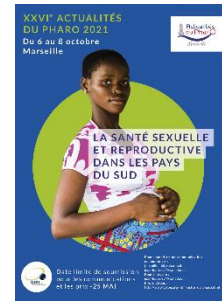


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Plasmodium ovale wallikeri and Plasmodium ovale curtisi: from the development of a differentiation method to the retrospective analysis of cases in the National Malaria Reference Centre, period 2013-2018

Keywords: paludisme, Plasmodium ovale wallikeri, Plasmodium ovale curtisi, qPCR-HRM, test de diagnostic rapide



Valentin JOSTE

valentin.joste@aphp.fr

Plasmodium ovale spp is one of five species of *Plasmodium* that can infect humans. One of its notable characteristics is its ability to cause relapses, which are defined as the reappearance of asexual forms of *Plasmodium ovale* spp in the peripheral blood after appropriate and well-monitored antimalarial treatment, without further contamination. Since 2010, this species has been separated into *Plasmodium ovale curtisi* and *Plasmodium ovale wallikeri* on the basis of distinct genetic sequences.

We have developed a qPCR-HRM method to distinguish them. Using this method, we identified 368 isolates of *Plasmodium ovale wallikeri* and 309 isolates of *Plasmodium ovale curtisi* received at the CNR du Paludisme between January 2013 and December 2018.

Epidemiological, clinical and biological data collected revealed more severe thrombocytopenia (94 G/L [70-130] vs 111 G/L [84-145], $p < 0.001$) and a shorter latency period (34 days [10-95] vs 72 days [18-208], $p < 0.001$) in *Plasmodium ovale wallikeri* infections. In addition, patients infected with *Plasmodium ovale wallikeri* were more often treated with artemisinin-based combination therapy (29.2% vs 17.1%, $p < 0.001$). Although not statistically significant, patients infected with *Plasmodium ovale wallikeri* tended to be hospitalised more frequently in intensive care units/continuing care units ($p = 0.134$) and to have severe thrombocytopenia ($p = 0.123$) than patients infected with *Plasmodium ovale curtisi*.

Regarding diagnostic methods, immunochromatographic techniques detecting aldolase were more sensitive than those detecting pLDH (47.8% vs 10.6%, $p < 0.001$).

Finally, we analysed the sequences of the *potra* gene in 90 isolates of *Plasmodium ovale* spp and found that this gene was not sufficiently polymorphic to be used for the genetic typing of revivals that are clinically and epidemiologically defined.