

Table for summary of the landscape of drug-resistant malaria in the DRC as of July 2023

Antimalarial drug	Malaria drug-resistance in the DRC as of June 2023
Quinine (QN)	<ul style="list-style-type: none"> QN-resistant malaria was not confirmed since there is still no validated molecular marker; but it was only suspected given several isolates carrying <i>Pf</i>CRT K76T and <i>Pf</i>MDR-1 D1246Y mutations.
Lumefantrine (L)	<ul style="list-style-type: none"> LU-resistant malaria was suspected given isolates potentially carrying <i>Pf</i>MDR1 the NFD haplotype which consists of N86, Y184F, and D1246 (but there is still no know validated marker for this resistance).
Mefloquine (MQ)	<ul style="list-style-type: none"> MQ-resistant malaria was not detected as no isolate was detected with amplified copy numbers of <i>pfmdr1</i> and <i>pfmdr2</i> genes.
Chloroquine (CQ)	<ul style="list-style-type: none"> Median 32.4% [IQR: 45.6] of isolates were CQ-resistant as they carried a <i>Pf</i>CRT K76T mutation predominately onto a background with CVIET haplotypes. <i>Pf</i>CRT K76T carriage by parasites substantially decreased from 2000 to 2020. Wide geographic variations in the prevalence of <i>Pf</i>CRT K76T parasites, however, was persisting in 2020 (1.8 to 89.5%) with increased risks of rebound due to the massive reintroduction and misuse of CQ for putative treatment or prevention of COVID-19.
Amodiaquine (AQ)	<ul style="list-style-type: none"> AQ-resistant malaria was not confirmed as no parasite isolate carried a <i>Pf</i>CRT SVMNT haplotype, but it was suspected since up several isolates carried <i>Pf</i>CRT N86Y and D1246Y mutations (and therefore possibly encoded the <u>YYY</u> haplotype consisting of N86Y, Y184 and D1246Y).
Piperaquine (PIP)	<ul style="list-style-type: none"> PIP-resistant malaria was not explored (i.e., corresponding <i>Pf</i>CRT mutations and gene amplification for <i>Pf</i>PM2 and <i>Pf</i>PM3 were not analyzed).
Artemisinin (ART) & derivatives	<ul style="list-style-type: none"> ART-resistant malaria was not established as only a single isolate (sampled in 2014) was detected with a R561H mutation that mediates for resistance. However, there is significant risk of local emergence or regional expansion of ART-resistant parasites from neighboring countries with reported emerging resistance (e.g., Uganda, Rwanda, and Tanzania) or from sites found with reduced levels of drug efficacy with ACTs. Isolates harboring mutations that structurally mimic known molecular markers of ART resistance need to be monitored and investigated.
Pyronaridine (PYR)	<ul style="list-style-type: none"> PYR-resistant malaria was not explored since corresponding mutations of the <i>Pf</i>MRP1 were not analyzed.
Proguanil (PRO)	<ul style="list-style-type: none"> The genetic background of the parasites suggests that PRO-resistant malaria is very common (e.g., >70% of parasites carry <i>Pf</i>DHFR S108N, N51I, and C59R), suggesting caution in the use of a chemoprophylaxis including PRO (e.g., PRO-AV combination) when traveling to the DRC.
Sulfadoxine-Pyriméthamine (S-P)	<ul style="list-style-type: none"> S-P resistant malaria was widespread at high frequencies but with a moderate molecular profile (<i>Pf</i>DHPS A437G: 88.0% [IQR: 33.6]; <i>Pf</i>DHPS K540E: 38.9% [IQR: 47.7]). Quintuple mutants (i.e., <u>IRN-GE</u>) were identified in 13.1% of parasites with highest prevalence in areas located in East parts of the country.