

A high-magnification electron micrograph showing a complex, yellowish, branching structure, likely a parasitic rhizoid or pseudopod, extending from a host cell. The host cell membrane is visible as a dark, wavy line. The background is black.

parasitus

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Foto de Portada

Trichomonas vaginalis (azul) conectados por citonemas (naranja) observados por microscopía electrónica de barrido.

Créditos: Nehuen Salas (INTECH, CONICET-UNSAM, Argentina), Antonio Pereira Neves (Instituto Aggeu Maglhães, Brasil) y Natalia De Miguel (INTECH, CONICET-UNSAM, Argentina).

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SIMPOSIO IV: Biología Molecular y Bioquímica

Imbalance of TbVps32 affects vesicular trafficking and cell cycle progression in procyclic forms of *T. brucei*

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Trypanosoma brucei is a eukaryotic parasite transmitted by tsetse flies that causes African trypanosomiasis, a devastating disease also known as sleeping sickness in humans, and Nagana in cattle. During its life cycle, this parasite alternates between the mammalian bloodstream forms and procyclic forms present in the insect vector, requiring specific adaptation to maintain homeostasis during this alternation. These adaptive mechanisms require the detection of extracellular signals and are facilitated by membrane trafficking. In this sense, *T. brucei* and other kinetoplastids have rewired components of the canonical endo-lysosomal machinery and have adapted processes such as endocytosis, exocytosis, and autophagy for efficient life cycle progression. The multivesicular bodies (MVB) are specialized late endosomes (LE) that function in targeting ubiquitinated cell surface proteins to the lysosome for degradation and are mainly composed of protein members of the Endosomal Sorting Complex Required for Transport (ESCRT). ESCRT is composed of four sub-complexes (0-III), with ESCRTIII being the most conserved among eukaryotic taxa. The Vps32 protein, also known as Vacuolar Sorting Protein 32, is a crucial component of the cellular machinery responsible for intracellular protein trafficking and sorting. It plays a pivotal role in maintaining the functionality and integrity of the endosomal-lysosomal system, a fundamental aspect of eukaryotic cell biology. Vps32 is the most abundant protein of ESCRT III and also has an important role in cytokinesis and vesicular trafficking as it was described in *Saccharomyces cerevisiae* and *Homo sapiens*.

African trypanosomes lack a morphologically well-defined MVB but contain orthologues of the ESCRT machinery that drive a diverse collection of membrane remodeling events. In fact, in *Trypanosoma brucei*, TbVps23 (ESCRTI) and TbVps4 (the terminal ESCRT ATPase) are both localized to the late endosome and play a role in lysosomal trafficking. In our laboratory, we have identified and studied several members of the Vps-protein family in *T. cruzi* and *T. brucei*. More recently, we identified the Vps32 orthologue in *T. brucei*, named TbVps32, which is shown to be associated with endocytic compartments. Through TbVps32 downregulation and the inducible expression of a tagged version of this protein (HA-TbVps32), we addressed the role of TbVps32 in vesicular transport to the lysosome and cell cycle progression. Knockdown of TbVps32 by interference RNA and HA-TbVps32 inducible over-expression resulted in the inhibition of cell growth in both cases, highlighting the relevance of fine-tuning the balance of this protein for the proper regulation of the ESCRT complex function. Moreover, trafficking of dextran, transferrin, and DQ-BSA in the endocytic pathway was impaired. Overall, we propose that TbVps32 participates in endocytic trafficking to the lysosome and is essential for *Trypanosoma brucei* survival.

Regulación epigenética en *Toxoplasma gondii*: papel del nucleosoma doble variante H2A.Z/H2B.Z

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Las histonas son proteínas fundamentales en una amplia variedad de procesos biológicos, regulando el grado de empaquetamiento del ADN, y haciendo gala de una variedad de modificaciones post-tradicionales (PTMs, por sus siglas en inglés) que son parte de un "código de histonas" interpretado por proteínas "lectoras" que modulan la estructura de la cromatina. Entre estas modificaciones, una de las más ampliamente