

Leishmania (Mundinia) spp.: from description to emergence as new human and animal Leishmania pathogens

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Abstract

During the last 20 years, *Leishmania (Mundinia) spp.* have emerged as new causative agents of human and animal leishmaniases. We provide a historical view of these parasites, from their initial description to their emergence as pathogens, to help avoiding future confusion in species assignment of these newly emerging pathogens.

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More than one billion people are at risk of contracting visceral leishmaniasis (VL) or cutaneous leishmaniasis (CL). VL causes 20 000 to 30 000 deaths annually, and CL affects the quality of life of millions, causing disability and permanent scarring after healing (<https://www.who.int/leishmaniasis/en/>). The first account of human leishmaniasis dates from the Middle Ages, but the discovery of *Leishmania* parasites as causative agents only occurred in modern times. Until recently, it was thought that the aetiologic agents responsible for leishmaniases belonged almost exclusively to the subgenus *Leishmania* in the Old and New Worlds and to the subgenus *Viannia* in the New World. This view is currently challenged [1].

Between 1995 and 2002, human and animal CL and VL caused by noncanonical *Leishmania* parasites were reported in geographically distant areas (Thailand, Martinique, Switzerland, Australia and Ghana). In Martinique, reports of cutaneous-like infections date back to 1917, but the aetiologic agent was not formally characterized until 2001 [2,3]. A draft genome of the isolate was released in 2013, and the species, named *L. martiniquensis*, was included in the *Leishmania* subgenus [3]. In Thailand, before the description of first autochthonous VL cases in 1999, leishmaniases were only diagnosed in travellers

returning from the Middle East. In 2008, a new species was suspected of being the aetiologic agent of VL cases in Thailand [4]. In West Africa, CL cases caused by *L. major* have been documented. In Ghana, from 2002 to 2003, a total of 8876 possible CL cases were reported, and *L. major* and another *Leishmania* sp. were identified [5]. Surprisingly, animal cases (horse, cow and red kangaroo) of CL were detected in North America, Europe and Australia [6–8]. The enigmatic *Leishmania* parasite responsible for CL in horses is genetically closed to the suspected new species identified in Thailand. The name '*Leishmania siamensis*' was used at the time [7]; nevertheless, given the lack of adherence to the international code for zoologic nomenclature, the name '*Leishmania siamensis*' is considered a nomen nudum. In 2014, clues emerged to incriminate *L. martiniquensis* in some CL and VL cases reported in Thailand since 1999 [9]. Surprisingly, all these pathogens were genetically related to a parasite, *Leishmania enriettii*, previously isolated from a guinea pig in Brazil [1,9]. In 2018, the subgenus *Mundinia* was created [1]. It encompasses *Leishmania* species responsible for human and animal diseases previously gathered in the *L. enriettii* complex, *L. (Mundinia) martiniquensis*, previously assigned to the subgenus *Leishmania* [1], and *L. (Mundinia) orientalis*, a newly described species responsible for CL in Thailand [1,10]. A schematic timeline the *Mundinia* subgenus of characterization is provided in Fig. 1.

Strikingly, the last 20 years have seen parasites of the subgenus *Mundinia* emerging as new human pathogens,

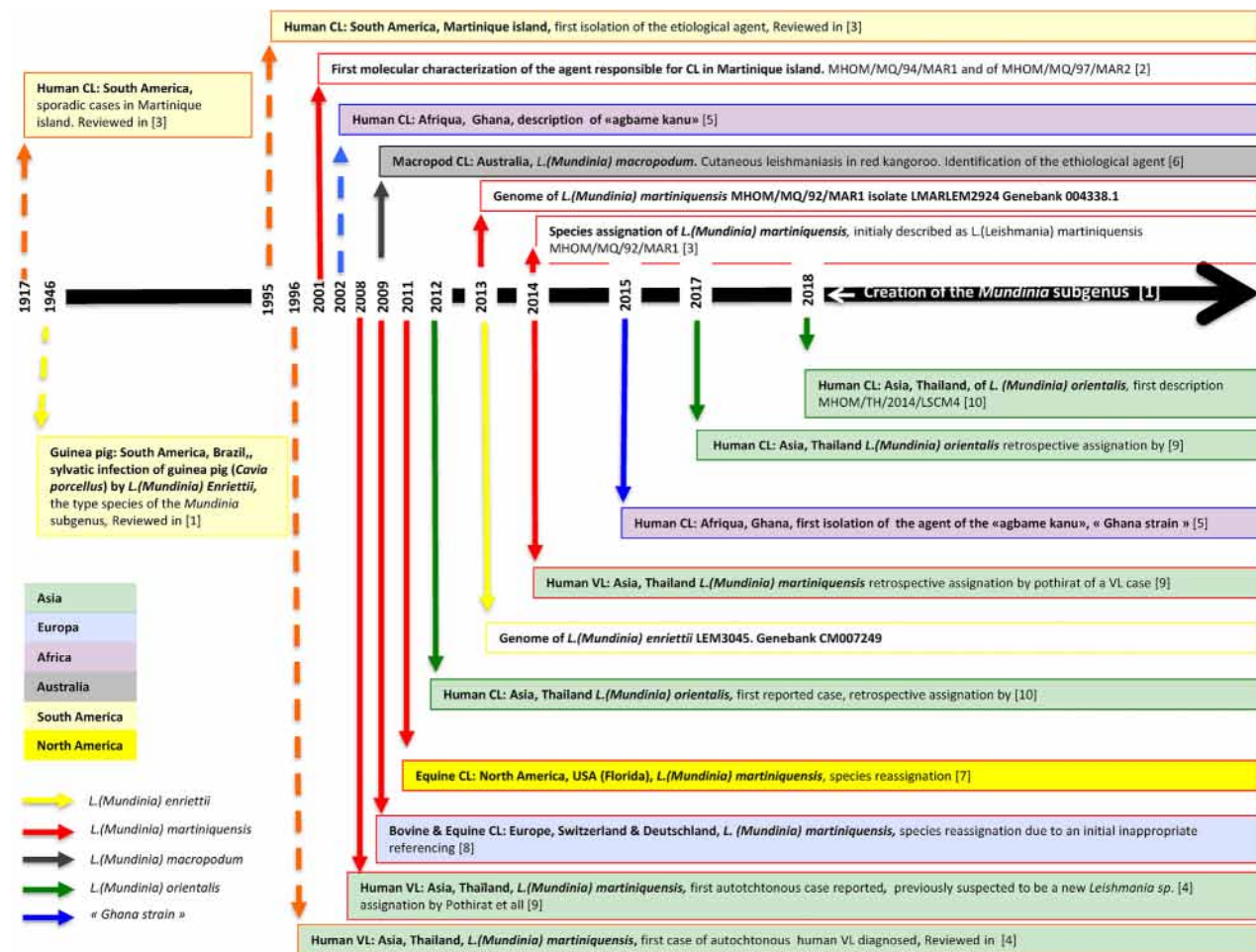


FIG. 1. Historical events leading to identification of *Leishmania (Mundinia)* spp. as newly emerging *Leishmania* pathogens worldwide. Dashed lines indicate absence of molecular identification of aetiologic agent. In Asia, members of the *Mundinia* (Shaw, Camargo and Teixeira 2016) subgenus are currently identified only in Thailand. In Africa, they were isolated in Ghana and are referred as Ghana strains. In Europe, presence was reported in Deutschland (Bavaria) and Switzerland; in North and South America, United States (Florida), Brazil (Curitiba, Sao Polo) and Martinique Island. Described species belonging to the *Mundinia* subgenus are: *Leishmania (Mundinia) enriettii* (Muniz and Medina 1948), *Leishmania (Mundinia) martiniquensis* (Desbois, Pratlong and Dedet, 2014), *Leishmania (Mundinia) orientalis* (Bates and Jariyapan 2018) and *Leishmania (Mundinia) macropodum* (Barratt, Kaufer and Ellis, 2017), plus parasites responsible for CL in Ghana (Ghana strain). CL, cutaneous leishmaniasis; VL, visceral leishmaniasis.

causing VL and CL in HIV⁺ and HIV⁻ patients. These parasites challenge our current knowledge of the worldwide distribution and physiopathology of leishmaniasis. To elucidate the underlying factors triggering the worldwide emergence of *L. (Mundinia)* spp. and to address the future risks for human and animal health, we must investigate the vectors and hosts involved in the transmission cycles of these pathogens.

Conflict of Interest

None declared.

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