Various pfcr and pfmdr1 genotypes of *Plasmodium falciparum* co-circulate with *P. malariae*, *P. ovale* sp and *P. vivax* in northern Angola

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**Background:** *Plasmodium falciparum* parasites have the ability of developing mechanisms to resist antimalarial drugs by suffering mutations in specific genes. Populations of *P. falciparum* that were previously dominated by chloroquine-resistant genotypes are now under the artemisinin-based combination drug pressure. *P. malariae*, *P. ovale curtisi* and *P. ovale wallikeri* are sympatric with *P. falciparum* and frequently presented as co-infections across the continent, but are often unreported.

**Material and methods:** The prevalence of human *Plasmodium* species was determined by nested PCR using DNA from blood spots collected during a cross sectional survey conducted within CISA (Health Research Center in Angola, translated) project’s Demographic Surveillance System (DSS) in northern Angola. *P. falciparum* was genotyped at resistance-associated loci in *pfcr* and *pfmdr1* by real-time PCR, or by direct sequencing of amplicons.

**Results:** From the 3316 collected samples, 541 (16.31%) contained *Plasmodium* sp. infections; from which 477 (88.17%) were *P. falciparum* alone, 6.47% were *P. falciparum* and *P. malariae* together, 3.69% harboured *P. ovale curtisi* or *P. ovale wallikeri* alone or in combination with other species and 1.11% comprised *P. vivax* alone (see table 1). Of 430 *P. falciparum* isolates genotyped for *pfcr*, 61.63% carried the wild-type allele CVMNK at codons 72 – 76, either alone or in combination with the resistant allele CVIET. No other *pfcr* allele was found. Wild-type alleles also dominated at codons 86, 184, 1034, 1042 and 1246 of the *pfmdr1* locus among the sequenced isolates (see figure 1).

**Discussion/Conclusion:** The use of molecular methods for species discrimination has provided an estimate of the prevalence of the different *Plasmodium* sp. Although *P. falciparum* is the predominant species, *P. vivax, P. malariae* and both *P. ovale* types also exist, frequently in mixed infections. Contrasting to previous studies conducted in Angola, *P. falciparum* comprised an approximately equal mix of chloroquine-sensitive and chloroquine-resistant parasites, suggesting changes in the parasite population, possibly due to either lower drug pressure due to poor access to treatment in rural areas, or a rapid impact of the national drug policy change.

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