PA-004 EFFECT OF ARTESUNATE MONOTHERAPY ON *PLASMODIUM FALCIPARUM* IN VIVO GENOMIC EXPRESSION

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Background Artemisinin-based combination therapies (ACTs) are the main treatment for malaria in endemic countries. *Plasmodium falciparum* resistance to artemisinins is described as

delayed parasite clearance, which is associated with mutations on the parasite K13 propeller gene. Both the mechanisms of action and mechanisms of resistance to artemisinins are poorly understood. Transcriptomic studies can help in improving our understanding of these processes. Here we explore *P. falciparum in vivo* RNA expression profile after a curative dose of artesunate monotherapy.

Methods During a prospective study of the efficacy of artesunate in monotherapy in children aged 1–10 years and presenting uncomplicated *P. falciparum* malaria in Bougoula-Hameau, Mali, venous blood was collected on PAXgen blood RNA tubes before treatment (H0) and one (H1), two (H2) and three hours (H3) after treatment. RNA was extracted from these respective blood samples and used for microarray experiments with *Plasmodium*/*Anopheles* GeneChips and the Affymetrix® platform.

Results A total of 23 samples from 6 patients were included in the final analysis after quality control using Affimetrix® and Qlucore® softwares. With a 2-groups comparison of H0/H after treatment, 236 genes were identified as differentially expressed. Overall 42 genes were up-regulated including a knob-associated histidine-rich protein, rifins (pf.12.409.0, pf.13_399.0), stevors (pf.3.184.0), RESA-like proteins with DNAJ domain and thioredoxins. Heat shock protein (Pf.5.258.0), a number of AP2 domain-containing genes (Pf.6.27.0, Pf.11.99.0), an ABC transporter (Pf.12.250.0), genes involved in cell cycle regulation and many exported protein genes with unknown function and membrane proteins genes were among the 194 down-regulated genes.

Conclusions Our data support a role for these genes in the *in vivo* response of *P. falciparum* to artesunate administration.