

Paracrine rescue of MYR1-deficient *Toxoplasma gondii* mutants reveals limitations of pooled *in vivo* CRISPR screens

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eLife Assessment

This **important** study shows that *Toxoplasma gondii* uses paracrine mechanisms, in addition to cell-intrinsic methods, to evade the host immune system, with MYR1 playing a key role in transporting effector molecules into host cells. The authors present **convincing** evidence that *in vivo*, MYR1-deficient parasites can be rescued by wild-type parasites, revealing a limitation in pooled CRISPR screens, where such paracrine effects may obscure the identification of key parasite pathways involved in immune evasion

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Abstract

Toxoplasma gondii is an intracellular parasite that subverts host cell functions via secreted virulence factors. Up to 70% of parasite-controlled changes in the host transcriptome rely on the MYR1 protein, which is required for the translocation of secreted proteins into the host cell. Mice infected with MYR1 knock-out (KO) strains survive infection, supporting a paramount function of MYR1-dependent secreted proteins in *Toxoplasma* virulence and proliferation. However, we have previously shown that MYR1 mutants have no growth defect in pooled *in vivo* CRISPR-Cas9 screens in mice, suggesting that the presence of parasites that are wild-type at the *myr1* locus in pooled screens can rescue the phenotype. Here, we demonstrate that MYR1 is not required for the survival in IFN- γ -activated murine macrophages, and that parasites lacking MYR1 are able to expand during the onset of infection. While Δ MYR1 parasites have restricted growth in single-strain murine infections, we show that the phenotype is rescued by co-infection with wild-type (WT) parasites *in vivo*, independent of host functional adaptive immunity or key pro-inflammatory cytokines. These data show that the major function of MYR1-dependent secreted proteins is not to protect the parasite from clearance within infected cells. Instead, MYR-dependent proteins generate a permissive niche in a paracrine manner, which rescues Δ MYR1 parasites within a pool of CRISPR mutants in mice. Our results highlight an important limitation of otherwise powerful *in vivo* CRISPR screens and point towards key functions for MYR1-dependent *Toxoplasma*-host interactions beyond the infected cell.

Significance statement

Pooled CRISPR screens are powerful tools to interrogate gene function in a high-throughput manner. Genes conferring fitness advantages or disadvantages upon disruption can be identified by sequencing. However, in *Toxoplasma gondii* pooled CRISPR screens in mice, fitness defects for some selected mutants drastically diverge from those observed in single-strain infections. Here, we show that a growth defect of a single *Toxoplasma* gene deletion mutant is rescued if co-infected with wildtype parasites. These results shine light on *Toxoplasma*'s ability to subvert the host response beyond the infected cell, and highlight an important limitation of pooled CRISPR screens in mice. This limitation is probably encountered in CRISPR screens in general where paracrine effects occur.

Introduction

Pooled CRISPR screens have been an extraordinarily powerful genetic tool to identify gene function in an unbiased manner using negative or positive selection. They have been applied in various cell culture conditions and *in vivo*, in combination with different genetic or chemical bottlenecks to identify genes in a specific setting (1). Fitness-conferring genes are identified by assessing the relative abundance of cells with different genetic perturbations within a pool of mutants upon selective pressure.

We have previously performed pooled CRISPR screens in mice with the intracellular parasite *Toxoplasma gondii*, to identify exported parasite proteins that are important for survival in his natural host (2, 3). For the majority of tested genes, the phenotypes observed in pooled CRISPR screens are concordant to those observed in single-strain infections using clonal mutants for those genes. To our surprise, however, we found that while some *Toxoplasma* genes are required for survival in single-strain mutant KO murine infections, this fitness defect phenotype is lost when the same mutants are part of a heterogenous mutant pool used for CRISPR screens in mice. We hypothesised that individual mutants can be rescued by paracrine effects triggered by other parasites in the pool, pointing towards a potential limitation of pooled CRISPR screens to detect a subset of important virulence factors in *Toxoplasma*. This limitation likely is not restricted to *Toxoplasma*, or other infectious contexts, but CRISPR screens in general where paracrine effects are operating.

Toxoplasma is a ubiquitous parasitic pathogen in all warm-blooded animals. *Toxoplasma* infection is widespread in livestock and wild animals, as well as in humans, where one third of the population is estimated to be seropositive (4). Following oral infection by oocysts or latent stage tissue cysts, the parasite grows as tachyzoites in intermediate hosts, before disseminating to distal organs. The host immune response is pivotal to reduce parasite burden caused by rapidly proliferating tachyzoites. However, it is not sufficient to completely clear infection, as surviving parasites can differentiate into the chronic bradyzoite forms and establish tissue cysts in the central nervous system and skeletal muscle cells (5). During the onset of infection, recognition of *Toxoplasma*-derived pathogen-associated molecular patterns (PAMPs) by host innate immune cells triggers the production of IL-12, amongst other pro-inflammatory mediators (6). IL-12 has a protective role during toxoplasmosis, primarily by triggering IFN- γ production in lymphocytes and thereby linking innate and adaptive immunity during infection (7). IFN- γ is a pivotal cytokine in conferring resistance against *Toxoplasma* infection since it induces expression of interferon-stimulated genes (ISGs) that limit intracellular parasite proliferation and curtail infection (8–10). These antimicrobial effects are enhanced by other pro-inflammatory cytokines. An example is TNF, which acts as a co-stimulatory signal to trigger IFN- γ production by

NK cells exposed to the parasite, and boosts the antimicrobial activity of IFN- γ -activated macrophages (11 [11](#)–13 [13](#)). Following *Toxoplasma* infection, host cells can also secrete chemokines such as CCL2, which drives recruitment of CCR2⁺Ly6C^{high} inflammatory monocytes from the bone marrow to the infected sites (14 [14](#), 15 [15](#)). There, they can differentiate into monocyte-derived dendritic cells or macrophages and act as an extra line of defence against the parasite (16 [16](#), 17 [17](#)).

In order to survive clearance by host immune cells and to disseminate within the infected host, *Toxoplasma* relies on an array of over 250 secreted proteins (18 [18](#)). Following invasion, *Toxoplasma* replicates inside a parasitophorous vacuole (PV) separated from the host cytoplasm by the PV membrane (PVM). During and after host cell invasion, *Toxoplasma* secretes proteins from the rhoptries and the dense granules. Secreted proteins from these organelles are not only pivotal for vacuole establishment, but also nutrient uptake, reprogramming of the infected cell and protection against the host immune response (19 [19](#)). In order to exert their effect, some *Toxoplasma* proteins secreted from dense granules must cross the PVM, likely via a multi-protein translocon that depends on MYR1 (20 [20](#)). GRA16, a dense granule effector that relies on MYR-dependent export to exit the PV and reach the host cytosol, was shown to drive upregulation of the transcription factor c-Myc in host cells (21 [21](#)). After the identification of MYR1 other putative components of the MYR translocon – MYR2, MYR3, MYR4, ROP17 – were identified, using their ability to trigger GRA16-dependent c-Myc induction in infected cells as a surrogate (22 [22](#)–24 [24](#)). It was subsequently suggested that most, if not all exported dense granule proteins that reach the host cell cytosol might depend on functional MYR1 for translocation (23 [23](#), 25 [25](#)). To date, seven virulence factors have been shown to be MYR1-dependent: IST, NSM, HCE1/TEEGR, GRA16, GRA18, GRA24 and GRA28. Once exported, these parasite proteins can interfere with host cell transcription and contribute to the establishment of permissive niches for *Toxoplasma* proliferation and survival via multiple downstream mechanisms. Examples include boosting resistance against IFN- γ -dependent antimicrobial mechanisms (IST (26 [26](#), 27 [27](#))), arresting the host cell cycle (HCE1/TEEGR (28 [28](#), 29 [29](#))), inhibiting programmed host cell death pathways (NSM (30 [30](#))) and modulating cytokine/chemokine secretion (GRA16, GRA18, GRA24, GRA28 (31 [31](#)–34 [34](#))).

Given the combined importance of exported dense granule effectors, it is not surprising that the vast majority of transcriptional changes in *Toxoplasma*-infected human fibroblasts are dependent on MYR1 (35 [35](#)), and that isogenic MYR1-deficient strains are avirulent in mice (20 [20](#)). In pooled *in vivo* CRISPR screens, however, we have shown that parasites lacking MYR1 had no fitness defect in a five-day infection experiment within the mouse peritoneum (2 [2](#), 3 [3](#)). This is in agreement with results from *in vivo* CRISPR screens performed in other labs using different parasite strains and mouse backgrounds where no (25 [25](#), 36 [36](#)), or only very mild growth defects (37 [37](#)) have been observed for MYR1. This divergence of results between isogenic infection, which clearly shows an important role for MYR1 in murine infections, and the pooled CRISPR screens, which show no defect of MYR1 mutants, led us to hypothesise that: 1) MYR1, and therefore proteins that rely on the MYR1 complex for translocation, are not essential for the cell-autonomous survival of parasites in macrophages, the main cell type infected in the first days of a peritoneal infection (38 [38](#)); and 2) Δ MYR1 parasites within a pool of mutants may be rescued by MYR1-competent parasites via a paracrine effect, setting up a parasite-permissive immune environment in which MYR1-deficient mutants can thrive.

Here, we verify both hypotheses, showing that MYR1 is not important for the *Toxoplasma* cell-autonomous survival within macrophages, and deploy co-infection strategies proving that MYR1-competent parasites can trans-rescue the growth defect of Δ MYR1 parasites *in vivo*. This rescue does not depend on the host adaptive immune response and surprisingly still occurs despite high levels of key pro-inflammatory cytokines. This knowledge is paramount to understand the biological function of MYR1-driven rewiring of the host cell, and consequently the function of MYR1-dependent effector proteins. It also highlights an important limitation of otherwise

powerful *in vivo* pooled CRISPR screens in *Toxoplasma*, where loss-of-function of a protein in one parasite can be rescued by other parasites in the pool. This limitation likely extends to CRISPR screens in other biological contexts in which paracrine effects operate.

Results

MYR1 is not essential for survival within IFN- γ -stimulated macrophages

To test whether MYR1 was required for the parasite cell-autonomous survival in immune cells, we infected IFN- γ -primed bone marrow-derived macrophages (BMDMs) with WT or MYR1 KO parasites established in the type II Prugnau (Pru) genetic background, and quantified infected cells after 24 h. As GRA12 was shown to be required for parasite survival in IFN- γ -stimulated macrophages (39) and had a strong growth defect in our pooled *in vivo* CRISPR screen (2), we included a Δ GRA12 strain in these experiments as positive control. As negative control, we included parasites lacking IST (SI Appendix, Fig. S1b), a known MYR1-dependent factor that inhibits the induction of interferon-stimulated genes. IST protects the parasites against intracellular restriction when the infection precedes IFN- γ activation, but not if *Toxoplasma* infects primed cells (26, 27). As expected, Δ GRA12 parasites showed a significant reduction in the proportion of infected cells in the presence of IFN- γ (Fig. 1a). Infection with Δ MYR1 was comparable to Δ IST and not significantly different to that of WT parasites, although a slight increase in restriction was observed for Δ IST and Δ MYR1. Our results are in line with findings from Wang and colleagues where deletion of MYR1 in a more virulent type I strain similarly causes no fitness defect in IFN- γ -activated macrophages (40).

To further validate the role of virulence factors in conferring parasite resistance against IFN- γ -mediated host defence, we assessed replication of Δ MYR1 or Δ GRA12 in competition with WT parasites over two lytic cycles in IFN- γ -treated or unprimed BMDMs, and in HFFs as control (Fig. 1b). As expected, Δ GRA12 was outcompeted by WT parasites exclusively in BMDMs pre-stimulated with IFN- γ , confirming its role to survive the cytokine-mediated clearance in macrophages (Fig. 1c). On the contrary, Δ MYR1 parasites displayed a fitness defect compared to WT parasites, regardless of the infected cell type and independently of IFN- γ treatment (Fig. 1c). This result is in line with the smaller size of the Δ MYR1 plaques established in HFFs compared to the parental strain (Fig. 1d), which recapitulates published data (22).

MYR1 mutants expand during the course of infection and can form tissue cysts *in vivo*

To investigate the growth of Δ MYR1 parasites *in vivo* and follow infection over time, we generated parasite strains expressing firefly luciferase (Luc) in the wild-type (WT-Luc) or Δ MYR1 backgrounds (Δ MYR1-Luc, SI Appendix Fig. S1c). We injected mice with 25,000 tachyzoites and monitored parasite growth over 7 days by intravital imaging (Fig. 2a). As expected from the reduced *in vitro* growth phenotype in HFFs and BMDMs, Δ MYR1-Luc showed reduced bioluminescent signal compared to WT-Luc parasites (Fig. 2b-c), confirming that the growth defect *in vitro* results in analogous phenotypes *in vivo*. Nevertheless, MYR1-deficient parasites were still able to expand in mice, as bioluminescence signal increased from day 3 to day 5 post infection (Fig. 2b-c). This initial increase of growth is similar to what was observed for Δ IST parasites (26, 27). Δ MYR1-Luc-infected mice that survived the acute phase of infection for four weeks p.i. carried a low number of cysts in the brain (3.4 cysts/brain on average; 0-13 cysts/brain detected, Fig. 1d). This is similar to previous observations (2) indicating that expression of luciferase does not decrease the ability to produce cysts and further supports the

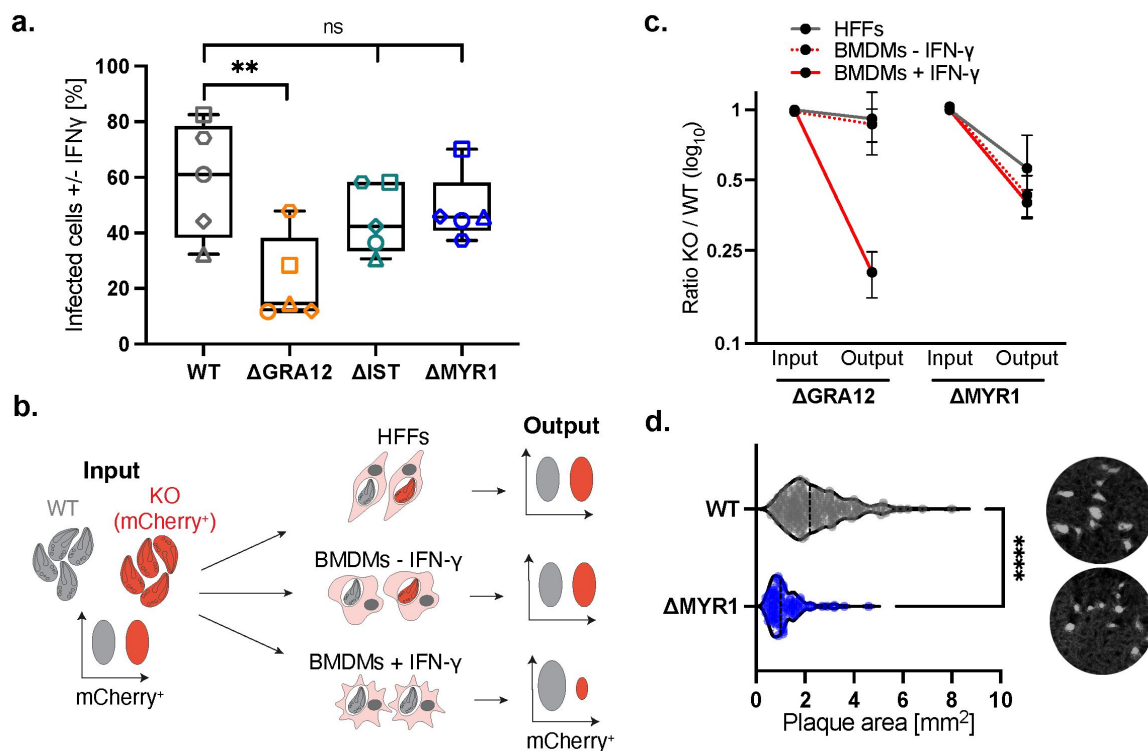


Fig 1.

MYR1 and MYR1-dependent factors are not contributing to *in vitro* *Toxoplasma* survival in IFN- γ -activated macrophages.

(a) BMDMs were stimulated with 100 U/ml IFN- γ for 24 h or left untreated, before infection with mCherry-expressing *Toxoplasma* strains for 24 h. Cells were fixed and imaged by high-content imaging, and the percentage of infected cells in IFN- γ -treated BMDMs compared to untreated controls is shown. WT refers to Pru Δ UPRT. The box-plot shows the median value and the whiskers show minimum and maximum values. Significance was tested with the One-way Anova test with the Benjamini, Krieger and Yekutieli FDR correction, n=5. (b) Schematic of the flow cytometer-based growth competition assay of an IFN- γ -dependent effector (e.g. GRA12). HFFs and BMDMs were co-infected with equal amounts of colourless WT and mCherry-expressing Δ GRA12 or Δ MYR1 strains. BMDMs were stimulated with 100 U/ml IFN- γ for 24 h or left untreated before infection. The mCherry signal was quantified by flow cytometry analysis and the ratio between the strains after two passages (output) was compared to the input. (c) Growth of competing mutant and WT parasites was assessed by flow cytometry. The normalised ratios of output versus input are shown. The average of two independent experiments with technical triplicates is shown. (d) Violin plot of the plaque size of parental Pru Δ KU80 and derived Pru Δ MYR1 strains. The bar represents the median value and representative images are reported on the right. Significance was tested using a two-tailed unpaired Welch's t-test, ** p<0.01, **** p<0.0001, n=2.

notion that Δ MYR1 parasites are able to form cysts, albeit at low numbers. As mice infected with WT parasites succumbed during the acute stage of infection, we cannot compare cyst numbers between the two strains.

MYR1-dependent secreted factor(s) rescue Δ MYR1 *in vivo* growth defect via a paracrine mechanism, independent of host adaptive immunity

We have shown that Δ MYR1 parasites have reduced *in vitro* and *in vivo* growth, despite not having any significant growth defect when in a pool with other mutants. Therefore, we hypothesised that MYR1-competent parasites within the KO pool generate a permissive environment that ultimately promotes growth of the Δ MYR1 mutants in a paracrine fashion. To test this hypothesis, we performed co-infection experiments where mice were injected with an inoculum containing a 20:80 ratio of Δ MYR1-Luc parasites with either WT parasites or Δ MYR1 mutants not expressing luciferase (**Fig. 3a**). This setting allows us to assess if the presence of WT parasites affects growth of Δ MYR1-Luc parasites within the peritoneum. Our results show that Δ MYR1-Luc parasites proliferate better in mice co-infected with WT parasites than with Δ MYR1 parasites (**Fig. 3b-c**). These results support a paracrine role of MYR1-mediated effectors *in vivo*.

To understand what mediates this trans-rescue phenotype, we assessed the production of selected pro-inflammatory cytokines important during *Toxoplasma* infection. Mice infected with a mix of Δ MYR1:WT or Δ MYR1: Δ MYR1 parasites display comparable levels of IL-12p40 in both peritoneum and serum at day 7 p.i. However, Δ MYR1:WT infections elicited higher levels of CCL2/MCP-1, TNF and especially IFN- γ compared to the Δ MYR1: Δ MYR1 mix (**Fig. 3d**, **SI Appendix Fig. S1d-f**).

Considering that Δ MYR1-Luc growth is rescued even when high levels of IFN- γ are produced in the peritoneal cavity, we wanted to assess whether disrupting IFN- γ -producing cell populations would impact the trans-rescue phenotype. Lymphocytes, in particular CD8⁺, Th1-committed CD4⁺ and $\gamma\delta$ T cells, are the main sources of IFN- γ during *Toxoplasma* infection (41). Thus, we applied the same mixed infection strategy in Rag2-deficient mice that do not produce mature T and B cells, and therefore fail to deploy adaptive immune responses (42) (**Fig. 3e**). As expected, an overall higher parasitaemia was detected in Rag2^{-/-} mice when compared to WT mice, due to the known role of the T and B cells to control infection. Nevertheless, in both Rag2^{-/-} and WT control mice Δ MYR1-Luc parasites proliferate more when mixed with WT parasites than with Δ MYR1 parasites (**Fig. 3f**). These results confirm that the host adaptive response is not essential for the trans-rescue of MYR1-deficient *Toxoplasma* during acute infection.

Discussion

In this work we show that deletion of MYR1, and by extension MYR1-dependent effectors, does not impact the ability of *Toxoplasma* to initiate an infection in mice and survive in IFN- γ -stimulated murine macrophages. While clonal Δ MYR1 mutants have a significantly reduced growth compared to WT parasites *in vivo*, co-infection with WT parasites increased their ability to proliferate. This finding supports results from pooled CRISPR-Cas9 screens, where loss-of-function mutants of *Myr1* and other genes previously shown to be involved in PV translocation of effector proteins, show no (2, 3, 25, 36) or only relatively minor fitness defects in mice (37). The rescue phenotype observed in mixed infections is very unlikely to occur through co-infection of host cells by WT and Δ MYR1 parasites, as in the peritoneal exudate from infected mice less than 2% of all infected cells were co-infected (data not shown). As such, our data indicates that some MYR1-dependent effectors cause changes in infected murine cells, that in turn provide a favourable environment for parasite growth in a paracrine manner. This is important as: 1) It shows that the

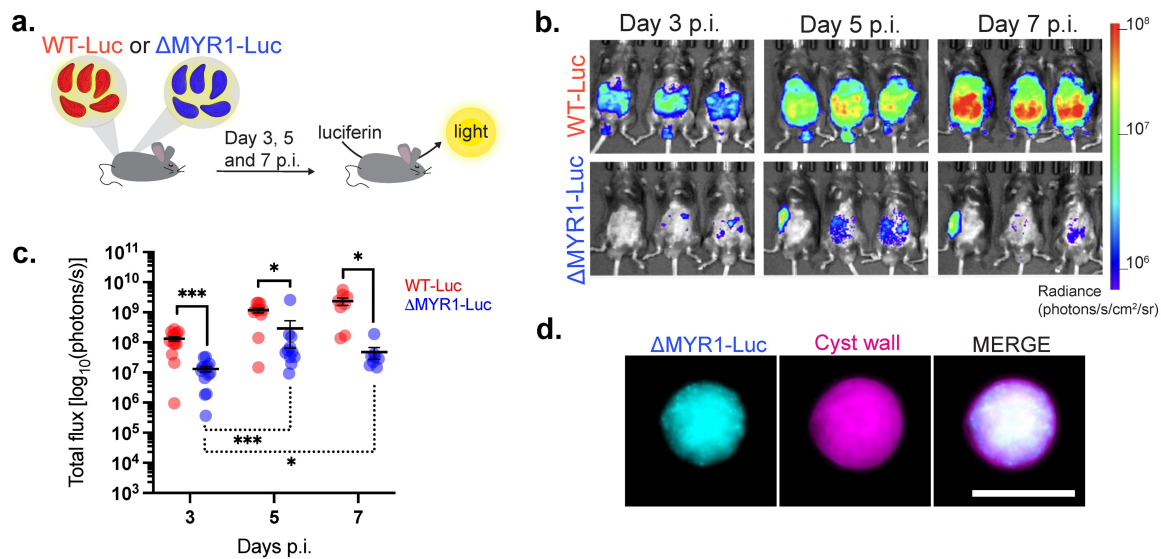


Fig. 2.

AMYR1 parasites expand in the murine host and form cysts *in vivo*.

(a) Mice were infected i.p. with luciferase-expressing *Toxoplasma* strains, WT-Luc or Δ MYR1-Luc, and whole-body intravital imaging was performed at days 3, 5 and 7 p.i. (b) Representative whole-body intravital imaging. (c) Graph shows the total bioluminescence signal converted to a logarithmic scale from two independent experiments. Statistical differences between the two strains at each timepoint were tested with the Mixed-effects model (REML) with Sidak post-hoc tests (continued lines). Significance for the Δ MYR1-Luc growth over time was tested with a One-Way Anova test (dotted line). Number of mice per group: day 3 p.i.: n=14; day 5 p.i.: n=11; day 7 p.i.: n=8. * $p < 0.05$, *** $p < 0.001$. (d) Representative fluorescent image of a brain cyst from a mouse infected with Δ MYR1-Luc. mCherry-expressing Δ MYR1-Luc parasites were detected by microscopy. Cyst wall was stained with the FITC-conjugated lectin DBA. The scale bar represents 25 μ m.

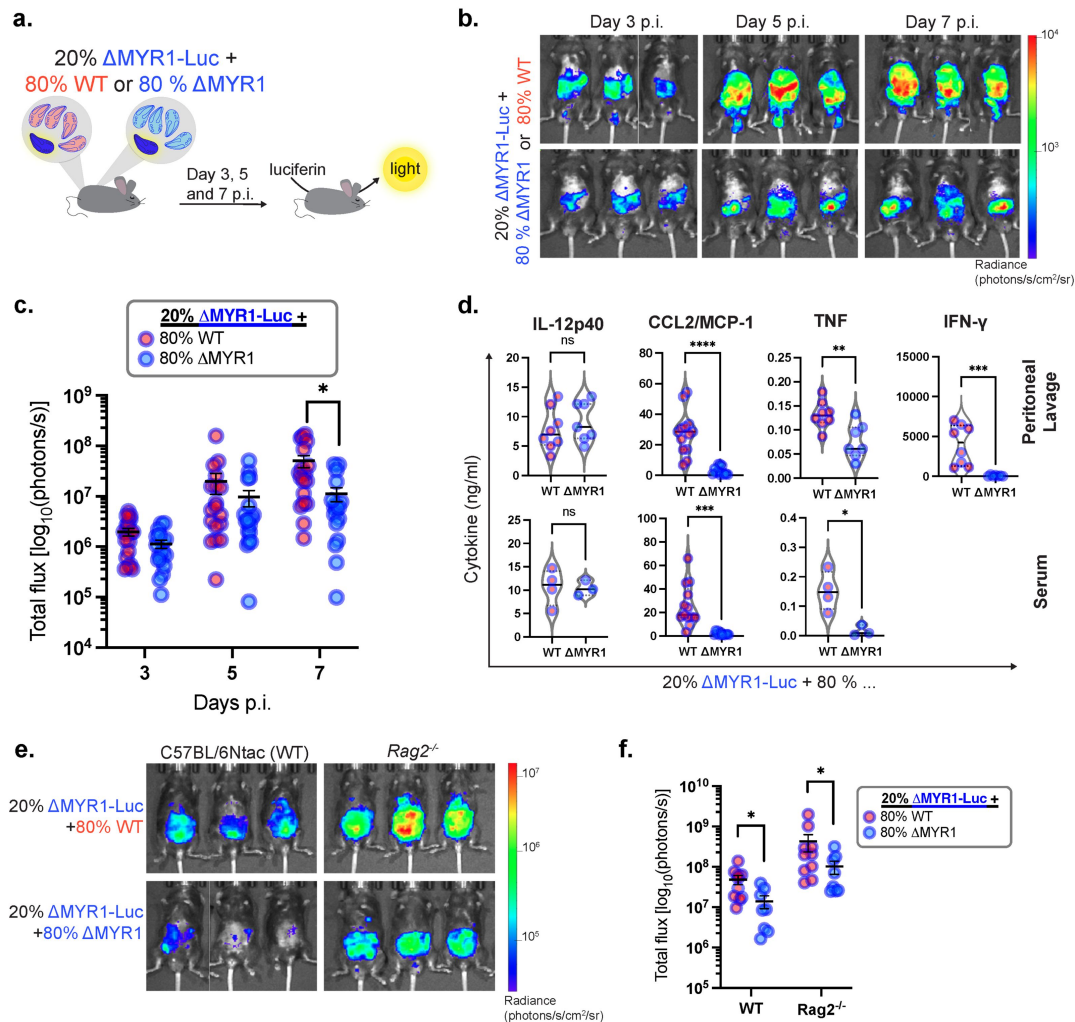


Fig 3.

The *in vivo* growth defect of Δ MYR1 is rescued by the presence of MYR1-competent parasites, independently of functional host adaptive immunity.

(a) Mice were infected i.p. with a mixed inoculum of *Toxoplasma* tachyzoites, containing a 20:80 ratio of luciferase-expressing Δ MYR1-Luc to WT or Δ MYR1 strains that do not express luciferase. Growth of Δ MYR1-Luc was monitored at 3, 5 and 7 days p.i. by whole-body intravital imaging. (b) Representative whole-body intravital imaging. (c) Total bioluminescence signal converted to a logarithmic scale from mice co-infected with Δ MYR1-Luc:WT (n=18) or Δ MYR1-Luc: Δ MYR1 (n=17). Graph shows cumulative data from four independent experiments. Significance was tested with a Two-way Repeated Measures ANOVA with Sidak post-hoc tests. (d) IL-12p40, CCL2/MCP-1, TNF and IFN- γ levels were detected in peritoneal lavage and serum of animals infected with mixed *Toxoplasma* inoculum (20:80 ratio) at day 7 p.i. by ELISA. The violin-plots show the median (continued black line) and quartiles (dotted grey lines). Significance was tested with the Welch's t-test (TNF, CCL2/MCP-1 and IL-12p40 ELISAs) and Mann-Whitney test (IFN- γ ELISAs). Samples from 2 to 3 independent experiments were assayed. Number of samples for CCL2: WT n=13 and Δ MYR1 n=12. Number of samples for other cytokines: peritoneal lavage samples: WT n=8 and Δ MYR1 n=7; serum samples: WT n=4 and Δ MYR1 n=3. Data with higher differences between inocula (CCL2 and IFN- γ) are displayed in a logarithmic scale in **SI Appendix Fig. S1d-f**. (e) Representative whole-body intravital imaging at day 7 p.i. of C57BL/6Ntac (WT) or RAG2-deficient (*Rag2*^{-/-}) mice infected i.p. with a mixed inoculum containing a 20:80 ratio of luciferase-expressing Δ MYR1-Luc tachyzoites to WT or Δ MYR1 strains that do not express luciferase. (f) Total bioluminescence signal converted to a logarithmic scale from mice co-infected with Δ MYR1-Luc:WT (n=10) or Δ MYR1-Luc: Δ MYR1 (n=8). Graph shows cumulative data from two independent experiments. Significance was tested with the Multiple Mann-Whitney test with a False Discovery Rate approach by a Two-stage step-method. * p<0.05, ** p<0.01, *** p<0.001, **** p<0.0001.

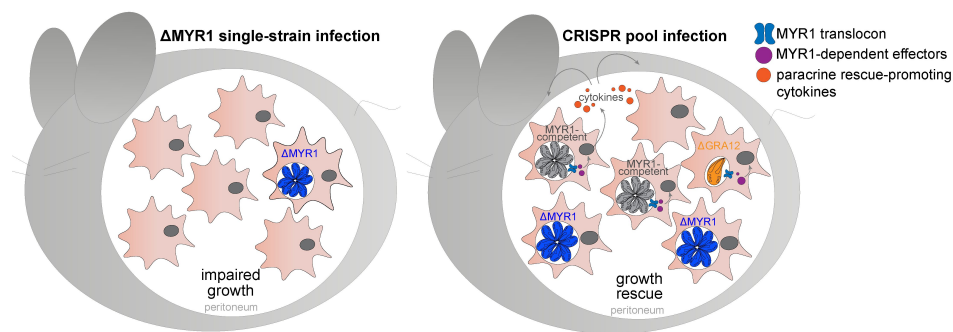


Fig 4.

Model illustrating paracrine rescue of Δ MYR1 parasites in pooled CRISPR screens.

Left panel: In single-strain infections Δ MYR1 parasites grow slowly within the peritoneum and are cleared. Right panel: Growth of Δ MYR1 parasites within a CRISPR pool is rescued by the presence of MYR-competent parasites. In cells infected with MYR1 competent parasites, MYR-dependent effectors enter the host cell, leading to secretion of cytokines that promote a favourable immune environment. MYR1 mutants are able to proliferate under these conditions (i.e are rescued *in trans*). However, *Toxoplasma* virulence factor mutants required for survival within a cell (cell-autonomous), such as GRA12, can not be rescued in trans.

major transcriptional changes caused by MYR-dependent effectors are not required for *Toxoplasma* to survive cell-autonomous immune responses in IFN- γ -primed cells; 2) Paracrine rescue in pooled CRISPR-Cas9 screens may mask a significant amount of proteins required for *Toxoplasma* survival; 3) It is likely that this “paracrine masking effect” can be found in CRISPR screens in other biological contexts, e.g.: other host-microbe interaction screens, and possibly even in non-infectious biological contexts, such as pooled CRISPR screen approaches to study cancer immunity and to discover regulators of innate and adaptive immunity crosstalk (reviewed in (43 [↗](#), 44 [↗](#))).

We found that the presence of WT parasites in a mixed inoculum with Δ MYR1 mutants elicited significantly higher levels of IFN- γ and TNF in the peritoneum than Δ MYR1 mutants alone. As IFN- γ was shown to be a major cytokine to limit *Toxoplasma* growth in a cell-autonomous manner, and that TNF acts mainly by enhancing the antimicrobial effects in IFN- γ -activated cells, one would expect that Δ MYR1-Luc parasites would be more restricted when injected in combination with WT parasites. However, we observed the opposite, as higher Δ MYR1-Luc parasitaemia was observed in Δ MYR1:WT than in Δ MYR1: Δ MYR1 mixes. These data provide further support that MYR1, and by extension MYR1-dependent effectors, do not protect *Toxoplasma* from the IFN- γ -mediated intracellular clearance in mice.

What could be the driving force of the rescue? We show that the adaptive immune system plays no role, pointing towards cells of the innate immune system. Higher CCL2 levels in mice infected with Δ MYR1:WT suggests higher inflammatory Ly6C^{high} monocytes recruitment to infected tissues (14 [↗](#), 15 [↗](#)). These cells could be responsible for the high levels of TNF and IFN- γ detected. While monocytes have been shown in multiple reports to be important for limiting *Toxoplasma* upon exposure to IFN- γ in infected niches (14 [↗](#), 17 [↗](#), 45 [↗](#)), it is possible that recruited monocytes also provide an important reservoir for parasites to grow in the peritoneum. However, how Δ MYR1 parasites are eventually cleared in homogenous infections in the absence of high levels of CCL2 is not yet known.

Individual MYR-related effectors that may be responsible for the paracrine rescue have not been investigated here and we hypothesise that the phenotype is likely the concerted result of multiple effectors that affect cytokine secretion. For example, previous studies showed that both GRA18 and GRA28 can induce release of CCL22 from infected cells (32 [↗](#), 46 [↗](#)), while GRA16 and HCE1/TEEGR impair NF- κ B signalling and the potential release of pro-inflammatory cytokines such as IL-6, IL-1 β and TNF (29 [↗](#), 47 [↗](#)). Regardless of the effector(s), our results highlight an important novel function of MYR1-dependent effectors by establishing a supportive environment *in trans* for *Toxoplasma* growth within the peritoneum.

We further confirm previous results using luciferase-expressing Δ MYR1 parasites that MYR1 appears to be dispensable for the formation and persistence of latent *Toxoplasma* stages *per se*. As MYR1 has been demonstrated to be dispensable for stage conversion *in vitro* (48 [↗](#)), the relatively low number of cysts is likely explained by a failure of Δ MYR1 parasites to efficiently disseminate and/or persist within the murine host (34 [↗](#)). In alternative, we hypothesise that the absence of CCL2 in Δ MYR1 infections limits recruitment of host cells that *Toxoplasma* can potentially use as vehicles to reach the brain.

This work also highlights the limitations of restriction-based CRISPR-screens in capturing the variety of pathogen’s mechanisms to survive host clearance. Novel applications of the CRISPR screens, for example in combination with single-cell RNA sequencing (49 [↗](#)) or with functional assays to explore immunological contexts (43 [↗](#)) could help understand how infected cells affect the neighbouring environment to support infection, and contribute to parasite survival, dissemination and persistence within the host. Here, we show that MYR1-dependent proteins play a critical role in promoting a favourable environment for growth beyond the infected cell in a paracrine manner. This is different to the injection of rhoptry effector proteins by *Toxoplasma* into

cells it does not invade, which requires parasite-host cell contact (50), and provides a novel angle on how the parasite can systematically alter the host environment in its favour during infection.

Our work draws attention to an understudied aspect of pathogen manipulation in complex multicellular settings which warrants further studies. The limitation we highlight here, that mutant phenotypes can be masked in pooled CRISPR screens, likely extends to other experimental setups where paracrine effects are possible.

Material and methods

Cell culture and parasite strains

Primary human foreskin fibroblasts (HFFs) (ATCC) were maintained in Dulbecco's modified Eagle's Medium (DMEM) with 4.5 g/L glucose and GlutaMAX-1 (Gibco Thermo Fisher Scientific) supplemented with 10% foetal bovine serum (FBS) (Gibco Thermo Fisher Scientific) at 37°C and 5% CO₂. To generate bone marrow-derived macrophages (BMDMs), bone marrow cells were extracted from femurs of C57BL/6J mice and differentiated to macrophages for 7 days at 37°C and 5% CO₂. Briefly, bone marrow cells were seeded in 15 cm² Petri dishes (Corning) and differentiated into BMDMs in RPMI 1640 medium (Gibco Thermo Fisher Scientific) supplemented with 20% L929 conditioned media (containing the murine macrophage colony stimulating factor (mM-CSF)), 50 µM 2-mercaptoethanol, Penicillin/Streptomycin (Thermo Fisher Scientific), and 10% FBS. For experiments BMDMs were grown in the above RPMI medium but lacking 2-mercaptoethanol (called working media further on). *Toxoplasma gondii* strains PruΔKU80 (51), PruΔUPRT::mCherry (3), PruΔGRA12::mCherry (2), PruΔMYR1::mCherry (2) and derived strains were maintained in confluent HFFs and passaged by syringe lysis through 23G needles every 2-3 days.

Generation of parasite lines

10⁶ freshly lysed parasites were transfected with 20-25 µg of DNA by electroporation using the 4D-Nucleofector (Lonza) with previously optimised protocols as described in Young *et al* (2). All primers used are listed in **SI Appendix Fig. S1a**. To generate pSAG1::Cas9sgIST the IST gRNA sequence was inserted into pSAG1::Cas9sgUPRT (52) by inverse PCR using primers 1&2. To generate the IST KO (PruΔIST::mCherry), PruΔKU80 parasites were co-transfected with pSAG1::CAS9sgIST and a Pro-GRAl::mCherry::T2A::HXGPRT::Ter-GRAl construct amplified with primers 3&4 containing 40 bp homology regions to the 5'- and 3'-untranslated regions of IST (ToxoDB TGME49_240060). 24 h after transfection, 50 µg/ml Mycophenolic acid (Merck) and Xanthine (Sigma) (M/X) were added to select for integration, and a clonal culture was verified by PCR with primers 5-8. To generate Luciferase expressing parasite lines, PruΔKU80 or PruΔMYR1::mCherry were co-transfected with pSAG1::CAS9sgUPRT and PciI digested pUPRT-ffLucHA to insert a HA-tagged Firefly luciferase gene (LucHA) into the *Uppt* locus and establish WT-Luc and ΔMYR1-Luc strains respectively. To generate pUPRT-ffLucHA, the GRA1 promoter region and firefly Luciferase sequences were amplified from pGRA (53) and pDHFR-Luc (54) plasmids respectively using primers 9&10 and 11&12 and combined with BamHI/XmaI digested pUPRT-HA in a Gibson reaction. 24 h post transfection 20 µg/ml FUDR (Sigma) was added to select for disruption of the *Uppt* locus and clones verified by PCR with primers 13&14.

Parasite growth in BMDMs

5×10⁴ BMDMs were seeded per well in 96-well Ibitreat black µ-plates (Ibidi GmbH) in working media. The following day cells were either treated with IFN-γ (100 U/mL, Peprotech) or left untreated. 24 h later cells were infected with the strains in triplicate at a multiplicity of infection (MOI) of 0.3, and the plate was centrifuged at 210 g for 3 min. At 3 h post infection (p.i.) the

medium was replaced to remove non-invaded parasites. Cells were fixed in 4% paraformaldehyde (PFA) at 24 h p.i., washed in PBS and stained with Far Red Cell Mask (1:2,000, Thermofisher Scientific). Plates were imaged on an Opera Phenix High-Content Screening System (PerkinElmer) with a 40x NA1.1 water immersion objective. 38 fields of view with 10 planes were imaged per well. Analysis was performed on a maximum projection of the planes and the percentage of infected cells was quantified over triplicate samples similarly to previously established protocols (3, 55).

Competition assay

5×10^5 BMDMs were seeded in 12-well plates in working media. The following day cells were either treated with 100 U/ml IFN- γ or left untreated. 24 h post treatment BMDMs were infected with a 1:1 mix of either WT (Pru Δ KU80) and Pru Δ GRA12::mCherry parasites or WT and Pru Δ MYR1::mCherry parasites at a MOI of 0.3 (1.5×10^5 parasites per well). Confluent HFFs in 12-well plates were similarly infected to evaluate defects in growth of the KO parasites. A sample of input parasites were fixed in 4% PFA to verify the starting ratio. 48 h p.i. cells were scraped and passed through a 27G needle, and the parasites inoculated onto HFF monolayers and grown for a further 3-4 days. For flow cytometry analysis, cells were lysed with 23G needles and the parasites passed through a 5 μ m filter before fixation in 4% PFA and staining with Hoechst 33342 (Thermofisher Scientific). Samples were analysed on a BD LSR Fortessa flow cytometer and with FlowJo software v10. Hoechst 33342 was excited by a 355 nm laser and detected by a 450/50 band pass filter. mCherry was excited by a 561 nm laser and detected by a 600 long pass filter and a 610/20 band pass filter. To eliminate debris from the analysis, events were gated on forward scatter, side scatter and Hoechst 33342 fluorescence. Parasites were identified by their nuclear staining and KO were discriminated by their mCherry signal. The ratios of KO/WT parasites (mCherry⁺/mCherry⁻) from two independent experiments, each in technical triplicates for each condition, were calculated and normalised by dividing by the input ratio, to allow comparison between strains and biological replicates.

Plaque assay

HFF were grown to confluency in T25 flasks and infected with 200 parasites to grow undisturbed for 10 days. Cells were fixed and stained in a solution with 0.5% (w/v) crystal violet (Sigma), 0.9% (w/v) ammonium oxalate (Sigma), 20% (v/v) methanol in distilled water, then washed with tap water. Plaques were imaged on a ChemiDoc imaging system (BioRad) and measured in FIJI (56).

Animal Ethics Statement

C57BL/6J (Jackson Laboratories), C57BL/6NTac and Rag2 N12 C57BL/6N (Rag2-deficient; Rag2^{-/-}, Taconic) mice were bred and housed under specific pathogen-free conditions in the biological research facility at the Francis Crick Institute. Mice maintenance and handling adhered to the Home Office UK Animals Scientific Procedures Act 1986. All work and procedures performed were approved by the UK Home Office and performed in accordance with the granted Project License (P1A20E3F9), the Francis Crick Institute Ethical Review Panel, and conforms to European Union directive 2010/63/EU.

In vivo infections

Male and female mice, aged 6-12 weeks were used in this study. For experiments, animals were sex- and age-matched. Mice were injected intraperitoneally (i.p.) with a total of 25,000 *Toxoplasma gondii* tachyzoites in 200 μ L PBS either as a single-strain inoculum (100% Pru Δ UPRT::LucHA or Pru Δ MYR1::LucHA), or as a mixed strain inoculum including 5,000 tachyzoites of luciferase-expressing strain Pru Δ MYR1::LucHA::mCherry (20%) and 20,000 tachyzoites of Pru Δ KU80 or Pru Δ MYR1::mCherry strains (80%). Mice were monitored and weighed regularly throughout the experiments. Parasite *in vivo* growth was monitored by intravital imaging (IVIS) at days 3, 5 and 7 p.i. Mice were injected i.p. with 100 μ L of 30 mg/ml luciferin (PerkinElmer) in PBS and were

anaesthetised (isoflurane 5% for induction and 2.5% afterwards) 15 min prior to bioluminescent imaging on an IVIS Spectrum CT (Perkin-Elmer). Animals were euthanised at day 7 p.i. or at humane endpoints, blood was collected by cardiac puncture and peritoneal exudate cells were harvested by peritoneal lavage through injection of 1 mL PBS i.p. Blood was transferred to serum separating tubes and centrifuged at 10,000 rpm for 10 min at 4°C to isolate serum, and peritoneal exudate was spun at 500 g for 5 min to remove the cellular component. IL-12p40 (#88-7120-88), TNF (#88-7324-88), IFN- γ (#88-7314-88) and CCL2/MCP-1 (#88-7391-88) levels were detected on serum and/or in suspension at peritoneal exudates of infected mice by ELISA, following manufacturer's protocol (ThermoFisher). To confirm cyst formation, the brain of mice surviving infection with Pru Δ MYR1::LucHA::mCherry tachyzoites were homogenised in 1 mL PBS and 300 μ L of the sample were stained with FITC-conjugated Dolichos Biflorus Agglutinin (DBA; 1: 200; Vector Laboratories #RL-1031) for 1 h at room temperature. Fluorescently labelled cysts were counted using a Ti-E Nikon microscope.

Data analysis

Data was analysed in GraphPad Prism v10. All data shown is presented as means $\pm$ SEM, except for violin plots, where median and quartiles are presented. Two-tailed unpaired Welch's t-test (Gaussian-distributed data) or Mann-Whitney test (non-Gaussian-distributed data) were used for statistical analysis of data with only two experimental groups. For analysis of data with three or more experimental groups, One-way or Two-way ANOVA were performed. When datasets did not follow a Gaussian distribution, data was transformed to a logarithmic scale and parametric statistical analysis was performed on transformed datasets (57 [\[4\]](#)). If logarithmic-transformed data still did not follow a Gaussian distribution, untransformed data was analysed by non-parametric tests (standard or multiple Mann-Whitney tests). Statistical significance was set as: ns – not statistically significant, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

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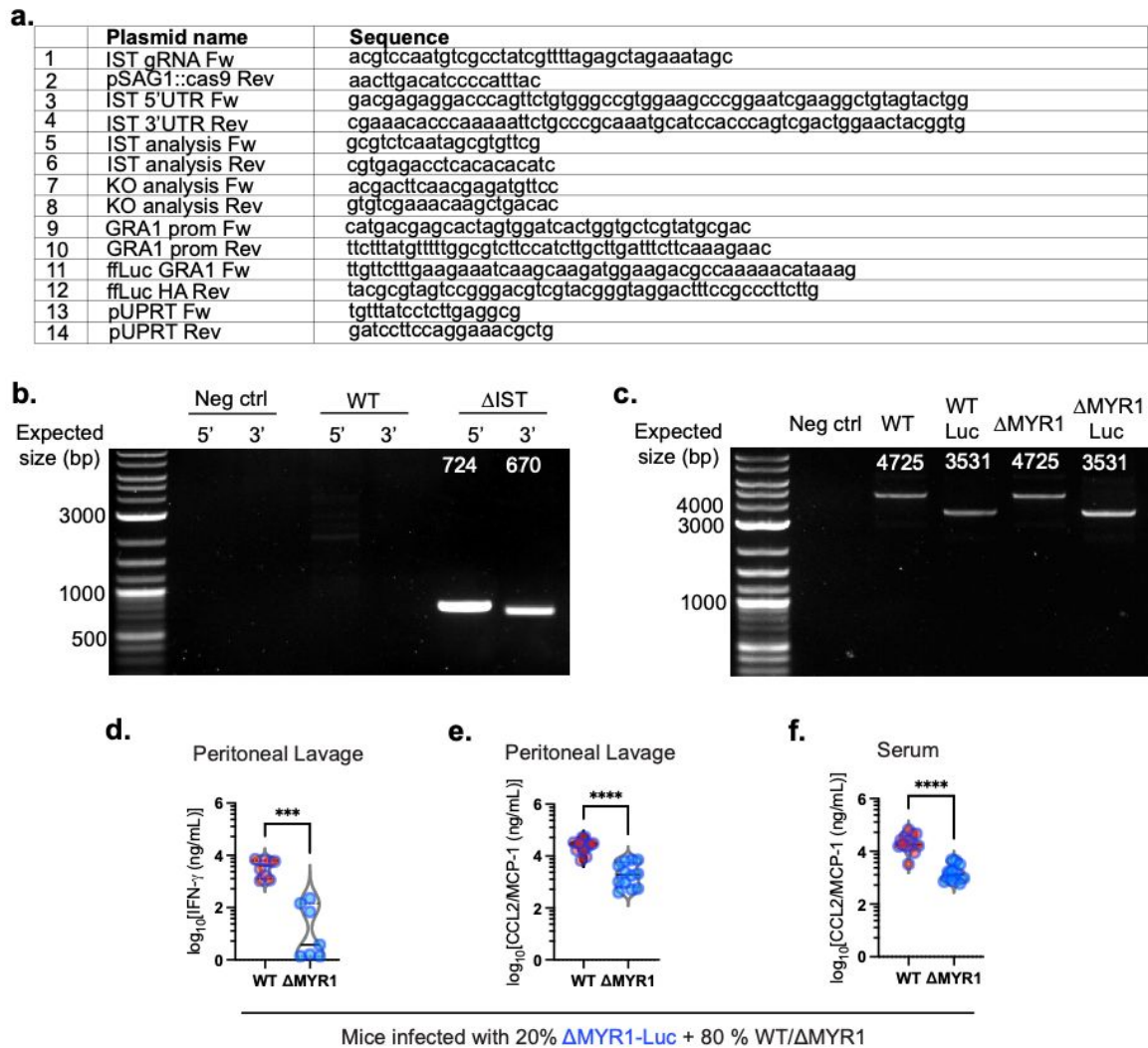
Additional information

Author Contributions

Conceptualisation: F.T., D.F., J.C.Y., M.T.; investigation: F.T., D.F., J.C.Y., S.B.; writing, review, editing: all authors; supervision: M.T.; funding acquisition: F.T., M.T.

Competing interests

The authors declare no competing interests.



SI Appendix Fig. S1.

(a) List of primers used in the study. (b) PCR validation of the Pru Δ IST strain compared to parental Pru Δ Ku80 (WT). (c) PCR validation of the luciferase-expressing WT-Luc and Δ MYR-Luc strains compared to their respective parental strains Pru Δ Ku80 (WT) and Pru Δ MYR1 (Δ MYR1). (d, e and f) IFN- γ at peritoneal lavage (d) and CCL2 at both peritoneal lavage (e) and serum (f), were detected by ELISA at day 7 p.i. with mixed *Toxoplasma* inocula (20:80 ratio) of luciferase-expressing Δ MYR1-Luc to WT or Δ MYR1 strains that do not express luciferase. The violin-plots display data shown in Fig. 3d converted to a logarithmic scale, with the median (continued black line) and quartile values (dotted grey lines) highlighted. Significance was tested with the Mann-Whitney test for IFN- γ , and by Welch's t-test for CCL2 data. The number of biological replicates (n) in each graph is the same as mentioned in the original graphs on Fig. 3d. *** p<0.001, **** p<0.0001.

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Reviewer #1 (Public review):

Previous studies have highlighted some of these paracrine activities of *Toxoplasma* - and Rasogi et al (mBio, 2020) used a single cell sequencing approach of cells infected in vitro with the WT or MYR KO parasites - and one of their conclusions was that MYR-1 dependent paracrine activities counteract ROP-dependent processes. Similarly, Chen et al (JEM 2020) highlighted that a particular rhoptry protein (ROP16) could be injected into uninfected macrophages and move them to an anti-inflammatory state that might benefit the parasite.

Caveats around immunity and as yet no insight into how this works. In Fig 2 there is a marked defect in the ability of the parasites to expand at day 2 and day 5. Together, these data sets suggest that this paracrine effect mediated by MYR-1 works early - well before the development of adaptive responses.

Comments on revisions:

The authors have provided their perspective on the original review. There were some previous comments that revolved around whether some of the early changes were masked by pooling data sets where they have reiterated that it is not statistically different. Would have been nice to have seen out addressed by having experiments that were appropriately powered. But it's their call.

<https://doi.org/10.7554/eLife.102592.2.sa2>

Reviewer #2 (Public review):

Summary:

In this manuscript by Torelli et al., the authors propose that the major function of MYR1 and MYR1-dependent secreted proteins is to contribute to parasite survival in a paracrine manner rather than to protect parasites from cell-autonomous immune response. The authors conclude that these paracrine effects rescue Δ MYR1 or knockouts of MYR1-dependent effectors within pooled in vivo CRISPR screens.

Strengths:

The authors raised a more general concern that pooled CRISPR screens (not only in *Toxoplasma* but also other microbes or cancers) would miss important genes by "paracrine masking effect". Although there is no doubt that pooled CRISPR screens (especially in vivo CRISPR screens) are powerful techniques, I think this topic could be of interest to those fields and researchers.

Weaknesses:

In this version, the reviewer is not entirely convinced of the 'paracrine masking effect' because the in vivo experiments should include appropriate controls (see major point 2) in the first submission.

After the revision, although no experiments were added, this reviewer considered that the points have been sufficiently discussed and commented on.

<https://doi.org/10.7554/eLife.102592.2.sa1>

Author response:

The following is the authors' response to the original reviews.

We thank the reviewers for their time and thoughtful comments on our manuscript.

We realised a preliminary version of Figure 2 was initially submitted, which we are replacing now with a novel version. Differences between the two figures are : 1) The schematic in Figure 2a was replaced with a new one in line with that of Figure 3a; 2) in Figure 2c details about the statistical analysis were removed from the legend and one datapoint that was erroneously removed at day 5 for the Δ MYR1-Luc condition was included. Regardless, these changes do not affect the results and the conclusions initially drawn.

Public Reviews:

Reviewer #1 (Public review):

Previous studies have highlighted some of these paracrine activities of Toxoplasma - and Rasogi et al (mBio, 2020) used a single cell sequencing approach of cells infected in vitro with the WT or MYR KO parasites - and one of their conclusions was that MYR-1 dependent paracrine activities counteract ROP-dependent processes.

Similarly, Chen et al (JEM 2020) highlighted that a particular rhoptry protein (ROP16) could be injected into uninfected macrophages and move them to an anti-inflammatory state that might benefit the parasite.

We are aware of both these studies, where the injection of rhoptry proteins into cells that the parasite does not invade alters the host transcriptional profile establishing a permissive environment. However, here we propose a different paracrine effect that goes beyond the injected/uninfected cell. Specifically, we propose that one or more MYR1-dependent effectors alter the cytokine secretion profile of infected cells, which leads to overall changes in the immune response such as cell types recruited to the site of infection, or the activation state.

There are caveats around immunity and as yet no insight into how this works. In Figure 2 there is a marked defect in the ability of the parasites to expand at day 2 and day 5. Together, these data sets suggest that this paracrine effect mediated by MYR-1 works early - well before the development of adaptive responses.

Yes, we also hypothesise an early effect based on the data. Growth continues until day 5 at least, and then plateaus towards day 7, which makes us believe that the effect takes place within the first 5 days. We agree with the reviewer that the MYR1-mediated rescue acts before the involvement of the adaptive immune response, which is supported by our results obtained in Rag2^{-/-} mice shown in Figure 3e.

Reviewer #2 (Public review):

Summary:

In this manuscript by Torelli et al., the authors propose that the major function of MYR1 and MYR1-dependent secreted proteins is to contribute to parasite survival in a paracrine manner rather than to protect parasites from cell-autonomous immune response. The authors conclude that these paracrine effects rescue Δ MYR1 or knockouts of MYR1-dependent effectors within pooled in vivo CRISPR screens.

Strengths:

The authors raised a more general concern that pooled CRISPR screens (not only in Toxoplasma but also other microbes or cancers) would miss important genes by "paracrine masking effect". Although there is no doubt that pooled CRISPR screens (especially in vivo CRISPR screens) are powerful techniques, I think this topic could be of interest to those fields and researchers.

Weaknesses:

In this version, the reviewer is not entirely convinced of the 'paracrine masking effect' because the in vivo experiments should include appropriate controls (see major point 2).

(1) It is convincing that co-infection of WT and Δ MYR1 parasites could rescue the growth of Δ MYR1 in mice shown by in vivo luciferase imaging. Also, this is consistent with Δ MYR1 parasites showing no in vivo fitness defect in the in vivo CRISPR screens conducted by several groups. Meanwhile, it has been reported previously and shown in this manuscript

that $\Delta MYR1$ parasites have an in vitro growth defect; however, $\Delta MYR1$ parasites show no in vitro fitness defect the in vitro pooled CRISPR screen. The authors show that the competition defect of $\Delta MYR1$ parasites cannot be rescued by co-infection with WT parasites in Figure 1c, which might indicate that no paracrine rescue occurred in an in vitro environment. The authors seem not to mention these discrepancies between in vitro CRISPR screens and in vitro competition assays. Why do $\Delta MYR1$ parasites possess neutral in vitro fitness scores in in vitro CRISPR screens? Could the authors describe a reasonable hypothesis?

The reviewer raises a very interesting point, which at this stage, we cannot fully explain. A technical explanation could be that the relatively small growth defect detected for clean KOs, is not well represented in the CRISPR screens due to the variability of guides, where smaller differences in growth are not reliably captured and hidden within the noise of the assays. Another technical explanation may be median-centering: if the majority of KOs in the pool have a small growth defect, median centering would push these towards a zero. We have observed and reported this phenomenon in Young et al., 2019 for libraries containing a larger fraction of genes with a negative fitness score. In the library used here focusing on secreted proteins, we have not observed a strong trend to negative fitness scores, but cannot exclude smaller shifts. Because we have no solid base to favour any of the above mentioned explanations, we have decided to not speculate too much on this in the manuscript. However, we wanted to show all the data as the difference between these results may not be technical, but biological, which could inform future studies or results by us and others.

(2) The authors developed a mixed infection assay with an inoculum containing a 20:80 ratio of $\Delta MYR1$ -Luc parasites with either WT parasites or $\Delta MYR1$ mutants not expressing luciferase, showing that the in vivo growth defect of $\Delta MYR1$ parasites is rescued by the presence of WT parasites. Since this experiment lacks appropriate controls, interpretation could be difficult. Is this phenomenon specific to MYR1? If a co-inoculum of $\Delta GRA12$ -Luc with either WT parasites or GRA12 parasites not expressing luciferase is included, the data could be appropriately interpreted.

We are not quite sure what appropriate controls the reviewer refers to. We show here in Figures 3c and 3f that increasing parasite load by co-infecting mice with $\Delta MYR1$ parasites is not sufficient to rescue $\Delta MYR1$ -Luc parasite growth. Co-infection with WT parasites, however, does result in increased $\Delta MYR1$ -Luc parasitaemia at day 7 p.i., indicating that MYR1 competence is required for the *in vivo* trans-rescue we describe. As $\Delta GRA12$ parasites have a very strong cell-autonomous restriction *in vitro* and severe growth defect *in vivo* (Torelli et al., BioRxiv), these parasites would be rapidly depleted, which is also observed in all CRISPR screens from various laboratories. Therefore we do not think that co-infection with GRA12-deficient parasites would be an informative experiment here. We do speculate that mutant parasites for other proteins required for export (i.e. MYR 2, 3, 4, ROP17) could also be trans-rescued in addition to mutants for other MYR-dependent proteins such as GRA24 and GRA28, which remodel cytokine secretion and could individually, or synergistically, affect host cell immunity. Dissecting which *Toxoplasma* factor/s and host cytokine signalling pathways drive this trans-rescue effect is highly interesting, but beyond the scope of this manuscript. Here, we focused on the basic concept that an individual mutant can be rescued in trans *in vivo*, which we think is of importance beyond the field of *Toxoplasma* research.

(3) In the Discussion part, the authors argue that the rescue phenotype of mixed infection is not due to co-infection of host cells (lines 307-310). This data is important to support the authors' paracrine hypothesis and should be shown in the main figure.

We understand the reviewer's concern for rescue by co-infection of the same cell, but we largely exclude this hypothesis as *Toxoplasma* cell-autonomous effectors, such as GRA12 and

ROP18, would also be rescued if that were to happen on a larger scale. We previously performed an *in vivo* experiment to assess co-infection rates of peritoneal exudate cells (PECs) by imaging using infection doses comparable to those used in the trans-rescue experiments. The total infection rate of PECs was 2.3%, so the overall number of infected cells per image was low, and not suitable for publication purposes. We tried to capture more cells using FACS analysis, however, PECs are highly autofluorescent in the yellow/green channels, which prevented us from drawing adequate conclusions using our GFP and mCherry strains. Because we see no rescue of GRA12 or ROP18 in CRISPR screens, and the overall *in vivo* co-infection rates were very low as observed by imaging, we did not think that generating strains expressing different fluorochromes compatible with standard FACS analysis, and then performing more *in vivo* experiments was best use of resources at the time.

(4) In the Discussion part, the authors assume that the rescue phenotype is the result of multiple MYR1-dependent effectors. I admit that this hypothesis could be possible since a recently published paper described the concerted action of numerous MYR1-dependent or independent effectors contributing to the hypermigration of infected cells (Ten Hoeve et al., mBio, 2024). I think this paragraph would be kind of overstated since the authors did not test any of the candidate effectors. Since the authors possess Δ IST parasites, they can test whether IST is involved in the "paracrine masking effect" or not to support their claim.

MYR1 deletion impairs the export of multiple *Toxoplasma* effectors into the host cell, including GRA16, GRA24, GRA28, HCE1/TEEGR etc, many of which can influence cytokine levels. As such, we speculate that it is a combination of multiple effector proteins that are responsible for the trans-rescue. As stated above, which parasite effectors, host cell types and cytokines are involved in the phenotype we describe are part of ongoing and future studies. Here, we wanted to focus on the key message, that in *in vivo* CRISPR screens, paracrine rescue of individual mutants can occur. While we will test IST mutants, it is probably not the top candidate as it only prevents upregulation of ISGs after exposure to IFN- γ , but has probably no role in already stimulated cells. As we still observe strong rescue past day 3, when IFN- γ levels are already elevated (Nishiyama 2020 Parasitol Int), IST probably plays no dominant role.

Recommendations for the authors:

Reviewer #1 (Recommendations for the authors):

(1) Figure 1 - it's not obvious what concentration of IFN-gamma is being used in these assays (sorry if this is stated somewhere else).

All *in vitro* experiments were performed with 100 U/ml IFN- γ as stated in the Material & Methods section, however added this information in the figure legend of Figure 1.

(2) Figure 3 This reviewer wonders if earlier differences are buried in the data sets. In Figure 3b it looks like there are early differences but this is lost in the collated data analysis in 3c. An early difference is quite apparent in Figure 2.

We agree with the reviewer that a difference is visible at day 3 and 5 in Figure 3b, however differences between experimental groups became statistically significant only at day 7 in Figure 3c (N = 4 biological replicates). We cannot compare results between Figure 3c and Figure 2c as the latter reports 100% WT or Δ MYR1 infections and not 20:80 mixes.

(3) The authors conclude from their in vitro studies that MYR-1 is not required for in vitro growth in IFN-g activated macrophages. Given that the WT parasites still rescue MYR KO parasites in RAG mice it does imply that this paracrine effect would impact early innate

responses. Since RAG mice do have a strong ILC/NK cell response that leads to the local production of IFN- γ it would seem like a reasonable candidate. Do the authors know if the MYR KO have improved growth in the absence of IFN- γ in vivo? This could be done using KO mice or with IFN- γ neutralization.

MYR1 displayed a neutral score in CRISPR screens in IFN- γ KO mice (Tachibana et al Cell Reports 2023), suggesting that lack of IFN- γ does not specifically improve MYR1 mutant growth compared to other mutants in a pool. We believe that the rescue is rather driven by other cytokines that have been shown to be altered in a MYR1 dependent manner (i.e CCL2, IL-6, IL-12). But as laid out before, this is subject of future studies.

This is a submission that might benefit from a graphical model of how the authors view this system working.

We agree with the reviewer and we added a graphical model to the manuscript.

Reviewer #2 (Recommendations for the authors):

*The authors previously published a study that combines CRISPR screens in *Toxoplasma* and host transcriptome by scRNA-seq (Butterworth et al., Cell Host Microbe 2023). I think the authors possess transcriptome of Δ MYR1-infected HFFs. Although I understand this screen is conducted in in-vitro culture and human fibroblasts, are there any differentially expressed genes or pathways that could explain the paracrine rescue phenomenon described in this manuscript?*

We thank the reviewer for this insightful comment, which is however hard to address. Thousands of host cell genes within multiple pathways are affected by MYR1 deletion (Naor et al. mBio 2018; Butterworth et al. Cell Host Microbe 2023). Therefore the PerturbSeq dataset is not helpful to pinpoint specific immune mechanisms of rescue, and is speculative without any experimentation to back it up. However, we added a sentence in line 350 of the discussion to highlight known MYR1-related effects on immune-related pathways. “Individual MYR-related effectors that may be responsible for the paracrine rescue have not been investigated here and we hypothesise that the phenotype is likely the concerted result of multiple effectors that affect cytokine secretion. For example, previous studies showed that both GRA18 and GRA28 can induce release of CCL22 from infected cells (He 2018 eLife; Rudzki 2021 mBio), while GRA16 and HCE1/TEEGR impair NF- κ B signalling and the potential release of pro-inflammatory cytokines such as IL-6, IL-1 β and TNF (Seo 2020 Int J Mol Sci; Braun 2019 Nat Microbiol). Regardless of the effector(s), our results highlight an important novel function of MYR1-dependent effectors by establishing a supportive environment in *trans* for *Toxoplasma* growth within the peritoneum.”

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