Indigenous Plasmodium ovale Malaria in Bangladesh

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Abstract. In spite of the high prevalence of malaria in Southeastern Bangladesh, there remains a significant shortage of information regarding the presence of five human malaria parasites: Plasmodium ovale, P. malariae, and P. knowlesi. The presence of P. ovale and P. knowlesi has previously never been reported from Bangladesh. We used a genus- and species-specific nested polymerase chain reaction, targeting highly conserved regions of the small subunit ribosomal RNA (SSU rRNA) gene, to investigate the presence of malaria parasites in a total number of 379 patient samples in a survey of patients with febrile illnesses in the Chittagong Hill Tracts in Southeastern Bangladesh. We identified the first cases of P. ovale in Bangladesh. They were confirmed by sequence analysis; 189 of 379 samples (49.9%; 95% confidence interval = 44.9–54.9%) were positive for Plasmodium sp. by PCR. P. falciparum monoinfections accounted for 68.3% (61.3–74.5%), followed by P. vivax (15.3%; 10.9–21.2%), P. malariae (1.6%; 0.5–4.6%), P. ovale (1.6%; 0.5–4.6%), and mixed infections (13.2%; 9.1–18.8%). We found no evidence of P. knowlesi in this region.

INTRODUCTION

Almost 1 million people die of malaria every year, and recent reports of emerging artemisinin resistance in Southeast Asia will add another challenge to malaria control efforts.1–3 High standards in the diagnosis of the malaria-causing Plasmodium species are essential to control and adequately treat malaria. Despite its known limitations, microscopy remains the gold standard in the diagnosis of the malaria-causing parasite. This may lead to a significant underestimation of the availability of polymerase chain reaction (PCR)-based techniques for the diagnosis of malaria, this parasite has recently been documented in Malaysia, Thailand, Myanmar, Singapore, and the Philippines.18–24 P. knowlesi has a daily (quotidian) asexual cycle, potentially resulting in life-threatening hyperparasitemia and hepatorenal dysfunction. A number of fatal cases have been reported from Malaysia.19 Identification of P. knowlesi solely based on microscopy remains difficult.18,25 Several Macaque species, including the traditional hosts of P. knowlesi, have their habitats in Bangladesh, and populations of critically endangered Macaca fascicularis are known to be endemic in the very southeastern parts of the country.26 The limited distribution of mosquitoes of the Anopheles leucophyrus group, the only known vector of P. knowlesi, restricts the current distribution of P. knowlesi to a limited area in Southeast and parts of South Asia, including the Chittagong Hill Tracts in Bangladesh.27,28

The primary aim of this study was to establish the prevalence of all five malaria species among febrile patients in the Chittagong Hill Tracts in Bangladesh with special emphasis on the three rare malaria species.

MATERIALS AND METHODS

Study population. Diagnostic samples were collected from febrile patients in the course of field surveys in Bandarban District in the Chittagong Hill Tracts in 2007/2008 and a hospital-based survey at the Malaria Research Initiative Bandarban (MARIB) field site in 2008/2009. Male and female volunteers of any age with acute fever or a history of fever within the past 72 hours were included in this study. Venous blood was only drawn from patients 8 years or older. Written informed consent was obtained from all study participants or their legal representatives before blood samples were collected. The study protocol was reviewed and approved by the Ethical Review Committee of the International Center for Diarrhoeal Disease Research, Bangladesh.

Malaria diagnosis. Thick and thin blood smears were prepared and examined in duplicate by two expert microscopists blinded to each other’s results after staining with Giemsa (Merck KGaA, Darmstadt, Germany). In thick films,
RESULTS

A total number of 189 of 379 [49.9%; 95% confidence interval (CI) = 44.9–54.9%] filter papers from patients with febrile illnesses gave positive results for *Plasmodium* spp. with genus-specific primers by nested PCR. All 159 samples classified as positive by microscopic examination were confirmed as being positive. In addition, 30 samples that were diagnosed as negative by microscopy were positive in the genus-specific nested PCR. Species-specific PCR showed that of 189 *Plasmodium* spp. positive samples, 154 (81.5%; 95% CI = 75.3–86.4%) were positive for *P. falciparum*, 50 (26.5%; 95% CI = 20.7–33.2%) were positive for *P. vivax*, 7 (3.7%; 95% CI = 1.8–7.4%) were positive for *P. malariae*, and 3 (1.6%; 95% CI = 0.5–4.6%) were positive for *P. ovale*. All samples tested negative for *P. knowlesi*.

We found 164 (86.8%; 95% CI = 81.2–91.1%) mono-infections and 25 (13.2%; 95% CI = 9.1–18.8%) mixed infections; 129 (68.3%; 95% CI = 61.3–74.5%) patients presented with *P. falciparum*, 29 (15.3%; 95% CI = 10.9–21.2%) with *P. vivax*, 3 (1.6%; 95% CI = 0.5–4.6%) with *P. malariae*, and 3 (1.6%; 95% CI = 0.5–4.6%) with *P. ovale* mono-infections. In addition, 21 (11.1%; 95% CI = 7.4–16.4%) patient samples contained DNA of both *P. falciparum* and *P. vivax*, 2 (1.1%; 95% CI = 0.3–3.8%) of *P. falciparum* and *P. malariae*, and 2 (1.1%; 95% CI = 0.3–3.8%) triple infections with *P. falciparum*, *P. vivax*, and *P. malariae* (Table 1). One patient presented with *P. ovale* two times in the course of this study. Based on the PCR results, 30 (7.9%; 95% CI = 5.5–10.8%) microscopy slides were classified as false negative, and none were false positive. Compared with the 25 PCR-confirmed samples with mixed malaria infections, only 9 (36%) were read as positive for mixed infections in microscopy, and only 6 (24%) were diagnosed as mixed infections by RDT.

All three samples positive for *P. ovale* in PCR were proven by DNA sequencing (GenBank Accession numbers: HM196277, HM196278) and after unblinding, were also found positive for *P. ovale* on microscopic reexamination.

DISCUSSION

For 2006, the World Health Organization estimated almost 3 million malaria cases and 15,000 deaths in Bangladesh in mostly unconfirmed cases. Among microscopy-confirmed malaria infections, *P. falciparum* was the dominant species, causing more than 70% of all malaria cases. A recent report based on microscopic diagnosis indicated that 70.3% of all malaria cases in the Chittagong Hill Tracts were caused by *P. falciparum*, 29.6% were caused by *P. vivax*, and only 0.01% were read as mixed infections. A study using microscopic and molecular methods for diagnosis conducted between 2000 and 2002 revealed that of those slides considered positive for *Plasmodium* spp., 84% were *P. falciparum* monoinfections or mixed infections, 15% were *P. vivax*, and 1% were *P. malariae*. Our study shows comparable results for *P. falciparum* monoinfections.

### Table 1

Comparison of malaria diagnosis by nested PCR, microscopy, and FalciVax-RDT

<table>
<thead>
<tr>
<th></th>
<th>Neg</th>
<th>Pf</th>
<th>Pr</th>
<th>Pm</th>
<th>Po</th>
<th>Pk</th>
<th>Pf + Pr</th>
<th>Pk + Pm</th>
<th>Pf + Pr + Pm</th>
</tr>
</thead>
<tbody>
<tr>
<td>PCR†</td>
<td>190</td>
<td>129</td>
<td>29</td>
<td>3</td>
<td>3</td>
<td>0</td>
<td>21</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>Microscopy*</td>
<td>220</td>
<td>122</td>
<td>29</td>
<td>3</td>
<td>3</td>
<td>0</td>
<td>6</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>RDT‡</td>
<td>228</td>
<td>108</td>
<td>15</td>
<td>15</td>
<td>0</td>
<td>0</td>
<td>6</td>
<td>6</td>
<td>6</td>
</tr>
</tbody>
</table>

* Neg = negative; Pr = *P. falciparum*, Pf = *P. vivax*, Pm = *P. malariae*, Po = *P. ovale*, Pk = *P. knowlesi*; Pr + Pf = *P. falciparum*, Pr + Pm = *P. falciparum* + *P. malariae*, Pr + Po = *P. falciparum* + *P. ovale*, Pr + Pr = *P. falciparum* + *P. vivax* + *P. malariae*.  
* n_{null} = 379; diagnosis of Pf, Pr, Po, Pk, Pm, and Pk + Pm is not possible with FalciVax-RDT.

† n = 379; diagnosis of Pf, Pr, Po, Pk, Pm, and Pk + Pm is not possible with FalciVax-RDT.
with 81.5% (of which 68.3% were monoinfections) and P. vivax with 26.5% (of which 15.3% were monoinfections). However, none of the earlier studies ever reported any cases of P. ovale.

We report the first three cases of P. ovale in Bangladesh. All of them were monoinfections and originated from the Chittagong Hill Tracts. Two of the positive samples found in this survey were seen in the same patient who originally tested negative in the RDT but was diagnosed with P. malariae based on microscopy (assuming that P. ovale was not an option, because it had never been seen in Bangladesh before). Two months after being treated for his suspected P. malariae infection, the patient returned with signs and symptoms consistent with malaria. This sample was confirmed to be P. ovale by molecular techniques, suggesting a relapse with P. ovale.

The nested PCR assay used in this study is highly sensitive with a documented limit of detection of 6 parasites/µL. P. ovale was found in 1.6% of the Plasmodium-positive samples. P. ovale had previously been reported from nearby Rakhine State in Myanmar. It has also been reported from other parts of Myanmar and a surprisingly high prevalence of up to 6.1% in Taninthyari Division in 1996. In the same study, P. malariae was reported from 15.2% of all cases. Other PCR-based studies in Southeast Asia report up to 4% of P. ovale malaria in Northeastern Cambodia and 1.03% in Thailand.

The impact of newly emerging pathogens in public health is increasing. Although our data do not confirm the presence of P. knowlesi in Bangladesh, our knowledge of the reservoir, vectors, and ecology of this malaria parasite indicates that Southeastern Bangladesh may be a an environment in which P. knowlesi is likely to be found. Human infections are easily mistaken for P. falciparum infections when the parasites are in the stage of young trophozoites. In studies based on microscopic diagnosis, it may also easily be mistaken for the morphologically similar parasite P. malariae. This parasite should, therefore, always be considered whenever patients are from or report a travel history to remote areas of Southeast Asia and are diagnosed with P. malariae malaria based on microscopic examination.

Relative to molecular, molecular methods not only tend to improve the sensitivity and specificity of diagnostic studies, but they also result in higher estimates of malaria prevalence, particularly for the rare species P. malariae and P. ovale, and higher rates of mixed infections. Studies conducted in Lao People’s Democratic Republic (PDR) (23.1%) and Northwestern Thailand (23–24%) in which molecular techniques were all used suggested the presence of high numbers of mixed infections.

In our survey, we found 25 cases (13.2% of all positive samples) of mixed infections, of which the combination of P. falciparum and P. vivax was most frequently seen. Triple infections with P. falciparum, P. vivax, and P. malariae are rare and were found in only two patients coming from the same small village (Nathogri, Rowanchari Subdistrict).

Accurate diagnosis of Plasmodium spp. is essential for optimizing malaria-treatment guidelines. Further studies assessing the prevalence of the rare species P. ovale, P. malariae, and P. knowlesi in South Asia are, therefore, urgently needed to better understand the species distribution and to allow for adapting treatment strategies.

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