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Introduction of tryptophan residues towards the cytoplasmic end of the *Trepanosoma brucei* Aquaporin

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A frican Trepanosoma brucei cause sleeping sickness in humans, a disease that is typically fatal without chemotherapy. Unfortunately, drug resistance is common and our understanding of the underlying mechanisms remains incomplete. In Trypanosoma, three aquaporins genes, AQP1-3, have been identified. Recent studies have shown that loss of AQP2, a channel with an unusual selectivity filter, is specifically responsible for MPXR, leading to the hypothesis that some of the clinical trypanocides, specifically pentamidine and the melaminophenyl arsenicals enter through these aquaporins. In T. brucei, the TbAQP2 protein was found to be a highly efficient transporter for pentamidine and melarsoprol and introduction of the corresponding gene into Leishmania mexicana made these parasites more than 1000-fold more sensitive to melarsoprol, and 40-fold more sensitive to pentamidine. Therefore, an understanding of the mechanisms of AQP2-mediated drug uptake in African trypanosomes will facilitate the advancement of diagnostic tools and perhaps at the same time the improvement of enhanced treatments. We report here the construction of several genetic mutations (single amino acid substitutions) in AQP2 to investigate their effects on the ability of the gene for drug sensitivity and drug transport. As part of this strategy, leucine residues were replaced by tryptophan in three suggested sites in the Tb AQP2 gene. The results of introducing tryptophan residues in L84 and L118 in the TbAQP2 showed some loss of pentamidine susceptibility compared to the wild-type cells, whereas L218 showed equal sensitivity to pentamidine compared to the wild-type cells.

Keywords: African trypanosomiasis, drug resistance, Leishmania spp, Trepanosoma brucei

Biography

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