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Isolated bc₁ Complex as a Screening System for Potential Anti-Malaria Drugs

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Malaria is responsible for 1–2 million deaths per year. Therefore, the development of new and inexpensive antimalaria drugs is required. The mitochondrial bc1 complex in protozoa was identified as a suitable drug target for malaria antibiotics. The mechanism is based on a stronger inhibition of the bc_1 complex in plasmodia than in mammalian bc_1 complex. Aim of this study was to set up a model system for the screening of compounds with possible anti-malaria activity. Due to the sequence homology of the bc_1 complex in plasmodia and Saccharomyces cerevisiae, its bc1 complex can be used as a model. Therefore, the membranebound bc1 complex was isolated via a detergent-based solubilization and chromatographic purification from bovine heart mitochondria and from yeast mitochondria as models for mammals and plasmodia, respectively. The measurement of the quinol : cytochrome c oxidoreductase activity in both complexes gave turnover numbers of about 200 s^{-1} indicating a functional enzyme preparation. Titration of the enzymatic activity with stigmatellin revealed an IC₅₀ of 2.15 \pm 0.28 nM for bovine and 1.80 \pm 0.19 nM for the yeast bc_1 complex indicating the nonselective toxicity of this compound. However, if the only available anti-malaria drug for this target atovaquone was used, an IC₅₀ of $12.4 \pm 1.08 \ \mu M$ for bovine and 4.52 ± 0.35 μM for yeast bc₁ complex was obtained. In contrast to stigmatellin, the drug atovaquone inhibits the yeast complex three times more than the mammalian bc_1 complex. These basic biochemical data indicate that the model consisting of isolated bovine and yeast bc_1 complex is suitable for the identification of new anti-malaria drugs.