Background. WHO recommended seasonal malaria chemoprevention (SMC) in 2012 for Sahel countries in Africa with the aim to reduce malaria among children less than 5 years of age by using sulphadoxine-pyrimethamine and amodiaquine (SP+AQ). This strategy was scaled up in Mali from 2012. The use of millions of doses of SP+AQ could generate potential Plasmodium falciparum resistance mutant parasites. The aim of this study was to monitor the prevalence of Pf\textit{dhfr}+Pf\textit{dhps}+Pf\textit{crt}+Pf\textit{mdr1} mutations in parasites infecting the target population.

Methods. Two cross-sectional surveys were conducted before (August 2012, n=662) and after (June 2014, n=670) a pilot implementation of SMC in the health district of Koutiala. Children aged 3–59 months received 3 and 4 rounds of curative doses of SP+AQ over two malaria seasons in 2012 and 2013, respectively. Genotypes of \textit{P. falciparum} Pf\textit{dhfr} codons 51, 59, 108 and 164; Pf\textit{dhps} codons 437 and 540, Pf\textit{crt} codon 76 and Pf\textit{mdr1} codon 86 were analysed by PCR on DNA of parasites from SMC population blood samples (after and before) and non-SMC patients aged 7 years or above (November 2014, n=500).

Results. In the SMC population 191 and 85 children before and after SMC implementation respectively were included in the molecular analysis. In the non-SMC patients 220 were successfully PCR analysed. In the SMC population, the prevalence of the six-mutation Pf\textit{crt} [Pf\textit{dhfr}-\textit{dhps} quintuple+Pf\textit{crt}-76T] genotype increased significantly after SMC implementation, from 0.0% to 7.1% ($p=0.0008$). The post-intervention prevalence of the six-mutation Pf\textit{mdr1} [Pf\textit{dhfr}-\textit{dhps} quintuple+Pf\textit{mdr1}-86Y] and the seven-mutation Pf\textit{crt}+Pf\textit{mdr1} [Pf\textit{dhfr}-\textit{dhps} quintuple+Pf\textit{mdr1}-86Y+Pf\textit{crt}-76T] genotypes were both 1.2% among the SMC population. No six-mutation and seven-mutation genotypes were observed neither among SMC population at baseline nor in the non-SMC patient population ($p=0.30$).

Conclusion. SMC increased the prevalence of the six-mutation Pf\textit{crt} genotype of \textit{P. falciparum} that can lead to resistance in a population exposed to SMC with SP+AQ.