Title: Tuft cell-derived acetylcholine regulates epithelial fluid secretion

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Abstract:

Tuft cells are solitary chemosensory epithelial cells that can sense lumenal stimuli at mucosal barriers and secrete effector molecules to regulate the physiology and immune state of their surrounding tissue. In the small intestine, tuft cells detect parasitic worms (helminths) and microbe-derived succinate, and signal to immune cells to trigger a Type 2 immune response that leads to extensive epithelial remodeling spanning several days. Acetylcholine (ACh) from airway tuft cells has been shown to stimulate acute changes in breathing and mucocilliary clearance, but its function in the intestine is unknown. Here we show that tuft cell chemosensing in the intestine leads to release of ACh, but that this does not contribute to immune cell activation or associated tissue remodeling. Instead, tuft cell-derived ACh triggers immediate fluid secretion from neighboring epithelial cells into the intestinal lumen. This tuft cell-regulated fluid secretion is amplified during Type 2 inflammation, and helminth clearance is delayed in mice lacking tuft cell ACh. The coupling of the chemosensory function of tuft cells with fluid secretion creates an epithelium-intrinsic response unit that effects a physiological change within seconds of activation. This response mechanism is shared by tuft cells across tissues, and serves to regulate the epithelial secretion that is both a hallmark of Type 2 immunity and an essential component of homeostatic maintenance at mucosal barriers.

Introduction:

The physiologic function and immune defense of mucosal tissues require fluid secretion, and epithelial cells employ multiple independent mechanisms to regulate this process. For example, cyclic AMP (cAMP) induces apical chloride (Cl⁻) secretion from epithelial cells through cystic fibrosis transmembrane conductance regulator (CFTR).[1] The resulting ionic gradient draws Na^+ and then water out of the tissue and into the lumen, where it hydrates mucus and can contribute to epithelial "flushing".[2,3] Loss-of-function mutations in CFTR cause cystic fibrosis, a disease characterized by viscous mucus, reduced lung function, and bacterial overgrowth.[1] Epithelial Cl⁻/water secretion can also occur via calcium-dependent ion channels, with muscarinic acetylcholine receptors (mAChR) in the basolateral membrane often inducing the necessary intracellular calcium flux.[2] Acetylcholine (ACh) is a canonical neurotransmitter synthesized by the enzyme choline acetyltransferase (*Chat*). Neurons innervating mucosal barriers can induce ACh-dependent fluid secretion, but non-neuronal sources of ACh have now been widely reported in other contexts.[3–7]

Among epithelial cells, tuft cells are the dominant source of ACh.[8,9] Found across mucosal tissues, they are a lineage of chemosensory cells that monitor the lumenal microenvironment and release effectors to regulate the mucosa. *Chat* expression is part of a transcriptional signature shared by all murine tuft cells[10,11] and ChAT protein has been detected in human tuft cells in the intestine and airways.[12,13] The function of tuft cell-derived ACh has also been studied in several tissues. For example, tuft cells in the nasal epithelium sense bitter and bacteria-derived ligands[14] and secrete ACh, which signals on neurons to induce neurogenic inflammation.[15] Tracheal tuft cells activate nicotinic ACh receptors (nAChRs) to cause a brief cessation in breathing[16] and mAChRs on neighboring epithelial cells to increase ciliary beat frequency[8,17] in response to similar ligands. Likewise, tuft cells in the urethra use ACh to activate neurons and regulate urine release.[18,19] However, the function of tuft cell-derived ACh in the intestine is unknown, nor has a link between tuft cells and fluid secretion been tested.

Small intestinal (SI) tuft cells play a critical role in the initiation of "Type 2" immune responses to helminth infection and colonization by *Tritrichomonas sp.*

protists.[20,21,22] Tuft cells express SUCNR1, the receptor for extracellular succinate,

which *Tritrichomonas sp.* and the microbiota secrete as a metabolite.[11,23,24] SUCNR1

signaling causes intracellular Ca^{2+} flux that opens the cation channel TRPM5. The

resulting Na^+ influx depolarizes the tuft cell and likely regulates secretion of most tuft

cell effector molecules.[25,26] *Sucnr1$^{-/-}$* mice fail to detect *Tritrichomonas sp.* colonization,

but the immune response to helminth infection is unaffected.[11,24] Nonetheless, sensing

of both helminths and protists is severely attenuated in *Trpm5$^{-/-}$* mice or *Pou2f3$^{-/-}$* mice

that lack tuft cells entirely.[11,20,22]

Once activated by lumenal signals, tuft cells produce IL-25 and, in some cases,

leukotriene C4 (LTC$_4$) to activate resident group 2 innate lymphoid cells (ILC2s) in the

underlying *lamina propria* (LP).[21,27] ILC2s secrete canonical Type 2 cytokines, including

IL-13, that collectively recruit Type 2 immune cells and coordinate intestinal remodeling.

Among its many targets, IL-13 produced by ILC2s signals on undifferentiated epithelial

cells to bias differentiation towards mucus-producing goblet cells and tuft cells.[20,21,28,29]

Given the 3-5 day turnover of the intestinal epithelium, this feed-forward process, known

as the tuft-ILC2 circuit, results in dramatic hyperplasia of both goblet cells and tuft cells,

the latter of which increase 10-fold.[20,21,22]

The Type 2 effector functions that clear worms from the intestine,[30,31] collectively

referred to as "weep and sweep," require the coordination of multiple signals. In addition

to increasing the number of tuft and goblet cells, IL-13 upregulates production of mucus

and anti-helminthic/microbial peptides in the epithelium,[32,33,34] increases fluid

secretion,[35] and increases expression of mAChRs on smooth muscle,[36,37,38] but actual

secretion ("weep") and muscle contraction ("sweep") generally require additional

signals. ACh is one molecule that can acutely activate both weep and sweep,[38] and

mAChRs are required for helminth clearance.[39,40] Conversely, helminths secrete ACh

esterases (AChE), likely in an attempt to inhibit weep and sweep responses.[41,42,43] The

sources of ACh in Type 2 immunity, however, are not defined.

By sensing lumenal signals and activating ILC2s, tuft cells serve as sentinels for

intestinal Type 2 immunity, but the fact that many more tuft cells are generated after the

agonist has been detected suggests an additional effector function for these cells. Here

we describe such an effector function, which is independent of ILC2s. We show that in

response to sensing of succinate or direct activation of TRPM5, tuft cells secrete ACh to
induce epithelial fluid secretion in the intestine and airways. During Type 2 tissue
remodeling, *Chat*+ tuft cells increase in number, enhancing the fluid secretion response.
Upon helminth infection, mice with *Chat*-deficient tuft cells experience delayed helminth
clearance despite normal tuft-ILC2 circuit activation. We conclude that tuft cell-derived
ACh regulates epithelial fluid secretion, and that this effector function can contribute to
Type 2 immune responses during helminth infection.
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Results:
SI tuft cells express Chat in a proximal to distal gradient
Neuronal *Chat* is important for intestinal function, but the role of *Chat* in intestinal
tuft cells has not been studied. To assess *Chat* expression by tuft cells in the SI at
single cell resolution, we employed *Chat-GFP* transgenic reporter mice. Immunolabeling
for GFP colocalized with the tuft cell marker DCLK1 in both the proximal SI (pSI; first 5-
10 cm) and distal SI (dSI; last 5-10 cm) (Fig. 1A). By flow cytometry, >99% of GFP+
epithelial cells stained for the tuft cell-specific *Il25-RFP* reporter (Fig. 1B). However, not
all tuft cells were GFP+ (Fig. S1A), and we observed a gradient in the frequency of
GFP+ tuft cells that increased from 40% of all tuft cells in the pSI to 80% in the dSI (Fig.
1C-D). The discovery of GFP-negative tuft cells was unexpected, as the *Chat* reporter
marks nearly 100% of tuft cells in other tissues.[8] To validate our findings, we crossed
Chat-Cre mice, in which Cre is expressed from the endogenous *Chat* locus, to
Rosa26::STOP^fl/fl::CAG-tdTomato (Ai9) mice for lineage tracing. Using CD24 and
Siglec-F to identify tuft cells, we again observed both reporter-positive and -negative tuft
cells, with an increased frequency of reporter-positive tuft cells in the distal compared to
the proximal SI (Fig. S1B).

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Figure 1: SI tuft cells express *Chat* in a proximal to distal gradient. (**A**) Representative images of
GFP(*Chat*) expression (green) by DCLK1+ tuft cells (magenta) in the proximal SI (pSI) and distal SI (dSI)
by immunofluorescence. White arrows indicate GFP(*Chat*)- tuft cells. Nuclei stained with DAPI (blue).
Scale bars: 50 μm (**B**) GFP+ epithelial cells (EpCAM+) are RFP(*Il25*)+ tuft cells. (**C** and **D**) (C)
Representative flow cytometry and (D) quantification of the percentage of GFP+ tuft cells by sequential 7
cm section across the length of the SI. In D, each symbol represents an individual mouse (columns
represent different tissues from same mouse) from three pooled experiments. *p < 0.05, **p < 0.01, ***p <
0.001 by one way ANOVA with Tukey's multiple comparisons test (D). mSI, medial SI. Graphs depict
mean +/- SEM. Also see Figure S1.

Given the binary nature of *Chat-GFP* expression in SI tuft cells, we hypothesized

that *Chat* might mark transcriptionally distinct tuft cell subsets. We therefore sorted

GFP+ and GFP- tuft cells, performed bulk RNA sequencing, and identified differentially

expressed genes (DEGs) (Fig. S1C, Table S1, Data File S1). Surprisingly, despite the

binary nature of GFP expression, *Chat* was downregulated only 2.8-fold (FDR = .0009)

in GFP- cells, suggesting translation is regulated via untranslated regions of the

endogenous *Chat* transcript that are retained in the transgene (Fig. S1C). More broadly,

even with a lenient fold-change (FC) cutoff of 2 (FDR <.01), there were only 105 DEGs.

None of the downregulated genes were part of the SI tuft cell signature,[44] but *Sucnr1*

(FC = 3.3, FDR = .0007) and the downstream G alpha subunit *Gnat3* (FC = 4.9, FDR =

.0001) were upregulated in GFP+ cells (Fig S1C, Table S1). Comparing *Chat*+ tuft cells

to previously reported intestinal tuft cell subsets "Tuft-1" and "Tuft-2",[9] we found greater

enrichment for Tuft-2 genes (Fig. S1D), but the best match was with a dSI tuft cell

signature we generated by sorting tuft cells from the proximal and distal 5 cm of

unmanipulated intestines (Fig. S1D-E, Table S2, Data File S2). This signature similarly

includes *Sucnr1* and *Gnat3,* and we hypothesize that transcriptional differences

between GFP+ and GFP- cells resulted mostly from a distal bias among sorted GFP+

cells, consistent with the gradient we observed (Fig. 1D).

We also considered the possibility that *Chat*- cells were an immature stage

before *Chat*+ cells, but while GFP+ cells predominated in the villi and GFP- cells in the

crypts, there were still GFP+ cells in the crypts (Fig. S1F) and GFP- cells at the villus

tips (Fig. S1G), making a developmental relationship unlikely. Both IL4ra-dependent

and IL4ra-independent tuft cells have been identified in the SI,[45] but we found many

Chat-GFP+ tuft cells in the SI of *Il4ra*^{-/-} mice, suggesting *Chat* expression is not

exclusive to IL-13-induced tuft cells (Fig. S1H). The mechanisms regulating *Chat*

expression in tuft cells therefore remain unknown.

Supplemental Figure 1: (**A**) Quantification of GFP+ tuft cells (RFP+) from pSI and dSI of *Chat-*

GFP;*Il25*[RFP/+] mice by immunofluorescence (IF). (**B**) Representative flow cytometry of traced tdTom+ tuft

cells (CD24+, Siglec-F+) from pSI and dSI of wild-type (WT) and *Ai9;Chat-Cre* mice. (**C**) Volcano plot

showing log2FC of genes expressed in *Chat*+ tuft cells (n=4) versus *Chat*- tuft cells (n=3) sorted from

whole SI of *Chat-GFP*;*Il25*[RFP/+] mice. (**D**) Gene set enrichment analysis comparing *Chat*+ tuft cell gene

expression to Tuft-1 and Tuft-2 consensus gene signatures and the dSI tuft cell signature from (**E**)

Volcano plot showing log2FC of genes expressed in tuft cells sorted from the dSI (n=4) versus tuft cells

sorted from the pSI (n=4) of B6 mice. (**F**) Representative immunofluorescence image showing GFP+

(green) tuft cells (RFP+, magenta) in the SI crypt (solid white arrows), next to one GFP- tuft cell (open

white arrow). Nuclei stained with DAPI (blue). Scale bars: 50 µm. (**G**) Representative

immunofluorescence image showing a GFP- (green) tuft cell (DCLK1+, magenta) at the villus tip (open

white arrow), past other GFP+ tuft cells (solid white arrows). Nuclei stained with DAPI (blue). Scale bars:

50 µm. (**H**) Quantification of GFP(*Chat*)+ tuft cells (DCLK1+) from denoted tissues of *Il4ra*^{-/-}*;Chat-GFP*

mice by immunofluorescence. In the graphs, each symbol represents an individual mouse (columns

represent different tissues from same mouse) from two pooled experiments. *p < 0.05, **p < 0.01, ***p <

0.001 by Mann-Whitney test (A) or one way ANOVA with Tukey's multiple comparisons test (G). mSI,

medial SI. Graphs depict mean +/- SEM.

ACh from tuft cells induces fluid secretion from the SI epithelium

ACh rapidly induces fluid, mucus, and antimicrobial peptide secretion when it

binds muscarinic ACh receptors (mAChRs) on SI epithelial cells.[4,46,47,48] Classically,

enteric neurons are considered the primary source of ACh that regulates SI

secretion,[4,49,50] but we hypothesized that tuft cells could link lumenal chemosensing to

epithelial secretion via basolateral release of ACh.

To make sensitive, real-time measurements of SI epithelial electrophysiology, we

employed Ussing chambers,[51] which have been used to measure ACh-induced

epithelial ion flux.[52] Two chambers containing physiologic buffer are separated by a

piece of SI epithelium and the voltage across the epithelium is clamped. When

negatively charged ions (e.g. Cl^-) are secreted into the lumenal chamber, current is

injected into the basolateral chamber to restore the voltage (Fig. 2A). This "short-circuit"

current, or Isc, is directly proportional to ion flux.[51]

To test whether tuft cells regulate ion flux, we mounted SI tissue from

unmanipulated mice in the Ussing chamber and stimulated with Na_2-succinate

(succinate), since it is the best-defined ligand for SI tuft cells.[11,23,24] When we stimulated

the lumenal side of the SI tissue with 10 mM succinate, we recorded a rapid increase in

the Isc that lasted several minutes before returning close to baseline (Fig. 2B). We

quantified this response by measuring the change in Isc from the baseline before

stimulation to its peak, known as the delta Isc (ΔIsc; see Fig. 2B inset). To control for

the addition of sodium, we tested NaCl at an equimolar concentration of sodium (20

mM). NaCl was sufficient to increase the Isc, but the response was

significantly smaller than the succinate response and failed to return to baseline. The

succinate response, on the other hand, had similar kinetics to the response elicited by

the ACh mimic carbachol (CCh), given basolaterally to maximally stimulate mAChRs

(Fig. 2B). The succinate response was greatly diminished in SI from $Sucnr1^{-/-}$ mice,

though a residual, likely sodium-dependent increase remained (Fig. S2A). To avoid the

sodium response, we used the synthetic SUCNR1 agonist cis-epoxysuccinic acid

(cESA),[53] which stimulated an Isc response comparable to succinate, but that was

entirely $Sucnr1$-dependent (Fig. S2A). We used cESA in place of succinate for most of

the subsequent Ussing experiments.

To further characterize the succinate/cESA Isc response, we began by testing

the role of epithelial polarity. cESA induced ion flux when given lumenally, but not

basolaterally, consistent with lumenal restriction of SUCNR1 in tuft cells (Fig. S2B).

Conversely, CCh stimulated ion flux when given basolaterally, but not lumenally,

consistent with basolateral restriction of mAChRs on intestinal epithelial cells (IECs).[4]

Since the Isc represents net ion flux across the epithelium, the increased Isc response

to succinate could be due to either increased lumenal secretion of negatively charged

anions (e.g. Cl^-, $HCO3^-$) or increased absorption of positively charged cations (e.g. Na^+,

K^+) from the lumen.[4] To test the contribution of Cl^- ions selectively, we replaced Cl^- with

gluconate, which cannot cross the epithelium,[51,54] and found that both the cESA and

CCh responses were abrogated (Fig. 2C). Bumetanide, an inhibitor of the basolateral

chloride transporter NKCC1 that is required for sustained Cl^- secretion,[1] likewise

decreased the response to cESA (Fig. S2C).

Figure 2: Tuft cell-derived ACh induces epithelial fluid secretion. (**A**) Ussing chamber schematic. (**B**)

Average Isc traces and quantification of the delta Isc (ΔIsc, see inset and bar graph) of WT dSI tissue

stimulated as indicated (10 mM Na_2-succinate and 20 mM NaCl, lumenal; 100 µM CCh, basolateral). (**C**)

ΔIsc values of WT dSI in presence of normal chloride- (Cl⁻) containing buffer or buffer selectively lacking

Cl⁻, stimulated as indicated (10 mM cESA, lumenal). (**D**) ΔIsc values of WT intact dSI compared to

stripped dSI and dSI pretreated 15 min with TTX (1 μM, basolateral), stimulated as indicated. (**E**) ΔIsc

values of dSI from mice of indicated genotypes stimulated as indicated. (**F**) ΔIsc values of WT dSI

compared to dSI pretreated 15 min with pan-CHRM inhibitor atropine (10 μM, basolateral), stimulated as

indicated. (**G** and **H**) ΔIsc values of dSI with (G) epithelial cell- (*Vil1-Cre*) and (H) tuft cell-specific

(*Pou2f3^{ERT2-Cre/+}*) *Chat* deletion, stimulated as indicated. (**I**) Model of tuft cell chemosensing of succinate

driving ACh-dependent fluid secretion independent of neurons. (**J**) ΔIsc values of WT pSI and dSI

stimulated as indicated. (**K**) Average Isc traces of pSI from WT or *Trpm5^{-/-}* mice stimulated as indicated (5

μM C8, basolateral). (**L** and **M**) ΔIsc values of WT tissues compared to (L) tissues from indicated

genotypes or (M) tissues pretreated 15 min with atropine (10 μM, basolateral), stimulated as indicated. In

the graphs, each symbol represents an individual mouse (one tissue or average of two) pooled from two

or more experiments. Groups represent sequential stimulations of the same tissue. *p < 0.05, **p < 0.01,

***p < 0.001, ****p < 0.001 by RM one way ANOVA with Tukey's multiple comparisons test (B), two way

ANOVA with Dunnett's multiple comparisons test (D, E, L), multiple Mann-Whitney tests with Holm

Sídák's multiple comparisons test (C, F, G, H, M). ns, not significant. Graphs depict mean +/- SEM. Also

see Figure S2.

Since enteric neurons are both a major source of ACh and major regulators of

fluid secretion in the intestine, we investigated the possibility that SI tuft cells activate

enteric neurons. Studies of *Chat*+ tuft cells in the airways have emphasized their close

contact with neurons and provided evidence that signaling can occur from tuft cells to

neurons, often via release of ACh.[15,16] We therefore looked for similar tuft-neuronal

connections by microscopy using the *Chat-GFP* reporter, which marks cholinergic

intestinal neurons as well as tuft cells. We found some instances where a GFP+ tuft cell

was approached by a GFP+ neuron, but we never saw neurons extend into the

epithelium and contact tuft cells, as they do in the airways (Fig. S2D). *Chat*+ neurons

represent only a subset of total intestinal neurons,[55] yet staining for the pan-neuronal

marker BIII tubulin (TUJ1) revealed no additional neuronal contacts (Fig. S2E),

suggesting that neuronal contacts with tuft cells, much less "synapses", are uncommon

in the SI.

Recognizing that signaling can occur without direct contact, we experimentally

tested the requirement for neurons in the succinate response. First, we disrupted

neuronal integrity by physically "stripping" the submucosa off the back of the epithelium

to eliminate most of the submucosal and all of the myenteric neuronal plexuses.[51]
Alternatively, we used tetrodotoxin (TTX) to inhibit neuronal action potentials in intact SI
tissue.[4] Neither treatment reduced the cESA or CCh responses; in the stripped tissue
the CCh response was instead increased, likely due to enhanced diffusion (Fig. 2D).
Altogether, our data show that succinate/cESA binds to SUCNR1 expressed apically on
epithelial cells and induces chloride-dependent fluid secretion, independently of enteric
neurons or submucosal tissue.
To confirm that tuft cells were the cells that sensed succinate/cESA to initiate the
secretion response, we stimulated dSI from tuft cell-deficient $Pou2f3^{-/-}$, and
chemosensing-deficient $Trpm5^{-/-}$ mice. As with SI tissue from $Sucnr1^{-/-}$ mice, tissues
from these mice failed to respond to cESA (Fig. 2E). Importantly, the CCh response was
intact in all knockout mice, demonstrating that the tissue's capacity for ACh-dependent
fluid secretion was unaltered. To test whether ACh was involved in the cESA response,
we pretreated the dSI with the pan-mAChR inhibitor atropine and found that this
completely blocked the cESA and CCh responses (Fig. 2F). Deletion of $Chat$ from IECs
using $Chat^{fl/fl};Vil1-Cre(Tg+)$ mice also abrogated the cESA response (Fig. 2G). Although
tuft cells are the only $Chat$-expressing IECs, we also deleted $Chat$ in tuft cells
specifically using $Chat^{fl/fl};Pou2f3^{Cre-ERT2/+}$ mice, and confirmed that tuft cell-derived ACh
production was required for cESA-induced fluid secretion (Fig. 2H).
Other tuft cell effectors (e.g. LTC_4 or PGD_2) have been implicated in acute responses
and tuft cells themselves express the receptor for IL-25,[11,56,57] but we excluded the
involvement of IL-25 and LTC_4 in ion flux using dSI from $Il25^{-/-}$ and $Alox5^{fl/fl};Vil1-$
$Cre1000(Tg+)$ mice, respectively (Fig. S2F,G). Pretreatment with the COX inhibitor
ibuprofen to block PGD_2 synthesis also did not affect the cESA response (Fig. S2H).
Furthermore, PGD_2, which has not been previously linked with fluid secretion but has
been reported to induce mucus secretion from goblet cells (GCs) in the colon,[56] did not
induce ion flux in the dSI (or the colon) when administered basolaterally (Fig. S2I). We
also investigated the possibility that tuft cells were signaling to neighboring cells via gap
junctions.[58] The gap junction inhibitor carbenoxolone partially blocked cAMP-driven fluid
secretion induced by IBMX + forskolin, but had no effect on cESA or CCh responses
(Fig. S2J). Thus, we have demonstrated that tuft cells in the dSI sense lumenal

succinate/cESA and release ACh basolaterally, which stimulates mAChR-dependent Cl⁻

ion secretion (Fig. 2I). The response is epithelium-intrinsic and does not involve enteric

neurons.

Supplemental Figure 2: (**A**) Average Isc traces of dSI from WT or *Sucnr1*^{-/-} mice stimulated as indicate

(Na$_2$-succinate and cESA, lumenal). (**B**) ΔIsc values of WT dSI stimulated as indicated. (**C**) ΔIsc values of

WT dSI pretreated 15 min with vehicle or bumetanide (100 µM, basolateral), stimulated as indicated (10

mM cESA lumenal; 100 µM CCh, basolateral). (**D**) Representative immunofluorescence image of a GFP+

(green) neuronal process (indicated by solid white arrow) approaching a GFP+/RFP+ (magenta) tuft cell

from the dSI of *Chat-GFP;Il25*[*RFP/+*] mice. Nuclei stained with DAPI (blue). Scale bars: 50 µm. (**E**)

Representative immunofluorescence image of GFP+ (green) neurons co-stained for BIII tubulin (TUJ1,

magenta) in the dSI. Nuclei stained with DAPI (blue). Scale bars: 50 µm. (**F**, **G**, and **H**) (F and G) ΔIsc

values of dSI from indicated genotypes or (H) WT dSI compared to dSI pretreated 15 min with ibuprofen

(10 µM, bilateral), stimulated as indicated. (**I**) ΔIsc values of WT tissues stimulated as indicated (PGD$_2$,

basolateral). (**J**) ΔIsc values for WT dSI compared to dSI pretreated 15 min with carbenoxolone (1 mM,

lumenal), stimulated as indicated (100 µM IBMX + 10 µM forskolin, bilateral). (**K**) ΔIsc values of WT pSI

stimulated as indicated (100 µM N-C11-G, lumenal). (**L**) Representative immunofluorescence image of

GFP+ (green) tuft cells expressing HA+ Gq-DREADDs (magenta) in the crypts and villi of the medial SI

(mSI). Nuclei stained with DAPI (blue). Scale bars: 50 µm. (**M**, **N**, and **O**) (M) ΔIsc values of indicated

tissues from unmanipulated mice or (N and O) indicated tissues from mice 7 days after start of tamoxifen

chow, stimulated as indicated (1 µM C21, bilateral). (**P**) ΔIsc values of WT pSI stimulated as indicated

(C8, bilateral). (**Q**) ΔIsc values of WT tissues from pSI and dSI stimulated as indicated. (**R**) Average Isc

traces of dSI stimulated as indicated (5 µM C8, basolateral). (**S**) Average Isc traces and ΔIsc values of

pSI stimulated as indicated (2.5 µM C8, basolateral). In the graphs, each symbol represents an individual

mouse (one tissue or average of two) pooled from two or more experiments. Groups represent sequential

stimulations of the same tissue. In (C) paired vehicle and bumetanide-treated tissues are from the same

mouse. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.001 by multiple Mann-Whitney tests with Holm

Sídák's multiple comparisons test (B, F-H, J, M-O, S), Wilcoxon matched-pairs signed rank test with Holm

Sídák's multiple comparisons test (C), or Mann-Whitney test (Q). ns, not significant. Graphs depict mean

+/- SEM.

A TRPM5 agonist induces tuft- and ACh-dependent fluid secretion in the pSI and

dSI

In characterizing the succinate response, we found that the pSI did not respond

to succinate stimulation (Fig. 2J). This finding is consistent with greater succinate

receptor (*Sucnr1*) expression in tuft cells from the dSI compared to the pSI (Table S2),[23]

and may also reflect the reduced frequency of *Chat*+ tuft cells in the pSI (Fig. 1D). Since

the pSI was responsive to CCh, we reasoned that pSI tuft cells could induce fluid

secretion if properly stimulated. We first tested several putative tuft cell ligands. Worm

excretory and secretory products from *Nippostrongylus brasiliensis* (*Nb*), known as

NES, failed to stimulate ion flux whether made from infective L3 larvae or adult worms

(data not shown). The bacterial metabolite N-C11-G did not induce ion flux either (Fig.

S2K). Next, we tried a chemogenetic approach with Gq- or Gi-coupled receptors that

respond only to synthetic ligands (DREADDs)[59] using constitutive (*Il25-Cre*) or inducible

(*Pou2f3^Cre-ERT2/+*) for tuft cell-specific expression. Although tuft cells expressed the HA

tag included in the DREADD constructs, stimulation with Compound 21[60] was

insufficient to drive a fluid secretion response in the pSI or dSI (Fig. S2L-O). Perhaps G

proteins required for DREADD function are not available in tuft cells or the signals

induced downstream of DREADD activation are not sufficient to induce ACh release.

Finally, we decided to stimulate TRPM5 directly, since all tuft cell chemosensing

pathways identified to date converge on TRPM5. We acquired a TRPM5 agonist

compound called Class 8 (C8),[61,62] and found that it induced ion flux in both the pSI and

dSI when administered lumenally or basolaterally, with a trend toward higher basolateral

responses (Fig. 2K, S2P-Q). The C8 response was similar to cESA- or CCh-induced ion

flux, and was TRPM5-dependent in the pSI and dSI (Fig. 2K-L, S2R). The C8 response

was also tuft cell- and ACh-dependent in both locations (Fig. 2L-M). In the pSI, C8

induced a slow TRPM5-independent increase in Isc (Fig. 2K), but this off-target effect

could be eliminated by lowering the dose of C8 (Fig. S2S). We conclude that in

response to direct TRPM5 activation, tuft cells in the pSI and dSI can release ACh to

induce fluid secretion from the intestinal epithelium.

Tuft cell-mediated fluid secretion occurs across mucosal tissues and is

detectable in vivo

We previously found that *Sucnr1* expression is even higher in tracheal tuft cells

than those of the SI,[11] so to test if tuft cells regulate fluid secretion at multiple mucosal

barriers, we stimulated tracheal tissue in the Ussing chamber with succinate. As in the

dSI, we found that this induced a rapid increase in the Isc that was *Pou2f3*-, *Sucnr1*-,

and *Trpm5*-dependent (Fig. 3A-B). In addition, the response was mAChR-dependent

(Fig. 3C). By comparison, the cecum and colon, where tuft cells express *Sucnr1* at low

levels,[11] responded only weakly to succinate stimulation and in a tuft-independent

manner (Fig. S3A). Colonic tissue did respond to TRPM5 agonism with C8, with a larger

response in the proximal colon (pCol) than the distal colon (dCol) (Fig. 3D-E). The

reported tuft ligand N-C11-G[56] did not stimulate fluid secretion from the dSI or dCol (Fig.

S3B), and also failed to elicit tuft-dependent leukotriene production from intestinal

epithelial monolayers (Fig. S3C). Therefore, tuft cell control of epithelial fluid secretion is

a common effector function across barrier tissues.

The Ussing chamber measures ion flux but cannot measure water movement

directly. We therefore wanted to test if activating tuft cells *in vivo* could induce fluid

secretion into the intestine. We dosed mice with C8 or vehicle in the morning and then

measured the wet weight of fecal pellets 3 hours later. In mice given vehicle, the fecal

water content declined, likely due to reduced water intake during the day. C8 treatment

prevented this decline, indicating sustained fluid secretion (Fig. 3F). Importantly, this

fluid secretion was dependent on epithelial *Chat* (Fig. 3G, S3D). Thus, activation of tuft

cells along the intestinal tract induces ACh-dependent ion flux that drives fluid secretion

into the intestinal lumen.

Figure 3: *Tuft cell-mediated fluid secretion occurs across mucosal tissues and is detectable in*

vivo. (**A** and **B**) (A) Average Isc traces and (B) ΔIsc values of trachea from mice of indicated genotypes

stimulated as indicated (1 mM Na₂-succinate, lumenal; 100 μM CCh, basolateral). (**C**) ΔIsc values of WT

trachea compared to trachea pretreated 15 min with atropine (10 μM, basolateral), stimulated as

indicated. (**D** and **E**) Average Isc traces and ΔIsc values of WT and *Pou2f3⁻/⁻* tissues stimulated as

indicated (5 μM C8, basolateral). (**F** and **G**) Quantification of water content of fecal pellets collected from

(A) WT or (B) *Chat-fl;Vil1-Cre(Tg+)* mice treated orally with vehicle or C8 (30 mg/kg) for the indicated

durations. In the graphs, each symbol represents an individual mouse (one tissue or average of two)

pooled from two or more experiments. Groups represent sequential stimulations or timepoints of the same

tissue or animal. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, ****$p < 0.001$ by, two way ANOVA with Tukey's

multiple comparisons test (B), or multiple Mann-Whitney tests with Holm Sídák's multiple comparisons

test (C-G). ns, not significant. Graphs depict mean +/- SEM. Also see Figure S3.

Supplemental Figure 3: (**A**) ΔIsc values of WT and *Pou2f3*$^{-/-}$ tissues stimulated as indicated (10 mM Na$_2$-

succinate and 20 mM NaCl, lumenal; 100 µM CCh, basolateral). (**B**) ΔIsc values of WT tissues stimulated

as indicated (100 µM N-C11-G, lumenal). (**C**) Cysteinyl leukotriene (CysLTs) production from WT and

Pou2f3$^{-/-}$ SI epithelial monolayers stimulated as indicated. (**D**) Quantification of water content of fecal

pellets collected from indicated mice immediately after oral treatment with C8 (30 mg/kg). In the graphs,

each symbol represents an individual mouse pooled from two or more experiments. In (A-B) groups

represent sequential stimulations of the same tissue and in (C) groups represent individual monolayers.

*p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.001 by multiple Mann-Whitney tests with Holm Sídák's

multiple comparisons test (A, D), or multiple unpaired t tests with Holm Sídák's multiple comparisons test

(C). ns, not significant. Graphs depict mean +/- SEM.

Tuft cell-derived ACh is not required for ILC2 activation

Having defined ACh-dependent fluid secretion as a tuft cell effector function in

unmanipulated mice, we next considered the role of tuft cell-derived ACh during Type 2

immunity. Consistent with previous reports in the airways,[63] we found that tamoxifen

partially suppressed Type 2 responses in the intestine. For example, treating protist-

colonized $Chat^{fl/fl};Pou2f3^{Cre-Ert2/+}$ mice with tamoxifen for one week reduced tuft cell

counts by nearly half in both WT and Cre+ mice (Fig. S4A). The effect of tamoxifen was

less noticeable during helminth infection, perhaps because this induces more Type 2

inflammation (Fig. S4B). Nonetheless, given these non-specific effects of tamoxifen, we

focused on identifying $Chat$-dependent effects by analyzing $Chat$-sufficient and $Chat$-

deficient mice that had all been treated with tamoxifen.

Previously characterized SI tuft cell effector molecules (e.g. IL-25 and LTC_4)

have primarily been shown to regulate ILC2 activation.[21,27] Also, recent studies have

reported that ILC2s express $Chat$ following activation and that ACh can potentiate their

production of cytokines and proliferation, perhaps via autocrine signaling[64,65]. We

therefore asked if tuft cell-derived ACh was signaling to ILC2s in addition to inducing

fluid secretion. We began by testing if ACh could enhance ILC2 activation using an *in*

vitro model of acute (6-hour) ILC2 stimulation.[27] Pairing ACh with IL-25 to mimic the

results of tuft cell activation, we failed to detect any ACh-dependent ILC2 activation as

measured by IL-13 reporter expression and secretion of IL-13 and IL-5 (Fig. S4C-D). By

contrast, LTC_4 greatly enhanced ILC2 activation when given with IL-25, as expected.

We conclude that ACh does not induce cytokine expression in ILC2s sorted from

unmanipulated mice and is therefore unlikely to contribute to their initial activation.

Supplemental Figure 4: (**A**) Schematic of tamoxifen (TAM) treatment of protist-colonized *Chat-fl;*

Pou2f3^ERT2-Cre/+ mice and quantification of dSI tuft counts by immunofluorescence at D7 after start of

treatment. (**B**) Quantification of pSI tuft counts by immunofluorescence of WT mice treated with or without

tamoxifen and infected with *Nb* for 7 days. (**C** and **D**) (C) Flow cytometric quantification of percent hCD4+

(IL-13+) SILP ILC2s and (D) IL-13 and IL-5 concentration in their supernatant after 6 hr *in vitro* culture

with the indicated conditions (0.1 ng/mL rIL-25, serial 10-fold dilutions of ACh from 10 mM to 0.1 μM, 1

nM LTC$_4$). (**E** and **F**) Quantification of number of hCD4+ (IL-13+) ILC2s, total ILC2s, and percent ILC2s at

the indicated timepoints, tissues, and genotypes. (**G**) Quantification of dSI tuft counts by

immunofluorescence from indicated mice treated with 150 mM succinate drinking water for 7 days. (**H**) SI

length from indicated mice vertically-colonized with *T. rainier* protists with or without 7 days of additional

150 mM succinate drinking water treatment. (**I**) Schematic of acute deletion of *Chat* from vertically *T.*

musculis (*Tm*) -colonized mice and quantification of dSI tuft counts by immunofluorescence 5 days after

start of treatment. In the (A-B, E-I), each symbol represents an individual mouse from two or more pooled

experiments. In (C and D) each symbol represents a technical replicate of cells sorted from pooled mice.

*p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.001 by multiple Mann-Whitney tests with Holm Sídák's

multiple comparisons test (A, F, H) or Mann-Whitney test (B, E, G, I). ns, not significant. Graphs depict

mean +/- SEM.

To test if tuft cell-derived ACh was involved in ILC2 activation *in vivo* and at later

timepoints, we generated *Chat^{fl/fl};Pou2f3^{ERT2-Cre/+}* mice that also expressed an IL-13

reporter (Smart13). We treated these mice with tamoxifen, infected with *Nb*, and

assessed early ILC2 activation in the LP 4 days post infection (dpi), about 2 days after

the worms arrive in the intestine. We found no difference in ILC2 activation or expansion

(Fig. 4A, S4E). Since *Chat* has been detected in activated but not resting ILC2s, we

also tested if tuft cell-derived ACh regulated ILC2s later during infection. Given the

difficulty of isolating viable cells from Type 2 inflamed SI, we assessed ILC2s in the

mesenteric lymph nodes at 5 and 7 dpi. Again, we saw equivalent activation and

expansion of ILC2s between *Chat*-sufficient and -deficient mice (Fig. 4B, S4F). We

conclude that tuft cell-derived ACh does not contribute to ILC2 activation during

helminth infection of the SI.

Tuft cell-derived ACh is not required for Type 2 intestinal remodeling

An effective immune response to helminths requires intestinal remodeling, such

as hyperplasia of tuft cells and mucus-producing GCs and lengthening of the SI.[23,66] IL-

13 is critical for this process, but ACh might also contribute. For example, ACh has been

implied in direct modulation of epithelial cell differentiation,[67,68] and could also impact

tissue remodeling via other AChR-expressing cells, such as neurons.[55]

Using tuft cell frequency, goblet cell frequency, and intestinal length as markers

of SI remodeling, we found little or no defect 7 days after *Nb* infection of mice with either

constitutive (*Vil1-Cre(Tg+)*) or acute (*Vil1-Cre-Ert2(Tg+)*) deletion of *Chat* in IECs (Fig.

4C-E). The same was true both 5 and 7 days after *Nb* infection when we used *Pou2f3-*

Cre-ERT2 for tuft cell-specific *Chat* deletion (Fig. 4F-H). Since tuft cell circuits are

distinct in the pSI and dSI,[11,27] we also tested Type 2 remodeling in the dSI 4 and 7

days after starting treatment with succinate-supplemented drinking water. As before,

there was little effect of either constitutive or inducible IEC *Chat* deletion (Fig. 4I-K;

S4G). Likewise, *Chat^fl/fl;Vil1-Cre(Tg+)* mice vertically colonized with protists had no

defect in tuft cell hyperplasia or SI length at homeostasis or following one week of

additional succinate drinking water treatment (Fig. 4L, S4H). Acute loss of *Chat* in

protist-colonized *Chat^fl/fl;Vil1-Cre-ERT2(Tg+)* mice also had no effect on tuft cell

hyperplasia 5 days later (Fig. S4I). In sum, Type 2 remodeling is broadly intact in the

absence of tuft cell ACh. We did observe small but significant decreases in tuft cell

hyperplasia or SI lengthening in some assays, but this effect was inconsistent and

minimal compared to loss of other tuft cell effector molecules (e.g. IL-25 and LTC$_4$).[21,27]

Figure 4: Tuft cell-derived ACh is not required for ILC2 activation or intestinal remodeling. (**A** and

B) (A) Representative flow cytometry and quantification of percent hCD4⁺ (IL-13⁺) ILC2s (Lin⁻, CD45⁺,

KLRG1$^+$, CD4$^-$) in the SI LP and (B) mesenteric lymph nodes (MLN) at the indicated *Nb* infection

timepoints. (**C**, **D**, and **E**) (C) Quantification of pSI tuft cells (DCLK1+) and (D) goblet cells (WGA+) by

immunofluorescence and (E) total SI length from the indicated mice at D7 of *Nb* infection. (**F**, **G**, and **H**)

Same analysis as in C-E in the indicated mice at the indicated *Nb* infection timepoints. (**I**, **J**, and **K**) Same

analysis as in C-E in the indicated mice at the indicated timepoints of 150 mM succinate drinking water

treatment. (**L**) Quantification of tuft cells (DCLK1+) by immunofluorescence from indicated mice vertically-

colonized with *T. rainier* protists with or without 7 days of additional 150 mM succinate drinking water

treatment. In the graphs, each symbol represents an individual mouse from two or more pooled

experiments. For graphs of tuft cell counts, horizontal dashed line signifies baseline tuft cell count in

unmanipulated mice. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.001 by Mann Whitney test (A) or

multiple Mann-Whitney tests with Holm Sídák's multiple comparisons test (B-L). ns, not significant.

Graphs depict mean +/- SEM. Also see Fig. S4.

Tuft cell hyperplasia results in enhanced ACh-dependent fluid secretion

The ability of tuft cells to induce fluid secretion in the steady state led us to ask

how it would change during Type 2 inflammation, when tuft cell numbers can increase

10-fold and fluid secretion might support worm clearance as part of the canonical weep

and sweep response. First, we asked whether the number and frequency of *Chat*+ tuft

cells changed with Type 2 inflammation. While the frequency of *Chat*+ tuft cells

decreased (Fig. S5A), this was more than compensated for by the hyperplasia, such

that the total number of *Chat*+ tuft cells per millimeter crypt/villus was increased in the

pSI and especially the dSI 7 days after either succinate-treatment or *Nb*-infection (Fig.

5A).

Next, we infected mice with *Nb* to induce tuft cell hyperplasia and quantified the

fluid secretion response to succinate in the pSI and dSI across the course of infection.

Although pSI tuft cells do not respond to succinate at steady state, we wondered if

those that emerge during infection might be responsive. The pSI did not become

responsive to succinate (or cESA) over the course of infection, but the dSI succinate

response increased by day 7, when tuft cell numbers peaked (Fig. 5B, S5B-C). The

increased response to succinate was less than the ~3-fold increase of *Chat*+ tuft cells

that we observed on D7 of *Nb* infection, likely because the epithelium's total capacity to

respond to ACh/CCh was reduced by Type 2 inflammation, as previously reported (Fig.

5B).[69]

Figure 5: Tuft cell hyperplasia results in enhanced ACh-dependent fluid secretion. (**A**)

Quantification of GFP(*Chat*)+ tuft cells (*Il25*-RFP+) from the pSI and dSI of WT mice untreated, treated

with 150 mM Na₂-succinate drinking water (succinate), or infected with *N. brasiliensis* (*Nb*) for 7 days. (**B**)

ΔIsc values of dSI from WT mice infected with *Nb* for the indicated number of days and stimulated as

indicated (10 mM succinate, lumenal; 100 μM CCh, basolateral). (**C**) Ratio of succinate ΔIsc values to

CCh ΔIsc values of dSI from (B). (**D**) Ratio of succinate ΔIsc values to CCh ΔIsc values of dSI of indicated

mice 7 days after *Nb* infection. (**E**) Ratio of cESA ΔIsc values to CCh ΔIsc values of dSI from WT mice

treated with succinate (as in A) or vertically colonized with *T. rainier* (*Tr*) protists. (**F** and **G**) Ratio of C8

ΔIsc values to CCh ΔIsc values of pSI from (F) WT or (G) mice of indicated genotypes mice at indicated

timepoints after *Nb* infection. (**H**) Quantification of water content of fecal pellets collected at indicated

timepoints post *T. musculis* (*Tm*) colonization of WT mice. In the graphs, each symbol represents an

individual mouse pooled from two or more experiments. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.001

by two way ANOVA with Dunnett's multiple comparisons test (A), Mann-Whitney test (B, D, F-G), one way

ANOVA (C, E), or multiple Mann-Whitney tests with Holm Sídák's multiple comparisons test (H). ns, not

significant. Graphs depict mean +/- SEM. Also see Fig. S5.

This effect could be quantified by measuring the ratio of succinate-induced ∆Isc to CCh-
induced ∆Isc (Fig. 5C), highlighting how hyperplasia allows tuft cells to capture a greater
proportion of the total epithelial ACh response. We confirmed that the increased
succinate response on day 7 still required epithelium-derived ACh (Fig. 5D, S5D) and
did not occur without *Sucnr1* (Fig. S5E). Enhanced succinate/cESA-induced fluid
secretion was also observed if tuft cell hyperplasia was established with oral succinate
or *Tritrichomonas* colonization (Fig. 5E). We found that tuft cell hyperplasia induced by
Nb infection also increased C8-dependent fluid secretion in both the pSI and dSI, and
that this required epithelial *Chat* (Fig. 5F-G, S5F-K).
To further test the hypothesis that increased numbers of tuft cells drive increased
succinate-induced fluid secretion during Type 2 remodeling, we turned to Balb/c mice.
Unmanipulated Balb/c mice are nearly tuft cell-deficient in the dSI, but activation of
ILC2s with exogenous IL-25 increases tuft cell numbers (Fig. S5L).[44] Accordingly,
unmanipulated Balb/c dSI did not respond to cESA in the Ussing chamber, but
responsiveness was induced by rIL-25 treatment, indicating that increased numbers of
ACh-producing tuft cells were needed (Fig. S5M).
Lastly, to test if *in vivo* fluid secretion was enhanced during Type 2 remodeling,
we measured the fecal water content of protist-colonized mice. Compared to
uncolonized mice, mice colonized with the succinate-producing protist *T. musculis* had
increased fecal water content by 14 and 20 days after colonization (Fig. 5H). This
suggested that tuft cells were repeatedly responding to protist-derived succinate and
inducing fluid secretion. Thus, the increased number of *Chat*+ tuft cells induced during
SI Type 2 inflammation drives increased ACh-dependent fluid secretion despite an
overall desensitization of the tissue to ACh.

Supplemental Figure 5: (**A**) Quantification of percent GFP(*Chat*)+ tuft cells and RFP(*Il25*)+ tuft cells from
the pSI and dSI of WT mice untreated, treated with 150 mM Na₂-succinate drinking water (succinate), or
infected with *N. brasiliensis* (*Nb*) for the duration indicated. (**B**) ΔIsc values of pSI from WT mice infected
with *Nb* for the indicated number of days and stimulated as indicated (10 mM succinate, lumenal; 100 µM
CCh, basolateral). (**C**) Quantification of tuft cells (DCLK1+) by immunofluorescence from medial SI (mSI)
of mice in (B). (**D**) ΔIsc values of dSI from mice of indicated genotypes infected with *Nb* for 7 days and
stimulated as indicated. (**E**) ΔIsc values of *Sucnr1⁻/⁻* dSI with or without 7 day *Nb* infection, stimulated as
indicated. (**F-G**) ΔIsc values of (F) pSI and (G) dSI from WT mice with or without 7 day *Nb* infection,
stimulated as indicated. (**H**) Ratio of C8 ΔIsc values to CCh ΔIsc values in (G). (**I and J**) ΔIsc values of (I)

pSI and (J) dSI from mice of indicated genotype infected with *Nb* for 7 days, stimulated as indicated. (**K**)

Ratio of C8 ΔIsc values to CCh ΔIsc values from (J). (**L**) Quantification of tuft cells (DCLK1+) by

immunofluorescence in the mSI of mice of indicated genotypes treated as indicated. (**M**) ΔIsc values of

dSI from mice in (L) stimulated as indicated. In the graphs, each symbol represents an individual mouse

(one tissue or average of two) from two or more pooled experiments. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$,

****$p < 0.001$ by two way ANOVA with Dunnett's multiple comparisons test (A) two way ANOVA with

Tukey's multiple comparisons test (M), Mann-Whitney test (B, H, K), one way ANOVA with Tukey's

multiple comparisons test (C, L), or multiple Mann-Whitney tests with Holm Sídák's multiple comparisons

test (D-G, I-J). ns, not significant. Graphs depict mean +/- SEM.

Tuft cell ACh regulates helminth clearance but not protist colonization

There is little evidence to suggest that tuft cell sensing of *Tritrichomonas sp.* and

the resulting Type 2 immune response in the SI alter the total abundance of protists,[22]

but we wondered if tuft cell induced fluid secretion might instead regulate protist

localization along the length of the SI, with the goal of containing protists to the dSI and

cecum. We therefore assessed the abundance of protists across the pSI, dSI, and

cecum of vertically-colonized *Chat^{fl/fl};Vil1-Cre* mice (Fig. S6A), hypothesizing an

increase of protists in the pSI of *Chat*-deficient mice. Constitutive deletion of *Chat* in tuft

cells had no effect on protist abundance or localization across the SI or cecum (Fig.

S6B). Treating protist-colonized mice with succinate to amplify Type 2 immunity also did

not uncover a phenotype (Fig. S6B), and acute deletion of *Chat* for 5 days likewise

failed to alter protist abundance or localization (Fig. S6C). Thus, the physiologic function

of protist sensing by tuft cells remains unclear.

Supplemental Figure 6: (**A**) Representative flow cytometry of cecal contents from uncolonized and protist-colonized mice showing gating of protists by size. The "Large" gate contains *Tritrichomonas sp.* protists. (**B**) Quantification of total protists by flow cytometry in indicated tissues of vertically-colonized mice of indicated genotypes left untreated or given 150 mM Na$_2$-succinate in drinking water for 7 days. (**C**) Quantification of total protists by flow cytometry in indicated tissues of vertically-colonized mice of indicated genotypes administered tamoxifen 5 days prior to analysis. (**D**) Quantification of total SI *Nb* in mice of indicated genotype infected with *Nb* for 7 days without tamoxifen administration. (**E** and **F**) (E) Quantification of tuft cells (DCLK1+) by immunofluorescence and (F) total SI length 8 days post *Nb* infection of mice of indicated genotype given a single dose of tamoxifen (125 mg/kg) on day 5. In the graphs, each symbol represents an individual mouse (one tissue or average of two) from two or more pooled experiments. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.001 by multiple Mann-Whitney tests with

On the other hand, the requirement for tuft cell sensing and downstream Type 2

immunity for clearing helminths from the SI is well established.[11,20,45] To test if tuft cell

ACh contributes to helminth clearance, despite not impacting ILC2 activation or tissue

remodeling, we assessed worm burden in mice lacking epithelial *Chat* at 7 dpi, a

timepoint when WT mice begin to clear worms from the SI. Indeed, both constitutive and

acute deletion of epithelial *Chat* led to an increased SI worm burden (Fig. 6A). Tuft-

specific *Chat* deletion using *Pou2f3-Cre-Ert2* led to the same clearance delay 7 dpi (Fig.

6B). Worm burdens were equivalent in CRE-positive and -negative mice 5 dpi,

suggesting normal colonization of the SI by *Nb* arriving from the lung. The delayed

clearance was also not due to the loss of one *Pou2f3* allele in *Chat*^{fl/fl}*;Pou2f3*[Cre-ERT2/+]

mice as they cleared worms normally when not treated with tamoxifen (Fig. S6D). In

order allow initiation of type 2 remodeling to proceed normally and delete tuft cell ACh

only during worm clearance, we waited until 5 dpi to administer a single dose of

tamoxifen to *Chat*^{fl/fl}*;Vil1-Cre-ERT2* mice. Consistent with our earlier observation that

tamoxifen suppresses intestinal Type 2 immunity, worm clearance in WT mice was

delayed to day 8, but we again found a *Chat*-dependent delay in worm clearance

despite normal intestinal remodeling. (Fig. 6C, Fig. S6E-F). Thus, we propose that tuft-

cell derived ACh contributes to worm clearance by the induction of epithelial fluid

secretion.

Figure 6: Tuft cell-derived ACh contributes to helminth clearance. (**A** and **B**) Quantification of total SI

Nb in mice of indicated genotypes at (A) 7 or (B) indicated days post infection. (**C**) Quantification of total

SI *Nb* 8 days post infection in mice of indicated genotypes given single dose of tamoxifen on D5. In the

graphs, each symbol represents an individual mouse pooled from two or more experiments. *p < 0.05,

**p < 0.01, ***p < 0.001, ****p < 0.001 by Mann-Whitney test (A, C), or multiple Mann-Whitney tests with

Holm Sídák's multiple comparisons test (B). ns, not significant. Graphs depict mean +/- SEM. Also see

Fig. S6.

Discussion

This study identifies an epithelium-intrinsic response unit that couples tuft cell

chemosensing to epithelial fluid secretion via the release of ACh from tuft cells. This

effector function is common to tuft cells in multiple tissues and is executed within

seconds of activation. In the SI, tuft cell-derived ACh is required for timely clearance of

helminth infection, but unlike all previously identified tuft cell effector functions, tuft cell-

derived ACh does not impact ILC2 activation nor downstream intestinal remodeling.

Instead, it appears that tuft cell ACh provides an acute signal that contributes to the

weep and sweep responses that push worms out of the intestine. The magnitude of tuft

cell-dependent fluid secretion correlates with the number of *Chat*+ tuft cells, suggesting

one possible function for the tuft cell hyperplasia that occurs even after initial sensing of

the helminth has been achieved.

Some details of tuft cell-regulated fluid secretion remain unresolved. For

example, we do not understand the regulation of *Chat* in SI tuft cells. It is unclear why

only a subset of SI tuft cells are *Chat*+, why there is a proximal to distal gradient of

Chat+ tuft cells, and why the frequency of *Chat*+ tuft cells decreases during Type 2

inflammation (although the total number increases due to tuft cell hyperplasia).

Furthermore, most tuft cells do not express *Slc5a7*, which encodes CHT1, the

transporter that neurons use to import choline for ACh synthesis, nor *Slc18a3*, which

encodes VAChT, a transporter that loads ACh into secretory vesicles in neurons.[70]

Lastly, it remains to be seen whether tuft cell-derived ACh also induces bicarbonate

secretion, as this often occurs together with chloride release and further supports the

unfolding of extracellular mucus.[71]

We have also not identified the precise ACh receptor(s) that mediate(s) the fluid

secretion response, although inhibition by atropine implicates a muscarinic rather than

nicotinic receptor. *Chrm1* and *Chrm3* are the only detectable muscarinic receptor

transcripts in unmanipulated SI epithelium[9,11] and *Nb* clearance is delayed in *Chrm3*^{-/-}

mice.[40] Induction of Type 2 cytokines is also impaired in these *Chrm3*^{-/-} mice, so

conditional *Chrm* alleles will be needed to identify in which cells the receptors are

required and for which aspects of Type 2 immunity.

While tuft cell-derived ACh was not required for ILC2 activation during helminth

infection and intestinal remodeling was largely intact, there were slight yet significant

defects in tuft cell numbers or SI length at some timepoints analyzed. Prior literature has

shown that deletion of *Chrm3* from the SI epithelium causes an *increase* in tuft cell

numbers at baseline but a *decrease* in tuft cells following irradiation.[67] Perhaps epithelial

ACh signaling has damage-induced functions that overlap with helminth-induced

intestinal remodeling. Regulation of intestinal epithelial differentiation by tuft cell-derived

ACh bears further study.

We have focused on tuft cell ACh signaling on enterocytes to drive fluid

secretion, but ACh receptors are expressed by many cells, including other types of

intestinal epithelial cells. Goblet cells undergo compound exocytosis of mucus in

response to ACh,[46,47,72] and the formation of goblet-associated antigen passages

(GAPs) has also been linked to ACh signaling.[73,74] Additionally, tuft cell ACh was

recently reported to induce mucus secretion from cholangiocytes in the gallbladder.[57]

We therefore extensively tested the hypothesis that ACh from SI tuft cells signals on

villus goblet cells to induce mucus secretion and GAP formation, but we could not find

any evidence that this occurs *in vivo* (data not shown). A recent study demonstrating

that muscarinic receptor expression is restricted to GCs at the base of SI crypts, and

that only these cells respond acutely to CCh,[75] may explain why we did not detect tuft

cell-dependent regulation of GC mucus secretion. While it remains possible that ACh

from SI crypt tuft cells regulates secretion by GCs (and Paneth cells), we generally

found fewer *Chat*+ tuft cells in the crypts than in the villi, and chemosensing pathways

are likely not yet functional in immature crypt tuft cells. Perhaps in the colon tuft cell

ACh regulates the function of sentinel GCs at crypt openings.[76] Lastly, ACh-regulated

smooth muscle contraction is critical for SI helminth clearance[28,37] and tuft cells have

been linked to smooth muscle function in other tissues.[19,57] The short extracellular half-

life of ACh combined with the distance between epithelial tuft cells and smooth muscles

that surround the SI make direct signaling unlikely. Nonetheless, while we did not see

evidence of direct contact between tuft cells and enteric neurons, they have been

previously reported in the SI[10,77,78] and thus we cannot rule out the possibility that tuft

cell ACh regulates smooth muscle contraction via the enteric nervous system.

During Type 2 inflammation in the SI, the maximal fluid secretion induced by ACh

is dramatically reduced,[69] possibly to prevent excessive fluid loss or diarrhea during

chronic helminth infection. At the same time, the number of *Chat*+ tuft cells increases,

such that tuft cell-regulated fluid secretion is maintained or even enhanced compared to

baseline. This re-wiring of ACh-regulated fluid secretion may represent a regulatory

mechanism that minimizes fluid loss due to endogenous signals while maintaining the

ability to respond to lumen-restricted agonists such as helminths via tuft cell sensing. In

that regard, tuft cells also have an advantage over mast cells and neurons, which can

induce enhanced fluid secretion during Type 2 inflammation via release of histamine

and/or prostaglandin E2,[69] but can only respond to ligands that penetrate the mucosal

barrier. Relatedly, it remains unclear whether the acetylcholinesterases secreted by

helminths can penetrate the mucosal barrier to target ACh in the tissue, or whether

helminths are only able to counter the effects of ACh during tissue-dwelling phases of

their lifecycle.

Although we have focused on the SI in this study, we propose tuft cells link

chemosensing to fluid secretion in all tissues. Indeed, with the exception of tuft-ILC2

circuit activation, all other known tuft cell effector functions occur instantaneously and

seem to mediate evasion (e.g. breathing cessation)[14,16] and expulsion (e.g. mucociliary

sweep) of microbes and other agonists.[8,17] Fluid secretion fits this paradigm. The

mucosal barrier must be constantly hydrated and fluid secretion can provide a flushing

effect. Based on the ligands tuft cells sense in different tissues, such mechanisms could

be important to clear allergens from the upper airways or bacteria from the trachea and

urethra. Tuft cell sensing may also reduce baseline fluid secretion, as one recent study

suggested.[79] The ligands and function of tuft cells in the colon are only just being

elucidated,[56] but we predict that tuft cell-regulated fluid secretion would help maintain a

healthy mucosal barrier here too. Tuft cell frequency is generally decreased in patients

with active inflammatory bowel disease,[80,81] consistent with a role for tuft cells in

preventing bacterial infiltration. Conversely, increased tuft cell frequency was detected

in colonic biopsies from patients with diarrhea-predominant irritable bowel syndrome, a

largely non-inflammatory condition of unknown origin.[82]

Why tuft cells sense succinate in either the SI or, as we have now demonstrated,

the trachea, remains unclear. We could not find any impact of tuft cell *Chat* deletion on

Tritrichomonas burden or distribution, but perhaps tuft cell-mediated fluid secretion,

together with IL-13-induced anti-microbial peptides and mucus production, acts more

locally to keep microbes away from the epithelium.[83] Succinate levels have also been

shown to increase in contexts of bacterial dysbiosis, and inducing tuft cell hyperplasia

with succinate treatment reduces inflammation in a model of ileitis.[80] As for the trachea,

aberrant release of cellular succinate into the airways, which occurs in some patients

with cystic fibrosis, can promote colonization and biofilm formation by the

pathosymbiont *Pseudomonas aeruginosa.*[84] Induction of CFTR-dependent fluid

secretion by prostaglandin E2 released from airway tuft cells has also been

suggested.[86] Thus, tracheal tuft cells may induce fluid secretion to flush away succinate

and other soluble molecules and to deter bacterial accumulation.

Therapeutically, benefit may be achieved by tuning tuft cell effector functions up

or down, depending on the context and need. For example, tuft cell-induced fluid

secretion may prove useful in treating cystic fibrosis patients in whom CFTR-dependent

fluid secretion is impaired, while certain patients suffering from diarrhea might benefit

from reduced tuft cell function. Future study should investigate the involvement of tuft

cell-induced fluid secretion in human disease.

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<u>Contributions:</u>

TEB designed and performed experiments, analyzed data, and wrote the paper with

JVM. LMW, DBS, MMM, DNK, and JWM assisted with experiments at the University of

Washington. CF and MBG performed *in vivo* Class 8 and *T. musculis* fecal water

content experiments at Stanford University with supervision and funding provided by

MRH. KAB and LMR performed pilot Ussing chamber experiments with supervision and

funding provided by JSD. AB, MS, and RM led the development and validation of the

Class 8 TRPM5 agonist at Takeda Pharmaceuticals in collaboration with Evotec. JVM

conceived of and supervised the study, analyzed data, acquired funding, and wrote the

paper with TEB.

<u>Methods:</u>

Study Design

All experiments were performed using randomly assigned mice without investigator

blinding. No data were excluded, except from Ussing chambers when mounted tissues

failed to respond to stimulation by a positive control (e.g. CCh). All data points reflect

biological replicates, except for *in vitro* ILC2 stimulations and epithelial monolayer

experiments where each data point is a technical replicate. Data were pooled from

multiple experiments unless otherwise noted. The number of independent experiments

is included in the figure legends.

Experimental Animals

Mice aged 6 weeks and older were used for all experiments. Mice were age-matched

within each experiment. Pooled results include both male and female mice of varying

ages unless otherwise indicated. Mouse strains used in this study are listed in Table S3.

Acute deletion of conditional alleles in mice was achieved by oral gavage with tamoxifen

dissolved in corn oil (100 mg/kg). *Chat^{fl/fl};Vil1-Cre-ERT2(Tg+)* mice were administered

tamoxifen on day -4 and 0 of infection with *N. brasiliensis* and on day -6 and -4 of

treatment with 150 mM succinate drinking water, or as noted in the text.

Chat^{fl/fl};Pou2f3^{Cre-ERT2/+} mice were administered tamoxifen every other day starting on

day -4 of *N. brasiliensis* infection or as noted in the text. *DREADD(Tg+); Pou2f3^{Cre-ERT2/+}*

mice were administered tamoxifen chow for 7 days prior to Ussing experiments. All mice

(CRE+ and CRE-) received tamoxifen treatment. All mice were maintained in specific

pathogen-free conditions at the University of Washington or Stanford University and

were confirmed to be free of *Tritrichomonas sp.* by microscopy and qPCR, unless

specifically colonized for experimental purposes. All procedures were conducted within

University of Washington or Stanford University (Class 8 gavage) IACUC guidelines

under approved protocols.

Measuring epithelial ion flux with Ussing chambers

Ussing chamber protocols were informed by Clarke et al.[51]

Tissue mounting: Mice 7-12 weeks of age were euthanized by CO_2 and segments of the

intestine (SI, cecum, colon) were harvested and flushed with cold Krebs Buffered

Ringer's solution + mannitol (10 mM D-mannitol, 115 mM NaCl, 2.4 mM K_2HPO_4, 0.4

mM KH_2PO_4, 25 mM $NaHCO_3$, 1.2 mM $CaCl_2$ dihydrate, 1.2 $MgCl_2$ hexahydrate; pH

7.25-7.4). Intestines (first 5 cm of pSI and last 5 cm of dSI) were fileted open along the

mesenteric line, trimmed and mounted to the pins of an Ussing chamber cassette with

aperture of 0.3 cm^2 (Physiologic Instruments, Reno, USA), avoiding Peyer's patches.

For some experiments the SI was pinned to a Sylgard-coated plate with the serosal side

up and the muscle layer scored with a scalpel and "stripped" away using forceps under

a dissection scope. The resulting epithelium-submucosa tissue was mounted in a

cassette as normal. For trachea preparations, the entire trachea was harvested,

surrounding tissue (esophagus) removed, and cut open lengthwise along the anterior

side (away from esophagus) for mounting in a 2 mm^2 aperture cassette (Physiologic

Instruments, Reno, USA). Cassettes containing tissues were mounted in Ussing

chambers (Physiologic Instruments, Reno, USA) and the lumenal chambers filled with 5

mL of KBR + mannitol and the basolateral chambers filled with 5 mL of KBR + glucose

(10 mM D-glucose, 115 mM NaCl, 2.4 mM K_2HPO_4, 0.4 mM KH_2PO_4, 25 mM $NaHCO_3$,

1.2 mM $CaCl_2$ dihydrate, 1.2 $MgCl_2$ hexahydrate; pH 7.25-7.4). The chambers were

warmed to 37C and bubbled with carbogen (95% O_2, 5% CO_2) for the duration of the

experiment. For Cl^- replacement experiments, Cl^- free KBR was used, in which

gluconate is substituted for Cl- (115 mM D-gluconic acid sodium salt, 2.4 mM K_2HPO_4,

0.4 mM KH_2PO_4, 25 mM $NaHCO_3$, 4 mM calcium D-gluconate monohydrate, 1.2 mM

magnesium D-gluconate hydrate; pH 7.25-7.4).

Measuring the short circuit current (Isc): Automatic voltage clamping was performed by

MultiChannel Voltage-Current Clamp (Physiologic Instruments, Reno, USA). Voltage

differences between electrodes and fluid resistance of the buffer were compensated

prior to insertion of the tissue cassette. Isc was measured by voltage clamp every 1

second and recorded using Acquire & Analyze software (Physiologic Instruments, Reno,

USA) and normalized to tissue area. After a 20 min equilibration period, tissues were

stimulated lumenally with Na_2-succinate (1, 10 mM) or cis-epoxysuccinic acid (10 mM),

basolaterally with 5 µM Class 8, or bilaterally with 1 µM Compound 21. For

succinate/cESA stimulation, subsequent stimulations were administered every 10 min;

for Class 8 the interval was increased to 15 min due to the slower kinetics of the

response. Subsequent stimulations included lumenal 20 mM NaCl, basolateral 100 µM

CCh, and bilateral cocktail of 100 µM 3-Isobutyl-1-methylxanthine (IBMX) + 10 µM

forskolin. Chemical inhibitors were administered 5 min after start of equilibration period

(15 min before first stimulation): basolateral 100 µM bumetanide, bilateral 10 µM

ibuprofen, basolateral 10 µM atropine, basolateral 1 µM tetrodotoxin, and lumenal 1 mM

carbenoxolone. ∆Isc values were calculated as the difference between the Isc

measurement at the peak of the stim response and the Isc measurement taken right

before adding the agonist. For tissues that did not respond to the agonist (e.g., knockout

mouse intestines, tissues treated with inhibitors) and therefore had no peak response,

the Isc value was taken at the same timepoint as the peak Isc value for the

corresponding WT or control tissue.

Measuring fecal water content

Mice were orally gavaged with vehicle (0.5% methylcellulose + 1% Tween 20) or 30

mg/kg Class 8, and fecal samples (2+ pellets) were taken at 0 and 3 hours post gavage.

For protist-colonized experiments, B6 mice were colonized with *T. musculis* protists and

fecal samples collected at 2, 7,14, and 20 days post colonization. Fecal samples were

dried at 60C overnight and % water content calculated as (1-(dry weight/wet

weight))*100.

Monolayer culture and cysteinyl leukotriene ELISA

Proximal small intestine was isolated and villi were gently scraped off with a glass

coverslip. Tissue was incubated for 30 minutes at 4° with 2mM EDTA to release

epithelial crypts, then washed twice with cold PBS and filtered through a 70 um strainer.

Crypts were resuspended in complete monolayer media (DMEM/F12 supplemented

with 2mM glutamine, 100U/mL penicillin, 100mg/mL streptomycin, 10mM HEPES, N2

supplement, B27 supplement, R-spondin (10% supernatants from R-spondin secreting

cells), Noggin (10% supernatant from Noggin secreting cells), 500mM N-acetylcysteine,

50ug/mL mEGF, and 10 µM Y27632). Plates were coated with 2% Matrigel in cold

DMEM/F12 and incubated at 37° for at least 30 minutes. Media was aspirated from the

plate, and 1000 crypts were plated per well of a 48-well plate. Crypts were incubated
overnight, and non-adherent cells were aspirated the next day. Test stimuli diluted in
HBSS containing Ca2+/Mg2+ were added to monolayers and stimulated at 37° for 30
minutes. Supernatants were collected and used for the Cysteinyl Leukotriene Express
ELISA kit (Cayman Chemical) according to manufacturer's protocol.
905

906 **Succinate and cytokine treatment**
907 For succinate experiments mice were given 150mM sodium succinate hexahydrate
908 (Thermo) ad libitum in drinking water for the indicated amount of time. Recombinant
909 murine IL-25 (500 ng; R&D) was given for 3 consecutive days intraperitoneally in 200 μL
910 PBS.
911

912 **Helminth infections and analysis**
913 *N. brasiliensis* larvae were raised and maintained as previously described.[85]
914 Mice were infected subcutaneously with 500 *N. brasiliensis* L3. At sacrifice, the entire SI
915 was fileted open and total worms counted under a stereomicroscope.
916

Protist colonization and analysis
Breeding pairs were colonized with *Tritrichomonas musculis* or *T. rainier* as previously
described.[87] Pups from colonized breeding pairs were analyzed. Protist numbers were
quantified by flow cytometry as described by Chudnovskiy et al.[88] Briefly, 10 cm of pSI
and dSI were flushed into a 15 mL conical with 10 mL RT PBS using a gavage needle.
Cecal contents were harvested into 15 mL conical, weighed, and then 10 mL RT PBS
added. Samples were let sit for 30 min at RT, vortexed, and then passed through a 70
μm filter. Protists were washed, stained with DAPI, then count beads added and data
collected on a FACSCanto II (BD Biosciences). Protist numbers per gram of cecal
content was calculated.
927

Intestinal tissue fixation and staining
Intestinal tissues were flushed with PBS and fixed in 4% paraformaldehyde for 3-4
hours at 4°C, washed with PBS, and incubated in 30% (w/v) sucrose overnight at 4°C.

Samples were then coiled into "Swiss rolls", embedded in Optimal Cutting Temperature

Compound (Tissue-Tek) and sectioned at 8 μm on a CM1950 cryostat (Leica).

Immunofluorescent staining was performed in PBS with 1% BSA at room temperature

as follows: 1 hr 10% donkey serum with 1:1000 Fc Block, 1 hr (or O/N at 4°C) primary

antibody, 5 min wash, 45 min secondary donkey antibody and/or WGA-488, 5 min

wash, and mounted with Vectashield plus DAPI (Vector Laboratories). Images were

acquired with an Axio Observer A1 (Zeiss) microscope with a 10X or 20X A Plan

objective. Tuft cell frequency was calculated using ImageJ software to manually quantify

DCLK1$^+$ cells per millimeter of crypt-villus axis. Goblet cell frequency was calculated

using ImageJ software to manually quantify total WGA+ cells in the villus (crypts were

excluded because WGA also labels Paneth cells) per millimeter of crypt villus axis. For

each replicate, four 10x images of the Swiss roll were analyzed and at least 25 total villi

counted.

Single-cell tissue preparation for flow cytometry

For single cell epithelial preparations from SI, tissues were flushed with PBS,

Peyer's patches removed, opened longitudinally, and rinsed with PBS. Tissue was cut

into small pieces, shaken vigorously for 20 seconds in 30 mL cold HBSS (Ca^{+2}/Mg^{+2}-

free) with 1 mM HEPES, drained, and then incubated rocking at 37°C for 10 min in 15

mL HBSS (Ca^{+2}/Mg^{+2}-free) supplemented with 3 mM EDTA and 1 mM HEPES. Tissues

were vortexed thoroughly and released epithelial cells passed through a 70 μm filter.

This process was repeated for a total of 3 rounds. Supernatants were pooled and

washed with HBSS (Ca^{+2}/Mg^{+2}-free) with 1 mM HEPES before staining for flow

cytometry.

For lamina propria (LP) preparations from uninfected mice, SI was processed as

above to remove the epithelial fraction. Tissues were then incubated shaking at 37°C for

30 minutes in 10 mL RPMI 1640 supplemented with 20% FCS, 1 mM HEPES, 0.05

mg/ml DNase I (Sigma Aldrich), and 1 mg/mL Collagenase A (Sigma Aldrich). Tissues

were vortexed and cells were passed through a 100 μm filter, then a 40 μm filter,

washing with cold HBSS (Ca^{+2}/Mg^{+2}-free) with 1 mM HEPES. Cells were washed and

stained for flow cytometry.

For LP preparations from *N. brasiliensis*-infected mice (D4), mice were

anaesthetized with 5% avertin. The peritoneal cavity was opened, the SI nicked at the

junction with the stomach and transected at the cecum and flushed with 20 mL of 37°C

HBSS (Ca^{+2}/Mg^{+2}-free) plus 1 mM HEPES. Then the mice were perfused through the

heart with 30 mL of 37°C HBSS (Ca^{+2}/Mg^{+2}-free) with 30 mM EDTA and 1 mM HEPES.

Three minutes after perfusion was completed, the first 10 cm of the proximal SI was

harvested, Peyer's patches removed, opened longitudinally, and cut into small pieces

and shaken vigorously for 20 seconds in 30 mL cold HBSS (Ca^{+2}/Mg^{+2}-free) with 1 mM

HEPES, then drained. Tissues were then digested and processed as above in

uninfected mice.

For mesenteric lymph node (MLN) preparations, SI-draining MLN were harvested

into RPMI + 5% FBS on ice, mashed through a 70 μm filter, the filter washed with RPMI

+ 5% FBS, and cells washed and stained for flow cytometry.

Flow cytometry and cell sorting

Single cell suspensions from tissues were prepared as described above. For flow

cytometry, SI epithelium and MLN samples were stained in DPBS (Ca^{+2}/Mg^{+2}-free) with

3% FCS and LP samples were stained in PBS (Ca^{+2}/Mg^{+2}-free) with 3% FCS, 2 mM

EDTA, and 0.02 mg/mL DNase I with antibodies to surface markers for 30 min at 4°C,

followed by DAPI (Roche) for dead cell exclusion. When cell counts were needed,

counting beads (Spherotech) were added prior to running flow cytometry. Samples were

run on a FACSCanto II or LSRII (BD Biosciences) and analyzed with FlowJo 10.8.1.

Samples were FSC-A/SSC-A gated to exclude debris, FSC-A/FSC-H gated to select

single cells, and gated to exclude dead cells. For cell sorting, single cell suspensions

were prepared and stained as described and sorted on an Aria III (BD Biosciences).

ILC2 Stimulation Assay

Entire SILP from several mice were pooled and ILC2s (EpCAM-, CD45$^+$, Lin(CD3, CD4,

CD5, CD8, CD11b, CD19, NK1.1, FcER1)$^-$, KLRG1$^+$) sorted as described. Sorted cells

were plated at 5000 cells per well in a 96-well plate and incubated at 37°C overnight in

10 ng/ml IL-7 (R&D Systems) and basal media composed of high glucose DMEM

supplemented with non-essential amino acids, 10% FBS, 100 U/mL penicillin,

100mg/mL streptomycin, 10mM HEPES, 1mM sodium pyruvate, 100μM 2-

mercaptoethanol, and 2mM L-glutamine. The next morning, media was replaced and

cells were stimulated with the indicated agonist. After a six-hour stimulation,

supernatant was collected and the cells were washed and stained with 1 uL/well of PE-

conjugated anti-human CD4 for 20 min at 4°C. Cells were washed, resuspended in

DAPI and analyzed on a CantoRUO (BD Biosciences). Cytokine levels in supernatants

were measured using Enhanced Sensitivity Flex Sets (BD Biosciences) for mouse IL-5

and IL-13 according to the manufacturer's protocol. Data was collected on an LSRII (BD

Biosciences).

1003

RNA Sequencing and Analysis

150-200 tuft cells were sorted directly into lysis buffer from the SMART-Seq v4 Ultra

Low Input RNA Kit (Takara) and cDNA generated following manufacturer's instructions.

Cells were sorted from four individual mice for each experiment. Sequencing libraries

were generated using the Nextera XT library preparation kit with multiplexing primers,

according to manufacturer's protocol (Illumina), and library quality assessed using

Tapestation (Agilent). High throughput sequencing was performed on NextSeq 2000

(Illumina), sequencing dual-indexed and paired-end 59 base pair reads. All samples

were in the same run with a target depth of 5 million reads. Base calls were processed

to FASTQs on BaseSpace (Illumina), and a base call quality-trimming step was applied

to remove low-confidence base calls from the ends of reads. The FASTQs were aligned

to the GRCm38 mouse reference genome, using STAR v.2.4.2a and gene counts were

generated using htseq-count. Further analysis of the data was performed using the

DIY.Transcriptomics (diytranscriptomics.com) pipeline, with experiment-specific

modifications. Samples were filtered to exclude genes with counts per million = 0 in 4 or

more samples and genes annotated as pseudogenes. Finally, samples were normalized

to each other. To identify differentially expressed genes, precision weights were first

applied to each gene based on its mean-variance relationship using VOOM,[89] then data

was normalized using the TMM method[90] in EdgeR.[91] Linear modeling and bayesian

stats were employed via Limma[92] to find genes that were up- or down-regulated by 2-

fold (Log2FC = 1) or more, with a false-discovery rate (FDR) of 0.01. The code and

results for these analyses are included as Data File S1 and S2.

1026

1027   **Statistical Analysis**

1028   Statistical analysis was performed as noted in figure legends using Prism 9 (GraphPad)

1029   software. Graphs show mean +/- SEM.

1030

1031 **Table S3**

Reagent or Resource	Source	Identifier
B6.Cg-Tg(RP23-268L19-EGFP)2Mik/J (Chat-GFP)	Jackson Laboratory	JAX #007902
B6.$Il25^{Flare25/Flare25}$ (Il25-RFP)	R. Locksley (PMID: 26675736)	NA
B6.$Il13^{Smart13/Smart13}$ (Smart13)	R. Locksley (PMID: 22138715)	NA
C57BL/6N-Pou2f3<tm1(KOMP)Vlcg>/Tcp ($Pou2f3^{-/-}$)	Canadian Mouse Mutant Repository	CMMR #ABDF
B6.129P2-Trpm5^{tm1Dgen}/J ($Trpm5^{-/-}$)	Jackson Laboratory	JAX #005848
B6.$Sucnr1^{-/-}$	In-house (PMID: 30021144)	NA
B6.$Il25^{-/-}$	A. McKenzie (PMID: 16606668)	NA
B6;129-Chat^{tm1Jrs}/J ($Chat^{fl/fl}$)	Jackson Laboratory	JAX #016920
B6.Cg-Tg(Vil1-cre)997Gum/J	Jackson Laboratory	JAX #004586
B6.Cg-Tg(Vil1-cre)1000Gum/J (Vil1-Cre1000)	Jackson Laboratory	JAX #021504
B6.Cg-Tg(Vil1-cre/ERT2)23Syr/J ($Vil1$-Cre-$Ert2$)	Jackson Laboratory	JAX #020282
B6(129S4)-$Pou2f3^{tm1.1(cre/ERT2)Imt}$/J (Pou2f3-Cre-Ert2)	Jackson Laboratory	JAX #037511
B6.129S-Chattm1(cre)Lowl/MwarJ ($Chat$-Cre)	Jackson Laboratory	JAX #031661
B6.$Il25$-Cre	R. Locksley (PMID: 35245089)	NA
B6.Cg-$Gt(ROSA)26Sor^{tm9(CAG-tdTomato)Hze}$/J (Ai9)	Jackson Laboratory	JAX #007909
B6N;129-Tg(CAG-CHRM3*,-mCitrine)1Ute/J (Gq-DREADD)	Jackson Laboratory	JAX #026220
B6.129-$Gt(ROSA)26Sor^{tm1(CAG-CHRM4*,-mCitrine)Ute}$/J (Gi-DREADD)	Jackson Laboratory	JAX #026219
B6.$Alox5^{fl/fl}$	In-house (PMID: 32160525)	NA
B6.$Il4ra^{fl/fl}$	F. Brombacher (PMID: 15142530)	NA

1032

1033 **Table S4**

Reagent or Resource	Dilution Factor	Source	Identifier
Rabbit α-DCLK1	1:1000	Abcam	Cat#ab31704
Rabbit α-TUJ1 (Beta-III tubulin)	1:500	Abcam	Cat#ab18207
Goat α-GFP	1:500	Novus Bio	Cat#NB100-1770
Rabbit α-dsRed	1:500	Clontech	Cat#632496
Rabbit α-HA, clone 16B12	1:1000	Biolegend	Cat#901516
WGA-488	1:150	Thermo	Cat#W11261
Donkey α-Rabbit IgG AF594	1:1000	Thermo	Cat#A-21207
Donkey α-Goat IgG AF488	1:500	Thermo	Cat#A-11055
CD16 / CD32, clone 2.4G2	1:1000	Tonbo	Cat# 70-0161-M001
CD3 PerCP-Cy5.5, clone 145-2C11	1:100	Biolegend	Cat#100328
CD3 BV421, clone 145-2C11	1:400	Biolegend	Cat#100335
CD4 BV711, clone RM4-5	1:250	Biolegend	Cat#100549
CD4 eF450, clone RM4-5	1:200	eBioscience	Cat# 48-0042-80
hCD4 PE, clone RPA-T4	1:50	Biolegend	Cat#300508
CD5 PerCP-Cy5.5, clone 53-7.3	1:500	Biolegend	Cat#100624
CD5 eF450, clone 53-7.3	1:400	Biolegend	Cat#100607
CD8 PerCP-Cy5.5, clone 53-6.7	1:200	Biolegend	Cat#100724
CD8 BV421, clone 53-6.7	1:400	Biolegend	Cat#100737
CD11b AF700, clone M1/70	1:250	Biolegend	Cat#101222
CD11b BV421, clone M1/70	1:400	Biolegend	Cat# 101235
CD19 PerCP-Cy5.5, clone 6D5	1:250	Biolegend	Cat#115533
CD19 BV421, clone 6D5	1:400	Biolegend	Cat# 115537

CD24 PE, clone M1/69	1:300	Biolegend	Cat#101807
CD24 PerCP-Cy5.5, clone M1/69	1:300	Biolegend	Cat#101824
CD45 BV605, clone 30F11	1:300	Biolegend	Cat#103155
CD45 BV650, clone 30F11	1:500	Biolegend	Cat#103151
EpCAM PE-Dazzle, clone G8.8	1:300	Biolegend	Cat#118235
EpCAM AF488, clone G8.8	1:300	Biolegend	Cat#118210
EpCAM PE-Cy7, clone G8.8	1:300	Biolegend	Cat#118215
FcER1 BV421, clone Mar-1	1:400	Biolegend	Cat#334623
IL17RB APC, clone 9B10	1:100	Biolegend	Cat#146307
KLRG1 PE-Cy7, clone 2F1	1:250	Biolegend	Cat#138416
NK1.1 PerCP-Cy5.5, clone PK136	1:100	Biolegend	Cat#108728
NK1.1 BV421, clone PK136	1:200	Biolegend	Cat#108731
Siglec-F APC-Cy7, clone E50-2440	1:100	BD	Cat#565527
Siglec-F AF647, clone E50-2440	1:100	BD	Cat# 562680
Thy1.2 (CD90.2) BV605, clone 53-2.1	1:500	Biolegend	Cat#140318

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