MA, USA), Acetyl-H4 (Cat. #06-866, Millipore, MA, USA), anti-H3K4me3 (Cat. #ab8580, Abcam, MA, USA), anti-H3K9me3 (Cat. #ab8898, Abcam, MA, USA) and anti-H3K27me3 (Cat. #6002, Abcam, MA, USA). The primer pairs used in these experiments are listed in Supplementary Table 1.

Methyl-DNA immunoprecipitation

The T cells were harvested after washing with PBS and genomic DNA was isolated using a DNeasy Blood and Tissue kit (Qiagen) and sheared by sonication to obtain DNA fragments of approximately 500 bp. Ten microgram of sheared DNA was heated at 95°C for 10 min and snap-chilled before mixing with 10 μ l of freshly prepared protein A and protein G Dynal magnetic beads (Invitrogen) that were pre-incubated with 5 μ g of either anti-5-methyl-cytidine antibody (Cat. #ab10805) or mouse IgG control antibody (Cat. #ab18413), both from Abcam, for a minimum of 4 hr and washed 3 times with ice-cold PBS plus 5% BSA.

The mixture was then incubated overnight in buffer (20 mM Tris-HCl [pH 8.1], 150 mM NaCl, 2 mM EDTA, 1% Triton X-100). The bead-DNA complexes were then washed three times in RIPA buffer (50 mM HEPES [pH 7.6], 1 mM EDTA, 0.7% Na deoxycholate, 1% NP-40, 0.5 M LiCl) followed by three times with TE buffer (10 mM Tris HCl [pH 8.0], 1 mM EDTA). Immunoprecipitated DNA was then extracted by heating at 65°C in 1% SDS, 0.1 M NaHCO₃ for at least 6 hr. DNA fragments were purified with a QIAquick DNA purification Kit (Qiagen) and analyzed using SYBR -green real time PCR. The primer pairs used in these experiments are listed in Supplementary Table 2.

Transfection and luciferase assays

HEK293 cells were grown in DMEM supplemented with 10% fetal bovine serum, and transfected using the FuGENE HD (Roche, USA) transfection reagent according to the manufacturer's instructions. *il22* promoter reporter construction was purchased from Dr. Renauld (Ludwig Institute for Cancer Research and Experimental Medicine Unit, Universite Catholique de Louvain, Brussels, Belgium). Vectors coding for AhR and c-Maf were purchased from Gene Copoeia Inc (MD, USA), the vector coding for constitutively activated STAT3 was provided by Dr. David Frank (Dana-Farber Cancer Institute, Boston, MA, USA). Firefly and renilla luciferase activity was analyzed 48 h after transfection using a dual luciferase assay kit (Promega, USA).

T-cell Transfer and Colitis induction

Sorted splenic CD4⁺ T cells from C57BL/6, AhR-d and IL21R knock out mice were transferred i.p. (10×10^6 cells/mouse) into double RAG2- IL-2RG-deficient mice. One month after T cell transfer, the recipient mice were checked for reconstitution of CD4⁺ T cells and colitis was induced with DSS. 3% DSS (MW:36.000-50.000. MP Biomedicals, LLC) was dissolved in drinking water and administered for 7 days, and weight was monitored daily. Eight days after the initiation of the treatment with DSS the mice were euthanized, the colons were dissected and their length measured from the ileocecal junction to the anal verge.

Histological evaluation of colitis

Colonic tissue was removed and used for histologic evaluation by 2 independent investigators in a blinded fashion. The total histologic score represents the sum of nonulcerative regions of epithelium and an infiltration score ranging from 0 to 6 as follows: epithelium: 0, normal morphology; 1, loss of goblet cells in small areas; 2, loss of goblet cells in large areas; infiltration: 0, no infiltration; 1, infiltration around crypt basis; 2, infiltration reaching the lamina muscularis mucosae; 3, extensive infiltration reaching the lamina muscularis mucosae and thickening of the mucosa with abundant edema; 4, infiltration of the lamina submucosa.

Ex vivo colon culture and ELISA

Sections of 1cm of the colon were excised, longitudinally halved and washed three times with sterile HBSS+Hepes medium (2% HEPES buffer, 1% penicillin/streptomycin and 0,05% gentamicin). The colon sections were placed into culture in complete Bruff's media

and cultured for 72h at 37°C with 5% CO₂. The supernatants were harvested and the concentrations of IL-22 (Antigenix America), IL-6 and IL-23 (eBioscience) were determined by ELISA according to manufacturer's instructions.

Statistical analysis

Statistical analysis was performed using the Prism software (Graph Pad software, La Jolla, CA, USA). P<0.05 were considered statistically significant.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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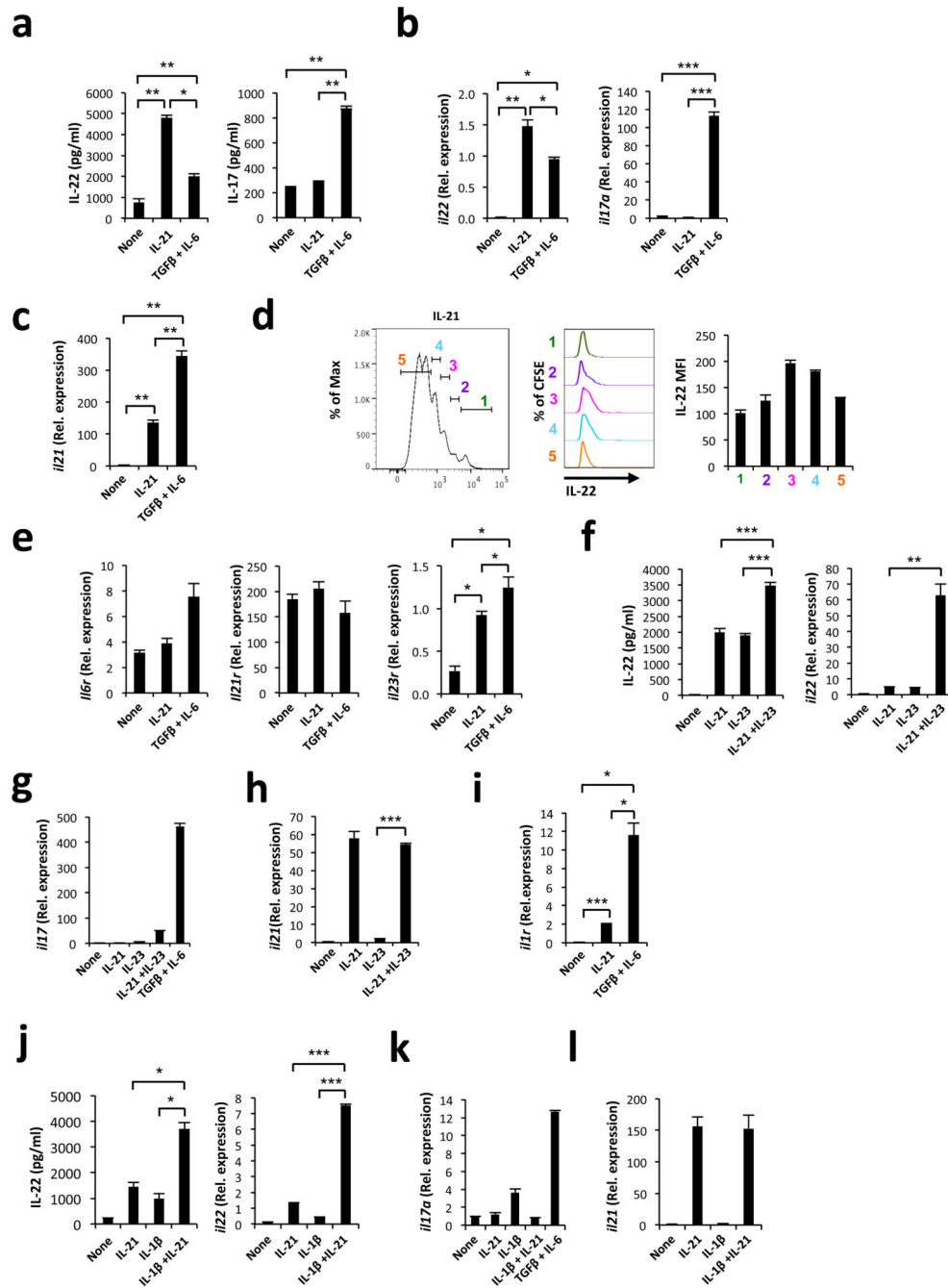


Figure 1. IL-21 promotes the differentiation of CD4+ T cells that produce IL-22 but not IL-17
 Naïve WT CD4+ T cells were stimulated *in vitro* with antibodies to CD3 and CD28 in the presence of different cytokines as indicated. **(a-b)** Effect of IL-21 in the production of IL-22 and IL-17 measured by ELISA in culture supernatants **(a)** and qPCR **(b)**. **(c)** Effect of IL-21 on the expression of *il21*. **(e)** Effect of IL-21 on the expression of *il6r*, *il21r*, *il23r*. **(d)** Relationship between cell division and IL-22 expression in CD4+ T cells. CFSE-labeled naïve CD4+ T cells were activated in the presence of IL-21 and the production of IL-22 was analyzed by intracellular staining. The data are shown as the Mean fluorescence intensity

(MFI) for IL-22 for each division cycle. **(e)** Effects of IL-21 on the expression of *il6r*, *il21r* and *il23r*. **(f-h)** Synergistic effects of IL-21 and IL-23 on IL-22 **(f)** and IL-17 **(g)** cytokine and *il21* expression **(h)**. **(i)** Effect of IL-21 on *il1r* expression. **(j-l)** Synergistic effects of IL-21 and IL-1 β on IL-22 **(j)**, *Il17a* **(k)** and *il21* **(l)** expression. mRNA expression is shown relative to *gapdh*. Results are representative of 3-5 independent experiments. * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ (one-way ANOVA).

Fig. 2a. mRNA expression is shown relative to *gapdh*. **(f)** Western blot analysis of the expression of AhR (95kDa) and ROR γ t (58kDa) on T cells activated in the presence of IL-21 or under Th17-polarizing conditions (left panel). Quantification of western blot reactivity (right panel). **(g)** Ingenuity Pathways Analysis of the transcriptional response of naïve CD4⁺ T cells to IL-21. * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ (one-way ANOVA).

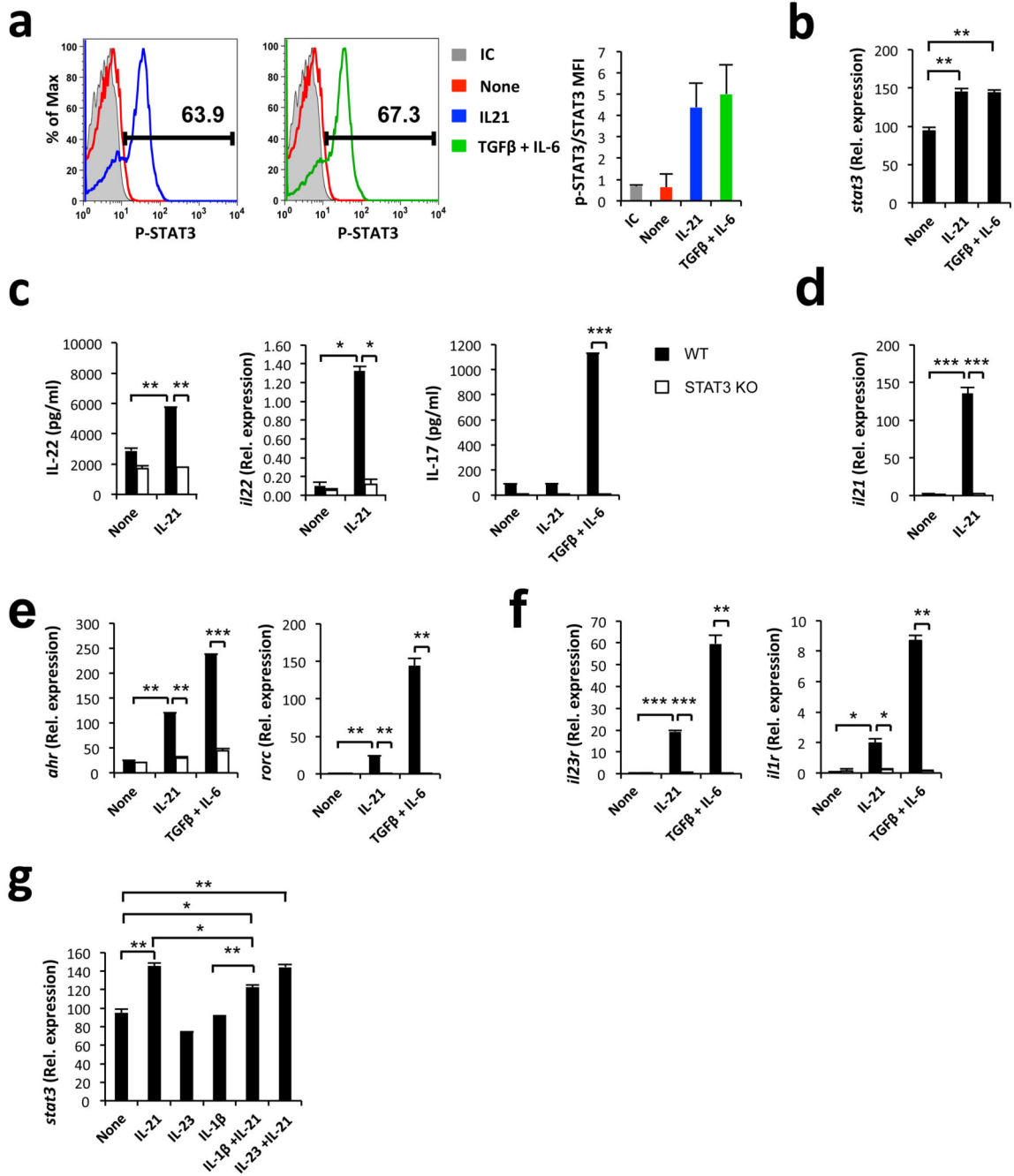


Figure 3. STAT3 controls the production of IL-22 by CD4+ T cells stimulated with IL-21 (a-b) Naïve WT CD4+ T cells were activated in the presence of IL-21 or IL-6 and TGFβ1. (a) FACS analysis of phosphorylated STAT3. Mean fluorescence intensity (MFI) of phosphorylated STAT3 normalized to total STAT3. (b) qPCR analysis of *stat3* expression. (c-f) Naïve WT and STAT3-deficient CD4+ T cells were activated in the presence of IL-21 or IL-6 and TGFβ1. (c) Effect of STAT3 deficiency on IL-22 and IL-17 production. (d) Effect of STAT3 deficiency on *il21* expression. (e-f) Effect of STAT3 deficiency on *ahr* and *rorc* expression (e) and the receptors *il1r*, *il23r* (f). (g) Induction of *stat3* by IL-1β, IL-21

IL-23, IL-1 β and IL-21 or IL-21 and IL-23. mRNA expression is shown relative to *gapdh*. Results are representative of 2-3 independent experiments. * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ (one-way ANOVA and Student's *t*- test).

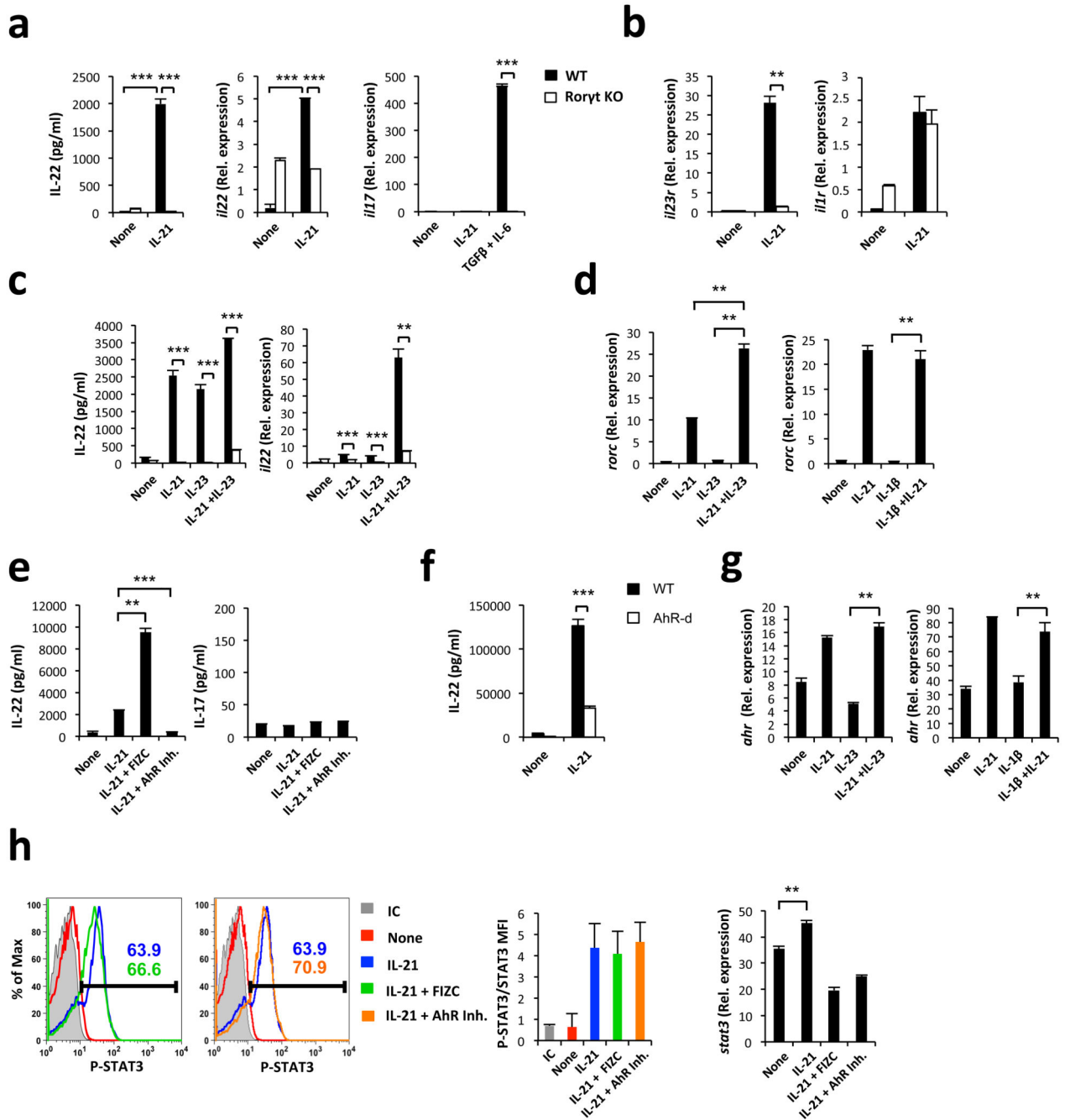


Figure 4. RORγt and AhR control IL-22 production by CD4+ T cells stimulated with IL-21 (a-c) Naïve WT and RORγt-deficient CD4+ T cells were activated in the presence of IL-21 or IL-6 and TGFβ1. (a) Effect of RORγt deficiency on IL-22 and IL-17 production. (b) Effect of RORγt deficiency on *il23r* and *il1r1* expression. (c) Effect of RORγt deficiency on the synergism between IL-21 and IL-23. (d) Effect of IL-1β and IL-23 in *rorc* expression. (e) Effect of the modulation of AhR activity on IL-22 and IL-17 production. (f) IL-22 production by WT and AhR-d CD4+ T cells activated in the presence of IL-21. (g) Modulation of *ahr* expression by IL-1β and IL-23. (h) Effect of AhR modulation on STAT3

phosphorylation and *stat3* expression. MFI of phosphorylated STAT3 normalized to total STAT3. mRNA expression is shown relative to *gapdh*. Representative results of 2-3 independent experiments. * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ (one-way ANOVA and Student's *t*- test).

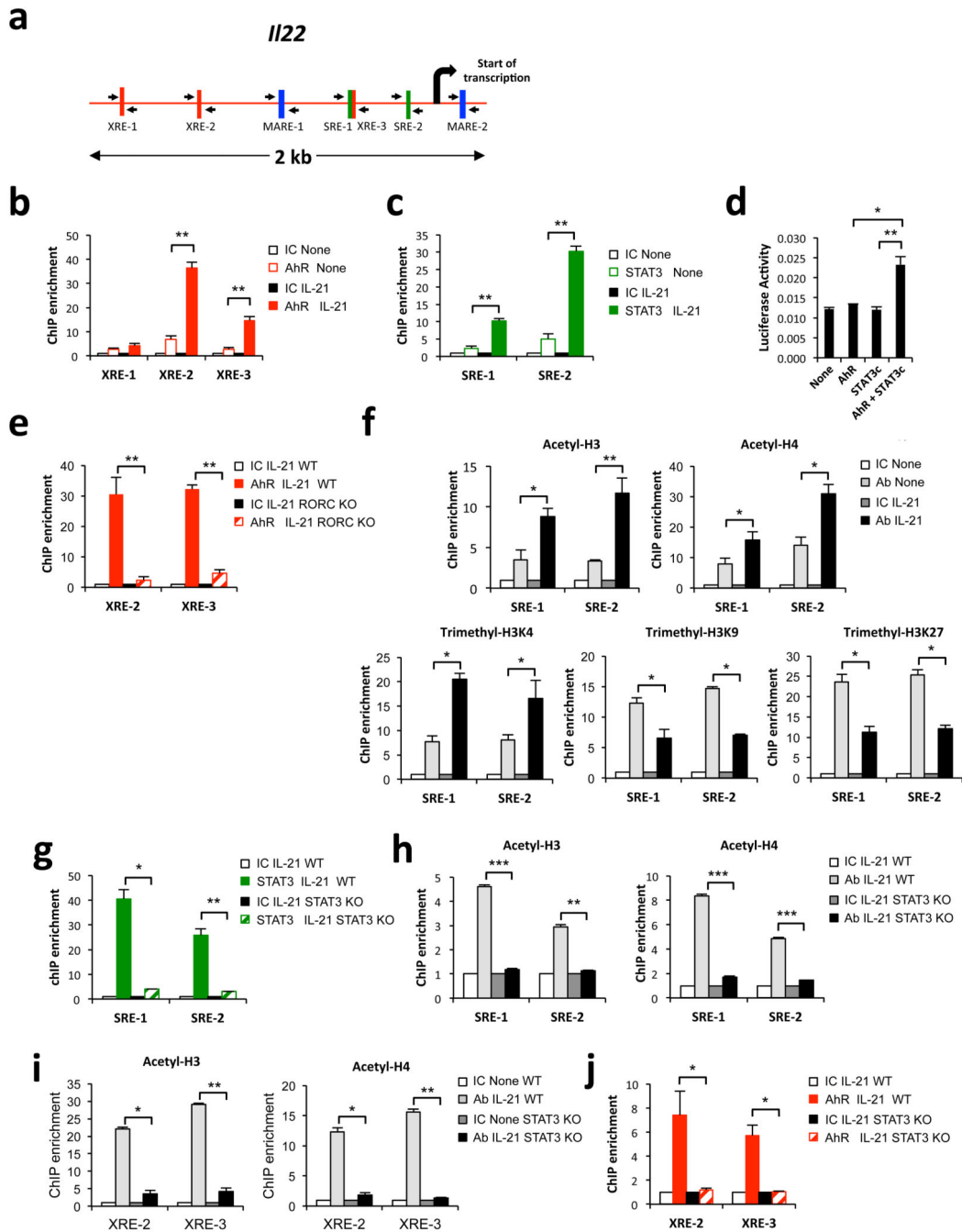


Figure 5. STAT3 controls AhR recruitment to the *il22* promoter in IL-21-stimulated CD4+ T cells
 (a) AhR, c-Maf and STAT3 binding sites in the *il22* promoter. (b-c) WT naïve CD4+ T cells were stimulated *in vitro* with antibodies to CD3 and CD28 in the presence or absence of IL-21. ChIP analysis of the interaction of AhR (b) and STAT3 (c) to the AhR and STAT3 binding sites in the *il22* promoter, respectively. (d) Regulation of the transcriptional activity of the *il22* promoter by AhR and STAT3. A reporter construct for the *il22* promoter (*il22*:Luc) was cotransfected in HEK293 cells with vector coding for AhR and/or

constitutively activated STAT3 (STAT3c). Firefly luciferase was determined and normalized to renilla luciferase activity. **(e)** ChIP analysis of the recruitment of AhR to the *il22* promoter in WT and ROR γ t-deficient CD4⁺ cells activated in the presence of IL-21. **(f)** WT naïve CD4⁺ T cells were stimulated *in vitro* with antibodies to CD3 and CD28 in the presence or absence of IL-21, and the epigenetic status of the *il22* promoter was analyzed by ChIP using antibodies to Acetyl-H3, Acetyl-H4 and H3 trimethylated at Lys4, Lys9 or Lys27. **(g-j)** ChIP analysis of the epigenetic status of the *il22* promoter in WT and STAT3-deficient CD4⁺ T cells activated in the presence of IL-21. STAT3 recruitment **(g)**, H3 and H4 acetylation in SREs **(h)** and XREs **(i)** and AhR recruitment **(j)** in the *il22* promoter. Results are representative of 2-3 independent experiments. * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ (one-way ANOVA).

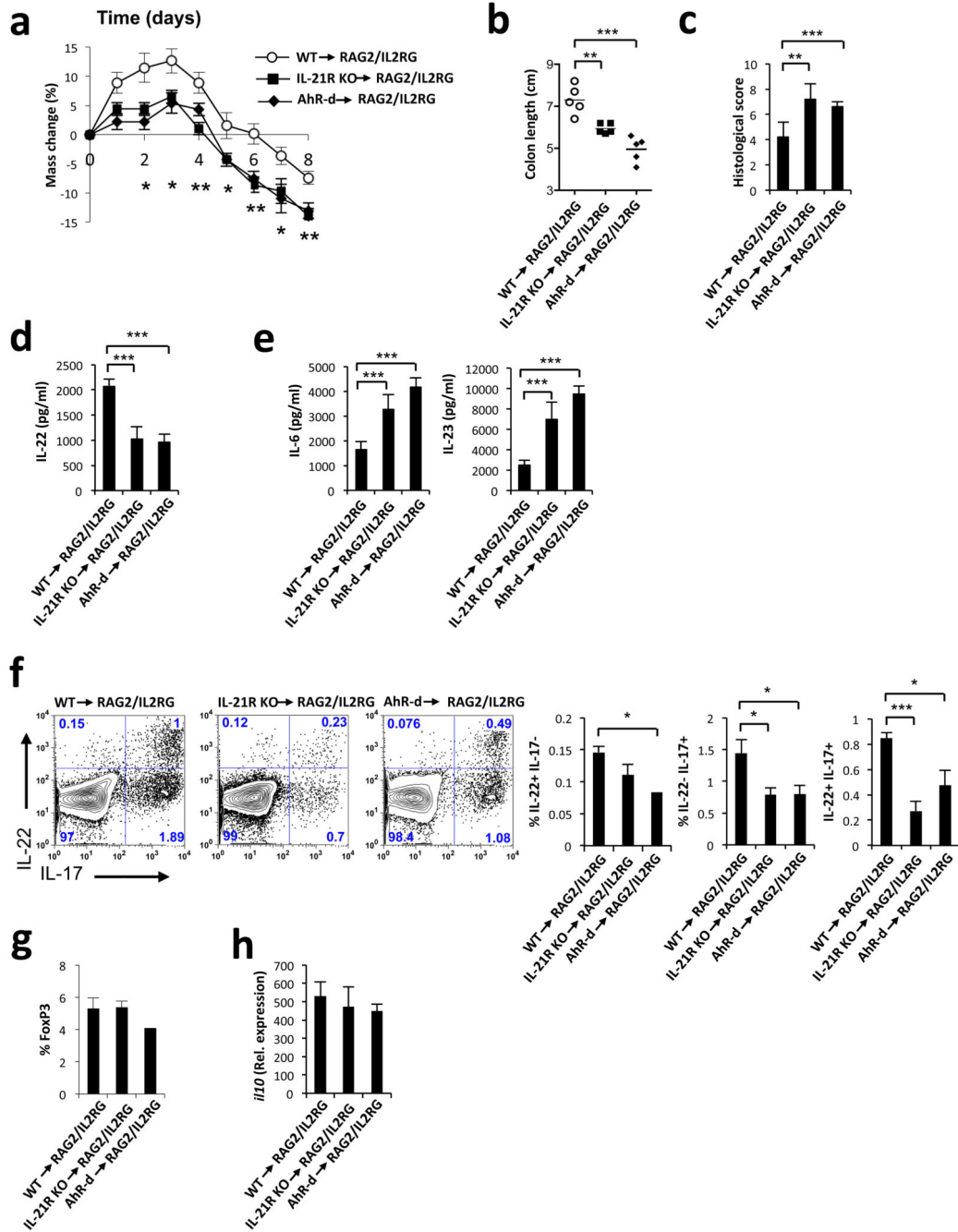


Figure 6. IL-21 and AhR control IL-22 + CD4+ T cells *in vivo* and limit mucosal inflammation
(a) RAG2/IL2RG mice transferred with WT, AhR-d or IL-21R deficient CD4+ T cells were given 3 % DSS *ad libitum* in their drinking water for 7 days. Body weight was assessed daily, and the percent mass change from day 0 was calculated. Mean ± s.e.m is shown, $n=5$ mice per group. Effect of genotype on disease course $P<0.0001$, $*P<0.01$ by two-way ANOVA. **(b)** Colon length at day 7 after treatment with DSS. **(c)** Colonic histological sections were scored as described in Methods. Values are mean ± s.e.m. **(d-e)** Colons were excised on day 7 after the initiation of treatment with DSS, cultured for 3 days and IL-22

(**d**), IL-6 and IL-23 (**e**) were quantified in the supernatants by ELISA. (**f-h**) Lymphocytes from the colonic lamina propria (LPL) were isolated. The frequency of IL-22+IL17-, IL-22+IL-17+, IL-22-IL-17+ T cells (**f**) and FoxP3+ Tregs (**g**) was analyzed by FACS and the expression of *il10* was measured by qPCR (**h**). mRNA expression is shown relative to the expression of *gapdh*. Results are representative of 3 independent experiments. * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$ (one-way ANOVA and two-way ANOVA).