1	Toxoplasma type II effector GRA15 has limited influence in vivo
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4	Running title: GRA15 has a minimal effect in vivo
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# 17 Abstract

18

19 Toxoplasma gondii is an intracellular parasite that establishes a long-term infection in the brain 20 of many warm-blooded hosts, including humans and rodents. Like all obligate intracellular 21 microbes, *Toxoplasma* uses many effector proteins to manipulate the host cell to ensure parasite 22 survival. While some of these effector proteins are universal to all *Toxoplasma* strains, some are 23 polymorphic between *Toxoplasma* strains. One such polymorphic effector is GRA15. The gra15 24 allele carried by type II strains activates host NF- $\kappa$ B signaling, leading to the release of cytokines 25 such as IL-12, TNF, and IL-1 $\beta$  from immune cells infected with type II parasites. Prior work 26 also suggested that GRA15 promotes early host control of parasites in vivo, but the effect of 27 GRA15 on parasite persistence in the brain and the peripheral immune response has not been 28 well defined. For this reason, we sought to address this gap by generating a new II $\Delta gra15$  strain 29 and comparing outcomes at 3 weeks post infection between WT and  $II\Delta gra15$  infected mice. We 30 found that the brain parasite burden and the number of macrophages/microglia and T cells in the 31 brain did not differ between WT and  $II\Delta gra15$  infected mice. In addition, while  $II\Delta gra15$ 32 infected mice had a lower number and frequency of splenic M1-like macrophages and frequency 33 of PD-1+ CTLA-4+ CD4+ T cells and NK cells compared to WT infected mice, the IFN-y+ CD4 34 and CD8 T cell populations were equivalent. In summary, our results suggest that in vivo GRA15 35 may have a subtle effect on the peripheral immune response, but this effect is not strong enough 36 to alter brain parasite burden or parenchymal immune cell number at 3 weeks post infection. 37

# 38 Introduction

40	To successfully establish a persistent infection, a microbe must take a "Goldilocks" route. The
41	microbe must evade host defenses enough to avoid microbial elimination while also preventing
42	host death from an overwhelming microbial burden or immune response. Thus, successful
43	persistent microbes evolve mechanisms for provoking "the right" amount of a host response
44	(1,2). Toxoplasma gondii is an eukaryotic intracellular parasite that persistently infects many
45	warm blooded animals-from birds to humans-including approximately 10-15% of the United
46	States population (3). Toxoplasma has achieved such success, in part, by manipulating host cell
47	signaling pathways through a variety of secreted effector proteins. These secreted effector
48	proteins are often known as ROPs and GRAs and are delivered by specialized secretory
49	organelles. Different ROPs and GRAs directly block immune clearance, alter the host cell cycle,
50	drive cytoskeletal remodeling, and alter apoptotic pathways (4-11). While many of these effector
51	proteins are the same in all Toxoplasma strains, some are polymorphic and show Toxoplasma
52	strain-specific effects (12,13). One such polymorphic effector protein is GRA15 (14).
53	During in vitro infection with type II Toxoplasma strains—but not with type I or type III
54	strains—GRA15 activates the NF- $\kappa$ B pathway, which leads to IL-12, IL-1 $\beta$ , and TNF release by
55	macrophages (15–18). GRA15 also limits parasite growth in IFN- $\gamma$ stimulated human and murine
56	fibroblasts in vitro by recruiting host defense proteins to the parasite's intracellular niche (15).
57	Consistent with GRA15 stimulating pro-inflammatory host responses that limit parasite
58	expansion, during acute infection, mice inoculated with type II parasites that lack GRA15 have
59	lower local IFN- $\gamma$ levels and higher parasite burdens compared to mice infected with wild-type
60	type II parasites (14).

61	While such findings might be expected to result in a higher systemic and brain parasite
62	burden during later stages of infection, the data are mixed. One paper found that $II\Delta gra15$
63	parasites showed no difference in cyst counts at 21 days post infection (dpi) compared to
64	parental parasites, while another paper found that $II\Delta gra15$ parasites showed a trend toward a
65	decrease in cyst count compared to WT parasites (19,20). Given these discrepant studies, we
66	sought to re-address the role of GRA15 in outcomes of type II infection, including assessing the
67	systemic and brain immune response as well as the brain parasite burden.
68	
69	Methods
70	
71	Ethics Statement
72	All procedures and experiments were carried out in accordance with the Public Health Service
73	Policy on Human Care and Use of Laboratory Animals and approved by the University of
74	Arizona's Institutional Animal Care and Use Committee (#12-391). All mice were bred and
75	housed in specific-pathogen-free University of Arizona Animal Care facilities.
76	
77	Parasite maintenance and generation of II\[] gra15 and
78	II∆gra15::GRA15
79 80	All parasite strains were maintained through serial passage in human foreskin fibroblasts (HFFs)
81	in DMEM supplemented with 10% FBS, 100 I.U./ml penicillin/streptomycin, and 2 mM

82 glutagro. All parasite strains were generated from a type II strain Pruginaud ( $Pru\Delta hpt$ ) in which

83 the endogenous hypoxanthine xanthine guanine phosphoribosyl transferase gene is deleted. The 84 wild type (WT) strain used throughout the paper expresses a Cre fusion protein that is injected 85 into host cells prior to parasite invasion (21). The II $\Delta gra15$  used throughout this work also 86 expresses the Cre fusion protein. 87 88 To disrupt GRA15 in II $\Delta hpt$  parasites, GRA15 targeting CRISPR plasmids (sgGRA15Up and 89 sgGRA15down) were generated from a sgUPRT plasmid (plasmid #54464) using a Q5 90 mutagenesis protocol (22). To generate a plasmid to insert hpt and toxofilin: cre into the GRA15 91 locus, upstream (500-bp) and downstream (500-bp) adjacent to the sgGRA15Up and 92 sgGRA15Down target sequences were used to flank *hpt* and *toxofilin:cre*. We then transfected 93 the IIAhpt parasites with the 1) sgGRA15Up CRISPR, 2) sgGRA15Down CRISPR, and 3)pTKO 94 plasmid (23) with GRA15 homology regions flanking hpt and toxofilin:cre. These parasites 95 underwent selection using media containing 25 mg/ml mycophenolic acid and 50 mg/ml of 96 xanthine prior to dilution to individual clones (24). Single clones were then screened for 97 disruption of the gra15 locus and confirmed to have lost NF-kB activation by 98 immunofluorescence. Clones were also confirmed to express toxofilin:cre by causing Cre-99 mediated recombination as previously described (25). 100

101 A complemented II $\Delta gra15$ ::GRA15 strain was made by inserting the GRA15 coding sequence 102 with 1000 bp upstream of the GRA15 TSS into a plasmid containing the selectable marker 103 bleomycin (26). The plasmid was linearized and transfected into II $\Delta gra15$  parasites. These 104 parasites were placed under selection in complete DMEM supplemented with 5 µg/ml zeocin 105 until lysing out. Lysed out parasites were incubated in 50 µg/ml zeocin media for 4 hours before

being transferred to HFFs containing the 5  $\mu$ g/ml zeocin media. This process was repeated three times prior to cloning by limiting dilution. Single clones were then screened for expression of *gra15* by Q-PCR and the ability to activate NF-κB pathway by immunofluorescence.

109

110 **Mice** 

111 Unless specifically noted, mice used in this study are Cre-reporter mice in a C57Bl/6J

112 background. Cells in these mice express GFP when cells undergo Cre-mediated recombination

113 (27). These mice were purchased from Jackson labs and bred in the University of Arizona

114 Animal Center (stock # 007906). BALB/cJ mice (Strain #:000651) were used for one

115 experiment. Male and female mice were intraperitoneally inoculated with 10,000 syringed lysed

parasites resuspended in 200 µl of UPS grade PBS. Unless otherwise stated, two cohorts were

used for each experiment. For 3 week post infection (wpi) studies, cohort one included 4-5 mice

per infection, aged 12-16 weeks, with initial weights between 18 and 33 grams. Cohort two

included 9-12 mice per infection, aged 6-10 weeks, with initial weights between 16 and 32

120 grams. For acute time points of 2- and 5-days post infection, each cohort contained 4-5 mice per

121 infection. Mice were given food and water ad libitum and provided moist chow to alleviate

suffering.

123

# 124 **Tissue preparation for histology and DNA extraction**

At the appropriate time points, mice were euthanized with CO<sub>2</sub>, without use of anesthesia, and
transcardially perfused with 20 ml cold PBS. Brains were removed and divided into two
hemispheres. The left hemisphere was drop fixed by placement in 4% paraformaldehyde (PFA).

The next day, PFA was removed and replaced with 30% sucrose. After sucrose embedding,
brains were sagittally sectioned to 40 µm sections using a microtome (Microm HM 430) and
stored in cryoprotectant media at -20° C until staining. The anterior ¼ of the right half of the
brain was sectioned coronally, placed in an Eppendorf tube, and flash frozen until used for DNA
extraction.

133

## 134 NF-κB activation assay

135 Syringe lysed parasites were added to confluent HFF monolayers grown on glass coverslips at an

136 MOI of 7.5 and spun down at 300 rpm for 1 minute. 24 hours post infection, cells were washed

and fixed for 15 minutes with 4% PFA followed by 5 min in ice cold methanol. Cells were then

138 blocked in 3% goat serum for 1 hour at room temperature and incubated in mouse anti-Sag1 (28)

139 [DG52] (gift from John Boothroyd, 1:5000) and anti-NF-κB (p65) (Santa Cruz Biotechnology,

140 sc-372, 1:1000) antibodies overnight at 4°C. The next day, cells were washed to remove excess

141 antibody and incubated in goat anti-mouse secondary antibody AF568 (Thermo Fischer

142 Scientific, A-11004, 1:500) and goat anti-rabbit AF488 (Life technologies, A-11008, 1:500) for

143 one hour. Coverslips were then washed 3 times in PBS, with the first wash containing Hoechst

144 (1:5000) to stain for host cell and parasite nuclei. Images were then obtained on an ECHO

145 Revolve fluorescent microscope to analyze nuclear NF-κB localization.

146 To measure NF-κB activation at early time points, syringe lysed parasites were filtered and

147 washed in 40 ml of cDMEM prior to addition to confluent HFF monolayers grown on glass

- 148 coverslips at an MOI of 5. Cells were fixed in 4% PFA at 1, 3, or 24 hrs post infection, blocked
- in 3% goat serum for 1 hour at room temperature and incubated in mouse anti-Sag1(28) [DG52]

- 150 and anti-NF-κB (Cell Signaling Technology, 8242S, 1:1000 antibodies) overnight at 4°C. The
- 151 subsequent steps followed the protocol described above.
- 152

## 153 Growth assay

- 154 Syringe lysed parasites were added to confluent HFF monolayers grown on glass coverslips at an
- 155 MOI of 1 and spun down at 300 rpm for 1 minute. 24 hours post infection, cells were washed in
- 156 PBS and fixed for 20 minutes in 4% PFA. Cells were then permeabilized, blocked, and stained
- using an anti-*Toxoplasma* antibody (Thermo Fischer, PA17252, 1:5000, goat anti-rabbit 568
- 158 Thermo Fischer, A11011, 1:500). To enumerate the number of parasites per vacuole, coverslips

159 were analyzed using an ECHO Revolve fluorescent microscope.

160

#### 161 Plaque assay

- 162 Confluent monolayers of HFF cells were infected with 250 parasites of the indicated strains in
- 163 cDMEM. After 10 days, media was removed, cultures were washed with PBS, and the

164 monolayers were fixed in ice cold methanol for 10 minutes. Fixed monolayers were then stained

165 with crystal violet for 10 minutes at room temperature.

166

# 167 Immunohistochemistry

168 For identification of macrophages/microglia, free floating brain sections were washed, treated in

169 H<sub>2</sub>O<sub>2</sub> for 40 minutes, washed again, blocked with goat serum, and incubated with polyclonal

170 rabbit anti-Iba-1 antibody overnight (Wako Pure Chemical Industries, 019-19741 Ltd. (1:3000)).

171 The next day, samples were washed, incubated for 1 hour in biotinylated goat anti-rabbit

172	antibody (Vector Laboratories, BA-1000 (1:500)). After washing off residual secondary
173	antibody, samples were incubated in ABC solution (Thermo Fisher, 32020) for 1 hour followed
174	by 60 second treatment with 3,3'-Diaminobenzidine (DAB)(Vector Laboratories, SK-4100).
175	Samples were then washed, mounted, and cover slipped prior to immune cell quantification.
176	

# 177 **Immunofluorescence**

178 For identification of T cells, free floating brain sections were washed in TBS, blocked with 3% 179 goat serum diluted in TBS for 1 hour, and then incubated overnight with hamster anti-CD3 180 antibody diluted in 1% goat serum/0.3% Triton-X100/TBS (BD Biosciences, 550277). The next 181 day samples were washed in TBS and incubated at room temperature in goat anti-hamster 647 182 (Life Technologies, A-21451). After a 4-hour incubation in secondary antibody, samples were 183 washed for 5 minutes in TBS/Hoechst (1:5000) followed by 2 subsequent washes in TBS. Brain 184 sections were then mounted, cover slipped with Fluoromount- $G^{TM}$  (Southern Biotech, 0100-01), 185 and z-stacks were obtained on an ECHO Revolve microscope using a 10x objective.

186

## 187 **Iba-1+ cell quantification**

To quantify Iba-1+ cells in brain sections, stained sections were imaged using light microscopy.
Eight images were obtained in a stereotyped pattern within the cortex of the brain section using a
20x objective. Three matched sections were imaged per mouse (24 images/mouse). Cells were
quantified manually using FIJI software. Individuals quantifying cells were blinded to infection
status of mice.

193

## 194 **T cell quantification**

Imaris software was used to quantify number of T cells within each 40 µm confocal image. The
spots tool was used to generate a threshold of detectable T cells and quantified by the program.
Individuals quantifying cells were blinded to infection status of mice.

198

# 199 Quantitative PCR

200 To quantify parasite burden, genomic DNA was isolated from the anterior quarter of the right

201 hemisphere (brain), the left lobe of the liver, or the distal quarter of the spleen using DNeasy

202 Blood and Tissue kit (Qiagen, 69504), following the manufacturer's protocol. The Toxoplasma

203 B1 gene was amplified using SYBR Green on the Eppendorf Mastercycler et realplex 2.2

system. Gapdh was used to normalize parasite DNA levels.

205

# 206 Cyst Stain

207 Sagittal brain sections were blocked in 3% goat serum diluted in 0.3% TritonX-100/TBS for 1 208 hour. These sections were then incubated with biotinylated Dolichos Biflorus Agglutinin (DBA) 209 (Vector laboratories 1031, 1:500) and a polyclonal rabbit anti-*Toxoplasma* antibody (Thermo 210 Fisher Scientific, PA17252, 1:5000) overnight at 4° C. Samples were then washed and incubated 211 with Streptavidin Cy5 (Life technologies, S21374, 1:500) and goat anti-rabbit 568 secondary 212 (Thermo Fisher Scientific, A11011, 1:500) for 4 hours at room temperature, after which samples 213 were washed to remove residual antibody. Hoechst (Thermo Fisher Scientific, H3570, 1:5000) 214 was added to the first TBS wash for 5 minutes to stain for nuclei. Sections were then washed two 215 more times, mounted on slides, and cover slipped using Fluoromount-G<sup>TM</sup>. The number of cysts 216 (DBA+, anti-Toxoplasma antibody+) was enumerated using an Echo Revolve fluorescent 217 microscope.

218

# 219 Single cell suspension for Flow Cytometry

- 220 At appropriate time points, mice were euthanized by CO<sub>2</sub> and intracardially perfused with 20 ml
- cold PBS. Spleens were then harvested for flow cytometry, maintained in complete RPMI (86%
- 222 RPMI, 10% FBS, 1% penicillin/streptomycin, 1% L-glutamine, 1% NEAA, 1% sodium
- 223 pyruvate, and <0.01%  $\beta$ -mercaptoethanol) and processed to generate single cell suspensions. For
- single cell suspension, spleens were passed through a 40 µm strainer and centrifuged at 1200
- rpm, 4°C, for 5 minutes. After removal of supernatant, red blood cells were lysed by addition of
- 1 ml ammonium chloride-potassium carbonate (ACK) lysis buffer (Life Technologies,
- A1049201). ACK was neutralized by the addition of cRPMI, centrifuged at 1200 rpm, 4°C, for 5
- 228 minutes. The supernatant was removed and the pellet resuspended in cRPMI. The number of
- viable cells was quantified by diluting  $10 \,\mu$ l of the single cell suspension in  $90 \,\mu$ l trypan blue and
- 230 counting on a hemocytometer. T cell panels to be quantified for IFN- $\gamma$  were treated with PMA,
- Ionomycin, and Brefeldin for 4 hours in 37°C incubator prior to washing, blocking, and staining.

232

# 233 Staining for Flow Cytometry

One million live cells of each sample were plated into a 96 well plate, washed in FACS buffer
(1% FBS/PBS), and blocked with Fc block (Biolegend, 101302) to prevent nonspecific staining.
Samples were then stained for a T cell panel or a macrophage panel. Samples were incubated in
antibody (1:100) diluted in FACS buffer for at least 30 minutes, protected from light, then
stained with live/dead Fixable yellow Dead Cell stain (Life Technologies, L34959). Samples
were then washed and fixed using intracellular staining permeabilization and fixation kit
(eBioscience, 00-5223-00). To stain for Foxp3, T-bet, Gata-3, and IFN-γ, the manufacturer's

- intracellular staining protocol was used (eBioscience, 00-5223-56; 00-5123-43; 00-8333-56).
- 242 Samples were then washed, run on a LSRII (University of Arizona Cancer Center Flow
- 243 Cytometry Core), and data analyzed using FlowJo<sup>TM</sup> Software.
- 244

# 245 Peritoneal Exudate Cells Isolation

246 Cre reporter mice were inoculated intraperitoneally with saline or 10,000 WT or  $II\Delta gra15$ 

247 parasites. At 2 and 5 dpi, peritoneal exudate cells were collected by injecting 5 ml of cold PBS

into the exposed peritoneal cavity, massaging the cavity, and recollecting PBS/cellular suspension.

249 PECS were then incubated in Fc block, stained for CD45, and run on the LSRII.

250

#### 251 Parasite RNA isolation

252 Confluent human foreskin fibroblasts were infected with indicated strains for 48 hours.
253 Monolayers were scraped, syringe lysed, and resuspended in TRIzol<sup>TM</sup>; RNA was extracted per
254 manufacturer's instructions (Thermo Fisher Scientific, 15596026). One µg of isolated RNA was
255 converted to cDNA using High-Capacity cDNA Reverse Transcriptase kit (Thermo Fisher
256 Scientific, 4368814). Q-PCR was performed on cDNA using GRA15 and TgActin specific
257 primers.

# 258 **Statistics**

Graphs were generated and statistical tests were run using Prism software version 9.4.1. All *in vivo* experiments in C57BL/6 mice were repeated with two independent cohorts; unless otherwise noted the data were analyzed with a two-way analysis of variance (ANOVA) with uncorrected Fisher's LSD. Infection of BALB/c mice was done once; data were analyzed with a T-test. For

intracellular growth assays and plaque assays, experiments were repeated three times and statistical
analysis was conducted on the composite data. For intracellular growth assay, a two-way ANOVA
with uncorrected Fisher's LSD was used, for plaque assays a one-way ANOVA was used.
Analysis of parasite genomes in the liver at 5 dpi showed one mouse from one cohort to be an
outlier as determined by the ROUT outlier test. Therefore, that mouse was removed for statistical
analysis.

269

# 270 **Results**

271

# GRA15 does not influence parasite burden or macrophage/microglia and T cell abundance in the brain at 3 wpi

275 To probe the influence of GRA15 during early chronic infection, we generated a type II strain 276 (Prugniaud or Pru) that lacked gra15 (II $\Delta$ gra15) and the appropriate complemented strain 277 (II $\Delta$ gra15::GRA15) using previously described CRISPR-Cas9 methodology (29). As the II $\Delta$ gra15 278 and II $\Delta gra15$ ::GRA15 strains express a rhoptry::Cre recombinase fusion protein, for the wild-type 279 (WT)/control strain, we used a Pru strain that has been engineered to express the same rhoptry::Cre 280 fusion protein (21). The II $\Delta gra15$  was confirmed to lack NF- $\kappa$ B activation and the complemented 281 strain restored NF- $\kappa$ B activity at 24 hours post infection (hpi) (S1 Fig A, B). At 1 and 3 hpi, none 282 of the strains induced NF-κB nuclear localization, regardless of GRA15 expression (S1 Fig C). To 283 assess GRA15's effect in vivo, Cre reporter mice that express GFP only after Cre-mediated 284 recombination (27) were inoculated with saline or WT, II $\Delta gra15$ , or II $\Delta gra15$ ::GRA15 parasites.

285 At 3 weeks post infection (wpi), spleen and brain were harvested. To assess overall brain parasite 286 burden, we performed Q-PCR for a Toxoplasma specific gene (B1) on genomic DNA isolated from the brain (23,30). We found no statistical difference between WT and  $II\Delta gra15$  infected brain 287 288 though the II $\Delta$ gra15::GRA15 infected brain consistently showed a lower parasite burden (Fig 1A). 289 As a second mechanism for assessing brain parasite burden, we quantified the number of cysts by 290 staining brain sections with Dolichos biflorous agglutinin (DBA), a lectin that stains sugar moieties 291 on components of the cyst wall (Fig 1B) (31). Consistent with the Q-PCR data, cyst counts from 292 WT and  $II\Delta gra15$  infected brain were not statistically different while cysts counts from 293 II $\Delta gra15$ ::GRA15 infected brain were lower (Fig 1C). Given that the II $\Delta gra15$ ::GRA15 strain 294 consistently appeared to be less capable of establishing an *in vivo* infection in multiple cohorts of 295 mice, we performed in vitro studies to determine if this strain had a growth defect and/or had an 296 unusual expression of gra15. Indeed, the II $\Delta$ gra15::GRA15 strain showed a replication defect at 297 24 hours post infection (S1 Fig D), though this difference did not translate into a defect in plaque 298 formation (S1 Fig E-G). In addition, we determined that the complemented strain expressed 299 approximately 5 fold more gra15 compared to the WT strain (S1 Fig H). Given the lytic cycle defect—which we expect would be exacerbated in vivo—and the increased expression of gra15 in 300 301 the II $\Delta$ gra15::GRA15 strain, we decided to move forward without the complement, as these 302 phenotypes introduce variables for which we cannot control.

As GRA15 influences macrophage phenotypes *in vitro* and a change in macrophage skewing might affect the neuroinflammatory response without altering brain parasite burden, we next sought to evaluate the brain immune response. We focused on macrophages/microglia and T cells because these are the primary immune cells to infiltrate and/or be activated in the brain upon *Toxoplasma* infection (29). To quantify the number of macrophages/microglia, we stained

308	tissue sections with anti-Iba1 antibodies, which stains a cytoskeletal protein (Iba1) expressed by
309	both macrophages and microglia. We then quantified the number of Iba1+ cells manually (29)
310	finding no difference in the number of Iba1+ cells in brain sections from WT and II $\Delta gra15$
311	infected mice (Fig 1D,E). To quantify T cells, we performed immunofluorescent assays for T
312	cells using an anti-CD3ɛ antibody. We then imaged the stained tissue sections and analyzed the
313	images with Imaris software, which is capable of segregating and counting the stained T cells in
314	an automated manner (Fig 1F,G). We found no difference in the number of $CD3\epsilon$ + cells in brain
315	sections from WT and II $\Delta gra15$ infected mice. Collectively, these data suggest that GRA15 does
316	not affect Toxoplasma's dissemination to or persistence in the brain at 3 wpi. GRA15 also does
317	not appear to alter the number of macrophage/microglia or T cells present in the brain at 3 wpi.
24.0	

318

## 319 GRA15 may influence M1-like polarization of macrophages at 3 wpi

320

321 While IHC allows us to quantify infiltrating immune cells, it cannot assess the polarization state 322 of immune cells, which can be done by flow cytometry. Given that GRA15 induces an M1-like 323 phenotype in infected macrophages in vitro (32), we were interested in determining how this 324 gene influences macrophage phenotypes in vivo. As prior data from our lab has shown that the 325 immune response within the spleen mirrors the immune response found in the brain at 3 wpi 326 (29), we used splenocytes for our analyses. To that end, we used the following markers to 327 segregate macrophages into pro-inflammatory macrophages (M1-like): CD45+, F4/80+/ CD11b<sup>hi</sup> 328 CD11c<sup>lo/int</sup>/ CD80+ CD86+ and wound-healing macrophages (M2): CD45+, F4/80+/ CD11b<sup>hi</sup> 329 CD11c<sup>lo/int</sup>/ CD206+/F4/80+ (gating scheme shown in S2 Fig). Given that we did not use iNOS 330 staining which is required to identify a true M1 macrophage, we refer to our CD80+ CD86+

331	population as M1-like macrophages. Consistent with the <i>in vitro</i> data, our analyses showed that,
332	compared to WT infected mice, II $\Delta gra15$ infected mice have fewer M1 macrophages (Fig
333	<b>2A,B</b> ). We did not detect differences in M2 macrophages ( <b>Fig 2C,D</b> ).
334	
335	GRA15 does not affect IFN- $\gamma$ producing T cell populations at 3 wpi
336	
337	M1/M1-like macrophages are expected to produce IL-12 (18,29,32). As IL-12 is one of many
338	signals that polarizes naïve CD4+ T cells to be T-bet+, IFN-7 producing Th1 cells, we
339	hypothesized that the lower number of M1-like macrophages provoked by $II\Delta gra15$ parasites
340	might result in decreases in IFN- $\gamma$ production by T cells (33,34). To test this possibility, we
341	profiled the splenic T cell compartment, assessing CD4 and CD8 numbers as well as their
342	capabilities to produce IFN- $\gamma$ (gating scheme is shown in <b>S3 Fig</b> ). We found no differences
343	between the groups in terms of the number or frequency of Th1, Th2, or Treg T cells (Fig 3A-F).
344	The number of IFN-γ producing CD4 and CD8 T cells was also not different (Fig 4).
345	Collectively, these data suggest that, at 3 wpi, GRA15 does not influence IFN-y production in
346	CD4 or CD8 T cells, despite potentially influencing M1-like macrophage number and frequency.
347	
348	GRA15 may influence the frequency of peripheral "exhausted" T
349	cells and NK cells at 3 weeks post infection in C57BL/6 mice
350	
351	As work from other labs have identified T cell exhaustion during chronic time points of
352	<i>Toxoplasma</i> infection (35,36) and because such analysis has not been done with $\Delta gra15$ strains,

353	we assessed the T cell compartment for exhausted T cells by looking for co-expression of
354	inhibitory markers PD-1 and CTLA-4 (FMO shown in S4 Fig). We found that mice infected with
355	II $\Delta gra15$ parasites generated a lower frequency of exhausted CD4+ T cells, though the total
356	number of exhausted CD4+ T cells only trended down in $II\Delta gra15$ infected mice (Fig 5A,B). As
357	NK cells have been shown to contribute to T cell exhaustion in the chronic phase of disease (37),
358	we also quantified NK cell number and frequency, finding a lower frequency of NK in the
359	II $\Delta gra15$ infected mice ( <b>Fig 5C, D</b> ). As with the exhausted T cells, the total number of NK cells
360	only trended down in II $\Delta gra15$ infected mice ( <b>Fig 5C, D</b> ).
361	
362	GRA15 may influence parasite dissemination during acute infection.

363

362

364 Given the published data suggesting a difference in parasite burden between WT and 365 II $\Delta gra15$  parasites at 5 dpi (14), we were surprised that we did not see a difference in parasite 366 burden in the brain at 3 wpi (Fig 1A,C). Therefore, we wondered if the previously reported 367 GRA15-associated phenotypes could only be seen early in infection. To address this question, 368 we inoculated Cre reporter mice intraperitoneally with saline or WT or  $II\Delta gra15$  parasites and 369 collected peritoneal exudate cells (PECS) and peritoneal fluid. Following the protocol from the 370 previously published report (14), we measured IFN- $\gamma$  in the peritoneal fluid, finding no 371 difference in IFN- $\gamma$  levels at 2 dpi (Fig 6A). While the prior study used bioluminescent imaging 372 to quantify parasite burden, our parasites were not compatible with such measurements (i.e., our 373 parasites do not express luciferase). Instead, as our parasite strains express a rhoptry::Cre fusion 374 protein and in Cre reporter mice the number of GFP+ cells correlates with the parasite burden 375 (29), we used the number of green fluorescent protein-expressing (GFP+) PECs as an indirect

376 measure of peritoneal parasite burden. Unlike the prior work, at 2 and 5 dpi, we found no 377 difference in the frequency of GFP+ CD45+ PECs between the two groups (Fig 6B). Though the 378 GFP+ PEC number were equivalent between WT and II $\Delta gra15$  infections at 2 and 5 dpi, Q-PCR 379 for Toxoplasma B1 on genomic DNA isolated from liver and spleen at 5 dpi was lower in the II∆gra15 infected mice (Fig 6C, D). In summary, unlike previously published data, we did not 380 381 find a decrease in IFN- $\gamma$  within the peritoneal cavity at 2 dpi, nor did we find evidence of an 382 increase in the number of II $\Delta gra15$  parasites compared to WT parasites at 2 or 5 dpi. On the 383 contrary, if anything, our Q-PCR data suggest the opposite. 384 Given that our findings were inconsistent with the prior work, we speculated that these 385 discrepancies arose from our using C57BL/6 mice while the prior work used BALB/c mice. We 386 were particularly interested in this possibility because BALB/c mice and C57BL/6 mice are 387 known to generate very different immune responses, with BALB/c mice being predisposed to a 388 Th2 response and C57BL/6 being predisposed to a Th1 response (38-40). To determine if 389 differences in mouse strain explained the discrepancy between our work and the prior work, we 390 inoculated a cohort of BALB/c mice with WT or II $\Delta gra15$  parasites and measured IFN- $\gamma$  levels 391 in the peritoneal cavity at 2 dpi. We found no difference in IFN- $\gamma$  levels between WT and 392 IIAgra15 infections in BALB/c mice (Fig 6E). However, consistent with BALB/c mice being 393 predisposed to generating a Th2 response, the IFN- $\gamma$  levels in peritoneal fluid of BALB/c mice 394 (Fig 6E) was approximately 10-fold lower than IFN- $\gamma$  levels in the peritoneal fluid of infected 395 C57BL/6 mice (Fig 6A). 396

# 397 **Discussion**

399	As GRA15 acutely modulates the secretion of IL-12 by infected macrophages in vitro
400	and has been reported to affect parasite growth and local IFN- $\gamma$ levels very early <i>in vivo</i>
401	(15,18,41), here we sought to understand the biological relevance of these changes beyond the
402	earliest days of infection by assessing brain outcomes at 3 wpi. We found that the brain parasite
403	burden, the number of macrophages/microglia and T cells in the brain, and splenic CD4 and CD8
404	IFN- $\gamma$ + T cells did not differ between WT and II $\Delta gra15$ strains. We did find several subtle
405	differences in splenocytes from WT and $II\Delta gra15$ infected mice (decreased M1-like
406	macrophages and frequency of PD-1+ CTLA-4+ CD4+ T cells and NK cells), but the biological
407	significance of these findings is unclear given the other equivalent outcomes. In summary, the
408	work presented here suggests that despite GRA15's well documented effects in vitro
409	(14,15,18,32), for the outcomes we measured, GRA15 has little effect on cerebral toxoplasmosis
410	and peripheral immune cell polarization in C57BL/6 mice at 3 wpi.
411	Our finding that GRA15 does not influence brain parasite burden, at least early in brain
412	infection, is consistent with a prior publication that also used an independently generated
413	II $\Delta$ gra15 strain (19). Conversely, a different publication that used strains generated by the lab
414	that originally identified the link between GRA15 and NF- $\kappa$ B found a trend (p>0.05) toward a
415	lower cyst burden at 4 wpi in mice infected with that $II\Delta gra15$ strain (14,20). Collectively, these
416	data suggest that GRA15 likely does not influence cyst burden early in brain infection, though
417	variation can be seen with knockouts from different labs.
418	Though we did not find GRA15-related differences in the brain parasite burden or
419	immune cells in the brain parenchyma, our identification of mice infected with $II\Delta gra15$ as
420	having a lower number and frequency of M1-like macrophages (Fig 2A,B) is consistent with the
421	in vitro data suggesting GRA15 plays a role in polarizing macrophages to an M1-like phenotype

422	(14). However, the rest of the results indicate that this difference in the M1-like compartment is
423	not sufficient to alter parasite abundance in the brain at 3 wpi. Our finding that $II\Delta gra15$ infected
424	mice have a lower frequency of "exhausted" CD4+ T cells is novel and interesting, especially
425	when viewed in the context that II $\Delta gra15$ infected mice had the same number of IFN- $\gamma$
426	producing CD4 and CD8 T cells as WT infected mice (i.e., no $II\Delta gra15$ effect on these
427	populations). While several possibilities might explain this discrepancy, one possibility is that
428	these PD-1+ CTLA-4+ CD4 T cells are not exhausted. Recent work suggests the identification of
429	exhausted cells using surface markers only is likely inadequate as PD-1 <sup>hi</sup> cells that also express
430	other inhibitory markers (e.g. TIM-3, CTLA-4) can be highly activated effector cells (i.e.,
431	express IFN- $\gamma$ ) that have not yet fully differentiated (42). As our flow panel that included PD-1
432	and CTLA-4 did not include IFN- $\gamma$ , we cannot determine if these cells were truly exhausted or
433	maintain effector function. Future studies will be required to definitively determine the status of
434	these cells.

435 The major limitation of this study, and every study that has examined type II gra15 436 knockout strains in mice (14,18–20), is the lack of an appropriate complemented strain in which 437 GRA15 has been ectopically expressed at the same level as in wild-type parasites. While a 438 complemented strain is not necessary for negative results (i.e., no difference between the wild-439 type and KO strain), complemented strains are important for phenotypes that differ between 440 wild-type and KO strains or between studies of independently generated KOs. For example, as 441 noted above, we found differences between mice infected with the wild-type and II $\Delta gra15$ 442 strains in the M1-like, "exhausted" CD4 T cell, and NK cell populations. Similarly, unlike prior 443 work, we did not find a decrease in peritoneal supernatant IFN-γ at 2 dpi in C57Bl/6 or BALB/c 444 mice infected with  $II\Delta gra15$  parasites compared to mice infected with WT parasites (Fig 6A, E).

While several possibilities might explain these differences, appropriate complemented strains
would help distinguish between GRA15 driven effects and effects driven by idiosyncratic
differences of individual knockout strains.

448 Why does GRA15—which has clear and consistent phenotypes in vitro (e.g., NF-κB 449 activation, IL-1 $\beta$  production)—have such a limited phenotype in mice? This discrepancy may 450 relate to Toxoplasma having evolved to survive across a range of intermediate hosts, leading to 451 redundancies in mechanisms to manipulate host signaling pathways. For example, *Toxoplasma* 452 proteins GRA83, GRA24, profilin, GRA7, and GRA15 are all linked to IL-12 production from 453 infected murine DCs and macrophages and are initiated through different ligand-receptor 454 interactions (6,14,15,18,43-45). Therefore, these redundancies in how parasites trigger IL-12 455 production in mice may compensate when parasites lack GRA15. On the other hand, species 456 that lack the receptors that murine cells use to detect *Toxoplasma* protein (e.g., humans lack 457 TLR11/12 which recognize the *Toxoplasma* protein profilin) may have a stronger dependency on 458 GRA15 signaling to generate IL-12 during infection. Thus, while GRA15 may not play an 459 essential role in mice up to 3 wpi, in a different host, GRA15 may be the difference between type 460 II parasite survival and clearance.

461

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617

#### 619 Figure 1. GRA15 does not influence brain parasite burden in the brain at 3 weeks post

620 infection. Mice were intraperitoneally (i.p.) inoculated with saline (control) or 10,000 WT,

- 621 II $\Delta$ gra15, or II $\Delta$ gra15:GRA15 parasites. Brains and spleens were harvested at 3 weeks post
- 622 infection (wpi). Mice from these infections were used in Figures 1-5. A. Graph of *Toxoplasma*
- brain burden as assessed by Q-PCR for the *Toxoplasma*-specific B1 gene. **B.** Representative
- 624 images of a brain tissue cyst stained with Dolichos biflorus agglutinin (DBA). *Top image* is DBA
- staining, *middle image* is staining with anti-*Toxoplasma* antibodies, and *bottom image* is merge.
- 626 C. Quantification of cyst numbers in 8 brain sections per mouse. D. Representative images of
- 627 Iba1+ cells (microglia/macrophages). Scale bar, 100 μm E. Quantification of the number of Iba-

1+ cells. **F**. Representative images of CD3 $\epsilon$ + cells (T cells). Scale bar, 100  $\mu$ m. Panels on right

- are enlarged insert of white box in left panels. G. Quantification of  $CD3\epsilon$ + cells. A, C, E, G.
- Bars, mean  $\pm$  SEM. N = 8 fields of view/section, 3 sections/mouse, 5-12 mice/group. For each

mouse, the number of cells/section was averaged to create a single point. Data representative oftwo independent experiments.

633

Figure 2. GRA15 may affect splenic M1-like macrophage population at 3 wpi. A, B. Splenic
 mononuclear cells were evaluated for the presence of M1-like macrophages (CD45+, F4/80+,

636 CD11b<sup>hi</sup>, CD11b<sup>lo/int</sup>, CD80+, CD86+) **C**, **D**. Splenic mononuclear cells were evaluated for the

637 presence of M2 macrophages (CD45+, F4/80+, CD11b<sup>hi</sup>, CD11c<sup>lo/int</sup>, CD206+ (MMR). Bars,

638 mean  $\pm$  SEM. N=11-12 mice/infected group. Data are representative of two independent

639 experiments.

640

Figure 3. GRA15 does not influence splenic Th2, Tregs, or Th1 CD4+ T cells populations at
3 wpi. A,B. Splenic CD4+ CD3+ T cells were evaluated for the presence Th2 T cells (CD3+

CD4+ Gata-3+) C,D. Splenic CD4+ CD3+ T cells were evaluated for the presence regulatory T
cells (CD3+ CD4+ Foxp3+) <b>E,F.</b> Splenic CD4+ CD3+ T cells were evaluated for the presence of
Th1 T cells (CD3+ CD4+ T-bet+) Bars, mean ± SEM. N=11-12 mice/infected group. Unlisted p
values were not significant. Data are representative of two independent experiments.
Figure 4. GRA15 does not influence IFN- $\gamma$ producing T cell populations at 3 wpi. A.
Splenic CD4+ CD3+ T cells were evaluated for their ability to make IFN- $\gamma$ <b>B</b> . Splenic CD8+
CD3+ T cells were evaluated for their ability to make IFN- $\gamma$ . Bars, mean $\pm$ SEM. N=11-12
mice/infected group. Data are representative of two independent experiments. Unlisted p values
were $\ge 0.05$ .
Figure 5. GRA15 may influence the frequency of peripheral "exhausted" T cells and NK
cells at 3 weeks post infection. A,B. Splenocytes were evaluated for the presence of CTLA-
4+/PD-1+ CD4+ T cells C,D. Splenocytes were evaluated for the presence of CD3- NK1.1+
cells. Bars, mean $\pm$ SEM. N=11-12 mice/infection strain. Data are representative of two
independent experiments.
Figure 6. GRA15 may increase parasite dissemination during acute infection. A-D. Cre
reporter mice were inoculated with 10,000 WT or $II\Delta gra15$ parasites. At denoted time points peritoneal
lavage was done to isolate peritoneal exudate cells (PECs). At 5 dpi liver and spleen tissue was also
collected for B1 analysis. A. ELISA of IFN- $\gamma$ found in the peritoneal cavity at 2 dpi. B. Frequency of
GFP+ CD45+ cells found within the peritoneal cavity at 2 and 5 dpi. C. Q-PCR of parasite genomes on
DNA isolated from liver at 5 dpi. <b>D.</b> Q-PCR of parasite genomes on DNA isolated from spleen at 5 dpi.
<b>E.</b> BALB/c mice were intraperitoneally inoculated with 5,000 WT or $II\Delta gra15$ parasites. Graph shows
levels of IFN- $\gamma$ detected by ELISA using peritoneal lavage fluid at 2 dpi. Bars, mean $\pm$ SEM. N = 4-5

- 668 mice/infection strain. B-D. Each dot represents a mouse. A-D. Data are representative of two
- 669 independent experiments, 4-5 mice/infection strain/cohort. Statistics: Two-way ANOVA, Fisher's LSD
- 670 multiple comparisons test. E. Statistics: T-test. N=5 mice per group, one experiment.







#### 675 **Figure 2**











679 680

#### 681 Figure 4







687 Figure 6









