

Evaluation of new multiplex PCR primers for the identification of Plasmodium species found in Sabah, Malaysia

Abstract

Background/aim: Malaria is a major public health problem, especially in the Southeast Asia region, caused by 5 species of Plasmodium (*P. falciparum*, *P. vivax*, *P. malariae*, *P. ovale*, and *P. knowlesi*). The aim of this study was to compare parasite species identification methods using the new multiplex polymerase chain reaction (PCR) against nested PCR and microscopy.

Materials and methods: Blood samples on filter papers were subject to conventional PCR methods using primers designed by us in multiplex PCR and previously designed primers of nested PCR. Both sets of results were compared with microscopic identification.

Results: Of the 129 samples identified as malaria-positive by microscopy, 15 samples were positive for *P. falciparum*, 14 for *P. vivax*, 6 for *P. knowlesi*, 72 for *P. malariae*, and 2 for mixed infection of *P. falciparum*/*P. malariae*. Both multiplex and nested PCR identified 12 *P. falciparum* single infections. For *P. vivax*, 9 were identified by multiplex and 12 by nested PCR. For 72 *P. malariae* cases, multiplex PCR identified 58 as *P. knowlesi* and 10 as *P. malariae* compared to nested PCR, which identified 59 as *P. knowlesi* and 7 as *P. malariae*.

Conclusion: Multiplex PCR could be used as alternative molecular diagnosis for the identification of all Plasmodium species as it requires a shorter time to screen a large number of samples.