Parasites lacking the micronemal protein MIC2 are deficient in surface attachment and host cell egress, but remain virulent in vivo [version 2; peer review: 3 approved]

Simon Gras¹*, Allison Jackson¹*, Stuart Woods², Gurman Pall¹, Jamie Whitelaw¹, Jacqueline M. Leung³,⁴, Gary E. Ward³, Craig W. Roberts², Markus Meissner 1

¹Wellcome Trust Centre For Molecular Parasitology, Institute of Infection, Immunity & Inflammation, Glasgow Biomedical Research Centre, University of Glasgow, Glasgow, G12 8TA, UK
²Strathclyde Institute of Pharmacy and Biomedical Sciences, Glasgow, G4 0RE, UK
³Department of Microbiology and Molecular Genetics, College of Medicine, University of Vermont, Burlington, VT, 05405, USA
⁴Department of Biology, Indiana University, Bloomington, IN, 47405, USA

* Equal contributors

Abstract
Background: Micronemal proteins of the thrombospondin-related anonymous protein (TRAP) family are believed to play essential roles during gliding motility and host cell invasion by apicomplexan parasites, and currently represent major vaccine candidates against Plasmodium falciparum, the causative agent of malaria. However, recent evidence suggests that they play multiple and different roles than previously assumed. Here, we analyse a null mutant for MIC2, the TRAP homolog in Toxoplasma gondii. Methods: We performed a careful analysis of parasite motility in a 3D-environment, attachment under shear stress conditions, host cell invasion and in vivo virulence. Results: We verified the role of MIC2 in efficient surface attachment, but were unable to identify any direct function of MIC2 in sustaining gliding motility or host cell invasion once initiated. Furthermore, we find that deletion of mic2 causes a slightly delayed infection in vivo, leading only to mild attenuation of virulence; like with wildtype parasites, inoculation with even low numbers of mic2 KO parasites causes lethal disease in mice. However, deletion of mic2 causes delayed host cell egress in vitro, possibly via disrupted signal transduction pathways. Conclusions: We confirm a critical role of MIC2 in parasite attachment to the surface, leading to reduced parasite motility and host cell invasion. However, MIC2 appears to not be critical for gliding motility or host cell invasion, since parasite speed during these processes is unaffected. Furthermore, deletion of MIC2 leads only to slight attenuation of the parasite.

Keywords
Toxoplasma, Microneme, Gliding motility, Host cell invasion, TRAP, MIC2, Plasmodium
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Introduction
Apicomplexan parasites are obligate intracellular parasites that invade the host cell in an active process that involves the parasite’s own acto-myosin system acting in concert with parasite-derived surface ligands (Meissner et al., 2013). These ligands are derived from secretory organelles, the micronemes, which are unique to apicomplexan parasites. Indeed, microneme secretion has been demonstrated in several studies to be linked to efficient parasite invasion and gliding motility, and it has been suggested that micronemal proteins act as force transmitters for the acto-myosin system, similar to the role of integrins in amoeboid cells (Bargieri et al., 2014; Tardieux & Baum, 2016). These proteins are then cleaved by rhomboid proteases (ROMs) to release the force independent analysis.

One crucial family of micronemal proteins is the thrombospondin-related proteins, such as TRAP, MTRAP, TSP and CTRP, which have been suggested to be essential for gliding motility and invasion in diverse life stages of Plasmodium spp. (Bartholdson et al., 2012; Baum et al., 2006; Dessens et al., 1999; Morahan et al., 2009; Moreira et al., 2008; Sultan et al., 1997). Similarly, the Toxoplasma gondii homolog of TRAP, MIC2, is thought to be required for gliding motility and invasion, and a conditional knockdown mutant for mic2 suggested that MIC2 is an important component of this machinery (Huynh & Carruthers, 2006). However, recent results questioned the importance of MIC2, since it is relatively straightforward to obtain clonal mic2 null mutants using reverse genetic tools, such as a conditional recombinase system (Andenmatten et al., 2013). Furthermore, a recent genome-wide CRISPR/Cas9 screen indicated a relatively minor contribution of mic2 to parasite fitness in vitro (Sidik et al., 2016). Given the huge repertoire of micronemal proteins, it is thus tempting to speculate that multiple redundancies exist among these proteins. Such a situation has been described for AMA1, a micronemal protein that is involved in host cell invasion, but is not essential (Bargieri et al., 2013; Lamarque et al., 2014).

A recent systematic dissection of other proteins involved in gliding motility, such as parasite actin, myosin A and its light chain MLC1, GAP45 and GAP40 has identified novel functions for these proteins and demonstrated that the gliding machinery is involved in the formation and release of attachment sites (Bargieri et al., 2014; Egarter et al., 2014a; Harding et al., 2016; Periz et al., 2016; Whitelaw et al., 2017). Furthermore, MIC2 is thought to interact with parasite F-actin via a connector protein that has been recently described and suggested to bind both the cytosolic tail of MIC2 and parasite F-actin (Jacot et al., 2016), which might well be involved in the regulation of attachment sites.

Given our evolving understanding of parasite motility mechanisms, we set out to re-analyse the functions of mic2 during the parasite’s asexual life cycle, both in vitro and in vivo. We confirm previous findings, demonstrating that MIC2 is involved in gliding motility and invasion (Huynh & Carruthers, 2006). This involvement is best demonstrated in attachment assays that suggest an important role for MIC2 in the generation of attachment sites that are required for efficient motility. However, while mic2KO parasites exhibited less motility and move on shorter distance, they reach the same maximal speeds as WT parasites. Similarly, fewer parasites lacking MIC2 invade host cells, but when they do invade they do so at speeds comparable to WT parasites. Like parasites deficient in other components of the acto-myosin system, with which MIC2 interacts, the mic2 KO parasites show delayed host cell egress. Mice have been widely used and an in vivo model of toxoplasmosis to test virulence of T. gondii in mammalian hosts. Unexpectedly, in vivo analysis demonstrates that they are only mildly attenuated and still induce lethal disease in mice. RNA sequencing analysis revealed that deletion of mic2 has a minor impact on the transcription levels of other micronemal, ROMs and motor complex proteins, as well as several proteins with no obvious connection to invasion or motility, suggesting a multifactorial adaptation to loss of MIC2.

Results
mic2 is an important but non-essential gene
We previously described the generation and initial characterisation of a null mutant for mic2 using the DiCre system (Andenmatten et al., 2013). In this mutant, the native mic2 gene has been replaced byloxP-flanked mic2 cDNA (loxPmic2). Upon Cre-mediated site-specific recombination, the mic2 cDNA was removed, and the reporter gene YFP placed under the control of the endogenous promoter, resulting in green fluorescent mic2 KO parasites (Figures 1A–C). Despite forming smaller plaques when compared to the WT RH strain, mic2 KO parasites can be easily isolated and maintained in culture, demonstrating that mic2 is an important, but non-essential gene in the Toxoplasma lytic cycle, as described previously (Andenmatten et al., 2013). No significant differences in plaque size were observed between loxPmic2 and WT T. gondii parasites (Figure 1D). To address the possibility of adaptation to mic2 loss, we compared freshly induced mic2 KO (1 lytic cycle, mic2 FKO) to mic2 KO parasites cultured for more than one year after induction. No significant difference in plaque size was observed between the two strains (Figure 1D). Proteolytic processing and trafficking of the MIC2-associated protein (M2AP) was previously shown to depend on MIC2 (Huynh & Carruthers, 2006). We confirmed that depletion of MIC2 leads to M2AP mislocalisation and constitutive secretion of unprocessed M2AP (Figure S1) with no significant effects on the localisation or secretion of other tested micronemal proteins.
Deletion of *mic2* leads to only minor changes in the expression of other known invasion machinery components

In the case of *ama1*, the removal of the gene leads to the upregulation of its homologue *ama2*, allowing compensation of the loss of *ama1* function ([Bargieri *et al.*, 2013; Lamarque *et al.*, 2014]). To test if removal of *mic2* leads to up- or downregulation of known components of the invasion machinery (i.e. other micronemal or glideosome proteins, actin, etc.), RNA sequencing analysis was performed to compare relative gene expression levels in RH, *loxP-mic2, mic2* KO and *ama1* KO. RH was used as a reference (100%) (Figure 2, Figure S2). In parallel, we confirmed for *ama1* KO that transcription levels of *ama2* were upregulated. We also observed increased transcription levels of various other genes in *ama1* KO that are implicated in invasion, such as *mic2, mic5, mic6, mic9, mic11,* and *rom5*, as well as downregulation of *mic3, mic17a, mic19, gap45, mic1* and *rom4*, suggesting that adaptation to *ama1* disruption in culture is multifactorial. Although *ama2* shows the strongest upregulation, the overall expression level of *ama2* remains very low compared to *ama1* (Figure S2, Table S1).

Fewer differences were seen between *loxP-mic2* and *mic2* KO parasites than were seen in *ama1* KO (Figure S2, Table S1). Other than *mic9* and *rom5*, deletion of *mic2* had little effect on the transcription level of the known MICs, glideosome or rhomboid genes examined. Furthermore, when we compared the whole transcriptomes, we observed similar changes in *ama1* KO and *mic2* KO, suggesting a potential multifactorial and overlapping adaptation process. The genes whose expression changed include several proteases, surface antigens and hypothetical proteins (Table S2 and Table S3). However, based on this analysis we were unable to identify a clear candidate that could compensate for loss of *mic2*.

Attachment is impaired in *mic2* KO parasites

We previously demonstrated that the acto-myosin system of the parasite is important for surface attachment and required for efficient initiation of gliding motility ([Whitelaw *et al.*, 2017]). Since MIC2 is connected to this system, we wished to investigate if a similar phenotype can be observed in *mic2* KO parasites. Using a standard attachment assay ([Whitelaw *et al.*, 2017]), we observed that the percentage of *mic2* KO parasites attached to host cells dropped to 20% in comparison to WT (Figure 3A), consistent with previous studies ([Harker *et al.*, 2014; Huynh & Carruthers, 2006]. We also estimated attachment strength using a fluidic shear stress assay on surfaces coated with collagen IV (Figure 3B). Parasites were
incubated without flow to allow them to attach to the surface. An initial flow of 0.5 dyn/cm² was applied to wash off unattached parasites and the remaining number of parasites for each strain was considered as the initial value (100%). In contrast to control parasites, mic2 KO parasites were washed off rapidly at low shear stress (39% vs. 86.6% parasites remaining for mic2 KO and WT, respectively at 2.5 dyn/cm²), consistent with previous results using the mic2 conditional knockdown (Harker et al., 2014). In summary, mic2 KO parasites have a deficiency in their capacity for surface attachment, which will inevitably affect gliding motility and host cell invasion.

Depletion of MIC2 has little impact on gliding speed
To analyse the role of MIC2 during gliding motility, we performed standard trail assays to determine the ratio of gliding to immotile parasites. Using this analysis, we confirmed that the majority (~60%) of mic2 KO parasites are incapable of initiating gliding compared to WT (Figure 4A), as previously reported (Huynh & Carruthers, 2006). By video microscopy, the three types of motility (circular, helical and twirling) (Håkansson et al., 1999) were observed (Video S1–Video S6). Time lapse analysis showed that once motility was initiated, depletion of MIC2 has an effect on both the average speed and average distance travelled by
Figure 4. Gliding initiation and gliding distance are affected by mic2 KO attachment defect but not maximal speed. A) Trail deposition assay of WT parasites compared to mic2 KO. Mean values of three independent assays are shown ± SEM and ** p-value <0.01 in a two-tailed Student's t-test. Scale bar 5 µm B) Kinetic analysis of 2D helical gliding. Data were analysed using auto-tracking software. Mean values of three independent assays are shown ± SEM, ***: p-value <0.001 in a two-tailed Student's t-test. C) Representative maximum intensity projections of 3D Matrigel-based motility assays comparing WT to mic2 KO parasites (left) and % of parasites moving (right) normalised to WT. Scale bar 50 µm D) Analysis of 3D trajectories; mean values of three independent assays are shown ± SD, ***: p-value <0.001 in two-way Anova with Sidak’s multiple comparisons test.
helically gliding parasites, while the maximal speed was not affected (Figure 4B). In the case of circularly gliding parasites, a reduction in the average distance travelled was seen for mic2 KO parasites, consistent with previous data (Huynh & Carruthers, 2006). Surprisingly, the average and maximum speeds of circular gliding increased compared to WT parasites (Figure S3).

Next, we wished to investigate gliding motility in a more physiological 3D environment (Figure 4C). In good agreement with the 2D-motility assays, fewer mic2 KO parasites initiated motility in a 3D matrix when compared to WT parasites. Furthermore, a significant reduction in average displacement (9.54 ± 1.17 µm vs. 16.66 ± 0.58 µm) and average speed (0.72 ± 0.16µm/s vs. 0.91 ± 0.08 µm/s) was observed in mic2 KO vs. WT parasites, respectively (Figure 4D). Again, no reduction in maximal speed was observed, indicating an “all-or-nothing” response (Figure 4D). Together, these data suggest that, similar to MyoA, MLC1 and F-Actin, the predominant function of MIC2 is in the establishment of attachment sites required for effective initiation of motility.

Depletion of MIC2 results in lower invasion rates, but has no influence on invasion speed

Next, we investigated the invasion process of mic2 KO parasites (Figure 5A) and found, as previously described (Huynh & Carruthers, 2006), that invasion is strongly inhibited, at 18 ± 3% relative to WT invasion levels. In this assay the overall failure of invasion is measured, which could be due to defects in host cell attachment, junction formation or host cell penetration. To differentiate between these individual steps, invasion rates were normalized to the total number of interacting parasites (i.e., attached plus invaded). Interestingly, in this case the invasion rates of WT and mic2 KO parasites are similar, demonstrating that the reduced invasion of mic2 KO parasites relative to WT parasites is mainly due to their failure to attach to the host cell (Figure 5B). Next, we assessed junction formation and penetration speeds (Figures 5C and D) and were unable to detect significant differences between WT and mic2 KO parasites. mic2 KO parasites invaded through a normal junction and penetrated the host cell at speeds similar to those of WT parasites (21.3 ± 11.7 s and 21.0 ± 6.9 s for WT and mic2 KO, respectively) (Video S7 and

![Figure 5](image-url)

**Figure 5. The mic2 KO defect in invasion is due to diminished attachment capacity.** A) mic2 KO and WT parasites were incubated for 1h with HFF cells, and invasion rate was calculated by comparing the number of mic2 KO vs. WT parasites invaded. Mean values of three independent assays are shown ± SEM. ***: p-value <0.001 in a two-tailed Student's t-test. B) Normalised invasion assays. For each strain (mic2 KO and WT), the number of invaded parasites was normalized to the total number of parasites observed (attached + invaded). Mean values of three independent assays are shown ± SEM. C) IFA of the junction protein RON2 and AMA1/YFP in mic2 KO and WT tachyzoites, scale bar 5 µm. n=3, total number of parasites observed >50. D) Penetration kinetics of mic2 KO and WT tachyzoites determined by time-lapse microscopy (n=25).
These results lead us to conclude that the invasion deficiency observed for mic2 KO parasites is due to impaired attachment to the host cell, as suggested previously (Huynh & Carruthers, 2006).

**Effect of mic2 deletion on intracellular parasites**

We also readdressed the function of MIC2 in intracellular development and egress. While intracellular replication of mic2 KO parasites appeared normal (Figure 6A), disruption of mic2 caused a significant delay in host cell egress (Figure 6B–D). When egress was artificially triggered with a Ca\(^{2+}\) ionophore (A23187), mic2 KO parasites were able to rupture the parasitophorous vacuole at levels comparable to WT (89 ± 2% vs. 84 ± 5% for WT and mic2 KO respectively) (Figure 6B). However, a higher proportion of mic2 KO parasites were unable to leave the host cell after lysing the parasitophorous vacuole membrane, suggesting a defect in initiating motility (Figure 6C and D, and Video S9–Video S10). This defect was still evident even at 30 min after induction, as only 37 ± 3% of mic2 KO had moved out of the vacuole compared to 95 ± 3% for WT.

**Figure 6.** Parasites lacking MIC2 replicate normally, but are defective in host cell egress. **A)** Replication analysis of mic2 KO parasites. Parasites were allowed to invade for 1 h prior to intracellular growth for 24 h and the number of parasites per parasitophorous vacuole was counted. Mean values of three independent assays are shown ± SEM. **B** and **C**) Parasite egress was artificially induced with Ca\(^{2+}\) ionophore (A23187) for 10 (B) and 30 min (C). For quantification, three outcomes were scored: parasites failed to lyse the vacuole (Intact PV), parasites lysed the vacuole but did not move (No movement) or classical egress (Movement out). Mean values of three independent egress assays are shown ± SEM. **D**) IFA illustrating a newly lysed vacuole (30 minutes post-induction) where antibody against SAG1 can only access part of the vacuole (top panels) and two fully lysed vacuoles, one showing little to no movement of mic2 KO parasites out of the vacuole (middle) and the other showing normal egress (bottom) Scale bar 5 µm.
mic2 KO parasites are less virulent than WT parasites but still lethal in mice
Previous data indicated that mic2 knockdown parasites are avirulent in mice (Huynh & Carruthers, 2006). To test whether this is also the case for the mic2 KO parasites, mice were infected intraperitoneally with mic2 KO, loxpmic2, killed WT tachyzoites (1×10⁴) or PBS. The mic2 KO parasites caused severe disease in mice leading to death or necessitating their euthanasia at humane endpoints by day 7 (Figure 7A). To verify that the cause of severe disease was due to parasite replication and to allow visualization of parasite burden in real time in vivo, we generated mic2 KO parasites stably expressing a red shift luciferase. Five days post-infection, the mic2 KO parasites were observed at similar anatomical locations, but with a less heavy parasite burden compared to similarly transfected loxpmic2 parasites (Figures 7B and C).

Discussion
Gliding motility and host cell invasion by apicomplexan parasites have been thought to critically depend on members of the thrombospondin-related anonymous protein (TRAP) family, which are transmembrane proteins derived from the micronemes (Huynh & Carruthers, 2006; Sultan et al., 1997). A huge body of research on these proteins led to the widely accepted model that they act as a link between the parasite’s cytoskeleton and the host cell by binding to surface receptors with their extracellular domain, and to parasite aldolase, which in turn interacts with parasite actin, via their C-terminal domain (Jewett & Sibley, 2003; Morahan et al., 2009). Aldolase was recently shown to be dispensable for gliding motility and invasion (Shen & Sibley, 2014b), but a new “connector” protein postulated to link the tail of MIC2 to actin has been described (Jacot et al., 2016). Nevertheless,
recent re-analysis of TRAP mutants suggested that these proteins do not necessarily function during motility as force transmitters, but rather in the regulated formation and release of adhesion sites (Hegge et al., 2010; Münter et al., 2009), since Plasmodium sporozoites remain motile in the absence of TRAP or TLP and can be chemically complemented on tuneable substrates (Hellmann et al., 2013). Furthermore, other members of the TRAP family have been demonstrated to have unexpected functions, unrelated to gliding motility or invasion. For example MTRAP has long been seen as the merozoite specific TRAP homolog that is required for merozoite invasion (Baum et al., 2006), but recent studies demonstrate that its crucial function lies in gametocyte egress (Bargieri et al., 2016; Kehrer et al., 2016). Furthermore, reassessment of other components of the gliding machinery in T. gondii, such as actin or MyoA, demonstrated that they play a crucial role in the formation of attachment sites, but not necessarily in force production per se (White law et al., 2017), and our current view of the mechanics of this complex system requires further analysis (Tardieux & Baum, 2016).

In the case of the TRAP-family protein MIC2, previous attempts to knock out the gene failed, suggesting an essential function (Huynh & Carruthers, 2006). A conditional knockdown mutant was therefore generated and used to demonstrate important roles for MIC2 in gliding motility, attachment to host cells, host cell invasion and virulence in vivo (Huynh & Carruthers, 2006). Using a conditional recombination system, however, we showed that it was possible to generate clonal null mutants for mic2 (Andematten et al., 2013), demonstrating that MIC2 is not an essential gene. This finding was corroborated by a recent genome-wide phenotypic screen based on CRISPR/Cas9, indicating that disruption of mic2 has only a mild phenotypic defect (phenotypic score = -1.17; Sidik et al., 2016).

Here, we assessed the functional consequences of deleting mic2. In contrast to other conditional null mutants generated using the DiCre system, such as the myoA KO, the isolation of clonal mic2 KO mutants was straightforward, indicating only minor competition between non-induced (mic2+) parasites and mic2 KO parasites (data not shown). Interestingly, we could not identify any long-term phenotypic adaptation due to prolonged culturing of mic2 KO parasites, since the phenotypes appear to remain unchanged over time. When we performed a comparative transcriptomic analysis, we found that deletion of mic2 had little effect on the transcription level of known MICs, motor or ROM proteins, while multiple proteases (lipases, methionine aminopeptidase), an uncharacterized EGF and PAN domain containing protein, SAG-related proteins and hypothetical proteins were found to be slightly upregulated in the mic2 KO (Table S2). These data suggest that the deletion of mic2 may result in a multifactorial adaptation that involves small differences in expression levels of seemingly unrelated genes. How rapidly such an adaptation occurs is not known; it is possible that the presence of other microneme proteins with partially overlapping functions immediately enables the parasite to tolerate the loss of mic2. Intriguingly, many of the seemingly unrelated genes upregulated in mic2 KO were also upregulated in ama1 KO (Table S2 and Table S3).

Like the parasites depleted of MIC2 by conditional knockdown (Huynh & Carruthers, 2006), mic2 KO parasites showed no defect in the trafficking and localization of other microneme proteins (with the notable exception of M2AP) and no effect on intracellular replication, but dramatic effects on host cell invasion, which are due primarily to decreased attachment. Both the conditional knockdown and the KO showed that the loss of MIC2 results in reduced 2D motility, likely through an effect on attachment, and that helical motility is more affected than circular motility. We have extended the motility analysis and shown that in both 2D and 3D, the defect appears to be one of motility initiation; once mic2 KO parasites start moving, they can reach the same maximal speeds as WT parasites. Interestingly a recent study compared adhesion of mic2 knockdown parasites under fluidic stress and concluded that only initial attachment, but not strengthening of attachment sites was affected (Harker et al., 2014). The invasion phenotype of the mic2 KO is similar to that of ama1 KO parasites, which also show reduced attachment to host cells, but penetration into the host cell at speeds similar to that of WT parasites (Bargieri et al., 2013). It remains to be seen if redundant proteins can compensate for gliding/invasion motility, but NOT attachment in the absence of MIC2, as suggested for AMA1 (Lamarque et al., 2014).

In contrast to the MIC2 conditional knockdowns (Huynh & Carruthers, 2006), we find that mic2 KO parasites have a significant delay in host cell egress. The reduced egress is not likely due to a complete inability of the parasite to move, since kinetic analysis of mic2 KO parasites demonstrates only partial motility defects in a 2D and 3D environment. Rather it appears that motility is initiated with a significant delay, and that the parasites stay connected to each other (data not visualised). Future experiments will be required to elucidate the role of MIC2 during egress in more detail and to determine whether the reduced ability of mic2 KO parasites to egress compared to the conditional knockdowns is due to residual expression of MIC2 in the conditional knockdown or to some other effect.

Most surprisingly, and in contrast to the results obtained for the MIC2 conditional knockdown (Huynh & Carruthers, 2006), we find that mic2 KO parasites are only mildly attenuated compared to WT RH parasites. The mic2 KO line (at least at the doses used in these studies) induces lethal disease in BALB/c mice. One explanation for the different findings could be that RH TATi ΔHX, the parasite line used to generate a knockdown for mic2 is already severely attenuated due to the expression of the Tet- transactivator. Indeed, in the study by Huynh & Carruthers, 2006, high doses (5 × 10⁴ tachyzoites) with RH TATi ΔHX were required to achieve normal time-to-death kinetics. It is thus possible that knockdown of mic2 in this strain reflects an enhancement of the already attenuated phenotype, while depletion in a WT background has only mild effects on parasite virulence. Alternatively, in our studies a reduced virulence of mic2 KO parasites is not evident because of the relatively high numbers of tachyzoites used to facilitate in vivo imaging. Consequently to fully compare the virulence LD₅₀ studies would be required. Nonetheless our studies demonstrate unequivocally that MIC2 is not necessary for in vivo infection and lethality in BALB/c.
mice. In vivo imaging and 3D diffuse tomographic reconstruction of mice infected with MIC2 deficient parasites transfected with a luciferase gene demonstrated that they grow in similar anatomical locations in mice as control parasites. However, dissemination and histopathological analyses would be necessary to rule out any potential differences in tissue tropism.

In summary, we find here that MIC2 acts as important, but not essential, attachment factor, and that reduced invasion and gliding rates are due to a decreased ability to initiate rather than to sustain motility. This is similar to the findings for other components of the acto-myosin system, such as actin, MyoA or MLC1, where it appears that formation of adhesion sites is one of the critical functions of this complex machinery (Whitelaw et al., 2017). Finally, our finding that deletion of mic2 causes only a mild attenuation of virulence in vivo will have implications for future vaccine design.

Materials and methods

Cloning DNA constructs: All primers used in this study were synthesised by Eurofins (UK) and are listed in Table S4. A red shift luciferase (Bruce Branchini, Connecticut College, USA) was amplified using Luc fw/rv primers and cloned under the p5RT70 promoter with a chloramphenicol resistant cassette.

**Mic2 inducible KO vector:** As previously described (Andennatten et al., 2013), to generate loxPMic2loxP-YFP-HX, the mic2 3’ UTR was amplified from genomic DNA using the primer pair 3’ UTR Mic2 fw/rv, and the PCR fragment was cloned into p5RT70loxPKillerRedloxPYFP-HX via SacI. The mic2 ORF (TGME49_201780) was amplified from cDNA using the primers Mic2 ORF fw/rv and was cloned into the parental vector p5RT70loxPKillerRedloxPYFP-HX using EcoRI and PacI. Finally, the mic2 5’ UTR containing the endogenous promoter was amplified from genomic DNA using the primer pair 5’ UTR Mic2 fw/rv and cloned into the final vector using ApaI and EcoRI.

**Culturing of parasites and host cells:** Human foreskin fibroblasts (HFFs) were grown on TC treated plastics plates and maintained in Dulbecco’s modified Eagle’s medium (DMEM) supplemented with 10% foetal bovine serum (FBS), 2 mM L-glutamine and 25 mg/ml gentamycin. Parasites were cultured in HFFs and maintained at 37°C and 5% CO₂.

**T. gondii transfection and selection:** The conditional mic2 knockout strain (ka80::diCre/endogenous mic2::loxP mic2loxP, referred to here as loxPMic2) was generated as previously described (Donald et al., 1996) by transfecting 60 μg of the plasmid loxPMic2loxP-YFP-HX into the ka80::diCre parasites to replace the endogenous copy of mic2, and parasites containing stable integration of this construct were selected using xanthine and mycophenolic acid, as previously described (Andennatten et al., 2013). The resulting loxPMic2 strain carries only one copy of mic2, which can be excised by adding rapamycin (50 nM in DMSO for 4 h before washout) to generate the mic2 null mutant (ka80::diCre/mic2−, referred to here as mic2 KO). The clonal mic2 KO line was isolated by performing serial dilutions on the clonal induced loxPMic2 strain after 4 h induction and subsequent removal of rapamycin. After verification of the integration, protein expression was checked by western blotting using anti-MIC2 and anti-catalase antibodies and IFA using anti-MIC2 antibodies and YFP expression. Red shift luciferase expressing loxPMic2 and mic2 KO were obtained by transfecting a Red-shift luciferase expressing plasmid using random integration. Parasites were then selected for chloramphenicol resistance and luciferase expression.

**RNA extraction and sequencing:** RH, loxPMic2, mic2 KO and amel KO RNA was extracted using the RNeasy® Mini Kit (Qiagen) in a biological triplicate. Eluate RNA concentration was determined by Nanodrop (Thermo Scientific). For sequencing, 4ug per sample was sent to NGS Laboratory, Glasgow Polymonics (University of Glasgow, Bearsden, UK). RNA was analysed after polyA library preparation using paired-end with a depth of sequencing of 25M bases on a Next Seq 500 sequencer. Results were analysed on Galaxy server, with software provided (http://heighliner.cvr.gla.ac.uk/login?redirect=%2F). After trimming, data were aligned to the T. gondii genome using TopHat2. After mapping, differential expression compared to RH was determined using Cuffdiff. For each analysis, data for the three biological triplicates were carried out under the same condition (loxPMic2, mic2 KO, amel KO) and compared to the triplicate of RH parasites using a quartile library normalization method, a pooled dispersion estimation method with a false discovery rate of 0.05. Individual FPKM of each sample was also extracted to control the analysis.

**Immunofluorescence analysis:** IFA was carried out as previously described (Egarter et al., 2014b). Briefly, parasites were allowed to invade and replicate in a HFF monolayer grown on glass coverslips. The intracellular parasites were fixed in 4% paraformaldehyde for 20 min at room temperature (RT). Afterwards coverslips were blocked and permeabilised in 2% BSA and 0.2% Triton X-100 in PBS for 20 min at RT. The staining was performed using the indicated combinations of primary antibodies for 1 h at RT, followed by the incubation with AlexaFluor 488-, AlexaFluor 594- or AlexaFluor 633-conjugated secondary antibodies (1:3000, Invitrogen–Molecular Probes) for another 45 min at RT. For a list of all antibodies used in this study see Table S5.

**Western-blots:** Freshly egress RH, loxPMic2 and mic2 KO parasites were harvested, filtered and washed before being resuspended in PBS containing Pierce™ Protease Inhibitor Mini Tablets, EDTA Free (Thermo Scientific) and Triton X-100 0.2%. Western blots were processed using the indicated combination of primary antibodies for 1 h at RT, followed by incubation with AlexaFluor 350-, AlexaFluor 488-, AlexaFluor 594- or AlexaFluor 633-conjugated secondary antibodies (1:3000, Invitrogen–Molecular Probes) for another 45 min at RT. For a list of all antibodies used in this study see Table S5.

Phenotypic characterisations

**Plaque assay:** Plaque assays were conducted as described previously (Egarter et al., 2014b). 1x10⁴ parasites were inoculated on a confluent monolayer of HFFs and incubated for 5 days at 37°C and 5% CO₂, after which the HFFs were washed once with PBS and fixed with ice cold MeOH for 20 minutes. HFFs were stained
with Giemsa with the plaque area measured using Fiji software version 1.8.0_66 (https://fiji.sc/). Mean values of three independent experiments +/- SD were determined.

Secretion assays: Microneme secretion was assayed by monitoring the release of MIC2, M2AP and MIC4 into the culture medium, as described previously (Huynh & Carruthers, 2006). Secretion was observed in absence (constitutive secretion) or presence of 2 μM A23187 (induced secretion) at 37°C.

Attachment assay: 1 ×10⁶ parasites were allowed to invade a confluent monolayer of HFF cells for 10 min. Cells were washed and fixed with cold 4% PFA (4°C). The total numbers of parasites within 15 fields of view (Objective 40X) were counted and compared between mic2 KO and WT. Mean values of three independent experiments +/- SD were determined.

Attachment under fluidic shear stress: Fresh extracellular parasites (4 ×10⁶ in total consisting of approximately equal numbers of control and KO) were loaded into collagen IV coated fluidic chambers (Ibidi IB-80192) and allowed to attach at 37°C for 20 minutes. PBS was pumped through the chamber using an “open loop flow” microfluidic pump (KD Scientific Legato 200 syringe pump) system, similar to that described by (Harker et al., 2014), to control flow rates and generate fluidic shear stress. In our setup, a flow rate of 1 ml/min achieves 3 dyn/cm² shear stress at the surface of the channel. Flow at 0.1 ml/min (equivalent to 0.3 dyn/cm²) was used to remove all non-attached parasites. At each fluidic shear stress level, control and mutant parasites were counted from 5 fields of view per experiment. Parasite count after the 0.1 ml/min wash was taken as 100% of attached parasites. Counts at all other rates of flow were normalised to the 100%. Data collected was analysed using Excel to assess significance of differences between control and mutants using Student’s t-test and further analysed using GraphPad Prism v. 6.01 software to display data as trends. Parasites in the chamber were monitored via a Zeiss Axio Vert.A1 microscope setup with a 40x objective combined with an AxioCam ICM1 camera and Zen capture software. Mean values of three independent experiments +/- SD were determined.

2D video motility assay: Time-lapse video microscopy was used to analyse the kinetics over a 2D surface similar as previously described. Briefly a glass-bottom live cell dish (Ibidi μ-dish 15mm-hb) was coated in 100% FBS for 2 hours at room temperature. Freshly egressed parasites were allowed to glide on FBS-coated glass slides for 30 min before they were fixed with 4% PFA and stained with α-SAG1 under non-permeabilising conditions. Mean values of three independent experiments +/- SD were determined.

3D motility assay: Tachyzoites were prepared and assayed as previously described (Leung et al., 2014). Three independent biological replicates, each with three technical replicates, were performed. Parameters calculated from 3D motility assays were analyzed using two-way ANOVA with Sidak’s multiple comparisons test, with GraphPad Prism v. 6.01. Where statistically significant, multiplicity adjusted P values for comparisons are indicated with asterisks.

Invasion and replication assay: 5×10⁴ freshly lysed parasites were allowed to invade a confluent layer of HFFs for 1 hour. Subsequently, five washing steps were performed for removal of extracellular parasites. Cells were then incubated for a further 24 hours before fixation with 4% PFA. Subsequently, parasites were stained with α-IMC1 antibody. For invasion, the number of vacuoles in 15 fields of view (Objective 40X) was counted. Invasion rates were normalised to RH Δhxgprt at 100%. For replication, 200 vacuoles were counted for the number of parasites per vacuole. Mean values of three independent experiments +/- SD were determined.

Red/Green assay: Classical “red/green” assays were performed as previously described by Huynh & Carruthers, 2006 to determine the percentage of invasion, independent of the attachment defect of mic2 KO. 1 × 10⁶ parasites were allowed to invade a confluent monolayer of HFF cells for 1 hour. Extracellular parasites were stained with α-SAG1 under non-permeabilising conditions. For both strains (mic2 KO and WT) independently of the other, the number of invaded parasites was compared to the total number of parasites observed (attached + invaded), allowing us to mitigate the attachment phenotype of mic2 KO. Mean values of three independent experiments +/- SD were determined.

Penetration time of invading parasites: Freshly egressed parasites were added to a confluent monolayer of HFFs grown on a glass-bottom live cell dish (Ibidi μ-dish 15mm-hb). Time-lapse images were taken at 1 image per second using a 40X objective in DIC for both RH Δhxgprt and mic2 KO parasites. For penetration times, 20 invasion events were analysed and scored from the initial start point of a visible junction to complete parasite internalisation.

Egress assay: Egress assays were performed as previously described (Black et al., 2000). Briefly, 5×10⁴ parasites were grown on HFF monolayers for 36 hours. Media was exchanged for pre–warmed, serum–free DMEM supplemented with 2 μM A23187
(in DMSO) to artificially induce egress. After 5 minutes the cells were fixed with 4% PFA and stained with anti-SAG1 antibody without detergent permeabilization. 200 vacuoles were counted for parasite egress. Mean values of three independent assays +/- SEM were determined.

**In vivo infection model**

All animal procedures conformed to guidelines from The Home Office of the UK Government under the Animals [Scientific Procedures] Act 1986. All work was covered by Licence PPL60/3929, “Mechanism of control of parasite infection” with approval by the University of Strathclyde ethical review board. BALB/c mice were bred in house at the Strathclyde Institute of Pharmacy and Biomedical Sciences, Glasgow, UK under specific pathogen free conditions. Mice were housed in polypropylene cages (13cm×35cm), containing Ecopure flakes and sizzle nest bedding (SDS Services) with access to water and CRM mouse chow (SDS Services) *ad libitum*. Care was taken to minimise suffering through provision of water soaked mouse chow. The minimum number of mice was used to give reliable qualitative results. Six to eight week old female mice (13.4–17.6g, mean 16.1g), grouped in cages of five, were used for infection studies. Mice were assigned randomly to groups by an independent worker with no knowledge of their experimental purpose. Prior to infection, all mice were weighed and subsequently monitored daily for morbidity and weight loss. Mice were euthanised when they reached the humane endpoints set out in the licence.

In initial phenotype studies, groups of five mice were each infected with 2×10⁵ WT or *loxPmic2* control or *mic2* KO tachyzoites in 200µl sterile PBS via intraperitoneal injection (IP). *In vivo* parasite burden was followed by bioluminescent imaging using *loxPmic2* and *mic2* KO expressing firefly luciferase. Mice were infected with 2×10⁵ tachyzoites via intraperitoneal injection in a volume of 400µl sterile PBS between 10.00–12.00 hrs. For imaging, the mice were dosed with 150mg/kg D-luciferin potassium salt solution (PerkinElmer), anesthetised with isoflurane and imaged (between 10.00 and 12.00 hrs) using an IVIS Spectrum (PerkinElmer). Isoflurane was used as this is the standard and recommended procedure by PerkinElmer the manufacturer of the IVIS. One minute exposures were taken twenty minutes post luciferin injection. Radiance data were quantified using Living Image software 4.0 (Perkin Elmer) and statistical significance determined by Mann-Whitney test.

**Data availability**

Complete Western blots for Figure 1 and Figure S1; raw count for all the assays (Plaque size, Attachment, Invasion, Replication, Egress, Flow, 2D video); raw galaxy results for *amal* KO-RH comparison; raw galaxy results for *mic2* KO-RH comparison; raw galaxy results for *loxPmic2-mic2* KO comparison are available on OSF: DOI, 10.17605/OSF.IO/FASQG (Meissner, 2017; https://osf.io/fasqg/).

**Author contributions**

Conceived and designed the experiments: SG, AJ, SW, GEW, CWR, MM. Performed the experiments: SG, AJ, SW, GP, JW, JML. Analyzed the data: SG, AJ, SW, CWR, MM, GEW. Wrote the paper: SG, CWR, GEW, MM. Supervised all aspects of the study: MM.

**Competing interests**

No competing interests were disclosed.

**Grant information**

This work was supported the Wellcome Trust [087582], [103875] and [085349]; an European Research Council-Starting grant [ERC-2012-StG 309255-EndoTox] to MM; US Public Health Service [AI105191] and [AI054961] to GW.

*The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.*

**Acknowledgements**

We would like to thank members of the Meissner lab for thoughtful discussions. We would also like to thank Prof. Dominque Soldati-Favre (University of Geneva), Prof. Vern Carruthers (University of Michigan), Dr Maryse Lebrun (University of Montpellier) and Dr Bruce Branchini (Connecticut College) for generously providing antibodies, parasite strains and the luciferase construct. We would like to thank Dr Nicholas Dickens and Dr Mussa Hassan (University of Glasgow) for help with the RNA preparation and sequencing analysis.

**Supplementary material**

**Figure S1:** Loss of *mic2* impacts localization and secretion of M2AP, but not other micronemal proteins. A) Localization by IFA of MIC proteins in *mic2* KO and WT tachyzoites; only M2AP localisation is altered. Scale bar: 2 µm. n=3, total number of vacuoles observed >300 B) *mic2* KO and WT tachyzoites were incubated in the absence (- ; constitutive secretion) or presence (+ ; induced secretion) of calcium ionophore, and the amount of MIC4 and M2AP secreted into the culture supernatant was determined by western blotting. Actin was used as a loading control. Black arrowhead indicates proM2AP and the empty arrowheads the processed forms (Huynh & Carruthers, 2006); note that proM2AP is not properly processed in the *mic2* KO.

[Click here to access the data.]
Figure S2: Mean FPKM of MICs in the different KO strains. Graphic representation of the mean FPKM value variation between RH (White), loxPmic2 (Black), mic2KO (Red) and ama1KO (Yellow) strains. The difference between each mutant and RH was calculated using CutDiff with a comparison of three independent biological replicates, using quartile library normalization method, a dispersion estimation method using “pooled” with the tree replicate and a false discovery rate of 0.05. Statistically significant differences are indicated by *. Error bar indicates the FPKM standard deviation within the replicate. MICS* FPKM value was divided by 2 for graphical purpose.

Click here to access the data.

Figure S3: Kinetic analysis of 2D circular gliding. Kinetic analysis obtained from live records of parasites undergoing circular gliding. Data were analyzed using Analysis was done using Fiji with the wrMTrckr version 1.04 tracking plugin (http://www.phage.dk/plugins/wrmtrck.html). Mean values of three independent assays are shown ± SEM. ***: p-value <0.001 in a two-tailed Student’s t-test.

Click here to access the data.

Supplementary Videos: Representative gliding, invading and egressing parasites. Video S1–S6, mic2 KO and RH parasites making circular, helical and twirling motion; Video S7–S8, mic2 KO and RH parasites invading host cells; Video S9–S10 mic2 KO and RH parasites egressing from host cells. Video were recorded at 1 frame per second.

Click here to access the data.

Supplementary Tables: RNA seq data and primer list. Table S1, RNA sequencing FPKM value of MICs in all strains (RH, loxPmic2, mic2 KO, ama1 KO). Table S2, RNA sequencing Accepted Hits between mic2 KO and RH. Table S3, RNA sequencing Accepted Hits between amal KO and RH. Table S4, Primers list used in the study. Table S5, antibodies used in the study. RH FPKM, mic2 KO FPKM and AMA1 FPKM, contain the FPKM of the three triplicates for all Toxoplasma genes for RH, mic2 KO and amal KO strains. MIC2KO-RH and AMA1KO-RH total results obtained after Cutfiff analysis between RH and mutants.

Click here to access the data.

References


Open Peer Review

Current Peer Review Status: ✔ ✔ ✔

Version 2

Reviewer Report 02 August 2017

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✔ Sebastian Lourido
Whitehead Institute for Biomedical Research, Cambridge, MA, USA

The authors have addressed all of the concerns I previously raised. In particular, they now provide the complete reports for their RNAseq experiments, which will allow other investigators to recreate the analyses for themselves. I have no further comments on the manuscript.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Parasitology, molecular biology, genome editing

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 02 August 2017

https://doi.org/10.21956/wellcomeopenres.13129.r24449

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✔ Vernon Carruthers
Department of Microbiology and Immunology, University of Michigan School of Medicine, Ann Arbor, MI, 48109, USA

My-Hang Huynh
Department of Microbiology and Immunology, University of Michigan School of Medicine, Ann Arbor, MI, USA
The authors have responded thoroughly to comments on the original submission and have revised the article in exemplary fashion. The article is now recommended for approval without further changes.

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Toxoplasma infection biology

We confirm that we have read this submission and believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.
Figure 5D: The "ns" on top of the graphs is hardly readable

Figure 7A: The black line for "Killed RH" is not visible

Figure S3: The Y-Axis description is missing for the second and third data set

The supplementary movie file cannot be opened

Additional remarks:

- Abstract – “MIC2 appears to not be critical for gliding motility …”. This is correct, but in the light of Fig. 4A, showing a 60% reduction in gliding motility, a re-phrasing of this sentence might be good to avoid confusion.

- Page 5: The up-regulation of various invasion-related genes in both the mic2 KO and the AMA1 KO could be -as suggested- connected to multifactorial compensation, although this has to analyze in detail and compared to additional KO strains lacking other invasion-related proteins. An alternative explanation could be that the “general” up-regulation is “noise” due to the perturbation of the functional protein network.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

We confirm that we have read this submission and believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Author Response 10 Jul 2017

Markus Meissner, University of Glasgow, Glasgow, UK

We thank the reviewers for their valuable comments, which helped us to improve our manuscript. We addressed all comments in our revision. See our response to the reviewers comments below (in bold)
Figure 3B: Please show SD also for the 0.5 dyn/cm² values

The value at 0.5 dyn/cm² value have been set for each experiment to 100% to be our starting point and allow us to visualise the variation under stronger flow. By doing so, no SD can be calculated for this point.

Figure 4A+C, Figure 6D: Please include scale bar information in the figure legend.

Information now included for all 3 panels

Fig. 4: Did the authors use a Students T-test (as described in the figure legend) or a two-way-Anova with Sidak’s multiple comparisons test as indicated in the Materials & Methods?

A two-way-Anova with Sidak’s multiple comparisons test as indicated in the Materials & Methods was used. The is now corrected in the text.

Figure 5C: This figure is confusing and not well embedded in the result section. It would be helpful to include co-localization of AMA1 and RON2 in the mic2 knock out cell line. Additionally, they could provide the information of the YFP expression in WT vs KO.

RON2 was used as a marker for the tight junction and was used ofr both WT and mic2 KO parasites to demonstrate normal junction formation. Ama-1 is only shown for WT to outline the parasite. In case of mic2KO parasites YFP expression is activation upon induction of DiCre, requiring no additional stain.

Figure 5D: The "ns" on top of the graphs is hardly readable

We changed this in the revision.

Figure S3: The Y-Axis description is missing for the second and third data set

We changed this in the revision.

The supplementary movie file cannot be opened

We have checked the files and they could be opened on our system.

Additional remarks:
Abstract – “MIC2 appears to not be critical for gliding motility …”. This is correct, but in the light of Fig. 4A, showing a 60% reduction in gliding motility, a re-phrasing of this sentence might be good to avoid confusion.

The sentence now reads “We verified the role of MIC2 in efficient surface attachment, but were unable to identify any direct function of MIC2 in sustaining gliding motility or host cell invasion once initiated.”

Page 5: The up-regulation of various invasion-related genes in both the mic2 KO and the AMA1 KO could be -as suggested- connected to multifactorial compensation, although this has to
analyze in detail and compared to additional KO strains lacking other invasion-related proteins. An alternative explanation could be that the “general” up-regulation is “noise” due to the perturbation of the functional protein network.

We agree with the reviews that a more thorough analysis of transcriptional changes in different null mutants for components of the invasion machinery is worthwhile for future investigations.

**Competing Interests:** No competing interests were declared.
direct comparisons between the complete and conditional knockouts, such differences might represent variability in how the experiments are performed or in the basal virulence of the parasites used (as noted by the authors).

Taken together, the current study provides a robust confirmation for the functions of MIC2 using the latest and most rigorous methods available in the field.

Major concerns:
1. RNA sequencing results are not presented in their entirety. Such an analysis should contain a full account of the sequencing reads mapped so that readers can draw their own conclusions from the data. The authors should include a figure comparing the expression of all genes in the three strains (each mutant to WT, for example) and a supplementary file with the RPKM for each gene in each sample.

2. Page 5. The statement that “no single candidate [gene was] capable of compensating for the loss of MIC2” is not supported by the experimental data, since all the possible candidates have not been directly tested.

3. Page 10. The statement that “MIC2 might be involved in a signaling cascade that triggers host cell egress or parasite/parasite interaction” is not supported by the data, and should be omitted from the discussion. There is no evidence for a role of MIC2 in signaling and the lack of egress after vacuole rupture is most consistent with the 3D motility data that they present.

Minor concerns:
1. Page 3. “a lower percentage of parasites devoid of MIC2 move for shorter distances” should read “a higher percentage of parasites” although the double negative is confusing.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
No

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Parasitology, molecular biology, genome editing
I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 10 Jul 2017

Markus Meissner, University of Glasgow, Glasgow, UK

We thank the reviewer for the comments, which helped to improve the manuscript. Please see our response below (in bold).

RNA sequencing results are not presented in their entirety. Such an analysis should contain a full account of the sequencing reads mapped so that readers can draw their own conclusions from the data. The authors should include a figure comparing the expression of all genes in the three strains (each mutant to WT, for example) and a supplementary file with the RPKM for each gene in each sample.”

We initially attempted to make an overview figure, as suggested by the reviewer in our initial submission. However, we found it rather distracting, since we were unable to observe any clear tendencies when comparing the transcriptomes of the different parasite strains. Instead, we decided to focus on known invasion related genes. We believe that adding a figure comparing the expression of all genes in the three strains (each mutant to WT, for example) would not help in answering the question if redundancies/adaptation exist in response to deletion of mic2. To allow interested readers to access all data, we added RPKM of all genes cutdiff between WT/mic2 and WT/AMA1 to the supplementary information.

Page 5. The statement that “no single candidate [gene was] capable of compensating for the loss of MIC2” is not supported by the experimental data, since all the possible candidates have not been directly tested.

The sentence now reads: "However, based on this analysis we were unable to identify a clear candidate that could compensate for los of mic2."

Page 10. The statement that “MIC2 might be involved in a signaling cascade that triggers host cell egress or parasite/parasite interaction” is not supported by the data, and should be omitted from the discussion. There is no evidence for a role of MIC2 in signaling and the lack of egress after vacuole rupture is most consistent with the 3D motility data that they present.

We agree with the reviewer that at this point it is a speculation and we decided to remove this statement in the discussion.

Minor concerns:
“Page 3. “a lower percentage of parasites devoid of MIC2 move for shorter distances” should read “a higher percentage of parasites” although the double negative is confusing.”

The sentence now reads “However, while mic2KO parasites exhibited less motility and move on shorter distance, they reach the same maximal speeds as WT parasites” for more clarity.
The Toxoplasma microneme protein MIC2 has been a central figure in the widely, albeit not uniformly, accepted model of gliding motility and active cell invasion. Previous work using a Tet-off conditional knockdown mutant suggested that MIC2 contributes substantially to gliding motility and attachment, which together result in an invasion defect. The current study largely corroborates the earlier findings, and includes additional analyses that more thoroughly establish a role for MIC2 in initiating gliding motility in both 2D and 3D gliding assays. Importantly, the study also includes assessment of transcriptional changes in MIC2 knockout parasites. Overall, data in the current study is of high quality, well controlled, and the phenotypic assessments are thorough and robust for most experiments. The conclusions are also generally well supported by the data, and the article is well written and accessible to a wide audience. Addressing the following aspects will further improve the study.

1. The most striking apparent difference between the conditional knockdown and the knockout is seen in infected mice. Infection studies with the conditional knockdown required injection of a relatively high inoculum of 50,000 tachyzoites to overcome the intrinsic virulence deficiency of the Tet regulated (Tati) strain, a fact that is discussed in the current study as the potential basis for the apparent discrepancy in assessment of virulence. 50,000 Tati parasites is the minimum dose needed to consistently observe lethal infection. Attaining lethal infection in 33% of mice infected with MIC2 conditional knockdown parasites required injection of 3x10^7 tachyzoites, which is 625 times higher than for the Tati strain. The current study uses a non-Tati strain that is presumably equally virulent to the RH strain, although this was not evaluated. RH strain has an effective LD100 of 1 viable tachyzoite via IP injection. However, assessment of virulence in this study was conducted by injecting 1,000 tachyzoites, which is 1000x the LD100. Most studies assess the virulence of mutants in an RH strain background by injecting 10-100 tachyzoites, and several more recent studies have utilized subcutaneous injection because this route renders it easier to detect a virulence deficiency. Accordingly, the conclusion that MIC2 knockout parasites have a minor virulence defect is not substantiated by the data as it currently stands without a more thorough assessment with lower inocula. In the absence of such an assessment, because a 1000x LD100 dose was used in the current study it theoretically remains possible that MIC2 knockout parasites have a loss of virulence that is similar or equal to that of MIC2 knockdown parasites. The authors
should either address this aspect with additional experiments, or acknowledge this possibility in the discussion. Also, it appears that the virulence experiment was only performed once, and with only 5 mice per group. Thus, reproducibility was not established, and the experiment is underpowered.

2. The authors conclude that MIC2 knockout parasites have a similar distribution in infected mice as WT parasites. There are two limitations to this conclusion. First, the resolution of whole body bioluminescence is very poor, and thus does not allow one to distinguish between organs unless the organs are removed and imaged individually. Second, IP infection with RH strain parasites results mostly in intraperitoneal replication, with limited dissemination prior to mortality. The authors should assess bioluminescence in individual organs or acknowledge limitations of using this approach and the strain in assessing dissemination.

3. The caption for Figure 4 states: "Maximal speed of gliding is not impacted by mic2 KO". This is somewhat misleading because it describes the findings of only 20% of the data in the figure. The figure has 10 panels or graphs, 8 of which show differences in gliding between WT and mic2 KO parasites. The figure caption should describe both the differences and the similarities.

4. Please provide y-axis labels for the middle and right panels of Fig S3. Also, for the sentence: “Surprisingly, the average and maximum speeds increased compared to WT parasites (Figure S3)” it should be explicitly indicated that this is for circular gliding.

5. Please describe in the materials and methods how the virulence experiment shown in Fig 7A was performed, including stating the number of times the experiment was performed and the number of animals in the experiment. Also, indicate in the legend of Fig 7 the inoculum for the bioluminescence experiment, and state in the methods the number of times the experiment was performed along with the number of mice used.

6. Examples shown in Fig 6D do not match the categories used for quantification in Fig. 6C. The authors should consider showing an example of an intact PV instead of the "Lysed" example. Also, it would be ideal to explicitly state in the materials and methods that for assessing egress the fixed monolayers were not detergent permeabilized.

References

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Partly

If applicable, is the statistical analysis and its interpretation appropriate?
Yes
Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Toxoplasma infection biology

We confirm that we have read this submission and believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however we have significant reservations, as outlined above.

**Author Response 10 Jul 2017**

**Markus Meissner,** University of Glasgow, Glasgow, UK

We would like to thank reviewer three for his comments. We share some of his concerns regarding virulence in mice and pointed this out more clearly in our revision. See our detailed response below (in bold):

The most striking apparent difference between the conditional knockdown and the knockout is seen in infected mice. Infection studies with the conditional knockdown required injection of a relatively high inoculum of 50,000 tachyzoites to overcome the intrinsic virulence deficiency of the Tet regulated (Tati) strain, a fact that is discussed in the current study as the potential basis for the apparent discrepancy in assessment of virulence. 50,000 Tati parasites is the minimum dose needed to consistently observe lethal infection. Attaining lethal infection in 33% of mice infected with MIC2 conditional knockdown parasites required injection of 3x10^7 tachyzoites, which is 625 times higher than for the Tati strain. The current study uses a non-Tati strain that is presumably equally virulent to the RH strain, although this was not evaluated. RH strain has an effective LD100 of 1 viable tachyzoite via IP injection. However, assessment of virulence in this study was conducted by injecting 1,000 tachyzoites, which is 1000x the LD100. Most studies assess the virulence of mutants in an RH strain background by injecting 10-100 tachyzoites, and several more recent studies have utilized subcutaneous injection because this route renders it easier to detect a virulence deficiency. Accordingly, the conclusion that MIC2 knockout parasites have a minor virulence defect is not substantiated by the data as it currently stands without a more thorough assessment with lower inocula. In the absence of such an assessment, because a 1000x LD100 dose was used in the current study it theoretically remains possible that MIC2 knockout parasites have a loss of virulence that is similar or equal to that of MIC2 knockdown parasites. The authors should either address this aspect with additional experiments, or acknowledge this possibility in the discussion. Also, it appears that the virulence experiment was only performed once, and with only 5 mice per group. Thus, reproducibility was not established, and the experiment is underpowered.

The authors conclude that MIC2 knockout parasites have a similar distribution in infected mice as WT parasites. There are two limitations to this conclusion. First, the resolution of whole body bioluminescence is very poor, and thus does not allow one to distinguish between organs unless the organs are removed and imaged individually. Second, IP infection with RH strain parasites results mostly in intraperitoneal replication, with limited dissemination prior to mortality. The
authors should assess bioluminescence in individual organs or acknowledge limitations of using this approach and the strain in assessing dissemination.

We agree with the reviewer that the results need to be interpreted with care and changed our discussion according to the reviewers suggestions. It reads now:

“Most surprisingly, and in contrast to the results obtained for the MIC2 conditional knockdown (Huynh & Carruthers, 2006), we find that mic2 KO parasites are only mildly attenuated compared to WT RH parasites. The mic2 KO line (at least at the doses used in these studies) induces lethal disease in BALB/c mice. The mic2 KO line induces lethal disease in BALB/c mice, and transfection of these parasites with a luciferase gene demonstrated that they grow in similar anatomical locations in mice as control parasites. One explanation for the different findings could be that RH TATi ΔHX, the parasite line used to generate a knockdown for mic2 is already severely attenuated due to the expression of the Tet-transactivator. Indeed, in the study by Huynh & Carruthers, 2006, high doses (5 × 10⁴ tachyzoites) with RH TATi ΔHX were required to achieve normal time-to-death kinetics. It is thus possible that knockdown of mic2 in this strain reflects an enhancement of the already attenuated phenotype, while depletion in a WT background has only mild effects on parasite virulence. Alternatively, in our studies a reduced virulence of mic2KO parasites is not evident because of the relatively high numbers of tachyzoites used to facilitate in vivo imaging. Consequently to fully compare the virulence LD50 studies would be required. Nonetheless our studies demonstrate unequivocally that MIC2 is not necessary for in vivo infection and lethality in BALB/c mice. In vivo imaging and 3D diffuse tomographic reconstruction of mice infected with MIC2 deficient parasites transfected with a luciferase gene demonstrated that they grow in similar anatomical locations in mice as control parasites. However, dissection and histopathological analyses would be necessary to rule out any potential differences in tissue trophism.”

The caption for Figure 4 states: “Maximal speed of gliding is not impacted by mic2 KO”. This is somewhat misleading because it describes the findings of only 20% of the data in the figure. The figure has 10 panels or graphs, 8 of which show differences in gliding between WT and mic2 KO parasites. The figure caption should describe both the differences and the similarities.

The capitation now read “Figure 4: Gliding initiation and gliding distance are affected by mic2 KO attachment defect but not maximal speed”

Please provide y-axis labels for the middle and right panels of Fig S3. Also, for the sentence: “Surprisingly, the average and maximum speeds increased compared to WT parasites (Figure S3)” it should be explicitly indicated that this is for circular gliding.

Modification have been made and the text now reads “Surprisingly, the average and maximum speeds of circular gliding increased compared to WT parasites (Figure S3).”

Please describe in the materials and methods how the virulence experiment shown in Fig 7A was performed, including stating the number of times the experiment was performed and the number of animals in the experiment. Also, indicate in the legend of Fig 7 the inoculum for the bioluminescence experiment, and state in the methods the number of times the experiment was performed along with the number of mice used.
We updated the Material Methods section and describe the virulence experiments in greater detail.

Examples shown in Fig 6D do not match the categories used for quantification in Fig. 6C. The authors should consider showing an example of an intact PV instead of the “Lysed” example. Also, it would be ideal to explicitly state in the materials and methods that for assessing egress the fixed monolayers were not detergent permeabilized.

We changed Figure 6D as suggested and updated Material and Methods as suggested.

Competing Interests: No competing interests were declared.