

Our findings add to the diversity of *Entamoeba* species found in humans. The incidence and effect of infection in infants by the newly recognized species *E. bangladeshi* await future epidemiologic studies.

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References

1. Mondal D, Haque R, Sack RB, Kirkpatrick BD, Petri WA Jr. Attribution of malnutrition to cause-specific diarrheal illness: evidence from a prospective study of preschool children in Mirpur, Dhaka, Bangladesh. *Am J Trop Med Hyg*. 2009;80:824–6.
2. Shimokawa C, Kabir M, Taniuchi M, Mondal M, Kobayashi S, Ali IK, et al. *Entamoeba moshkovskii* is associated with diarrhea in infants and causes diarrhea and colitis in mice. *J Infect Dis*. 2012 Jun 21; [Epub ahead of print]. <http://dx.doi.org/10.1093/infdis/jis414>
3. Haque R, Mondal D, Karim A, Molla IH, Rahim A, Faruque ASG, et al. Prospective case-control study of the association between common enteric protozoal parasites and diarrhea in Bangladesh. *Clin Infect Dis*. 2009;48:1191–7. <http://dx.doi.org/10.1086/597580>
4. Petri WA Jr, Haque R. *Entamoeba* species, including Amebiasis. In: Mandell GL, JE Bennett, R Dolin, eds. *Mandell, Douglas, and Bennett's principles and practice of infectious diseases*, 7th ed. Philadelphia: Churchill Livingstone; 2010. p. 3411–25.
5. Ali IKM, Zaki M, Clark CG. Use of PCR amplification of tRNA gene-linked short tandem repeats for genotyping *Entamoeba histolytica*. *J Clin Microbiol*. 2005;43:5842–7. <http://dx.doi.org/10.1128/JCM.43.12.5842-5847.2005>
6. Stensvold CR, Lebbad M, Victory EL, Verweij JJ, Tannich E, Alfellani M, et al. Increased sampling reveals novel lineages of *Entamoeba*: consequences of genetic diversity and host specificity for taxonomy and molecular detection. *Protist*. 2011;162:525–41. <http://dx.doi.org/10.1016/j.protis.2010.11.002>
7. Ali IKM, Hossain MB, Roy S, Ayeh-Kumi PF, Petri WA, Haque R, et al. *Entamoeba moshkovskii* infections in children, Bangladesh. *Emerg Infect Dis*. 2003;9:580–4. <http://dx.doi.org/10.3201/eid0905.020548>
8. Haque R, Kabir M, Noor Z, Rahman SMM, Mondal D, Alam F, et al. Diagnosis of amebic liver abscess and amebic colitis by detection of *Entamoeba histolytica* DNA in blood, urine, and saliva by a real-time PCR assay. *J Clin Microbiol*. 2010;48:2798–801. <http://dx.doi.org/10.1128/JCM.00152-10>
9. Haque R, Ali IK, Akther S, Petri WA Jr. Comparison of PCR, isoenzyme analysis, and antigen detection for diagnosis of *Entamoeba histolytica* infection. *J Clin Microbiol*. 1998;36:449–52.
10. Haque R, Faruque AS, Hahn P, Lyster DM, Petri WA. *Entamoeba histolytica* and *Entamoeba dispar* infection in children in Bangladesh. *J Infect Dis*. 1997;175:734–6. <http://dx.doi.org/10.1093/infdis/175.3.734>

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Autochthonous *Leishmania siamensis* in Horse, Florida, USA

To the Editor: *Leishmania siamensis*, a recently described species, was identified as the cause of autochthonous visceral leishmaniasis in 2 men in southern Thailand (1,2). Cutaneous leishmaniasis has been reported in horses in Europe and South America. Lesions in horses are solitary or multiple nodules that are often ulcerated and most commonly occur on the head, pinnae, legs, and neck. Other clinical signs are usually absent. In South America, biochemical characterization has identified *L. braziliensis* in horses (3). Leishmaniasis has been reported in horses in Puerto Rico (4), and equine leishmaniasis has been described, but no reports have been published, in the United States. *L. infantum* has been reported in equine cutaneous leishmaniasis in Europe (5). A report from central Europe recently identified an organism with 98% nucleotide identity over the ITS (internal transcribed spacer) 1 region to *L. siamensis* as the cause of cutaneous leishmaniasis in 4 horses (6). *L. siamensis* was also identified in a case of cutaneous bovine leishmaniasis in Switzerland (7).

In August 2011, a 10-year-old, 505-kg Morgan horse mare in Florida, USA, with no history of travel outside the eastern United States was evaluated at the University of Florida for an ulcerated mass in the left pinna. When, 6 months earlier, the owner had noticed the mass, it was ≈1 cm in diameter, firm, raised, and covered with hair. Three months later, the ear was unchanged, and the mare was successfully impregnated. Over the subsequent 2 months, the mass began to grow and ulcerate. At that time, veterinary consultation was obtained and a biopsy performed. Histologic

study showed that the dermis was hyperplastic and diffusely infiltrated with neutrophils, macrophages, and lymphocytes (online Technical Appendix Figure 1, wwwnc.cdc.gov/EID/article/18/9/12-0184-Techapp.pdf). Numerous intracytoplasmic protozoal organisms with a small nucleoid and smaller kinetoplast most consistent with *Leishmania* sp. were observed in macrophages. No treatment was pursued. After 45 days, the mare was seen at the University of Florida because of progression of the lesions. The mass on the internal aspect of the pinna was 6 cm × 3 cm and ulcerated, and 3 new firm 1 cm-diameter nodules were observed on the outer pinna of the same ear. Multiple soft, less-defined, 1 cm to 3 cm-diameter nodules were observed along both sides of the neck, shoulders, and withers. No other abnormalities were observed on physical examination or thoracic and abdominal ultrasound, and lymph nodes were not enlarged. Ultrasound confirmed a ≈90 day viable pregnancy. Complete blood count and plasma chemistry were within normal limits.

Tissue aspirates were taken of the multiple ear lesions and of the nodules along the neck and shoulder. From the ulcerated lesion, marked mixed, predominantly neutrophilic inflammation was seen, and rare neutrophils and macrophages contained intracellular protozoal organisms consistent with *Leishmania* sp. amastigotes (online Technical Appendix Figure 2). These organisms were 4–5 μm in diameter and round with pale basophilic cytoplasm. They had an eccentrically placed, basophilic, oval nucleus and a small, basophilic, rod-shaped kinetoplast oriented perpendicular to the long axis of the oval nucleus. No organisms were seen in any other aspirates.

Fresh tissue was submitted for PCR, which has been determined suitable for detecting Old World leishmaniasis in dogs (8). Results

were negative. Given the clear clinical, cytologic, and histologic evidence for cutaneous leishmaniasis, additional consensus PCR was performed as described (9), targeting the ITS1 region. Direct sequencing was performed by using the BigDye Terminator Kit (Applied Biosystems, Foster City, CA, USA) and analyzed on ABI 3130 automated DNA sequencers (Applied Biosystems) at the University of Florida Interdisciplinary Center for Biotechnology Research Sequencing Facilities (Gainesville, FL, USA). The resultant sequence was 310 bp after primers were edited out. Sequence alignment yielded a genotype with 99% identity to the first *L. siamensis* isolate (GenBank accession no. EF200012) and 100% identity to 2 more recently submitted sequences from human visceral leishmaniasis isolates from Thailand (GenBank accession nos. JQ001751 and JQ001752) (online Technical Appendix). The sequence was submitted to GenBank (accession no. JQ617283).

The mare delivered a stillborn foal at 350 days' gestation. Histopathology did not reveal any infectious organisms in the fetal tissues; however, the chorioallantois showed moderate villous atrophy, which was presumed to be the cause of fetal death. One month after foaling, the mare's cutaneous lesions were 90% resolved.

Because the mare in this report was born in the United States and had never left the country, this case appears to be autochthonous. Mode of transmission is unknown. Phlebotomine sand flies found in Florida include *Lutzomyia shannoni*, *Lu. cubensis*, *Lu. vexator*, and *Lu. cruciata*. *Lutzomyia* sp. are competent vectors of *Leishmania* spp. in other areas of the world. However, the vector for reported cases of *L. siamensis* in other regions has not been identified. Although leishmaniasis is infrequently diagnosed in any species in Florida, models have shown that with climate change, the range of sand flies and accompanying leishmaniasis

in North America is expected to expand substantially (10). This report raises many avenues for further investigation: the prevalence of leishmaniasis in horses in the United States, understanding of the life cycle and vectors, and the zoonotic potential of this *Leishmania* species.

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References

1. Sukmee T, Siripattanapipong S, Mungthin M, Worapong J, Rangsin R, Samung Y, et al. A suspected new species of *Leishmania*, the causative agent of visceral leishmaniasis in a Thai patient. *Int J Parasitol*. 2008;38:617–22. <http://dx.doi.org/10.1016/j.ijpara.2007.12.003>
2. Suankratay C, Suwanpimolkul G, Wilde H, Siriyasatien P. Autochthonous visceral leishmaniasis in a human immunodeficiency virus (HIV)-infected patient: the first in Thailand and review of the literature. *Am J Trop Med Hyg*. 2010;82:4–8. <http://dx.doi.org/10.4269/ajtmh.2010.09-0434>
3. Barbosa-Santos EGO, Marzochi MCA, Urtado W, Queirós F, Chicarino J, Pacheco RS. Leishmaniasis disseminated by *Leishmania braziliensis* in a mare (*Equus caballus*): immunotherapy and chemotherapy assays. *Mem Inst Oswaldo Cruz*. 1994;89:217–20. <http://dx.doi.org/10.1590/S0074-02761994000200018>
4. Ramos-Vara JA, Ortiz-Santiago B, Segalès J, Dunstan RW. Cutaneous leishmaniasis in two horses. *Vet Pathol*. 1996;33:731–4. <http://dx.doi.org/10.1177/030098589603300619>
5. Solano-Gallego L, Fernández-Bellón H, Serra R, Gállego M, Ramis A, Fondévila D, et al. Cutaneous leishmaniasis in three horses in Spain. *Equine Vet J*. 2003;35:320–3. <http://dx.doi.org/10.2746/042516403776148336>

6. Müller N, Welle M, Lobsiger L, Stoffel MH, Boghenbor KK, Hilbe M, et al. Occurrence of *Leishmania* sp. in cutaneous lesions of horses in Central Europe. *Vet Parasitol.* 2009;166:346–51. <http://dx.doi.org/10.1016/j.vetpar.2009.09.001>
7. Lobsiger L, Müller N, Schweizer T, Frey CF, Wiederkehr D, Zumkehr B, et al. An autochthonous case of cutaneous bovine leishmaniasis in Switzerland. *Vet Parasitol.* 2010;169:408–14. <http://dx.doi.org/10.1016/j.vetpar.2010.01.022>
8. Gaskin AA, Schantz P, Jackson J, Birkenheuer A, Tomlinson L, Gramiccia M, et al. Visceral leishmaniasis in a New York foxhound kennel. *J Vet Intern Med.* 2002;16:34–44. <http://dx.doi.org/10.1111/j.1939-1676.2002.tb01604.x>
9. el Tai NO, Osman OF, el Fari M, Presber W, Schönian G. Genetic heterogeneity of ribosomal internal transcribed spacer in clinical samples of *Leishmania donovani* spotted on filter paper as revealed by single-strand conformation polymorphisms and sequencing. *Trans R Soc Trop Med Hyg.* 2000;94:575–9. [http://dx.doi.org/10.1016/S0035-9203\(00\)90093-2](http://dx.doi.org/10.1016/S0035-9203(00)90093-2)
10. González C, Wang O, Strutz SE, Gonzalez-Salazar C, Sanchez-Cordero V, Sarkar S. Climate change and risk of leishmaniasis in North America: predictions from ecological niche models of vector and reservoir species. *PLoS Negl Trop Dis.* 2010;4:e585. <http://dx.doi.org/10.1371/journal.pntd.0000585>

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Novel Vectors of Malaria Parasites in the Western Highlands of Kenya

To the Editor: The primary malaria control techniques, indoor application of residual insecticides and insecticide-treated bed nets, are used on the basis of previously assumed key characteristics of behaviors of vectors of malaria parasites, i.e.,

resting and feeding indoors (1). Any deviation from the typical activities of a species related to exophagy (feeding outdoors) and exophily (living and resting indoors) (2) or to population replacement, followed by increased outdoor biting or resting (3), may undermine malaria control efforts. Identification of mosquitoes that transmit malaria parasites has, for the most part, relied on the use of outdated morphologic keys (4,5) and, more recently, species-diagnostic PCR (6). Cryptic species or subpopulations that exhibit divergent behaviors (7) may be responsible for maintaining malaria parasite transmission, and without adequate discriminatory techniques, these vectors may be misidentified and their key behavioral differences overlooked.

We evaluated indoor and outdoor trapping methods for anopheline mosquitoes in Bigege village, in Kisii Central District in the highlands of western Kenya, which are prone to periodic malaria epidemics. During May–August 2010, we captured 422 female *Anopheles* spp. mosquitoes, primarily from indoor and outdoor light traps. Of these, we identified 161 (38.2%) as species previously described as vectors in the area (*An. gambiae* sensu latu, *An. funestus* s.l., or *An. coustani* [8]) by using the standard morphologic key for sub-Saharan species (4). We identified another 52 (12.3%) as species not associated with malaria parasite transmission (1), but 209 (49.5%) could not be definitively identified. We extracted DNA from 418 mosquitoes and analyzed it for sibling species of the *An. gambiae* complex by using a diagnostic PCR (6). Of the 418 DNA samples tested, 80 (19.1%) were identified as *An. arabiensis*; 2 specimens were identified as *An. gambiae* s.s. (0.4%) but the remaining 336 (80.3%) could not be identified by PCR because no amplification product was observed.

To identify these specimens further, we performed molecular

characterization by sequencing the ribosomal second internal transcribed spacer (ITS2) and the mitochondrial CO1 loci. Of the 422 female *Anopheles* mosquito specimens, we sequenced DNA from 348, of which 74 (21.3%), 33 (9.5%), and 25 (7.2%) corresponded to GenBank sequences of *An. arabiensis*, *An. coustani*, and *An. funestus* mosquitoes, respectively. However, 216 (62.1%) could not be matched (<90% identity) to any of the 224 ITS2 or 164 CO1 published sequences of anopheline vectors or nonvectors. These 216 specimens could be grouped into several separate clades, distinct from known vectors in the area (Figure). Specimens were grouped by ITS2 sequence. These groups were ranked by abundance and arbitrarily named species A–J. Of the 348 sequenced DNA specimens, the most abundant group having identical but novel ITS2 and CO1 sequences (species A, n = 147, 42.2%) could not be matched definitively to a single species by using the morphologic key. The mosquitoes in this group were most frequently caught outdoors (132, 89.8%). For 64 of a total of 192 traps, collections were made every 2 hours between 6:30 PM and 6:30 AM for 64 nights. Of 30 specimens of species A from these collections, 22 (73.3%) were caught outdoors before 10:30 PM. Data we have collected on human sleeping patterns from this area suggest that a significant proportion of the population is still outdoors before 10:30 PM and therefore exposed to these vectors.

Five of 293 mosquitoes tested had ELISA results positive for *Plasmodium falciparum* sporozoites. All 5 had no previously published ITS2 or CO1 sequences, nor could they be identified by morphologic features. All were collected outdoors. Four of the 5 were in the sequence A group (online Technical Appendix, wwwnc.cdc.gov/EID/pdfs/12-0283-Techapp.pdf), and 1 belonged to species I (Figure). The sporozoite

Autochthonous *Leishmania siamensis* in Horse, Florida, USA

Technical Appendix

Multiple alignment with Fast Fourier Transform of *Leishmania siamensis* ITS1 sequences. Nucleotides with differences are shown in red.

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Horse FL      ATTACA-CCAAAAACATACAGG-TAGAGA-GTAGTAGAATACATCTACTCGGGGAGGCATGTTTTTCCG-ATATGCCTTTCCACATACACAAACACAGCAATATATATGT
Bovine|GQ281282 ATTACA-CCAAAAACATACAGGCTAGAGA-GTAGTAGAATACATCTACTCGGGGAGGCATGTTTTTCCG-ATATGCCTTTCCACATACACAAACACAGCAATATATATGT
Horse|GQ281281 ATTACA-CCAAAAACATACAGGCTAGAGA-GTAGTAGAATACATCTACTCGGGGAGGCATGTTTTTCCG-ATATGCCTTTCCACATACACAAACACAGCAATATATATGT
Human|JQ001751 ATTACA-CCAAAAACATACAGG-TAGAGA-GTAGTAGAATACATCTACTCGGGGAGGCATGTTTTTCCG-ATATGCCTTTCCACATACACAAACACAGCAATATATATGT
Human|JQ001752 ATTACA-CCAAAAACATACAGG-TAGAGA-GTAGTAGAATACATCTACTCGGGGAGGCATGTTTTTCCG-ATATGCCTTTCCACATACACAAACACAGCAATATATATGT
Human|GQ293226 ATTACA-CCAAAAACATACAGG-TAGAGA-GTAGTAGAATACATCTACTCGGGGAGGCATGTTTTTCCG-ATATGCCTTTCCACATACACAAACACAGCAATATATATGT
Human|GQ226034 ATTACA-CCAAAAACATACAGG-TAGAGA-GTAGTAGAATACATCTACTCGGGGAGGCATGTTTTTCCG-ATATGCCTTTCCACATACACAAACACAGCAATATATATGT
Human ref|EF200012 ATTACACCACAAAAACATACAGG-TAGAGAGGTAGTAGAATACATCTACTCGGGGAGGCATGTTTTTCCGTATATGCCTTTCCACATACACAAACACAGCAATATATATGT
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Horse FL      ATATATATACGTATATTGCTATACCCAAAAACCATACCGTAAAAAGCAAAAAGGCCGGTCGACGCCAAATGCCGCGCGTATACAGTGAAAAAGTCCGTTTCGTTACGGCTCTTT
Bovine|GQ281282 ATATATATACGTATATTGCTATACCCAAAAACCATACCGTAAAAAGCAAAAAGGCCGGTCGACGCCAAATGCCGCGCGTATACAGTGAAAAAGTCCGTTTCGTTACGGCTCTTT
Horse|GQ281281 ATATATATACGTATATTGCTATACCCAAAAACCATACCGTAAAAAGCAAAAAGGCCGGTCGACGCCAAATGCCGCGCGTATACAGTGAAAAAGTCCGTTTCGTTACGGCTCTTT
Human|JQ001751 ATATATATACGTATATTGCTATACCCAAAAACCATACCGTAAAAAGCAAAAAGGCCGGTCGACGCCAAATGCCGCGCGTATACAGTGAAAAAGTCCGTTTCGTTACGGCTCTTT
Human|JQ001752 ATATATATACGTATATTGCTATACCCAAAAACCATACCGTAAAAAGCAAAAAGGCCGGTCGACGCCAAATGCCGCGCGTATACAGTGAAAAAGTCCGTTTCGTTACGGCTCTTT
Human|GQ293226 ATATATATACGTATATTGCTATACCCAAAAACCATACCGTAAAAAGCAAAAAGGCCGGTCGACGCCAAATGCCGCGCGTATACAGTGAAAAAGTCCGTTTCGTTACGGCTCTTT
Human|GQ226034 ATATATATACGTATATTGCTATACCCAAAAACCATACCGTAAAAAGCAAAAAGGCCGGTCGACGCCAAATGCCGCGCGTATACAGTGAAAAAGTCCGTTTCGTTACGGCTCTTT
Human ref|EF200012 ATATATATACGTATATTGCTATACCCAAAAACCATACCGTAAAAAGCAAAAAGGCCGGTCGACGCCAAATGCCGCGCGTATACAGTGAAAAAGTCCGTTTCGTTACGGCTCTTT
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Horse FL      CTCTCTCGCGGGTGTGTGTGTGGATAACGGCTCACATAACGTGTGCGCATGGA-TGACTTGGCTTCCTATTTTCGTTGAAGAACGCAGTA
Bovine|GQ281282 CTCTCTCGCGGGTGTGTGTGTGTGGATAACGGCTCACATAACGTGTGCGCATGGA-TGACTTGGCTTCCTATTTTCGTTGAAGAACGCAGTA
Horse|GQ281281 CTCTCTCGCGGGTGTGTGTGTGTGGATAACGGCTCACATAACGTGTGCGCATGGA-TGACTTGGCTTCCTATTTTCGTTGAAGAACGCAGTA
Human|JQ001751 CTCTCTCGCGGGTGTGTGTGTGTGGATAACGGCTCACATAACGTGTGCGCATGGA-TGACTTGG-----
Human|JQ001752 CTCTCTCGCGGGTGTGTGTGTGTGGATAACGGCTCACATAACGTGTGCGCATGGA-TGACTTGG-----
Human|GQ293226 CTCTCTCGCGGGTGTGTGTGTGTGGATAACGGCTCACATAACGTGTGCGCATGGA-TGACTTGG-----
Human|GQ226034 CTCTCTCGCGGGTGTGTGTGTGTGGATAACGGCTCACATAACGTGTGCGCATGGA-TGACTTGG-----
Human ref|EF200012 CTCTCTCGCGGGTGTGTGTGTGTGGATAACGGCTCACATAACGTGTGCGCATGGA-TGACTTGGCTTCCTATTTTCGTTGAAGAACGCAGTA
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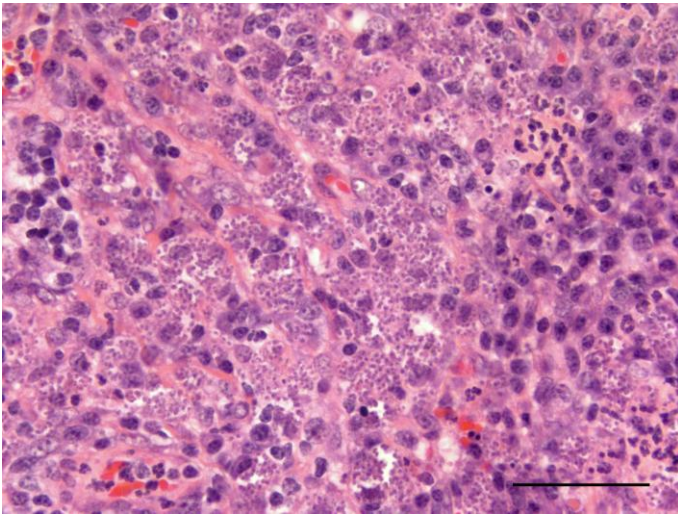



Figure 1. Histologic section of an ulcerated mass from a horse with cutaneous leishmaniasis. Macrophage cytoplasms contain myriad protozoa, each with a small nucleoid and a smaller kinetoplast. Original magnification $\times 50$.

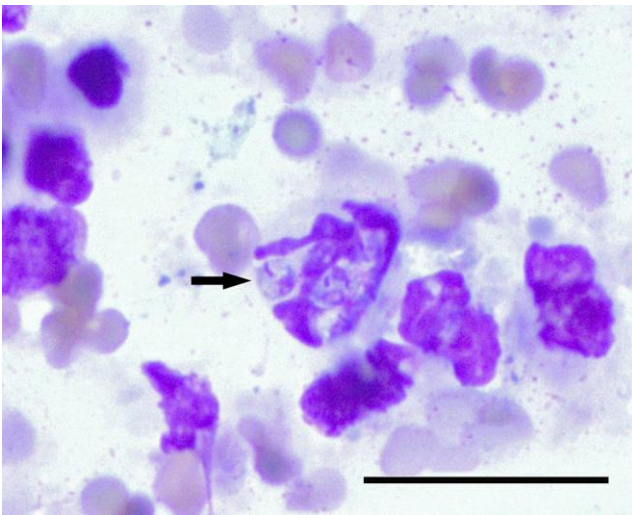


Figure 2. Fine needle aspirate of an ulcerated mass from a horse with cutaneous leishmaniasis exhibiting an intracellular amastigote (arrow). Original magnification $\times 100$.