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therefore they required high lysosomal activity to cope with their metabolism. In this line evidence, previously we demonstrated the occurrence of a single functional ortholog of the MiT/TFE family transcription factors in Echinococcus larval stages, Eg-TFEB, a bHLH-ZIP-type protein with a modular sequence involved in lysosomal biogénesis, autophagy and exocytosis. Based on Eg-TFEB conserved structure and its high level of endogenous expression, in situ immunodetection resulted appropriate as a method to verify its subcellular localization in the parasite. Eg-TFEB conserve a Ser199 residue phosphorylatable by TOR (equivalent to Ser211 of Homo sapiens TFEB), through which can to inhibit its activity by promoting its retention in the cytoplasm. During starvation and mTOR inactivation, TFEB is dephosphorylated and translocated to the nucleus, where it can promote the expression of its target genes. Rapamycin, hydroxychloroquine and metformin act as Eg-TFEB activators, promoting its nuclear localization. In this scenario, Eg-TFEB binds to palindromic CLEAR motifs (GTCACGTGAC) present in promoters of target genes, activating transcriptional expression and favoring processes such as autophagy (atg5, atg7, atg8.2 and atg12), lysosomal (lal-1, lal-2, atp6V1 and clcn7), metabolic activity (glut-1 and glut1-4), and even its own transcription. Contrarily to expectations, calcineurin is not involved in the activation of Eg-TFEB, due to its subcellular localization unchanged in presence of cyclosporine A. Finally, this work describes the *in vitro* dose-dependent anti-echinococcal effects exerted by eltrombopag (FDA-approved drug) on metacestodes, drug that specifically binds to helix-loop-helix region disrupting the TFEB-DNA interaction, highlighting TFEB as a druggable target for autophagy, a promising strategy for anti-cestodal therapy.

BPA-22

Identification and functional characterization of SQSTM1/p62 and its importance in the autophagy process in *Echinococcus granulosus*

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Echinococcus granulosus is the causative agent of human cystic echinococcosis, a zoonotic infection endemic in many areas throughout the world. Once an individual is infected, this cestode forms metacestodes, which grow in host organs, thus, causing the disease. Identification of new drug targets is urgently required given the toxicity and poor efficacy of available drugs. The protein SQSTM1/p62 plays an important role in selective autophagy in different cellular systems, under stress situations as drug exposure, hypoxia and starvation. In this work we identified, re-named, and deposited in GenBank a putative orthologous gene of *sqtsm*1/*p*62 in *E. granulosus* (ID2837631), based on BLAST searches against the parasite genome (E-value cutoff 1^{e-25}), the occurrence of conserved structural domains, and the transcriptional induction and *in situ* immunodetection under conditions of autophagy activation. The full-length open reading frame of Eg-p62 predicts a protein with 35% identity to the human ortholog (AAH01874 and Q13501), with a conserved domain structure containing the domains PB1 (homodimerization site with characteristic charged residues), ZZ (conserved amino-acids involved in autophagy regulation), IDR (binding sites for Raptor, LC3 and KEAP1) and UBA with ubiquitinated protein binding sites, allowing self-degradation and proteolysis of other ubiquitin-tagged proteins. By *in toto* immune-localization assays and using autophagy-inducing-drugs such as rapamycin and hydroxychloroquine, we observed huge spherical aggregates (0.5-3 µm) around the nucleus in metacestodes and protoscoleces, and a positive signal in calcareous corpuscles and protonephridia. In addition, by qPCR analysis, we found that these drugs induced a two-threefold increase in Eg-*sqstm*1/*p*62 mRNA levels compared to untreated parasites. Here, we discuss the effects of Eg-p62 on the proteostatic status and aggrephagy in cestodes.