Abstract

Copper serves as a cofactor for many important enzymes due to its redox properties. However, the presence of free copper ions in the cell can lead to undesired effects such as protein aggregation and loss of iron-sulfur clusters, ultimately resulting in cell death. Therefore, the intracellular concentration of copper in parasitic organisms is strictly controlled. Copper metabolism in parasitic organisms is not well understood, hence this work focuses on *Trypanosoma brucei*, the causative agent of sleeping sickness and the disease in cattle called nagana. The aim of this thesis was to investigate how copper is transported in the cell and to test its toxicity in *T. brucei*. Understanding copper transport in the cell could lead to the development of drugs disrupting copper homeostasis and exploit of its toxic properties.

In this diploma thesis, the function of the P1B-type ATPase of *T. brucei* in copper transport was described based on functional complementation. Successfully, the expression of the P1B-type ATPase was reduced using RNA interference in *T. brucei*. The decreased expression of this transporter led to increased sensitivity to copper, indicating its role in copper detoxification. Furthermore, we demonstrated the higher resistance to copper and its increased requirement in the metabolism of the insect form of *T. brucei* compared to the bloodstream form using inductively coupled plasma mass spectrometry and quantification of copper toxicity. The expression of *T. brucei* P1B-type ATPase was also monitored at increased and decreased copper concentrations using mass spectrometry.