Abstract

Introduction: Despite efforts to control malaria, around 10% of the world population is at risk of acquiring this disease. Plasmodium falciparum accounts for the majority of severe cases and deaths. Malaria control programs have failed due to the therapeutic failure of first-line antimalarials and to parasite resistance. Thus, new and better therapeutic alternatives are required. Proteomic analysis allows determination of protein expression levels under drug pressure, leading to the identification of new therapeutic drug targets and their mechanisms of action. Objective: The aim of this study was to analyze qualitatively the expression of P. falciparum trophozoite proteins (strain ITG2), after exposure to antimalarial drugs, through a proteomic approach. Materials and methods: In vitro cultured synchronized parasites were treated with quinine, mefloquine and the natural antiplasmodial diosgenone. Protein extracts were prepared and analyzed by two-dimensional electrophoresis. The differentially expressed proteins were selected and identified by MALDI-TOF mass spectrometry. Results: The following proteins were identified among those differentially expressed in the parasite in the presence of the drugs tested: enolase (PF10_0155), calcium-binding protein (PF11_0098), chaperonin (PFL0740c), the host cell invasion protein (PF10_0268) and proteins related to redox processes (MAL8P1.17). These findings are consistent with results of previous studies where the parasite was submitted to pressure with other antimalarial drugs. Conclusion: The observed changes in the P. falciparum trophozoite protein profile induced by antimalarial drugs involved proteins mainly related to the general stress response.

Keywords

Plasmodium falciparum, proteome, quinine, mefloquine.