

Wide distribution of *Plasmodium ovale* in Myanmar

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Summary

The presence of *Plasmodium ovale* has never been previously reported in Myanmar. Using blood samples obtained in many villages across the country between 1996 and 2000, molecular diagnosis of *Plasmodium* species was made with semi- or full-nested polymerase chain reaction (PCR) with species-specific primers, followed by agarose gel electrophoresis to detect amplification products. The presence of *P. ovale* was also confirmed with the another PCR-based diagnosis, the microtiterplate hybridization (MPH) method using species-specific probes. Both methods target the A type of the small subunit ribosomal RNA gene of the four human malaria parasites. *Plasmodium ovale* DNA was amplified in samples from 65 (4.9%) of 1323 PCR-positive patients, with perfect agreement between results obtained by nested PCR and MPH. Only four *P. ovale*-infected patients had single-species infection; all others were coinfecting with *P. falciparum*, *P. vivax* and/or *P. malariae*. Quadruple infections were observed in six subjects. Parasites with typical *P. ovale* morphology were found in only 19 patients by conventional microscopy of Giemsa-stained thin smears or fluorescence microscopy of acridine orange-stained thin smears. *Plasmodium ovale* infections were found in villages situated in the southern, central and western regions of Myanmar, suggesting that *P. ovale* may be widely distributed in this country.