Molecular diagnosis of Plasmodium

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Historically, the detection and identification of malaria parasites in the blood of the mammalian host, and indeed, in mosquitoes, was carried out based on parasite morphology as examined by light microscopy. Although the detection of parasites by thick blood smear microscopy can be highly sensitive when carried out by experienced microscopists, identification of parasite *species*, especially at low parasite densities, is notoriously difficult. Since the beginning of the 1990s, molecular biological detection and identification techniques, most notably based on polymerase chain reaction (PCR) amplification of parasite DNA has revolutionised the identification of malaria parasites, and vastly increased our understanding of the prevalence and distribution of the various species infectious to man. Very recently, within the last few years, however, the established PCR detection and identification techniques have encountered a hitherto unexpected phenomenon; the zoonotic infection of humans by parasites previously thought to infect only non-human primates. This phenomenon, combined with the need to survey sylvatic host-parasite systems in order to pre-empt the next potential zoonotic jump have required a reappraisal of the current PCR detection and species identification assays. Here we will consider the limitations of the current methodology, and suggest some alternatives, using as an example, a recent case of a cryptic parasitism of captive monkeys in Vietnam.