Characterization of the Chloroquine Resistance Transporter Homologue in Toxoplasma gondii

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Mutations in the Plasmodium falciparum chloroquine resistance transporter (PfCRT) protein confer resistance to the antimalarial drug chloroquine. PfCRT localizes to the parasite digestive vacuole, the site of chloroquine action, where it mediates resistance by transporting chloroquine out of the digestive vacuole. PfCRT belongs to a family of transporter proteins called the chloroquine resistance transporter family. CRT family proteins are found throughout the Apicomplexa, in some protists, and in plants. Despite the importance of PfCRT in drug resistance, little is known about the evolution or native function of CRT proteins. The apicomplexan parasite Plasmodium falciparum contains one CRT family protein. We demonstrate that T. gondii CRT (TgCRT) colocalizes with markers for the vacuolar (VAC) compartment in these parasites. The TgCRT-containing VAC is a highly dynamic organelle, changing its morphology and protein composition between intracellular and extracellular forms of the parasite. Regulated knockdown of TgCRT expression resulted in modest reduction in parasite fitness and swelling of the VAC, indicating that TgCRT contributes to parasite growth and VAC physiology. Together, our findings provide new information on the role of CRT family proteins in apicomplexan parasites.

In the intraerythrocytic life stage, Plasmodium falciparum parasites make a living by gaining energy from serum-derived glucose and consuming hemoglobin from the host erythrocyte as a source of amino acids (1). The hemoglobin is endocytosed and transported to the parasite’s digestive vacuole (DV), a lysosome-like compartment containing peptidases that break down hemoglobin into its constituent amino acids (2). This digestion process releases toxic heme subunits from the hemoglobin protein into the DV. The parasite detoxifies these subunits by incorporating them into an inert crystalline substance called hemozoin (3). The antimalarial drug chloroquine accumulates in this digestive vacuole, where it acts by interfering with heme detoxification. Chloroquine inhibits the formation of hemozoin, causing toxic heme subunits to build up within the DV, eventually resulting in parasite death (4).

Resistance to chloroquine is widespread and is mediated by mutations in the so-called P. falciparum chloroquine resistance transporter (PfCRT) (5, 6). PfCRT is a multi-pass membrane transporter that localizes to the DV (5). Mutant PfCRT proteins are able to transport chloroquine out of the DV, removing it from its site of action and thereby abating its toxic effects on the parasite (7). PfCRT belongs to a family of transporter proteins called the CRT family, which is part of the large drug/metabolite transporter superfamily (8, 9). Homologues of PfCRT are found in all apicomplexan parasites, as well as in a range of other protists and plants. The plant Arabidopsis thaliana contains three PfCRT homologues called chloroquinelline transporters (CLT) (10). These homologues localize to the A. thaliana plastid and regulate glutathione metabolism, likely by transporting glutathione and γ-glutamylcysteine between the cytoplasm and the plastid lumen (10).

The apicomplexan parasite Toxoplasma gondii contains one homolog of PfCRT (TgCRT). Like A. thaliana, both P. falciparum and T. gondii possess a plastid, termed the apicoplast. Unlike P. falciparum, T. gondii does not contain a large digestive vacuole, and the extent to which T. gondii uses endocytosis to sequester metabolites from its host cell in a manner akin to Plasmodium remains unclear.

In the work described in this paper, we investigated the localization and function(s) of TgCRT to gain insights into the evolution and role of this family of transporters. We demonstrated that, in intracellular parasites, TgCRT localized to highly dynamic vesicles that overlapped the markers for a lysosome-like vacuolar compartment called the VAC (11). In extracellular parasites, TgCRT localized to one or a few larger, vacuole-like compartments that also overlapped the VAC markers. We generated a regulatable knockdown of TgCRT expression and demonstrated that, while TgCRT was not essential to the growth of T. gondii in vitro, the loss of TgCRT resulted in a reduction in parasite fitness and dilation of the VAC compartment.

MATERIALS AND METHODS

Identification of TgCRT. A BLASTP sequence similarity search using PfCRT (accession number PF3D7_07090000, available at www.plasmodb.org) as a query sequence identified the TgCRT genomic locus. This region partially corresponds to that encoded by the annotated gene TGE49_313930 (www.toxodb.org). Alignment of the predicted sequence to those of other CRT-like proteins suggested the gene model was incorrect. We therefore designed the primers 5'-ACTGCTCCACTGTTTTGCTTCG and 5'-GACATGGCTGTAAAGGTCTTCG to amplify the entire open reading frame of TgCRT by PCR, using cDNA from RHΔHXGPRT strain.
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T. gondii parasites as the template. We cloned and sequenced the resulting PCR product.

**Alignment and phylogenetic analysis.** CRT homologues from a range of organisms were identified by a BLASTP sequence similarity search with P/TgCRT as the query sequence. We generated an initial alignment using ClustalW 2.0.12 (12), followed by manual adjustment in JALVIEW version 11.0 (13). The maximum likelihood tree was created using PhyML version 3.0 (14).

**Plasmid construction and parasite transfections.** Details on the construction of the various plasmids generated in this study, the selection procedures to generate the various parasite strains, and the Southern blotting approach are presented in the supplemental material.

**Parasite culturing.** Parasites were cultured in human foreskin fibroblast (HFF) cells grown in Dulbecco’s modified Eagle’s medium supplemented with 1% fetal calf serum and antibiotics. Where relevant, we added antihyedrotectyacrine (ATC) to a final concentration of 0.5 μg/ml.

**SDS-PAGE and Western blotting.** SDS-PAGE and Western blotting were performed as described previously (15). Membranes were probed with the following primary antibodies: rat antihemagglutinin (anti-HA) antibody (clone 3F10, 1:1,000 dilution; Roche Applied Science), mouse anti-green fluorescent protein (GFP) antibody (1:1,000; BD Biosciences), rabbit anti-TgTOM40 antibody (1:1,000) (G.G.V.D., unpublished data), rabbit anti-TgCPN60 antibody (1:5,000) (16), and mouse anti-TgGRAB antibody (1:100,000) (a kind gift from Gary Ward, University of Vermont). We then blotted the following secondary antibodies: anti-rabbit horseradish peroxidase (HRP) antibody (1:10,000), anti-rat HRP antibody (1:1,000), and anti-mouse HRP antibody (1:200). Protein bands were visualized using the Amersham ECL plus Western blotting detection system (GE Healthcare). The mass of each band was calculated from an Rf plot.

To generate antibodies specific to TgCRT, we PCR amplified a region encompassing the C-terminal 198 amino acids of the TgCRT protein using the primers 5’-GGGGTCCTGCGGCTGATCATGATGAAACGCC CGCC and 5’-CTTTGTCCTGCTTATATATACGTCCGTGGT CGC. We inserted the resultant fragment into the pAV421 vector (18) by ligation-independent cloning and introduced the plasmid into Escherichia coli strain BL21. The recombinant protein was purified by affinity chromatography using a Ni-nitrilotriacetic acid (NTA) agarose resin (Qiagen). We generated polyclonal antisera by inoculation into rabbits (Institute of Medical and Veterinary Science, Adelaide, South Australia). We used the antibody for Western blotting at a 1:200 dilution.

**Sodium carbonate analysis.** Intact membranes were isolated from clonal parasites expressing TgCRT with a 3-HA epitope tag (TgCRT-HA) by incubation in 100 mM Na2CO3 at pH 11.5 as described previously (15). Proteins extracted from both the membrane and soluble fraction were analyzed by SDS-PAGE and Western blotting as described previously (15).

**Microscopy.** Immunofluorescence assays were performed as described previously (15). The primary antibodies were rat anti-HA antibody (clone 3F10, 1:100 dilution; Roche Applied Science), mouse anti-ccmyc antibody (clone 9E10, 1:200; Thermo Scientific), rabbit anti-TgCRT antibody (1:2,000) (G.G.V.D., unpublished data), rabbit anti-TgCPN60 antibody (1:1,000), mouse anti-TgGRAB antibody (1:100,000) (a kind gift from Gary Ward, University of Vermont) (17), mouse anti-TgCRT antibody (1:2,000 dilution; Abcam), with the CAT protein only present in parental parasites by labeling with mouse anti-chloramphenicol acetyltransferase (CAT) antibodies (Abcam), with the CAT protein only present in i7TgCRT/D7TgCRT strain parasites.

**Quantification of VAC size.** Wild-type (RH) and i7TgCRT/D7TgCRT parasites were treated with 0.5 μg/ml ATC for 2 days. Freshly lysed parasites were added to HFF cells, allowed to settle for 15 min at room temperature, and then incubated at 37°C for 30 min for invasion. Noninvaded parasites were washed away with phosphate-buffered saline. Infected HFF cells were fixed with 4% paraformaldehyde and stained with affinity-purified rabbit anti-TgCPL antibodies (11) at a 1:100 dilution. Images were captured with a Zeiss Axiosvid Observer Z1 inverted fluorescence microscope equipped with a 100×, 1.3-numerical-aperture objective lens and an AxioCam MRm camera. The diameters of VAC compartments were quantified using Zeiss Axiosvision 4.3 software. For nonspherical VACs, we measured the widest diameter. P values were calculated using an unpaired Student’s t-test.

**GenBank nucleotide sequence accession number.** The corrected TgCRT cDNA sequence has been deposited in GenBank under accession number KJ130040.

**RESULTS**

T. gondii contains one CRT family protein. To identify possible homologues of P/TgCRT in Toxoplasma gondii, we performed BLAST searches of the T. gondii genome (www.toxodb.org) using P/TgCRT as a query sequence. We identified a single putative CRT homologue encoded on chromosome XI and called this TgCRT. This
corresponded to a gene previously included in an alignment of CRTs from a range of organisms (22). To determine the correct coding sequence of TgCRT, we amplified the entire open reading frame, using cDNA as a template. This revealed that the TgCRT model presented in toxoDB is incorrect. The correct sequence encodes a protein of 890 amino acids, with a predicted mass of 92 kDa.

To elucidate the evolutionary relationships between CRT family proteins, we performed a phylogenetic analysis on CRT family proteins from apicomplexans, oomycetes, plants, red algae, and amoebae. This revealed that TgCRT branches with CRT homologues from related coccidian parasites, such as Eimeria tenella and Neospora caninum (see Fig. S1A in the supplemental material). We identified single CRT family proteins from each apicomplexan parasite that we examined, but the phylogenetic tree was not sufficiently resolved to determine whether these represent a monophyletic group. A multiple sequence alignment (see Fig. S1B) reveals that the similarity of TgCRT to other CRT family proteins resides in the central region of the protein, which spans the 10 predicted transmembrane helices. Compared to CRT family proteins from other organisms, coccidian CRT proteins harbor extended N and C termini (see Fig. S1C). A key mutation that confers chloroquine resistance in PfCRT is the conversion of lysine 76 to a threonine (K76T) (5, 23). Intriguingly, TgCRT and other coccidian CRTs harbor a threonine in this position (see Fig. S1B). TgCRT, however, resembles wild-type PfCRT at several other positions with a known role in conferring chloroquine transport activity, such as N76 and N326 (see Fig. S1B) (23). TgCRT contains numerous other regions that are conserved in CRT homologues from other organisms, including a cysteine-rich motif in the loop between transmembrane domains 7 and 8 (see Fig. S1D).

TgCRT localizes to a population of dynamic vesicles. To examine the localization of TgCRT, we inserted an HA3 epitope tag at the 3′ end of the native TgCRT open reading frame in Δkat80 T. gondii parasites (24, 25). We observed TgCRT-HA3 localizing to multiple small puncta in intracellular parasites (Fig. 1A). Western blot analysis of the resulting cell line revealed a protein with an observed mass of 87 kDa (Fig. 1B), congruent with the predicted mass of 92 kDa. Like other CRT family proteins, TgCRT contains multiple predicted transmembrane domains (see Fig. S1B and C in the supplemental material). To establish whether TgCRT is a membrane-bound protein, we carried out a Na2CO3 partitioning assay on the parasite line expressing TgCRT-HA3 (26). This assay segregates integral membrane proteins from soluble and peripheral membrane proteins. TgCRT-HA3 partitioned into the integral membrane fraction (Fig. 1C), consistent with TgCRT being a transmembrane protein. We conclude that TgCRT is an integral membrane protein that resides in small, membrane-bound vesicles in intracellular parasites.

To investigate the identity of the putative TgCRT-containing vesicles, we coabeled TgCRT-HA3 with markers for several well-described organelles in T. gondii tachyzoites, including the apicoplast, mitochondrion, dense granules, and micronemes (Fig. 2A to D). TgCRT-HA3 did not colocalize with any of these markers.

Earlier studies revealed that the proton-pumping vacuolar ATPase of T. gondii (TgV-ATP) localizes to small vesicles that were described as acidocalcisomes (27). To determine whether TgCRT colocalizes with TgV-ATP, we inserted a c-myc epitope tag into the 3′ end of the open reading frame of subunit B of the V-ATP (TgV-ATP-cmyc). We transfected this construct into the parasite line already expressing TgCRT-HA3. Immunofluorescence assays carried out on the resulting parasite line showed that TgCRT-HA3 and TgV-ATP-cmyc partially overlap in intracellular tachyzoites (Fig. 2E, arrowheads). We next coabeled TgCRT-HA3 with antibodies against vacuolar pyrophosphatase-1 (VP1), a marker for the late endosomes in intracellular parasites (11, 28). We observed essentially no overlap between these structures (Fig. 2F). As a second marker for late endosomes, we coabeled TgCRT-HA3 parasites with antibodies against TgNHE3, a Na+/H+ exchanger (29). Again, we observed no overlap between these organselles (Fig. 2G).

The vesicular pattern of TgCRT labeling resembled that of the fragmented VAC compartment described in intracellular parasites (11). We therefore coabeled TgCRT-HA3-expressing parasites with antibodies against TgCPI, a marker for the VAC. This revealed considerable overlap between the two compartments (Fig. 2H), suggesting that TgCRT is associated with the VAC.

TgCRT-containing organelles change morphology in extracellular parasites. The lytic cycle of T. gondii alternates between intracellular dividing cells and motile extracellular stages. The VAC is highly dynamic in intracellular tachyzoites (11). During most stages of the parasite lytic cycle, the VAC is fragmented into multiple smaller vesicular structures, but it is seen as one or more larger vacuolar structures in extracellular parasites. To observe TgCRT localization in extracellular parasites, we performed immunofluorescence assays on parasites expressing TgCRT-HA3 and TgV-ATP-cmyc (Fig. 3A) or on TgCRT-HA3-expressing parasites coabeled with antibodies against TgVP1 (Fig. 3B), TgNHE3 (Fig. 3C), or TgCPI (Fig. 3D). Interestingly, the morphology of the TgCRT-containing compartment is markedly different in extracellular tachyzoites. Consistent with previous observations of the VAC (11), TgCRT-HA3 localization appears as one or a few

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**FIG 1** TgCRT is an integral membrane protein that localizes to multiple vesicles in intracellular parasites. (A) Immunofluorescence assay of cells expressing C-terminally tagged native TgCRT (TgCRT-HA3) labeled with antibodies against the HA epitope (green) and the inner membrane complex (IMC; red). Scale bar, 3 μm. (B) Anti-HA Western blot of cell line expressing TgCRT-HA3, revealing a single protein band of an estimated 87 kDa. (C) Western blot of a sodium carbonate extraction of TgCRT-HA3-expressing parasites showing total (T), soluble (S), and membrane (M) proteins. TgCRT partitions into the membrane fraction. TgTOM40 and TgCPN60 are used as controls for membrane and soluble proteins, respectively.
larger vacuolar organelles in extracellular parasites (Fig. 3). Conversely, TgV-ATP-cmyc appears to localize to the plasma membrane and cytoplasm rather than to any defined vesicular structures (Fig. 3A).

Previous studies have defined TgVP1 and TgNHE3 as markers for the plant-like vacuole (PLV) (28, 29) in extracellular parasites. We find that TgVP1 and TgNHE3 localize to a large vacuolar structure in extracellular parasites that shows a close spatial association with the TgCRT-HA localization (Fig. 3B and C), although in our hands, these structures are not overlapping. TgCRT and TgCPL retain their colocalization in extracellular parasites (Fig. 3D), consistent with TgCRT localization to the VAC.

To further explore the change in morphology between extracellular and intracellular tachyzoites, we generated a parasite line where TgCRT was fused to green fluorescent protein (GFP). This allowed us to visualize the VAC in live parasites. Live-cell fluorescence images of intracellular T. gondii expressing TgCRT-GFP reveal the presence of multiple small vesicles in intracellular parasites (Fig. 4A), mirroring what we observed in epitope-tagged parasites. In extracellular parasites, TgCRT-GFP localizes to a larger vesicle and, occasionally, some smaller vesicles (Fig. 4B). Western blotting reveals that TgCRT-GFP exists as a single protein of 120 kDa, similar to the predicted mass of 124 kDa (Fig. 4C).

Having established TgCRT-GFP as a robust marker for the VAC compartment in live parasites, we next set out to characterize the dynamics of the changes that occur in this compartment between extra- and intracellular stages by performing time-lapse imaging of TgCRT-GFP parasites. We allowed parasites to invade host cells and then imaged single-cell vacuoles every 15 min for 7 h (Fig. 4D; see also Movie S1 in the supplemental material). During this time frame of intracellular growth, the large VAC compartment observed in extracellular parasites fragments substantially. Notably, the VAC is fragmented before the parasite undergoes its first round of cell division (Fig. 4D). To quantify fragmentation of the VAC, we counted TgCRT-GFP-containing vesicles in parasites at regular time intervals postinvasion (Fig. 4E). In extracellular parasites (time zero), TgCRT-GFP exists in an average of approximately three separate compartments, typically one larger compartment and some smaller ones. Eight hours postinvasion, parasites typically have over a dozen smaller TgCRT-GFP-containing vesicles. The relationship between vesicle number and time postinvasion has a statistically significant Spearman’s rank correlation coefficient of 0.752 (P < 0.0001), suggesting a strong correlation between time after invasion and vesicle number.

The role of TgCRT in parasite fitness and VAC morphology. P/CRT has proven recalcitrant to genetic ablation, suggesting that it may be essential to parasite survival (30). To determine whether TgCRT is important for growth in T. gondii, we first generated a parasite strain expressing an anhydrotetracycline (ATc)-regulated TgCRT gene in TATi strain T. gondii parasites (31). This parental cell line, termed iTgCRT/CtTgCRT, expresses both native and ATc-regulatable copies of TgCRT. We then deleted the 5’ region of the native TgCRT locus by double homologous recombination, using a previously described cosmid recombinering system (32) to generate a parasite line, termed iTgCRT/ΔTgCRT, that expresses only the ATc-regulatable copy of TgCRT. Southern blot analysis of the resulting cell line demonstrated successful disruption of the native TgCRT locus (see Fig. S2 in the supplemental material).

To measure the regulation of TgCRT in the iTgCRT/ΔTgCRT
cell line, we incubated parasites in the absence of ATc (day 0) or the presence of ATc for 1, 2, and 3 days and then performed Western blotting to detect the HA-tagged TgCRT protein. After 1 day on ATc, TgCRT levels are greatly reduced, and after 2 days, the protein is undetectable (Fig. 5A), demonstrating robust down-regulation of the protein in the iTgCRT/eTgCRT cell line. To compare the levels of ATc-regulated TgCRT expression to the wild-type TgCRT level, we generated polyclonal antibodies against TgCRT and probed proteins extracted from iTgCRT/eTgCRT and iTgCRT/eTgCRT/H9004TgCRT cell lines grown with and without ATc. In the absence of ATc in both cell lines, we observed bands of the expected mass for TgCRT (Fig. 5B). When we knocked down iTgCRT expression through the addition of ATc in the iTgCRT/eTgCRT cell line, we observed a band corresponding to the expected mass for native TgCRT but at a reduced intensity compared to that obtained when the ATc-regulatable copy of TgCRT is expressed (Fig. 5B). This suggests that there is overexpression of TgCRT from the ATc-regulated promoter. Nevertheless, when we cultured iTgCRT/ΔTgCRT in the presence of ATc, TgCRT protein was undetectable (Fig. 5B), indicating that the iTgCRT/ΔTgCRT strain allows strong depletion of TgCRT protein upon the addition of ATc.

To elucidate the importance of TgCRT for parasite growth and viability, we performed plaque assays on the iTgCRT/ΔTgCRT and iTgCRT/eTgCRT parasite lines. Parasites were added to a monolayer of human foreskin fibroblast cells and grown for 9 days in the presence or absence of ATc. Over this time, parasites will form zones of clearance in the host cell monolayer, which become apparent upon staining with crystal violet dye. The sizes of the plaques indicate how well the parasites have grown during this time. We found that iTgCRT/ΔTgCRT grew in both the absence and presence of ATc, suggesting that TgCRT is not essential for parasite growth (Fig. 6A). Quantification of plaque size revealed that plaques of the iTgCRT/ΔTgCRT parasite line grown in the presence of ATc were on average smaller than those of iTgCRT/ΔTgCRT parasites grown in the absence of ATc (P < 0.0001).
This effect is likely specifically due to the depletion of TgCRT from this cell line, since we observed little difference in plaque size upon the addition of ATc to the parental iTgCRT/eTgCRT cell line \((P > 0.05)\) (Fig. 6B).

As a more quantitative measure of parasite growth, we introduced a superbright tdTomato fluorescent protein into the iTgCRT/eTgCRT cell line. We added parasites to wells of a 96-well plate and measured the fluorescence intensity of each well on a daily basis, with the fluorescence in each well correlating directly to parasite growth \((15, 21)\). The iTgCRT/ΔTgCRT parasites grew \(\sim 30\%\) more slowly in the presence of ATc (Fig. 6C), again supporting a minor role for TgCRT in parasite growth.

These data suggested a fitness cost associated with the loss of TgCRT in T. gondii parasites. To test this, we performed a competition assay where parental iTgCRT/eTgCRT and iTgCRT/ΔTgCRT mutant parasites were mixed in a 1:1 ratio and then grown in the presence or absence of ATc. We could distinguish mutant from parental parasites by performing immunofluorescence assays to detect the presence of chloramphenicol acetyltransferase, which is only present in the mutant. We monitored the parasites over 24 days. During this time, the ratio of the two
parasite strains grown in the absence of ATc remained approximately 1:1 (Fig. 6D). In contrast, iTgCRT/ΔTgCRT mutant parasites were rapidly outcompeted in the presence of ATc, with less than 5% remaining after 24 days (Fig. 6D).

Our data indicate that TgCRT is not essential for parasite growth but that loss of TgCRT does incur a fitness cost on the parasite. We also demonstrate that TgCRT localizes to the VAC compartment. We wondered whether loss of TgCRT would result in morphological changes to the VAC. To test this, we performed immunofluorescence assays to label the VAC in wild-type (RH) and iTgCRT/ΔTgCRT parasites grown in the absence and presence of ATc. We focused on recently invaded parasites in which the VAC was still in its larger, extracellularlike form. We noted the VAC appeared larger in parasites lacking TgCRT. We focused on recently invaded parasites in which the VAC was still in its larger, extracellularlike form. We noted that the loss of ATc was on average 1.3 μm in diameter, significantly larger than the average 0.73-μm diameter found in parasites grown without ATc (Fig. 7B) (*P < 0.0001). We observed no such difference in wild-type parasites. Together, these results suggest that the loss of TgCRT leads to an enlargement of the VAC compartment, suggesting an effect on the physiology of this organelle.

**DISCUSSION**

The CRT protein family is found in a diverse array of eukaryotes. In plants, chloroquine-like transporters localize to the plastid, where they appear to play a role in glutathione homeostasis and metabolism, possibly by mediating glutathione export from the organelle (10). In erythrocytic stages of *Plasmodium*, CRT proteins localize to the digestive vacuole (DV) (5), a lysosome-like organelle that functions primarily in the digestion of hemoglobin (33, 34). The DV houses a suite of proteases that digest hemoglobin into its constituent amino acids, which are then utilized for parasite growth (1, 33). In *Plasmodium*, chloroquine accumulates in the DV and interferes with the polymerization of heme released from hemoglobin (4, 35). Heme in its free state is highly toxic to the parasite (36). Failure to polymerize heme results in swelling of the DV and rapid parasite death (37, 38). Mutant CRT alleles in *P. falciparum* confer resistance to the major antimalarial drug chloroquine by transporting chloroquine from the DV (5, 7).

In this study, we characterized the CRT homologue from the model apicomplexan *T. gondii*, revealing that TgCRT localizes to the recently described VAC compartment (11). The VAC is a proteolytic compartment that houses cathepsin-like cysteine proteases, such as TgCPL and TgCPB (11, 39). Using a live-cell-imaging approach, we demonstrated that the VAC is a highly dynamic compartment. In extracellular and recently invaded parasites, it typically exists as a single large compartment, which then apparently fragments into a dozen or more smaller TgCRT-containing vesicles during parasite replication.

We demonstrate here that the TgCRT-labeled VAC is distinct from the plant-like vacuole (PLV) in intra- and extracellular parasites. TgVP1 was described as the seminal marker of the PLV in *T. gondii* (28). In a parallel study, TgCPL was reported to be a marker of the VAC (11). Both studies reported that intracellular replicating parasites show TgVP1 associated with markers of late endosomes, whereas TgCPB was seen in multiple vesicular structures attributed to fragmentation of the resident organelle (11, 28). However, in extracellular parasites, these markers were reported to colocalize in the PLV in one study (28) but were observed separately in the VAC (TgCPL) and late endosome (TgVP1) in the parallel study (11). The discrepant findings were attributed to the dynamic nature of these endolysosomal organelles and possible fusion of the VAC with late endosomes to form the PLV. Regardless, these studies provided evidence for multiple functions of the PLV and VAC organelles, including roles in regulating ion balance in response to changes in the extracellular environment and proteolytic processing or digestion of proteins. In this study, we have used the term VAC when referring to a compartment(s) associated with TgCPL, while PLV has been used to indicate structures associated with TgVP1.

The proteomic makeup of the VAC appears quite dynamic. The vacuolar H⁺-pumping ATPase associates with some TgCRT-containing vesicles in intracellular parasites, suggesting that these are acidic compartments. In extracellular parasites, however, the association between the VAC and the vacuolar H⁺-pumping ATPase is not apparent. In a previous study, we demonstrated that the VAC is a highly dynamic compartment. In extracellular and recently invaded parasites, it typically exists as a single large compartment, which then apparently fragments into a dozen or more smaller TgCRT-containing vesicles during parasite replication.

The intracellular TgCRT-associated VAC compartments exhibit numerous intriguing similarities to the DV of *Plasmodium* (Fig. 8). In addition to the presence of CRT homologues in both the VAC and DV, both compartments house cathepsin proteases, TgCPL and TgCPB in the case of the VAC and falcipains 2a, 2b, and 3 in the case of the DV (40). During intracellular replication, both compartments also harbor a V-type H⁺-pumping ATPase that likely functions in maintaining the acidity of the organelle
Given these similarities, we hypothesize that the common ancestor of *Plasmodium* and *Toxoplasma* may have harbored an acidic lysosome-like vacuole that gave rise to the VAC in *T. gondii* and the DV in *Plasmodium* (Fig. 8). Despite this possible shared ancestry, some of the functions of the DV and VAC differ in their respective parasites. The DV of *Plasmodium* functions primarily in the proteolytic digestion of hemoglobin. Endocytic vesicles carrying hemoglobin from the erythrocyte form at a cytosome and are internalized into the parasite (42). These endocytic vesicles are acidified and contain proteases that can digest hemoglobin. Ultimately, the endocytic vesicles fuse to form the larger DV, where the bulk of hemoglobin digestion in the parasite takes place (42).

TgCRT is not essential for *T. gondii* growth, but depletion of TgCRT imparts a fitness cost on parasites. (A) Plaque assays of iTgCRT/eTgCRT and iTgCRT/ΔTgCRT cell lines grown in the absence and presence of ATc. (B) Quantification of the relative areas of plaques in the parental and mutant cell lines grown in the absence and presence of ATc. These are represented as box and whisker plots, with the medians indicated by vertical bars, the 1st and 3rd quartiles forming the box, and whiskers indicating the minimum and maximum values. ****, $P < 0.0001$; n.s., not significant. (C) Fluorescence growth assay of iTgCRT/ΔTgCRT parasites grown in the absence and presence of ATc over 7 days. Error bars each represent one standard deviation from the mean of three technical replicates. (D) Competition assay of iTgCRT/eTgCRT and iTgCRT/ΔTgCRT parasites grown in the absence and presence of ATc. Parasites were mixed in a 1:1 ratio at the start of the experiment, and the percentages of iTgCRT/ΔTgCRT parasites in the population were monitored over 24 days, as a percentage of parasites expressing the CAT protein. Error bars each indicate one standard deviation from the mean.

Although the role of mutant *PfCRT* alleles in chloroquine transport is clear (7), the native function of CRT homologues in apicomplexans remains to be elucidated. Unpublished attempts to knock out *PfCRT* were unsuccessful (30), suggesting that *PfCRT* may be essential for *P. falciparum* survival in erythrocytic stages. Knockdown of chloroquine-resistant *PfCRT* protein levels to approximately 65% of the wild-type levels lessened parasite...
resistance to chloroquine and led to an alkalinization of the DV (30), suggesting a possible role for CRT in acidification of this compartment. Plant chloroquine-like transporters function in transporting glutathione, and a recent study implicates chloroquine-resistant PfCRT (but not chloroquine-sensitive PfCRT) in glutathione transport into the DV (10, 44).

In this study, we demonstrate that TgCRT is not essential for the growth of T. gondii under standard in vitro culture conditions. Although our data suggest robust knockdown of TgCRT in the iTgCRT/ΔTgCRT parasite line compared to wild-type levels (Fig. 6B), we cannot rule out that a small amount of TgCRT is expressed that is sufficient for TgCRT function. Nevertheless,
competition growth assays revealed that the loss of TgCRT imparts a fitness cost to the parasite. Intriguingly, a reduction in TgCRT levels results in an enlargement of the VAC compartment. The reasons for this remain unclear. It is possible that TgCRT has a role in the biogenesis or homeostasis of the VAC. For example, the loss of TgCRT may influence the pH of the VAC (much like depletion of PFCRT alters the pH in the DV of Plasmodium [30]), which in turn could influence ion regulation and lead to swelling of the organelle. Notably, we have previously demonstrated that treatment of T. gondii with agents that cause alkalization of acidic compartments (bafilomycin A1, which inhibits V-type H⁺-ATPases, and chloroquine) disrupts some of the functions of the VAC and leads to swelling of this compartment (11).

It is equally possible that the loss of TgCRT leads to an accumulation of the native substrate transported by TgCRT, which in turn causes VAC swelling. Another possibility is that TgCRT, like plant chloroquine-like transporters and chloroquine resistance alleles of PFCRT (10, 44), has a role in transporting glutathione. Dysregulation of glutathione functions in the VAC may then lead to the swelling of this organelle.

P. falciparum parasites harboring chloroquine resistance alleles of PFCRT are less fit than strains with chloroquine-sensitive PFCRT. Cessation of chloroquine treatment in areas where chloroquine-resistant (e.g., see reference 45). More recently, this reemergence has been duplicated in a laboratory environment (46). The latter study performed competition growth assays with chloroquine-sensitive and -resistant strains of P. falciparum in the absence of chloroquine. The study found that chloroquine-sensitive strains almost entirely outcompeted resistant strains over an ~70-day time frame (46). This mirrors our findings with T. gondii parasites that were depleted of TgCRT. The same study examined the metabolic differences between chloroquine-sensitive and -resistant strains of P. falciparum and found that parasites harboring chloroquine resistance alleles accumulated hemoglobin-derived peptides (46). This suggests that parasites carrying mutated forms of PFCRT are less efficient in catabolizing hemoglobin, which may in turn affect parasite amino acid pools and result in the observed decrease in fitness.

Less clear is how these observed phenotypes correspond to the function of PFCRT (46). As we have proposed for the effects of the TgCRT mutant on VAC function, it is possible that mutated forms of PFCRT perturbed DV function and this led to impairment of hemoglobin digestion. Another possibility is that PFCRT functions as a peptidase (or amino acid transporter), with impairment of the transporter then leading to the accumulation of peptides in the DV. In this context, it is certainly intriguing that glutathione, which is transported by plant chloroquine-like transporters (10), is a tripeptide. Could TgCRT be functioning as a peptidase or amino acid transporter? Given the presence of proteases like TgCPL and TgCBP, it is conceivable that one function of the VAC is in protein catabolism, with peptides or amino acids derived from this process contributing to overall parasite amino acid pools. T. gondii is auxotrophic for many amino acids (47), which are primarily derived from the growth medium by in vitro cultures. We tested whether TgCRT knockdown parasites had impaired growth in amino acid-depleted medium but observed no differences compared to the growth of parasites that expressed TgCRT (not shown). This does not rule out the possibility that TgCRT functions as a peptidase or amino acid transporter—it could be that the contribution of the VAC to overall amino acid pools is minimal or that peptide or amino acid transport from the VAC is important to maintain VAC functions.

In this study, we have examined the localization and possible functions of TgCRT, with a view to elucidating the origin and evolution of CRT family proteins. CRT family proteins localize to lysosome-like vacuolar organelles in both T. gondii and Plasmodium. In T. gondii, the VAC compartment to which TgCRT localizes is a highly dynamic structure, potentially involved in numerous roles within the parasite. CRT family proteins exist in a range of other organisms, presenting opportunities to further explore the function(s) of this important group of transporters.

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