Proteomic analysis of acidocalcisomes of *Trypanosoma brucei* uncovers their role in phosphate metabolism, cation homeostasis, and calcium signaling

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Abbreviations: CDF, cation diffusion facilitator; Ccc1, Ca²⁺-sensitive cross-complementer 1; IP₃R, inositol 1, 4, 5-trisphosphate receptor; PolyP, polyphosphate; PPX, exopolyphosphatase; VIT, vacuolar iron transporter; VTC, vacuolar transporter chaperone.

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Trypanosoma brucei, the causative agent of African trypanosomiasis, is a unicellular parasite that possesses lysosome-related organelles known as acidocalcisomes. These organelles have been found from bacteria to human cells, and are characterized by their acidic nature and high calcium and polyphosphate (polyP) content. Our proteomic analysis of acidocalcisomes of T. brucei procyclic stages, together with in situ epitope-tagging and immunofluorescence assays with specific antibodies against selected proteins, established the presence of 2 H^+ pumps, a vacuolar H^+ -ATPase and a vacuolar H⁺-pyrophosphatase, that acidify the organelles as well as of a number of transporters and channels involved in phosphate metabolism, cation uptake and calcium signaling. Together with recent work in other organisms, these results provide direct evidence that acidocalcisomes are especially adapted to accumulate polyP bound to cations and for calcium signaling.

Acidocalcisomes were first identified in trypanosomes^{1,2} and later found from bacteria to human cells.³ Although originally described in bacteria as metachromatic⁴ or volutin⁵ granules they were though to lack a surrounding membrane. The discovery that in some bacteria^{6,7} they possess a proton pump and are able to accumulate protons (H⁺) and calcium ions (Ca²⁺) established them as real organelles and led to the recognition that, together with lipid droplets,⁸ they are the only organelles present in both prokaryotes and eukaryotes.⁹

Acidocalcisomes belong to the group of lysosome-related organelles¹⁰ and their acidification is driven by either a vacuolar H⁺-ATPase or a vacuolar H⁺-pyrophosphatase or, in the case of trypanosomes, by both.9 However, a definitive demonstration of the co-localization of these proton pumps in T. brucei was not established until our recent work.¹¹ In this regard, acidocalcisomes of T. brucei share the property of being acidified by 2 proton pumps with the plant vacuole,¹² the plantlike vacuole of *Toxoplasma gondii*,¹³ and the digestive food vacuole of the malaria parasites.14 An acidic acidocalcisome pH is required to maintain polyP in its polymeric state because their alkalinization results in polyP hydrolysis.¹⁵ PolyP is a polyanion of 3 to thousands of orthophosphate monomers and binding with organic (basic amino acids, polyamines) or inorganic (calcium, magnesium, sodium, potassium, zinc, iron) cations neutralizes its negative charges.

Here, we discuss our recent proteomic analysis of acidocalcisomes of T. brucei¹¹ to further clarify their important role in phosphate and cation homeostasis, and Ca^{2+} signaling. Of the 2 best-studied life stages of this organism, the procyclic stages found in the vector, and the bloodstream forms found in the mammalian host, we chose the procyclic stages, which are richer in acidocalcisomes.¹⁶ To isolate acidocalcisomes we used a modification of protocols described before.^{17,18} Cells were broken by abrasion with silicon carbide in a mortar and after subcellular fractionation that included 2 iodixanol gradient centrifugations, a fraction highly enriched acidocalcisomes was isolated, in as

established by marker enzyme assays, marker antibody immunoblotting and electron microscopy analyses (Fig. 1 and detailed in ref. 11). After SDS-PAGE of the proteins, bands were cut, digested ingel with trypsin and peptides analyzed by LC-MS/MS. Bioinformatic analysis of the resulting peptides allowed the identification of a set of candidate proteins whose acidocalcisome localization was validated by in situ epitope-tagging and western blot analyses using specific antibodies (Fig. 1). Knockdown by RNA interference (RNAi) of the expression of 4 of the genes encoding these proteins (vacuolar H⁺-ATPase subunits a and d, vacuolar iron transporter, and zinc transporter) was done to investigate their requirement for cell growth in procyclic and bloodstream forms of the parasite. Growth was greatly inhibited in both life cycle stages after knockdown of the V-H⁺-ATPase subunits or of the vacuolar iron transporter.

Of the 580 proteins identified with protein probability > 0.95, (listed in¹¹) over 40 were selected for further study on the basis of their presence in acidocalcisomes of other organisms, or on specific properties like presence of transmembrane domains or similarity to transporters of cations or metabolites known to be present in acidocalcisomes or lysosome-related organelles. Five proteins previously identified as localized to the acidocalcisomes by immunofluorescence assays (IFA) using epitope tagged proteins or specific antibodies, were found in the acidocalcisome proteome: vacuolar H⁺ pyrophosphatase (TbVP1),¹⁹ plasma membrane-type vacuolar Ca²⁺-ATPase (PMCA, TbPMC1),²⁰ inositol 1,4,5-trisphosphate receptor (TbIP₃R),²¹ vacuolar transporter chaperone 4 (TbVtc4),²² and vacuolar soluble pyrophosphatase (TbVSP1).²³ Four proteins were found in the acidocalcisome proteome and their localization validated by IFA using epitope-tagged proteins: vacuolar H^+ -ATPase subunits *a* and *d* (TbVAa and TbVAd), acid phosphatase (TbAP), and phosphate transporter (TbPho91). Four proteins that localize to acidocalcisomes or acidocalcisome-like organelles of other species, such as Zn transporter (TbZnT),²⁴ vacuolar iron transporter (TbVIT1),²⁵ polyamine trans-porter (TbPOT1),²⁶ and vacuolar transporter chaperone 1 (TbVtc1)^{27,28} were not detected in the acidocalcisome proteome but were validated by IFA as localized to acidocalcisomes.¹¹ Finally, 5 proteins were detected in the acidocalcisome proteome but were localized to different organelles such as mitochondria (ABC transporter, TbABCT), nuclear membrane (hypothetical protein, TbNP), Golgi and lysosomes (Golgi /lysosome glycoprotein 1, TbGLP1), lysosomes (polyamine transporter 2, TbPOT2), and flagellar tip (cation/proton antiporter, TbFTP).¹¹

Although the acidocalcisome proteome contained 580 proteins most of them corresponded to proteins known to localize in other subcellular compartments.¹¹ This "contamination" is not unexpected because acidocalcisomes are usually observed in close contact with other organelles and intracellular structures such as the nucleus, mitochondria, subpellicular mitcrotubules, and lipid inclusions²⁹ and parts of these structures and organelles could co-sediment with acidocalcisomes. In this regard, contact sites between organelles has been widely described.³⁰ Of the proteins validated as acidocalcisome proteins, only 2 are soluble, TbVSP1, and TbAP.

Several proteins were identified in both the T. brucei¹¹ and the Cyanidioschyzon merolae¹⁸ acidocalcisome proteomes such as acid phosphatase, vacuolar H⁺-ATPase subunits a and d, vacuolar pyrophosphatase, zinc transporter, vacuolar iron transand vacuolar porter, transporter chaperone 1. There is also considerable overlap of acidocalcisome proteins with proteins localized in the yeast vacuole: V-H⁺-ATPase subunits, Ca²⁺-ATPase Pmc1p (ortholog of TbPMC1), Vtc1p and Vtc4p (orthologs of TbVtc1 and TbVtc4), Ca²⁺-sensitive cross-complementer 1 or Ccc1p (ortholog of TbVIT1), zinc transporter Zrc1p (ortholog of TbZnT), and phosphate transporter Pho91p (ortholog of TbPho91), and to the Arabidopsis thaliana vacuole: V-H+-



Figure 1. Flow chart shows steps for characterizing acidocalcisome proteome of *Trypanosoma brucei*. An integrated approach for functional analyses of the newly identified acidocalcisome proteins is proposed.

ATPase subunits, vacuolar H^+ -pyrophosphatase, vacuolar iron transporter 1 (ortholog to TbVIT1), and metal tolerance protein 1 (ortholog to TbZnT). These results suggest a close relationship between these organelles.

The analysis of the acidocalcisome proteome reveals potential roles of the organelle in several metabolic and signaling pathways¹¹ (Fig. 2). A role in Ca²⁺ signaling is supported by the presence of mechanisms for Ca^{2+} uptake and release. Ca^{2+} uptake is driven by the plasma membrane-type Ca^{2+} -ATPase (TbPMC1). This pump acts as a Ca²⁺/H⁺ countertransporting ATPase requiring an acidic intraorganellar pH for efficient Ca^{2+} uptake.^{20,31} The mechanism for Ca²⁺ release is represented by the inositol 1,4,5-trisphosphate receptor (TbIP₃R).²¹ A previous study localized this channel to the acidocalcisomes using endogenous epitope tagging,²¹ which was confirmed in this work¹¹ using specific antibodies. This appears to be in contrast to the apparent endoplasmic reticulum localization

of the channel in *T. cruzi*,³² although this has been disputed.³³

Acidocalcisomes are also important for phosphate metabolism (Fig. 2). In addition to enzymes involved in PPi and polyP hydrolysis, like the vacuolar soluble pyrophosphatase (TbVSP1)²³ and the exopolyphosphatase (PPX) activity previously reported in acidocalcisomes of T. cruzi,¹⁵ our work confirmed the localization of 2 components of the vacuolar transporter chaperone (VTC) complex, TbVtc1²⁸ and TbVtc4,^{22,34} in *T. brucei* acidocalcisomes.¹¹ The VTC complex, which was first described in the yeast vacuole, where it has 4 components (Vtc1-4p),³⁵ is involved in the synthesis and translocation of polyP to acidocalcisomes^{22,34} and acidocalcisome-like vacuoles of yeast^{35,36} and Chlamydomonas reinhardtii.²⁷ In addition to this Pi entry mechanism there is also evidence for a P_i release mechanism as suggested by the identification of a Na⁺/P_i symporter (TbPho91) with similarity to the Pho91p transporter localized in the yeast vacuole and responsible for P_i efflux.³⁷





Furthermore, an acidocalcisome acid phosphatase (TbAP) which could be involved in P_i release from organic molecules (R- P_i), including perhaps polyP, is also found in acidocalcisomes.¹¹

Given the polyanionic nature of polyP it is not surprising that acidocalcisomes need to accumulate cations to compensate all those negative charges (Fig. 2). Previous studies revealed the presence of Na⁺/H⁺ and Ca²⁺/H⁺ exchangers in acidocalcisomes of procyclic forms of *T. brucei*, 38,39 and in the new report¹¹ we describe the localization in acidocalcisomes of a putative Zn²⁺ transporter (TbZnT). TbZnT is homolog to a previously described T. cruzi zinc transporter²⁴ and member of the cation diffusion facilitator (CDF) family that includes transporters involved in Zn²⁺, Cd²⁺, Co²⁺, and/or Ni²⁺ transport in exchange for protons.⁴⁰ Acidocalcisomes also possess a protein (TbVIT1) with similarity to the vacuolar iron transporter (Vit1p) from yeast²⁵ and plant⁴¹ vacuoles involved in Fe²⁺ and Mn²⁺ sequestration. Finally a putative polyamine transporter (TbPOT1) partially localizes to the acidocalcisomes.¹¹ Polyamines, which have several positive charges, are known to be abundant in the acidocalcisome-like vacuole of yeast.⁴² Interestingly, it was recently reported that during zinc limitation acidocalcisomes of C. reinardtii43 also accumulate copper, which was proposed as a mechanism to avoid protein mismetallation.44

In conclusion, acidocalcisomes are rich in polyP and cations and in addition to this storage function, most of its functions in trypanosomes could probably be attributed to their components including their role in pH¹⁹ and osmotic⁴⁵ regulation, response to stress,¹⁵ autophagy,⁴⁶ growth and infectivity.^{45,47} As several of the newly identified acidocalcisome proteins (V-H⁺-ATPase subunits a and d, TbVIT1) are essential for growth of procyclic and bloodstream forms of T. brucei,11 and acidocalcisomes possess proteins with no similarity to mammalian proteins like the vacuolar H⁺-pyrophosphatase, and the VTC complex, the newly identified pathways could be appropriate targets for chemotherapy.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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