

Break the malaria transmission chain: Identification of the reservoir and treatment (IRT)



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Background

Malaria remains a public health problem. Several studies have shown a lower prevalence in endemic countries. The epidemiological studies are quite needed to develop new strategies for disease control and even its eradication.

Aim

The present study was conducted according to the IRT protocol (Detection and treatment of all *P. falciparum* infections, use of vector control means and surveillance of the emergence of antimalarial drug-resistance) in a rural setting of southeastern Gabon named Dienga.

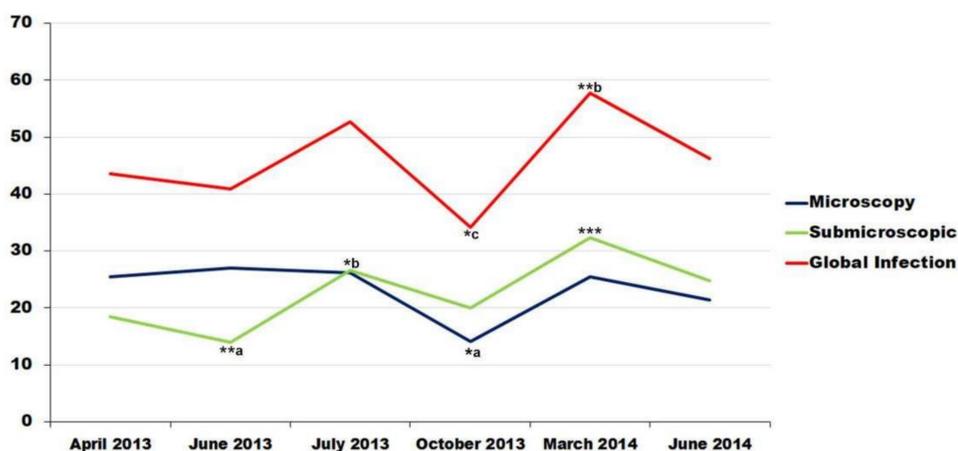
Methods

From March to May, *P. falciparum* infection was sought by microscope (ME) and PCR STEVOR gen, in 375 subjects (≥ 3 years old) living in Dienga, during 6 passages (P1, P2, P3, P4, P5 and P6). Demographic data, along with behaviors and attitudes towards malaria, blood samples were collected in Dienga. The laboratory analyzes were carried out at the CIRMF in Franceville, the town located at 200 km from DIENGA. Any cases detected were treated (curative and adjunctive therapies).

Results

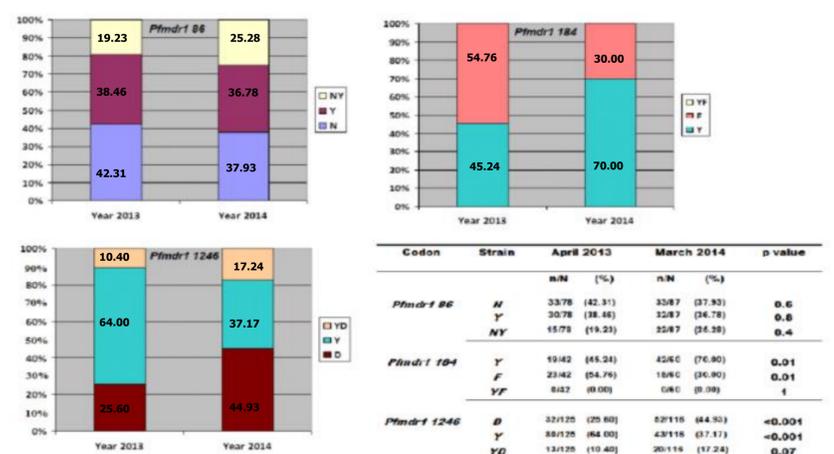
The prevalence of *P. falciparum* infection in P1 (April 2013), P2 (June 2013), P3 (July 2013), P4 (October 2013), P5 (March 2014) and P6 (June 2014) was respectively 43.5% (25.1% ME+, 18.4% PCR+); 40.9% (27.0% ME+, 13.9% PCR+), 52.7% (26.1% ME+, 26.6% PCR+); 34.1% (14.1% ME+, 20% PCR+), 57.7% (25.4% ME+, 32.3% PCR+); and 46.2% (21.4% ME+, 24.8% PCR+). P4 and P5 prevalences were statically different throughout all passages (Figure 1).

Figure 1. Global prevalence of malaria infection in Dienga



Asymptomatic infections were the most frequent (96%). Gametocytes were detected in levels ranging from 5.9% to 13.9%. Insecticide-treated nets, indoor residual insecticides, and self-medication were used by respectively 33.2%, 17.7% and 12.1% of the study population. The average age was 40.33 years old, a sex ratio of 0.99 with 93 years old the largest age. The polymorphism of *P. falciparum* multidrug resistance -1 gene (*Pfmdr1*) was investigated. Among the three codons 86, 184 and 1246 of *Pfmdr1*, the wild-type alleles were the most prevalent in 2014.

Figure 2. Distribution of *PfMDR1* polymorphism over the study period



Conclusion

These data show that the prevalence of *P. falciparum* malaria was not impacted by treatment due to the irregularity of research trips. The lack of funds was the major cause of the failure which was based on the scrupulous respect of its design. High rate of asymptomatic infections testifies the immensity of *P. falciparum* malaria reservoir in Dienga in this time. The fluctuations in the infection rates observed have been linked to the climate (depending of the rainy (P5) or dry season (P4)). Data from Dienga showed moderate variations in the distribution of *Pfmdr1* genotypes and a high haplotype diversity suggesting the low ACT drug pressure on parasites in this locality. The IRT remains a good example of malaria eradication, if we respect all its protocol.