Co-infection with *Toxoplasma gondii* leads to a loss of resistance in *Heligmosomoides*

***bakeri* trickle-infected mice due to ineffective granulomas**

Breton Fougere[1,2*], Anupama Ariyaratne[1,2*], Naomi Chege[1,2], Shashini Perera[1,2], Emma

Forrester[1,2], Mayara de Cassia Luzzi[1,2], Joel Bowron[1,2], Aralia Leon Coria[1,2], Edina

Szabo[1,2], Constance A. M. Finney[1,2]

[1]Department of Biological Sciences, Faculty of Science, University of Calgary, Calgary,

Alberta, Canada.

[2]Host-Parasite Interactions Research Training Network, University of Calgary, Calgary,

Alberta, Canada.

*Co-authors

Corresponding Author: Constance A. M. Finney, constance.finney@ucalgary.ca, Faculty

of Science, Department of Biological Sciences, University of Calgary, 2500 University

Drive N.W., Calgary, Alberta, Canada.

Keywords: parasitic worm infections, Toxoplasma, nematodes, granuloma, innate

immunity, antibody responses, trickle infection, co-infection

ABSTRACT

The intestinal roundworm *Heligmosomoides bakeri* causes chronic infection in

susceptible (C57Bl/6) mice; however, repeat (trickle) infection confers immunity and

facilitates worm clearance. We previously showed that this acquired immunity is

associated with a strong Th2 response, notably the enhanced production of intestinal

granulomas. Here we demonstrate that elevated proportions of IgG_1-bound eosinophils

and macrophages are observed around the developing tissue worms of trickle-infected

female C57Bl/6 mice compared to bolus infected animals. Levels of IgG_{2c}, IgA or IgE

were not detected in the granulomas. Increased proportions of $SiglecF^+$ and $CD206^+$

cells, but not $Ly6G^+$ and/or $NK1.1^+$ cells, were also found in the granulomas of trickle-

infected mice. However, in the natural world rather than the laboratory setting,

immune environments are more nuanced. We examined the impact of a mixed immune

environment on trickle infection-induced immunity, using a pre-infection with

Toxoplasma gondii. The mixed immune environment resulted in fewer and smaller

granulomas with a lack of IgG_1-bound cells as well as reduced proportions of $SiglecF^+$

and $CD206^+$ cells, measured by immunofluorescence and flow cytometry. This was

associated with a higher worm burden in the co-infected animals. Our data confirm the

importance of intestinal granulomas and parasite-specific antibody for parasite

clearance. They highlight why it may be more difficult to clear worms in the field than in

the laboratory.

AUTHOR'S SUMMARY

Despite decades of research on intestinal parasitic worms, we are still unable to clearly

point to why so many people (approximately 1.8 billion) and most livestock/wild animals

are infected with these parasites. We have made progress in understanding how the

immune system responds to parasitic worms, and how these parasites manipulate our

immune system. However, identifying effective clearance mechanisms is complex and

context dependent. We have used models of trickle infection (multiple low doses of

parasites) and co-infection (two intestinal parasites) to simulate how people/animals

get infected in the real world. Using these models, we have confirmed the host/parasite

interface (the granuloma) within the intestinal tissue to be key in determining the host's

ability to clear worms. The lack of specific immune cells and antibodies within the

granuloma was associated with chronic infection. Our results help explain why intestinal

parasitic worms are so prevalent and why it may be difficult to clear worms in natural

settings.

INTRODUCTION

Gastrointestinal nematodes (GINs) are ubiquitous. They are highly prevalent in humans

[1], livestock (reviewed in [2]) and pets [3]. Despite the low mortality associated with these

parasites, they significantly impact human and animal health (reviewed in [4–6]). Infected

hosts mount strong anti-GIN immune responses, but the efficacy of the response is

dependent on genetics, infection dynamics and the environment, and we have yet to

find treatments that clear worms and prevent reinfection. Understanding effective

clearance mechanisms by the host in natural settings is key to developing strategies to

stimulate sterile immunity.

Heligmosomoides bakeri (Hb), formerly *Heligmosomoides polygyrus* [7], is a rodent model

gastrointestinal nematode parasite which has been extensively used to understand

host/parasite interactions in related livestock and human parasites [8]. For the first 7-10

days of infection, Hb develops within the tissue. After 10 days, adults emerge into the

lumen, where they remain coiled around the intestinal villi for the duration of infection.

Hb infection stimulates a strong Th2 response, ultimately dependant on the production

of IL-4 and IL-13, and IL-4 receptor signalling for effective clearance [9,10]. Tissue dwelling

parasite stages induce an influx of immune cells to the site of infection culminating in

the formation of an intestinal granuloma (reviewed in [11]). The levels of IL-4/IL-13, and

the size and number of granulomas are associated with the resistant/susceptibility

phenotype of different mouse strains [12,13].

Immune protection from reinfection, observed in laboratory models of vaccination

and/or secondary infections, has been linked to effective immune responses against

tissue dwelling Hb stages [14–16]. Within the granuloma, the host response simultaneously

immobilises, damages and/or kills the parasites while healing the damage caused by the

growing worm (reviewed in [11]). Due to their size, parasitic worms cannot be

phagocytosed by immune cells; antibody-bound myeloid cells, namely SiglecF+

eosinophils and CD206+ macrophages, within the granuloma have been implicated in

protection (reviewed in [11]).

Resistant strains of mice develop faster and stronger parasite-specific antibody

responses to Hb, as compared to susceptible strains [12,13]. More specifically, elevated

levels of IgG_1, IgA and IgE have been linked to worm clearance [17–20]. Passive transfer of

serum, more specifically IgG_1, from infected mice decreases adult worm numbers as

well as their fitness [21–24]. Mice lacking IgG, and to a lesser extent IgA, but not IgE, have

increased worm burdens upon secondary infection compared to wild-type animals [18]. In

support of this, macrophages isolated from Hb-induced granulomas from challenge

infected mice are bound to IgG isotypes (IgG_1 and IgG_3) but not IgE [15]. They also express

high levels of FcγRs, and mice lacking FcγRs (unable to bind IgG antibodies) have

increased parasite loads [16].

While it's clear that in the context of a Th2 immune environment generated in a

laboratory-based experimental model, susceptible strains of mice can mount strong

immune responses to reinfections with Hb [13,18], in natural settings, where immune

environments are more nuanced, Hb prevalence is high [25–27]. One of the many factors

that influence immune environments is co-infection, a common occurrence in the

natural world [28].

The overarching aim of our study was to examine the impact a mixed immune response

on effective clearance of Hb. As an obligate intracellular parasite, *Toxoplasma gondii*

(Tg) elicits a strong inflammatory response in the small intestine during infection, with

elevated IL-12 and IFNγ levels (as reviewed in [29]). Following infection of the intestinal

mucosa, IL-12 producing monocytes and neutrophils are recruited to the small intestine,

where they recruit ILC1s and T cells, both potent producers of IFNγ. Research suggests

that previous Tg infection skews Hb-specific CD4$^+$ T cell and IgG antibody responses

towards a more Th1 phenotype, with no impact on worm burden [30]. However, this

previous study focused on a primary chronic infection (28 days post infection - D28) and

did not address potential impacts to the host/parasite interface in the granuloma. We

used the more realistic trickle model of TgHb confection and show that TgHb infected

animals have a reduction in the size and number of granulomas, and that their

granulomas have fewer myeloid cells and more specifically, IgG$_1$-bound myeloid cells.

The lack of functional granulomas was associated with increased worm burdens. Our

data confirm the importance of intestinal granulomas in the context of re-infection, and

highlight why it may be more difficult to clear worms in the field than in the laboratory.

MATERIALS AND METHODS

Mice, Parasites and Antigens

Female BALB/c and C57Bl/6 mice aged 6-10 weeks were bred and maintained in the Life

and Environmental Science Animal Resource Centre (LESARC) in the Department of

Biological Sciences, University of Calgary, Canada. Original stocks were obtained from

Charles River, Canada. Mice were acclimatised for a minimum of two days when moved

to our experimental room and housed in groups of 3-5 in individually vented cages. All

experiments were approved under protocol # AC17-0083 and AC19-0121 by the

University of Calgary's Life and Environmental Sciences Animal Care Committee. All

protocols for animal use and euthanasia were in accordance with the Canadian Council

for Animal Care (Canada). Enrichment was provided in the form of plastic housing,

bedding and for parasite passage animals, a variety of veterinary approved small treats

(seeds, nuts, etc) and/or supportive nutrition (DietGel).

Mice were orally infected by gavage with 200 third stage *Heligmosomoides bakeri* larvae

(maintained in house, stock was a gift from Dr. Allen Shostak, University of Alberta,

Canada and Dr Lisa Reynolds, University of Victoria, Canada) and euthanized at either

D5, D7, D21 or D28. Larvae were obtained from fecal cultures after approximately 8-9

days of incubation at room temperature. Mice were infected according to the bolus or

trickle infection regimes (Figures 1A & 4A). To avoid differences in counts during the

trickle infections, on D0, two identical solutions were made up (200 worms/100µl). One

was used to infect the bolus infected mice on D0 and one was used for the trickle-

infected mice. The solution for the trickle-infected animals was divided into ten equal

parts. Each part was made up to 100ul using water. Animals were gavaged with a diluted

solution on days 0, 2, 4, 6, 8, 10, 12, 14, 16 and 18. Using the 10 doses, trickle-infected

animals received 200 larvae in total over 18 days.

The Me49 strain of *Toxoplasma gondii* (Tg) (maintained in house, original stock was a

gift from Dr. Georgia Perona Wright, University of British Columbia, Canada) was

maintained in male C57BL/6 and CD1 mice by alternating bimonthly passage into new

animals. Cysts were obtained from the brains of these animals a month after infection.

Ten cysts were orally administered per mouse (female C57BL/6) followed by Hb larvae

14 days later. Mice were euthanized 21 or 28 days post Hb infection (Fig 7A).

Sample size was calculated based on numbers used in our previous work [13] or for the

flow cytometry of granuloma cells, on infecting enough animals to obtain the required

amount of cells. No animals for which we obtained data were excluded from analysis.

However, criteria had been set. We would have excluded all animals developing

pathologies unrelated to infections during the experiment or observed during necropsy

(e.g. tumours). Animals were not randomised. Co-infections and trickle infections

require many manipulations. Our experience is that using confounders increases

mistakenly providing the incorrect treatment to the mice.

All mice were monitored daily. Humane endpoints were defined as: general decline of

health, respiratory distress, severe neurological signs, loss of body weight > 20% or

recommendation from the facility veterinarian. Animals were euthanised within 24

hours of humane endpoints being observed. For TgHb animals, a small number of

animals were found dead before the 28 days post-Hb infection. This happened towards

the end of the experiment, usually in the early morning, after a check of humane

endpoints the previous day.

Hb antigen was prepared by collecting live adult worms from 14/21 or 28-day infected

mice using modified Baerman's apparatus. Worms were washed multiple times and

homogenized in PBS using a glass homogenizer. The resulting solution was centrifuged

(13, 000 g, 10 minutes, 4°C) and the supernatant filtered (0.2mm filter, Nalgene). The

protein concentration was calculated using the Bradford assay. The antigen was stored

at 15 mg/ml at -80°C.

We collected immune serum from trickle infected mice euthanized at D14 using a

previously published trickle infection model [13]. We transferred 100ul intravenously to

bolus infected mice at day 0, day 2, day 4 and day 6.

Worm and Granuloma Counts

Small intestines of infected mice were harvested and opened longitudinally. The number of adult worms present in the intestinal lumen along the length of the small intestine was counted under a dissection microscope. Macroscopic granulomas were counted by eye under a dissection microscope with the small intestine intact.

Granuloma size

Consecutive formalin fixed paraffin embedded mouse small intestinal sections were stained with H & E by the University of Calgary's Veterinary Diagnostic Services Unit. Stained tissue sections were analyzed visually using the Leica DMRB light microscope and/or the OLMYPUS SZX10 microscope. Images of granuloma were captured using the QCapture and the cellSens software and processed using the ImageJ software, in a blinded manner. Whole granuloma and necrotic centre size were measured for each granuloma on the slide. Granuloma area was calculated using ImageJ. Granuloma were outlined using the freehand perimeter tool and area was calculated using a pre-determined measurement scale.

Serum ELISAs

Blood samples were left to clot for 30 minutes and then centrifuged twice at 11, 000 g at

4°C for 10 minutes. Serum was collected and used either fresh or stored at -80°C. Total

IgE (BD, 555248) and IgA (capture antibody, BD, 556969, detection antibody, BD,

556978) and IgG1 levels (capture antibody, BD, 553440, detection antibody, BD,

553441) were measured by ELISA according to manufacturer's instructions.

Antigen specific antibody responses were also measured by ELISA. ELISA microplates

were coated with 10 mg/ml *H. bakeri* antigen in carbonate buffer (0.1mM NaHCO3, pH

9.6), overnight at 4°C. Plates were blocked with 2% BSA in TBS/ 0.05% tween 20 for 2

hours at 37°C. Sera were diluted in TBS Tween and added to wells overnight at 4°C.

Antigen-specific IgG1 was detected with HRP-conjugated corresponding detection

antibodies (anti-IgG1, BD, 553441) with TMB peroxidase substrate (T3405, Sigma). The

reaction was stopped using 1M H2SO4 solution and the color change was read at

450nm.

Intestinal tissue homogenate ELISAs

Small intestines were opened longitudinally and washed with PBS to remove luminal

content. The mucosal surface was identified under a dissecting microscope. The mucosal

surface (with its mucus) was gently scraped using a glass slide. Scrapings were weighed,

added to 500 ml lysis buffer (10 mM tris HCl, 0.025% sodium azide, 1% tween 80, 0.02%

phenylmethylsulfonyl fluoride) with one complete protease inhibitor tablet (Roche

diagnostics GmbH, Germany) and homogenized using a bead beater (40 seconds at

speed 6 using the Fast-prep-24 bead beater, MP biomedical). The homogenate was

centrifuged at 11, 000 g at 4°C for one hour. Supernatants were collected and used fresh

or stored at -80°C. IgA (IgA (capture antibody, BD 556969, detection antibody, BD

556978), IL-4 (R & D systems, DY404 kit), IL-13 (R & D systems, DY413 kit) and IL-21 (R &

D systems, DY594 kit) was measured by ELISA according to manufacturer's guidelines.

All IL-21 ELISAs were performed on fresh, unfrozen material [31].

MLN and SPL Cell isolation, *in vitro* re-stimulation assay and cytokine ELISAs

Mesenteric lymph nodes (MLN) and spleens (SPL) were mechanically dissociated into

single cell suspensions. Cells were counted using a Beckman-Coulter ViCell XR. MLN and

SPL were cultured at 1 x 10^6 cells/ml for 48 hours in RPMI medium, 10% FCS, 1% L-

glutamine, 1% penicillin/ streptomycin (supplemented RPMI 1640) in the presence of 10

mg/ml *H. bakeri* antigen or 2 mg/ml concanavalin A (Sigma) at 37^oC with 5% CO2.

Supernatants were collected for cytokine measurements. Measurements for antigen-

specific production were not included in the analysis unless cytokine production was

observed in the wells with concanavalin A stimulation. ELISAs were performed according

to manufacturer's guidelines (R & D systems, DY404 kit for IL-4 and DY413 kit for IL-13).

Transit time

Gastrointestinal transit time was measured one day prior to euthanasia. Mice were

fasted for 6 hours and 200 ml of 5% Evans blue (Sigma) in 5% gum arabic (ACROS

organics) was orally gavaged using a ball tip 20 gauge 1.5'', 2.25mm curved animal

feeding needle. Each mouse was labelled, with the time of dye administration recorded.

Mice were transferred to clean empty cages and the time to pass the first blue fecal

pellet was recorded. Gastrointestinal transit time was calculated for each mouse.

Immunofluorescence

Whole small intestines were fixed in formalin for a minimum of 48 hours, washed in

saline for a minimum of 48 hrs and processed to obtain paraffin embedded tissue

blocks. 6um sections were cut by the Diagnostic Services Unit, UCalgary. The sections

were stained for H&E or with either anti-mouse IgG_1 (BD 562026), anti-mouse IgA (BD

559354), anti-mouse IgE (BD 553415), anti-mouse IgG_{2c} (Invitrogen SA5-10221) or their

respective isotypes overnight at 4°C. Slides were mounted with FluoroshieldTM with

DAPI (Sigma-Aldrich F6057). Images were acquired using the Zeiss Axio ZoomV.16

stereoscopic microscope (Bio Core Facility, University of Calgary) or the Thorlabs Tide

whole- slide scanning microscope (Live cell imaging Facility, University of Calgary).

Brightfield and fluorescence images were taken either under the 2.3x objective with the

AxioCam High Resolution color (HRc) and High-Resolution mono (HRm) cameras, or the

20x/0.75 NA objective of the slidescanner respectively. Zeiss Zen (blue edition) software

or Thorlabs Tide LS image acquisition software was used. DAPI, FITC and Texas Red

fluorophores were used. Brightness and contrast were adjusted similarly for all

photographs in photoshop.

Granuloma Digestion for Flow cytometry

Granulomas were identified along the small intestine as tissue (containing worms) or

lumen (chronic granuloma not containing worms) using a dissection microscope.

Granulomas from 5 mice were pooled by infection type (trickle/bolus/co-infected) and

granuloma type (tissue/lumen). Isolated granulomas were incubated with DNAse (Roche

10104159001) and 1:50 Liberase (Roche 0540102001)) at 37°C for 90 minutes. After

incubation, granulomas filtered, washed, centrifuged and stored at 4°C until use.

Cells were counted using a Vi-CELLTM XR Cell Analyzer (Beckman Coulter 731196). $1x10^6$

cells (100µL) were used per sample. Samples were stained with fixable viability stain

(BD, 565388 or BD 564406) for 15 minutes at RT in dark, blocked with rat anti-mouse

CD16/32 (BD 553142) for 5 minutes at 4°C in the dark and stained for surface markers

for 20 minutes at 4°C in the dark. For the granuloma panel, cells were stained for CD3

(BD 560591), CD19 (BD 612781), NK1.1 (BD 564143), SiglecF (BD 552126), CD206 (BD

565250), Ly6G (BD 740953), CD11b (BD 563553), and IgG1 (BD 553443).

For intracellular staining (IgG_1 and IgA), samples were fixed, permeabilized and stained

for IgG_1 (BD 553443) and IgA (BD 743293) or isotype controls (BD 554684, BD 562868)

for 30 minutes at 4°C. Samples were then washed and centrifuged. Resuspended

samples were run on an LSRFortessaTM X20 (BD Biosciences) flow cytometer. Data was

acquired using FACSDivaTM software, and analysis of cell populations was performed

using FlowJoTM software (v10.7.1).

MLN and Peyer's Patches Isolation for Flow Cytometry.

Peyer's patches (PP) and MLN were removed from the small intestine under the

dissection microscope. Cells were mechanically dissociated into single cell suspensions.

PP and MLN cells were counted using a Vi-CELLTM XR Cell Analyzer (Beckman Coulter

731196). $1x10^6$ cells (100μL) were used per sample. Samples were stained with fixable

viability stain (BD 564406) for 15 minutes at RT in dark, blocked with rat anti-mouse

CD16/32 (BD 553142) for 5 minutes at 4°C in the dark and stained for surface markers

for 20 minutes at 4°C in the dark. For the plasma cell panel, cells were stained for CD3

(BD 566495), IgD (BD 558597), B220 (BD 561880), CD19 (BD 612781), and CD138 (BD

563193/565176).

RNA/DNA Extraction and Quantitative PCR

RNA and gDNA were extracted from 4 equal snap frozen sections of the SI (sections 1-4,

where 1 is the most proximal section and 4 the most distal from the stomach) by

crushing the tissue in Trizol (Ambion, Life Technologies) using a pestle and mortar on dry

ice. We followed manufacturer guidelines for RNA extraction. To measure cytokine

levels in the RNA samples, cDNA was prepared using DNase 1 (RNase-free, New England

Biolabs), and iScript Reverse Transcription Supermix for RT-qPCR (Bio-Rad) or

AdvanTech 5x Revese Transcription master mix (Diamed).

Primers for quantitative PCR were obtained from Integrated DNA Technologies (San

Diego) for IL-13 (GATCTGTGTCTCTCCCTCTGA forward, GTCCACACTCCATACCATGC

reverse), IFNγ (TCAAGTGGCATAGATGTGGAAGAA forward, TGGCTCTGCAGGATTTTCATG

reverse), IL-10 (GTCATCGATTTCTCCCCTGTG forward, ATGGCCTTGTAGACACCTTG

reverse) and 18S rRNA (GCAATTATTCCCCATGAACG forward, GGCCTCACTAAACCATCCAA

reverse). Samples were run in triplicate on a Bio-Rad CFX96 real time system C1000

touch thermocycler. Relative quantification of the cytokine genes of interest was

measured with the delta-delta cycle threshold quantification method [32], with 18S rRNA

for normalization. Data are expressed as a fold change relative to 18S rRNA levels for

each animal.

ELIspot Assay

Plates were then coated with either purified rat-anti mouse IgG1 (BD 553440) or Hb

antigen and incubated overnight at 4°C. Plates were washed and blocked with media for

2 hours at 37°C with 5% CO_2. MLN cells added in triplicate at 5×10^3 cells/mL to measure

total IgG1 producing cells. For quantifying *H. bakeri* antigen-specific IgG1 producing

cells, a total of 2×10^6 cells were cultured overnight at 37°C with 5% CO_2. For detection,

IgG1 (BD 553441) was incubated for 2 hours at RT, followed by a Streptavidin-HRP

(horseradish peroxidase; BD 554066) incubation for 1 hour at RT. Spots were allowed to

develop for 5-7 minutes once the substrate solution had been added, before stopping

the reaction. Plates were allowed to dry for 24-48 hours, before spots were counted

manually under a dissecting microscope.

Statistical Analysis

Graphpad Prism software (La Jolla, CA, USA) was used for all statistical analysis. To

compare multiple groups (three or more), we performed a normality test (D'Agostino

and Pearson test, unless N too small, in which case Anderson-Darling or Shapiro-Wilk).

ANOVA or Kruskal-Wallis tests were performed on parametric/non-parametric pooled

data, and when significant, Sidak's/Dunn's Multiple comparisons were performed on Hb

vs. HbTg and Tg vs. HbTg. For comparisons of 2 groups, statistical significance was

assessed by either an unpaired t test (for data sets with normally distributed data) or

Mann-Whitney's U test (for non-parametric data) or paired t test (for paired data sets

with normally distributed data). Data are presented as median and individual data

points, unless otherwise specified.

RESULTS

The resistant phenotype in trickle infected C57Bl/6 mice is not associated with

increased Th2 cytokine or antibody levels.

We have previously shown that using a trickle regimen, C57Bl/6 mice harbour fewer Hb

worms and have more granulomas than bolus infected mice [13]. Using a more robust

trickle model (more doses and later time points, Fig. 1A), we show even starker

differences depending on the mode of infection. After 28 days (D28), the Hb worm

burden (primary outcome) of the trickle-infected group was below 5 worms in 8/10

animals compared to a mean of 76 in bolus infected animals (Fig 1B). The granuloma

number was also higher in trickle infected animals, with 9/10 mice having more

granulomas than the bolus infected mouse with the most granulomas (32 granulomas,

Fig. 1C). Despite granuloma size being associated with susceptibility/resistance

phenotypes [12], we found that this parameter was not affected by the mode of infection.

Neither the size of the whole granuloma, nor the size of the internal necrotic centre

changed with the mode of infection (Fig 1D and 1E). However, as we have previously

shown with trickle infection [13], granuloma composition differs between bolus and trickle

infected animals. Macrophages numbers are similar (Fig 1F) but eosinophil numbers are

increased (Fig 1G). In resistant Balb/c animals, we see no differences in worm burden or

granuloma number between bolus and trickle infected animals (Sup Fig 1A and 1B).

A strong Th2 response is responsible for anti-parasitic worm immunity. Increased levels

of IL-4 and IL-13 in the MLN (mesenteric lymph nodes) and SPL (spleen) are commonly

reported in bolus infected animals and have been directly linked to parasite

clearance[9,10,33-35]. However, in trickle infected animals, previous studies have not linked

reduced parasite burdens to an increase in these cytokines [13,36]. We found no

differences in the levels of IL-4 and/or IL-13 between bolus and trickle infected mice,

apart from IL-13 in the SPL (Fig 2A-F). SPL IL-13 levels were recorded per cell and likely

decreased in the trickle infected animals in response to the low worm burden. When

accounting for differences in total cell number (Fig 2E and 2F), IL-4 and IL-13 levels in the

MLN and SPL in trickle and bolus infected animals remain similar. Levels of IL-4 and IL-13

were undetectable in the serum, as previously observed [13]. Again, in resistant Balb/c

animals, we see no differences between bolus and trickle infected animals in any of the

parameters measured, apart from spleen IL-13 (Sup Fig 1C-H).

Th2 immune responses can also be observed closer to the host/parasite interface, in the

Peyer's patches (PP) and the small intestine (SI). Levels of the Hb antigen-specific IL-4

and IL-13 were again similar between bolus and trickle infected animals (Fig 2G-J). No

levels of IL-5, IL-9 or IL-10 were detectable in intestinal tissue from control or infected

mice, as previously observed [13]. Increased mucus production [37], intestinal smooth

muscle contractility [38] and IL-21 levels [39] have all been associated with parasite

clearance. However, none of these parameters differed between the two infected

groups in the SI (Fig. 2K-M).

Resistance to Hb has also been linked to increased parasite-specific IgG_1, IgA and IgE

levels [18]. Total IgG_1 and IgE levels were increased in the serum of infected vs. naïve mice

(Fig 3A and 3B). However, the levels did not change with the mode of infection. No

difference was observed in the levels of parasite specific IgG_1 either (Fig 3C). Levels of

intestinal IgA did not differ between naïve, bolus infected or trickle infected animals (Fig

3D). No detectable levels of Hb larval or adult parasite antigen specific IgE, IgG_{2c} or IgA

were observed in the serum of bolus- or trickle-infected mice. In resistant Balb/c

animals, we see no differences between bolus and trickle infected animals in IgE or IgG_1

levels (Sup Fig 1I-K).

By D28 of infection, all worms had migrated from the tissue to the lumen. Our results

are therefore unsurprising in light of the importance of immunity against developing

tissue parasite stages, which are best observed at the host/parasite interface early

during infection. We next focused our efforts on studying immune responses within the

granuloma during acute infection.

Cell-bound IgG_1 antibodies accumulate around encysted larvae in the granulomas of

trickle-infected C57Bl/6 mice.

By D10 most, if not all, parasites have matured into adults, and left the tissue to inhabit

the lumen. Previous research has demonstrated that the resistance to Hb attained by

the host after vaccination and/or secondary infection is aimed at incoming larvae [14,15].

To study immune responses against larvae in the trickle infected animals, we euthanised

mice at D21 instead of D28 (3 instead of 10 days after the final parasite dose). This

ensured there were both developing parasites in the tissue and adults in the lumen. We

matched these to an early (D5) and late (D21) bolus infection (Fig 4A).

Tissue dwelling stages are immobilised/damaged/destroyed by antibody-bound cells

within the granulomas (reviewed in [11]). To quantify antibody levels within granulomas,

we isolated worm containing (acute) and non-worm containing (chronic) granulomas

and measured antibody levels on the isolated cells by flow cytometry (Sup Fig 2 for

gating strategy). Acute granulomas from trickle infected animals had the highest levels

of $CD11b^+IgG_1^+$ cells (Fig 4B and 4C). We confirmed these findings by staining for

antibodies in intestinal tissue sections isolated from infected mice (Fig 4D-F).

Interestingly, we only detected IgG_1 within the acute granulomas, and did not observe

any IgG_{2c} (Fig 2E), which has previously been linked to trapping developing worms

within granulomas upon secondary infection [15]. We did not observe IgA or IgE (Fig 2F)

within the granulomas either, confirming that IgG_1 is the key antibody subtype

associated with resistance in our model. Our results are in accordance with previous

work studying vaccination mediated protection [14].

Chronic granulomas had very low/background levels of IgG_1 (Fig 4G-I). However, despite

this, the granulomas from trickle infected animals were bigger (Fig 4J), with necrotic

centres of similar size (Fig 4K). Since this difference was not apparent at D28, the

observation is likely due to granuloma age. Once the worms have left the granulomas

and/or been killed within it, granulomas resorb. Chronic granulomas in the bolus

infected animals are all ~18 days old (granulomas start forming within 3 days of

infection), those in the trickle infected animals range in age from 8-18 days.

To assess whether the differences in granuloma antibody levels were due to differences

in antibody production, we measured plasma cell antibody levels at D21 in the MLN and

PP, the closest antibody-producing sites to the granulomas (Fig 5, Sup Fig 3 for gating

strategy). Plasma cell percentages in the MLN and PP of trickle infected mice were

decreased compared to bolus-infected mice; their numbers in the MLN followed this

trend (Fig 5A-D). We focused on IgA and IgG_1 levels because previous work has

demonstrated that, in a secondary infection, animals lacking these antibodies have

higher worm burden than wildtype animals [18]. At D21, intracellular IgG_1^+ plasma cell

percentages in the MLN (Fig 5E) and PP (Fig 5F) in trickle infected mice were increased

compared to naïve animals but decreased compared to bolus infected animals. Cell

numbers in the MLN followed this trend (Fig 5G). As expected, percentages in the MLN

were far greater than in the PP [18]. The decrease could be attributed to a lack of parasite

stimulation in the trickle infected animals, which have significantly lower worm burdens.

No differences were found between trickle and bolus infected animals with regards to

IgA^+ plasma cell percentages and/or numbers in the MLN and/or PP (Fig 5I-K). The

amount of soluble antibody produced per cell, measured by mean fluorescence index

(MFI) ratios, did not differ for either the antibody type (IgG_1 or IgA) or the immune site

(MLN or PP) between bolus and trickle infected mice (Fig 5L-O).

We have already demonstrated that IgG_1 serum and granuloma levels and serum IgA are

undetectable in bolus infected animals at the tissue worm stage (D7), when acute

granulomas are present [13]. This contrasts with trickle infected animals, which have

acquired partial resistance (Fig 1), have elevated levels of IgG_1^+ PP and MLN plasma cells

(Fig 5), and increased levels of serum and granuloma IgG_1 (Fig 3 and 4) during tissue

worm development. However, when we passively transferred serum from trickle

infected mice to bolus infected animals, we did not detect IgG_1 within their acute

granulomas (Sup Fig 4), suggesting that cells, and not only antibodies, present in the

granuloma have an important role to play. This supports the idea that sterile immunity

may require either extremely high antibody titers, or the activation of additional

protective effector cell populations [14].

IgG-bound macrophages and eosinophils are the cells of the granuloma responsible for

parasite damage/death (reviewed in [11]). We found that within the IgG_1^+ cells of the

trickle infected animals, $SiglecF^+$ (eosinophils) and $CD206^+$ (macrophages) cells

accounted for approximately 50% of the antibody bound cells (Fig 6A, Sup Fig 2 for

gating strategy). When comparing the composition of the whole acute granulomas from

trickle and bolus infected animals, trickle infected animals had a far higher proportion of

$SiglecF^+$ (Fig 6B) and $CD206^+$ cells (Fig 6C) than bolus infected mice. Proportions of $Ly6G^+$

(neutrophils, Fig 6C) and NK1.1[+] (NK cells, Fig 6D) cells remained unchanged between

the two groups.

Resistance in trickle infected mice is therefore associated with the presence of both

antibodies and SiglecF^{+}/CD206^{+} cells at the host/parasite interface during tissue

development. However, if repeated infections provide protection from Hb, why is this

not reflected in nature, where repeated infections are common? Wild rodents have a

high incidence of Hb [25,26] and, more generally, intestinal worms are common parasites of

humans [1], livestock (reviewed in [2]) and pets [3].

Resistance to Hb in trickle infected animals is lost when they are pre-infected with Tg

In natural settings, co-infection is common [28]. This translates to complex host immune

environments. To integrate the increased complexity produced by a mixed immune

response and potential co-infections into our research, we used *Toxoplasma gondii* (Tg)

as a potent inflammatory parasite. The order and time between infections was

optimized to ensure minimal pathology while retaining characteristic immune

signatures: animals were pre-infected with 10 Tg cysts 14 days prior to trickle Hb

infection (Fig 7A). In a previous study using the bolus model of infection, pre-infection

with Tg skewed the immune response to a mixed Th1/Th2 Hp immune response by D28.

Focusing on the sections with the most granulomas (first half of the small intestine, with

SI1 equating to the duodenum and SI2 to the first part of the jejunum), at D21, we found

that intestinal levels of *ifnγ* and *il10* gene expression were increased in the jejunum of

HbTg trickle infected mice, while *il13* levels were not different (Fig 7B-G). We wanted to

determine whether this more complex immune environment would disrupt the effective

anti-larval immunity observed during trickle infection, and impact worm burden.

In this context, we found that pre infection with Tg led to higher worm burdens at both

D21 and D28 (Fig 7H). Unsurprisingly, the increased parasite burden was associated with

fewer granulomas (Fig 7I) of smaller size (Fig 7J). Taking a closer look at the tissue

granulomas from TgHb animals, we found they had decreased levels of IgG_1^+ cells at

D21, as observed by flow cytometry (Fig 8A and 8B) and immunofluorescence (Fig 8C).

The overall cellular composition of granulomas was also altered: proportions of $SiglecF^+$

and $CD206^+$ cells were decreased (Fig 8D and 8E); proportions of $Ly6G^+$ (Fig 8F) and

$NK1.1^+$ (Fig 8G) cells remained unchanged. Histology confirmed our flow cytometry

findings: HbTg animals had fewer eosinophils (Fig 8H). Interestingly, total macrophages

numbers were similar between the two groups (Fig 8I). However, this is likely because

similar numbers of macrophages are recruited to the granulomas in both groups.

However, in HbTg animals, the influx of CD206+ macrophages is reduced is

counterbalanced by the influx of other more inflammatory macrophages.

To study whether reduced antibody production was responsible for reduced granuloma

antibody levels, we measured plasma cell antibody levels at D21 in the MLN using flow

cytometry (Fig 9). While total MLN cell numbers were decreased in co-infected animals

(Fig 9A), plasma cell percentage and numbers were increased (Fig 9B and 9C). The

proportion of MLN IgG_1^+ plasma cells was also increased in TgHb animals (Fig 9D),

although their number and antibody production level per cell (MFI) were similar

between the two groups (Fig 9E and 9F). However, when focusing on antigen specific

IgG_1 producing cells using ELIspot, TgHb animals had far fewer cells than Hb animals: a

maximum of 93 vs a mean of 318 (Fig 9G). The difference was not apparent when

measuring total IgG_1 (Fig 9H). Finally MLN IgA^+ plasma cells were decreased in number

(Fig 9I) but not in proportion (Fig 9J) or in their capacity to make IgA (MFI, Fig 9K).

Therefore, in co-infected animals, increased worm burdens are associated with a

reduction in the efficacy of granulomas: they lack the presence of $SiglecF^+$ and $CD206^+$

cells as well as parasite specific IgG_1.

DISCUSSION

The pattern of resilience/resistance observed in the laboratory is not what is observed

in naturally infected populations of animals – instead, GINs are widespread in wild

populations. As an example, studies in wild mice have reported a greater than 60%

prevalence with one or more helminth parasites [25–27] and in a recent Albertan survey,

100% of cattle herds were found to be infected with intestinal nematodes [40]. This is

likely due to stark differences in laboratory conditions compared to natural

environments. Factors such as nutrition, age, genetics and environment all play a role.

Importantly, so do immune history and co- infection, which can affect the immune

system's ability to respond to a parasite infection.

GIN infections typically occur over extended periods of time, with small amounts of

parasite taken up regularly during feeding. The mode of infection is an important factor

in the ensuing immune responses. Multiple low dose, or trickle infections, have long

been associated with increased resistance to helminth parasites, resulting in a

"resistant"/resilient phenotype in animals that are normally considered susceptible [13,41–

44]. This acquired resistance can remain long-term, with trickle infected animals

maintaining their ability to eliminate worms during subsequent challenge infections [41].

Here, we show that effective granulomas are key to eliminating incoming GIN larvae:

anti-GIN antibodies must be produced in time to target tissue developing parasites and

directed to the host/parasite interface where they can bind activated myeloid cells to

immobilise/damage/kill the parasites. Bolus and TgHb trickle infected animals had high

worm burdens. In bolus-infected susceptible animals, the antibodies were not produced

in time to reach the acute granulomas before the worm exited the tissue. In TgHb

trickle-infected animals, granuloma formation was impacted by a reduction in the influx

of GIN-specific antibody and myeloid cells to the host-parasite interface.

Granulomas are formed as a response to tissue invading Hb and consist mainly of

macrophages and eosinophils. The exact mechanisms by which tissue developing

parasites are immobilised/damaged/destroyed within the granulomas *in vivo* have not

been fully characterised. A study involving *Nippostrongylus brasiliensis* (closely related

to Hb) infection in mice found that following primary inoculation with the parasite, Th2-

primed macrophages remained in the lung (site of parasite development) and facilitated

rapid larval clearance upon reinfection [45]. Trickle infection of *N. brasiliensis* in its natural

host, the rat, results in increased lung macrophages and eosinophils [46]. We found

increased levels of CD206$^+$ cells in the tissue granulomas of trickle infected mice

suggesting that long-lived, previously sensitized CD206$^+$ macrophages may also play a

direct role in the clearance of Hb tissue stages from the intestine in these animals.

During *Litomosoides sigmodontis* infection, a parasite which does not cause granulomas

but develops in the pleural cavity, CD206$^+$ pleural cavity macrophage populations

increase due to the proliferation of tissue-resident macrophages and, to a lesser extent,

the re-programming of recruited inflammatory macrophages [47]. One caveat of our work

is that we did not assess markers of tissue residence or recruitment on granuloma

macrophages. Without this information, no definite conclusion can be made about the

origins of the cells that are required for the effective anti-larval immune response seen

in trickle-infected animals.

In vitro and in the presence of immune serum, CD11b on bone marrow derived

macrophages can directly bind Hb larvae using complement 3 [16]. This allows FcγR1 to

interact with parasite bound IgG$_{2a/c}$ (but not IgG$_1$) antibodies to immobilize the larvae [15].

However, while immune serum allows macrophages to bind to Hp larvae *in vitro*, it does

not impact infectivity, suggesting that macrophages are important only in parasite

immobilisation and not damage/killing. The authors hypothesised that this rapid

activation via $IgG_{2a/c}$ and Fc receptors would likely be important against tissue dwelling

parasites during acute infection, but this has yet to be proved as the main mechanism of

parasite immobilisation *in vivo*. In accordance with the authors, we observed $CD11b^+$

antibody-bound macrophages within the worm-containing granulomas of trickle-

infected mice. However, only IgG_1, and not $IgG2_c$, was observed in the granulomas

which supports previous reports identifying IgG_1 as the protective mechanism in

vaccinated mice [48]. Despite their proximity to Hb's infective niche, we saw no increase in

IgG_1^+ plasma cells in the PP of Hb infected animals. This is likely due to parasite-derived

immunomodulatory molecules preventing Th2 polarization at this site, as PP in direct

contact with Hb larvae show significant expansion of Treg populations [49].

A recent systematic review has concluded that IgA is associated with partial protection

from helminths in mice, rats and sheep [50]. Mechanism of protection include

entrapment, neutralization, and eosinophil-mediated ADCC. Mice infected with Hb have

elevated IgA levels during primary [17] and repeated [44] infections; mice lacking IgA and

infected with Hb in a drug cure/reinfection model do not clear parasites as effectively as

wildtype animals [18]. We did not observe IgA within the granulomas of trickle infected

animals and did not associate IgA with tissue parasite immobilisation/damage/

clearance.

The role of eosinophils during helminth infection has long been debated (reviewed in

[51]). *In vitro* studies have demonstrated that peritoneal and bone marrow derived

eosinophils can respectively adhere to [52] and limit the motility of parasitic worm larvae

through extracellular traps [53]. Eosinophils obtained from the mammary washes of sheep

can kill *Haemonchus contortus* (closely related to Hb) *in vitro* in the presence of

antibody; efficacy was increased in the presence of complement and by using 'primed'

eosinophils from previously infected sheep [54]. *In vivo,* studies using transgenic animals

show that killing by toxic granules is also important: EPX- and MBP1-deficient Balb/c

mice have higher worm burdens than wildtype mice after *L. sigmodontis* infection [55].

Data from *H. contortus* immunised sheep supports these findings: tissue larvae in the

vicinity of eosinophils were found to be at varying stages of damage [56]. However, in Hb

infected mice, parasite loads in mice lacking eosinophils (Balb/c Δdbl- GATA-1 and

C57Bl/6 PHIL) are similar to wild type animals [57] and others have shown that eosinophils

do not adhere to Hb *in vitro* [16], questioning the importance of this cell type in parasite

killing. Despite having similar worm burdens, Δdbl- GATA-1 mice challenged with Hb

after vaccination had significantly higher numbers of live larvae trapped in their

intestinal wall compared to their wild-type counterparts [48]. This suggests that

eosinophils are responsible for killing but not immobilising tissue-dwelling parasite

stages. The cells likely work in concert with macrophages to limit the number of tissue

dwelling parasites that develop into adults, which explains their elevated numbers in the

granulomas of trickle infected animals.

We have previously shown that by 10 days of infection with Tg, a strong increase in IFNγ

and IL-10 develops along the whole small intestine, the PP, MLN, SPL and the liver [58].

This immune environment impacts the ability of C57Bl/6 mice to mount an effective

immune response against a trickle Hb infection. We observed fewer and smaller

granulomas; they contained a lesser proportion of $CD206^+$, $SiglecF^+$ and IgG_1-bound

cells. To the naked eye, the acute granulomas were not as well formed, and the chronic

granulomas did not have the characteristic bead-like appearance that is associated with

bolus/trickle infections. Interestingly, in wild mice, granulomas are rarely observed by

eye (Pers. Comms. Dr Simon Babayan). This could be due to differences in parasite

lifecycles (*H. polygyrus* vs. *H. bakeri*), host responses (wood mice vs. laboratory mice) or

could suggest that a more complex immune environment impacts the formation of

these structures.

In a model of allergic inflammation, pre-infection with Tg resulted in decreased serum

allergen-specific IgG_1 levels [59]. Despite similar levels of IgG_1-producing plasma cells and

IgG_1 production, HbTg infected animals also had reduced antigen specific (Hb) IgG_1^+

MLN plasma cell levels compared to Hb trickle infected mice, which helps explain why

we observed very little IgG_1^+ in the granulomas of TgHb infected mice. These results

reflect gastrointestinal nematode infections in the wild whereby *H. polygyrus* infected

mice co-infected with the coccidian *Eimeria* had lower *H. polygyrus*-specific serum IgG_1^+

titers than *H. polygyrus* only infected mice [26]. HbTg infected animals also had elevated

proportions and numbers of plasma cells, indicating the induction of a polyclonal

antibody response against both pathogens, rather than a strong Hb-specific response.

The production of polyclonal antibodies during Hb infection has previously been shown

to reduce fecundity of adult worms in the intestinal lumen but not to reduce worm

burden [18], supporting our findings.

Despite receiving the same multiple small dose infection as trickle infected animals, the

proportion of SiglecF$^+$ and CD206$^+$ cells in the granulomas from co-infected animals was

severely reduced, indicating that Tg significantly impaired the recruitment of these cells

to the granulomas. TgHb bolus infected mice have been shown to simultaneously

decrease proportions of Th2 (GATA3$^+$CD4$^+$) cells and drastically increase proportions of

Th1 (T-Bet$^+$CD4$^+$ and T-Bet$^+$CD8$^+$) cells in the small intestine, mesenteric lymph nodes,

and spleen [30]. Hb-specific CD4$^+$ T cells produce IFNγ rather than IL-4 or IL-13 *in vitro*. This

observed shift would also impact other cells. For example, intestinal epithelial cells

recruit eosinophils to the small intestine through the production of eotaxin-1, following

activation in a Th2 environment [60]. The impairment of Th2 cytokine production would

therefore directly affect the recruitment and activation of eosinophils and CD206$^+$

macrophages, both of which are dependent on Th2 cytokine signaling (reviewed in [61,62]).

This has also been observed in the context of *N. brasiliensis*. When pre-infected with the

apicomplexan *Plasmodium chabaudi* (related to Tg), *N. brasiliensis* co-infected animals

had reduced CD206$^+$ macrophage accumulation at the site of parasite development, the

lung [63]. When Tg was the pre-infecting parasite, increased shedding of eggs (both in

amount of eggs and length of time) was observed in the co-infected animals [64].

Increased worm fecundity was also observed in TgHb infected animals using the bolus

infection model [30], but unlike with the trickle model, no difference in worm burden was

detected.

Recent work has demonstrated that larval trapping after secondary infection does not

require macrophages, rather it is intestinal epithelial cells that play a critical role in this

regard [65]. The exact molecules involved remain to be identified, although the process

was reliant on IL-4R signalling. The TgHb mice had significantly increased levels of

intestinal *ifnγ* levels throughout the experiment which may have hampered the IEC IL-4R

signalling required for effective clearance.

NK and neutrophils proportions did not change with the mode of infection. Recent work

has argued that NK cells are essential for host protection during the acute phase of Hb

infection. Removing NK cells did not impact worm burden or fitness in the bolus mode

of infection, rather intestinal injury was increased [66]. Ly6G$^+$ cells have been identified

within the granulomas of Hb infected animals [67,68]. However, immunity to Hb following

vaccination was unaffected by the loss of neutrophils induced by antibody treatment in

C57Bl/6 animals [48], and neutrophil populations did not increase in the lungs of mice with

a secondary *N. brasiliensis* infection [45].

One limitation of our study is that we did not assess whether differences in the

microbiome could account for the changes we observed. In the laboratory setting, Tg

infection (Me49, oral gavage) leads to dysbiosis, characterised by an increase in

proinflammatory Pseudomonadota species and a reduction of beneficial commensal

species, that persists into the chronic stage of infection [69]. By contrast, Hb infection in

C57Bl/6 mice leads to duodenal increases in the abundance of the immunoregulatory

Lactobacillus species [70] and infections in germ free mice result in increased worm

burdens [71]. However, in experiments using the trickle, rather than bolus, infection

model it was demonstrated that mice infected with *Trichuris muris* recovered alpha

diversity following the development of resistance [41]. Interestingly, in mice infected with

T. muris which were then moved outdoors and acquired an enriched microbiome, the

authors measured a decrease in Th2 and increase in Th1 immunity associated with

increased worm burdens and biomass [72], somewhat reflecting the more nuanced

immune environments created in our co-infection model. However, it is also important

to remember that other factors, unrelated to host biology, such as temperature and

humidity which are strong moderators of the microbiome [73], may play a significant role

in infection outcome in the wild. And that restricting studies to Th1 vs. Th2 in a

particular setting at a particular timepoint likely oversimplifies the mechanisms

underlying the optimal host response [74]. However, compared to both the typical

experimental infection (bolus) and the single infection grazing type infection (trickle),

the co-infection trickle model described here more realistically reflects immune

responses in real-world infections. Feeding through grazing exposes hosts to a variety of

pathogens. While our two-parasite system is not nearly as complex as real-world

infections, our research begins to explain the overwhelming prevalence of helminth

infections worldwide.

ACKNOWLEDGEMENTS

COMPETING INTERESTS STATEMENT

The authors declare that they have no known competing financial interests or personal

relationships that could have appeared to influence the work reported in this paper.

DATA ACCESS

All data not available in the manuscript or supplemental materials are available from the

corresponding author upon request.

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FIGURE LEGENDS

Figure 1: Characteristics of the H. bakeri trickle infection model in C57Bl/6 mice.

C57Bl/6 mice were infected with 200 *H. bakeri* according to the bolus and trickle

infection regimes. (A) Trickle infection regime: mice are infected with 200 larvae in total,

but in multiple doses over the course of infection (in blue). Doses of 20 larvae are

trickled on days 0, 2, 4, 6, 8, 10, 12, 14, 16 and 18 post-infection This leaves a 10-day

window after the final dose to allow parasites to fully develop into adults and migrate

from the intestinal tissue to the intestinal lumen. Bolus infected mice were infected with

200 larvae at day 0 (in red). Adult worms (B) and granulomas (C) were counted in the

small intestine at D28. Mice were infected according to the bolus (red) and trickle (blue)

regimes. Total granuloma area (D) and the granuloma necrotic centre (E) were

measured on H and E stained slides of whole small intestine. Macrophages (F) and

eosinophil (G) were counted within the center of the granulomas at x400 magnification.

Cells were counted for one field of view (FOV) per granuloma. Graphs represent pooled

data from a minimum of 2 experiments, bars represent the median, with a minimum of

3 mice per group per experiment. A normality test (D'Agostino & Pearson) was

performed, followed by a Kruskal Wallis/Anova (with post-tests) and Mann Whitney/T-

test to test for statistical significance between trickle and bolus groups, n.s. = not

significant, *** = p<0.001, **** = p<0.001.

Figure 2: Th2 response in the SPL, MLN, PP and SI during H. bakeri trickle infection in

C57Bl/6 mice. C57Bl/6 mice were infected with 200 *H. bakeri* larvae according to the

bolus and trickle infection regimes. At D28, single cell suspensions were isolated from

the spleen (SPL) ,mesenteric lymph nodes (MLN) and Peyers Patches (PP) and cultured

for 48 hours in the presence of Hb antigen. (A-D) IL-4 and IL-13 MLN and SPL cytokine

levels were measured in the supernatant by ELISA. Total cell numbers were calculated

for the MLN (E) and SPL (F). IL-4 (G) and IL-13 (H) PP cytokine levels were measured in

the supernatant by ELISA. (I-M) Small intestines were dissected and scraped using a

glass slide leaving only the serosa. (I-J) IL-4, and IL-13, were measured in the intestinal

scrapings by ELISA. (K) The intestinal scrapings were weighed for each mouse and

normalised to control animals. (L) Mice were fasted for 6 hours followed by Evans Blue

administration. Time from dye administration to the passing of dyed fecal pellets was

measured and normalised to control animals. (M) IL-21 was measured in the intestinal

scrapings by ELISA. Mice were infected according to the bolus (red) and trickle (blue)

regimes. Naive mice are represented by grey circles. Graphs represent pooled data from

2 experiments, bars represent the median, with a minimum of 3 mice per group per

experiment. A normality test (D'Agostino & Pearson) was performed, followed by a

Kruskal Wallis/Anova (with post-tests) for statistical significance between trickle and

bolus groups, n.s. = not significant, * = $p<0.05$, ** = $p<0.01$, *** = $p<0.001$, **** =

$p<0.001$.

1010

Figure 3: Antibody levels during H. bakeri trickle infection in C57Bl/6 mice. C57Bl/6

mice were infected with 200 *H. bakeri* larvae according to the bolus and trickle infection

regimes. At D28, blood was collected and serum obtained. (A) Total serum IgE, (B) Total

serum IgG_1, (C) Parasite-specific serum IgG_1 and (D) Total intestinal IgA were measured

by ELISA. Levels in naïve controls were undetectable for parasite specific IgG_1. Graphs

represent pooled data from a minimum of 2 experiments, bars represent the median,

with a minimum of 3 mice per group per experiment. A normality test (D'Agostino &

Pearson) was performed, followed by a Kruskal Wallis/Anova (with post-tests) and

Mann Whitney/T-test to test for statistical significance between trickle and bolus

groups, n.s. = not significant, ** = $p<0.01$, *** = $p<0.001$.

1021

Figure 4: IgG$_1$ in the granulomas of trickle-H. bakeri infected C57Bl/6 mice. C57Bl/6

mice were infected with 200 *H. bakeri* according to bolus and/or trickle models of

infection. (A) Trickle infection regimen (worm-containing granulomas): mice are infected

with 200 larvae in total but spread out over infection (in blue). Mice are euthanised on

day 21, doses of 20 larvae are trickled on days 0, 2, 4, 6, 8, 10, 12, 14, 16 and 18 post-

infection. There is a 3 day window after the final dose to allow parasites to start

developing in the mucosa and observe the formation of granulomas around them, as

well as having mature worms in the lumen. For the comparative bolus infections, we are

using animals infected for 5 (tissue worms only) and 21 (worms found in the lumen only)

days. (B & H) Granulomas were isolated from the small intestine of 5 mice per group.

Granulomas from the individual animals were pooled to form one sample per group.

Cells were obtained by tissue digestion of the pooled samples and stained by flow

cytometry. (B) The percentage of CD11b$^+$IgG$_1^+$ cells as a proportion of live granuloma

cells (with T and B cells removed) from acute granulomas was calculated for three

independent experiments. (C) Representative flow cytometry plots showing IgG$_1$ and

CD11b expression on live granuloma cells from acute granulomas. (D-G) Formalin fixed,

paraffin-embedded sections were obtained from small intestine swiss rolls. These

sections were co-stained with DAPI and either anti-mouse (D) IgG$_1$, (E) IgG$_{2c}$, (F) IgA/IgE

and (G) IgG$_1$. Scale bar=100µm. Antibody stain (left), isotype control stain (right).

Representative granulomas (white lines) containing worms (acute granulomas, D-F) or

not containing worms (chronic granulomas, G) from trickle and bolus infected mice. (H)

The percentage of CD11b$^+$IgG$_1^+$ cells as a proportion of live granuloma cells (with T and B

cells removed) from chronic granulomas was calculated for three independent

experiments. (I) Representative flow cytometry plots showing IgG$_1$ and CD11b

expression on live granuloma cells from chronic granulomas. (J) Total granuloma area

(K) and the granuloma necrotic centre were measured for chronic granulomas on H and

E stained formalin fixed sections from whole small intestine swiss rolls. Graphs

represent pooled data from a minimum of 2 experiments, bars represent the median,

with a minimum of 3 mice per group per experiment. A normality test (D'Agostino &

Pearson) was performed, followed by Mann Whitney/T-test to test for statistical

significance between trickle and bolus groups, n.s. = not significant, * = $p<0.05$, ** =

$p<0.01$.

1054

Figure 5: MLN and PP plasma cell antibody production during H. bakeri infection in

C57Bl/6 mice. C57Bl/6 mice were infected with 200 *H. bakeri* larvae according to the

bolus and trickle infection regimes. Mice were euthanized at D21. Mesenteric lymph

node (MLN) and Peyer's Patches (PP) were isolated to obtain single cell suspensions

which were analysed by flow cytometry. (A) The proportion of MLN CD138$^+$ (plasma)

cells. (B) Representative histogram showing CD138 expression. (C) The proportion of PP

CD138$^+$ cells. (D) The number of MLN CD138$^+$ cells. The proportion of MLN (E) and PP (F)

CD138$^+$ cells expressing intracellular IgG$_1$. (G) The number of MLN CD138$^+$ cells

expressing intracellular IgG1. (H) Representative flow plots showing IgA and IgG

expression on MLN CD138$^+$ cells. The proportion of MLN (I) and PP (J) CD138$^+$ cells

expressing intracellular IgA. (K) The number of MLN CD138$^+$ cells expressing intracellular

IgA. The IgG$_1$ MFI of MLN (L) and PP (M) CD138$^+$ cells expressing intracellular IgG1. The

IgG$_1$ MFI of MLN (N) and PP (O) CD138$^+$ cells expressing intracellular IgG1. Graphs

represent pooled data from a minimum of 3 experiments, bars represent the median,

with a minimum of 5 mice per group per experiment. A normality test (D'Agostino &

Pearson) was performed, followed by a Kruskal Wallis/Anova (with post tests) and Mann

Whitney/T-test to test for statistical significance between trickle and bolus groups, n.s. =

not significant, * = p<0.05, ** = p<0.01, *** = p<0.001, **** = p<0.001.

1073

Figure 6: Acute granuloma cell composition. C57Bl/6 mice were infected with 200 *H.*

bakeri according to bolus and/or trickle models of infection and euthanised at D21.

Granulomas were isolated from the small intestine of 5 mice per group. Granulomas

from the individual animals were pooled to form one sample per group. Cells were

obtained by tissue digestion of the pooled samples and surface stained by flow

cytometry. (A) Proportions of IgG$_1$-bound cells (SiglecF$^+$, CD206$^+$, Ly6G$^+$ and NK1.1$^+$)

were calculated within the acute (worm containing) granulomas of trickle infected mice.

Numbers reflect the mean of five independent experiments. Proportions of acute

granuloma (B) SiglecF$^+$, (C) CD206$^+$, (D) Ly6G$^+$ and (E) NK1.1$^+$ cells within bolus and trickle

infected mice were calculated for three independent experiments. A paired T-test to

test for statistical significance between trickle and bolus groups was performed, n.s. =

not significant, * = p<0.05, *** = p<0.001.

1086

Figure 7: The T. gondii/H. bakeri trickle coinfection model in C57Bl/6 mice. C57Bl/6

mice were infected with 200 *H. polygyrus* according to the coinfection and trickle

infection regimes. (A) Coinfection trickle infection regime: mice are infected with 20

Me49 *T. gondii* cysts 14 days prior to *H. bakeri* infection which consists of 200 larvae in

total, but in multiple doses over the course of infection (in grey). Doses of 20 larvae are

trickled on days 0, 2, 4, 6, 8, 10, 12, 14, 16 and 18 post-infection Animals are euthanised

on D21 (3 day window after the final dose), where tissue and lumen parasites can be

observed. Animals are also euthanised on D28 (10-day window after the final dose),

where only lumen parasites are found. Mice were infected according to the Hb (blue)

and TgHb (purple) regimes. (B-G) RNA was extracted was from the small intestine, which

had been cut into four equal portions. The duodenum (SI1) and jejunum (SI2) were

used. Gene expression was measured by quantitative RT-PCR for *il13* (B & C), *ifn γ* (D & E)

and *Il10* (F & G). Adult worms (H) and granulomas (I) were counted in the small intestine

at D21 and D28. (J) Granuloma area in C57Bl/6 mice was measured on H and E stained

sections from whole small intestine swiss rolls. Graphs represent pooled data from a

minimum of 2 experiments, bars represent the median, with a minimum of 4 mice per

group per experiment. A normality test was performed, followed by a Kruskal

Wallis/Anova (with post-tests) and Mann Whitney to test for statistical significance

between Hb and HbTg groups, n.s. = not significant, ** = $p < 0.01$, ***= $p < 0.001$, **** =

$p < 0.0001$.

1107

Figure 8: Granuloma characteristics in the T. gondii/H. bakeri trickle coinfection model

in C57Bl/6 mice. C57Bl/6 mice were infected with 200 *H. bakeri* according to the trickle

single or co-infection models, and euthanised on D21. Co-infected animals are infected

with 10 cysts of Me49 *T. gondii* 14 days before the first *H. bakeri* dose. Granulomas

were isolated from the small intestine of 5 mice per group. Granulomas from the

individual animals were pooled to form one sample per group. Cells were obtained by

tissue digestion of the pooled samples and stained by flow cytometry. (A) The

percentage of $CD11b^+IgG_1^+$ cells as a proportion of live granuloma cells (with T and B

cells removed) from acute granulomas was calculated for three independent

experiments. (B) Representative flow cytometry plots showing IgG_1 and CD11b

expression on live granuloma cells from acute granulomas. (C) Formalin fixed, paraffin-

embedded sections were obtained from small intestine swiss rolls. These sections were

co-stained with DAPI and anti-mouse IgG_1. Scale bar=100µm. Antibody stain (left),

isotype control stain (right). Representative granulomas (white lines) containing worms

(acute granulomas) from trickle and co-infected mice. (D) Proportions of acute

granuloma (D) $SiglecF^+$, (E) $CD206^+$, (F) $Ly6G^+$ and (G) $NK1.1^+$ cells within trickle and co-

infected mice were calculated for three independent experiments. A paired T-test to

test for statistical significance between two groups was performed, n.s. = not significant,

* = p<0.05. Granulomas were identified on H and E stained slides of whole small

intestine. Eosinophils (H) and macrophages (I) were counted within the center of the

granulomas at x400 magnification. Cells were counted for one field of view (FOV) per

granuloma. A normality test was performed, followed by a Kruskal Wallis/Anova (with

post-tests) to test for statistical significance between trickle and co-infected groups, n.s.

= not significant, * = p<0.05, **** = p<0.001.

1132

Figure 9: Plasma cell and antibody dynamics in T. gondii/H. bakeri trickle co-infected

C57Bl/6 mice. C57Bl/6 mice were infected with 200 *H. bakeri* according to the trickle

single or co-infection models, and euthanised on D21. Co-infected animals are infected

with 10 cysts of Me49 *T. gondii* 14 days before the first *H. bakeri* dose. Mesenteric

lymph nodes (MLN) were isolated to obtain single cell suspensions which were analysed

by flow cytometry. (A) The number of total viable MLN cells. (B) The proportion of

$CD138^+$ (plasma) cells. (C) The number of $CD138^+$ cells. (D) The proportion of $CD138^+$

cells expressing intracellular IgG_1. (E) The number of $CD138^+$ cells expressing

intracellular IgG_1. (F) The IgG_1 MFI of $CD138^+$ cells expressing intracellular IgG_1. The

number of MLN *H. bakeri*-specific (G) and total (H) IgG_1 producing cells assessed by

ELISPOT. (I) The proportion of $CD138^+$ cells expressing intracellular IgA. (J) The number

of $CD138^+$ cells expressing intracellular IgA. (K) The IgA MFI of $CD138^+$ cells expressing

intracellular IgG_1. Graphs represent pooled data from a minimum of 2 experiments, bars

represent the median, with a minimum of 5 mice per group per experiment. A normality

test (D'Agostino & Pearson) was performed, followed by a Kruskal Wallis/Anova (with

post-tests) and Mann Whitney/T-test to test for statistical significance between Hb and

TgHb groups, n.s. = not significant, * = p<0.05, ** = p<0.01, **** = p<0.001.

1150

Supplemental Figure 1: Characteristics of the H. bakeri trickle infection model in Balb/c

mice. Balb/c mice were infected with 200 *H. bakeri* according to the bolus and trickle

infection regimes. Adult worms (A) and granulomas (B) were counted in the small

intestine at D28. Mice were infected according to the bolus (red) and trickle (blue)

regimes. Single cell suspensions were isolated from the spleen (SPL) and mesenteric

lymph nodes (MLN) and cultured for 48 hours in the presence of Hb antigen. MLN/SPL

cell numbers were calculated (C & F), and IL-4 (D & G) and IL-13 (E & H) cytokine levels

were measured in the supernatant by ELISA. (I) Total serum IgE, (J) total serum IgG_1 and

(K) parasite-specific serum IgG_1 were measured by ELISA. Levels in naïve controls were

undetectable for parasite specific IgG_1. A normality test (D'Agostino & Pearson) was

performed, followed by a Kruskal Wallis/Anova (with post-tests) and Mann Whitney/T-

test to test for statistical significance between trickle and bolus groups, n.s. = not

significant, ** = p<0.01, *** = p<0.001, **** = p<0.001.

1164

Supplementary Figure 2: Gating strategy for IgG_1^+ granuloma cells. Granulomas (acute

and chronic) were isolated from the small intestine of 5 mice per group. Granulomas

from the individual animals were pooled to form one sample per group. Cells were

obtained by tissue digestion of the pooled samples and surface stained by flow

cytometry. Gating strategy involved removing doublets using FSC and SSC. Dead cells

(positive for viability stain) were excluded. B and T cells were excluded by removing

$CD3^+$ and $CD19^+$ cells from the analysis. Antibody-bound cells were identified as

$CD11b^+IgG_1^+$ cells using appropriate controls. To identify specific cell types, eosinophils

were identified as SiglecF$^+$, macrophages as CD206$^+$, neutrophils as Ly6G$^+$ and NK cells as

NK1.1$^+$, using appropriate controls.

1175

1176

Supplementary Figure 3: Gating strategy for IgG$_1$ and IgA producing plasma cells.

Organs were isolated to obtain single cell suspensions which were analysed by flow

cytometry. Gating strategy involved removing doublets using FSC and SSC. Dead cells

(positive for viability stain) were excluded. IgD$^+$CD3$^-$ cells were excluded by removing

CD3$^+$ and IgD$^+$ cells from the analysis. IgG$_1$$^+$CD138$^+$ and IgA$^+$CD138$^+$ populations were

identified using appropriate controls.

1183

Supplementary Figure 4: IgG$_1$$^+$ cells in the granulomas of D7 bolus infected mice.

Serum was administered intravenously at D0, D2, D4, D6 to bolus infected animals.

Formalin fixed paraffin embedded small intestine swiss rolls were obtained on D7 and

co-stained with anti-mouse IgG$_1$ and DAPI. Top: mice who received trickle immune

serum obtained from trickle infected mice. Bottom: mice who received non-immune

control serum obtained from naïve animals. Experiment was performed once with 5

mice per group, and representative images are presented. Scale bar=100μm.

Figure 1

Figure 5

A. Pie chart legend: SiglecF+ 26%, CD206+ 27%, Ly6G+ 10%, NK1.1+ 1%, Other 36%

B. % SiglecF+ — Bolus vs Trickle — ***

C. % CD206+ — Bolus vs Trickle — *

D. % Ly6G+ — Bolus vs Trickle — ns

E. % NK1.1+ — Bolus vs Trickle — ns

Figure 7