

Predominance of *Leptospira wolffii* in north-central Bangladesh, 2019

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Abstract

Leptospira was detected in 48.9% of blood samples from 182 febrile patients in north-central Bangladesh in 2019. Most *Leptospira* were classified as *L. wolffii* (93%) on the basis of phylogenetic analysis of 16S ribosomal RNA genes, while others were assigned to *L. borgpetersenii* and *L. meyeri*.

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Keywords: 16S rRNA, Bangladesh, *Leptospira borgpetersenii*, *Leptospira meyeri*, *Leptospira wolffii*

Original Submission: 18 June 2020; **Revised Submission:**

14 September 2020; **Accepted:** 16 September 2020

Article published online: 19 September 2020

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Leptospirosis is the most common anthropozoonosis worldwide. It is caused by a pathogenic species of the genus *Leptospira*, with an estimated 1.03 million cases and 58 900 deaths annually [1]. In developing countries, this disease remains largely underestimated as a result of the variability of its clinical manifestation and the unavailability of appropriate laboratory diagnostic facilities. In Bangladesh, the prevalence of leptospirosis among febrile illnesses has been described mostly by using serologic tests [2–4]. In our previous study, *L. interrogans* was first genetically identified as a major *Leptospira* species in north-

central Bangladesh [5]. On the basis of those results, we conducted an extended epidemiologic study of *Leptospira*.

Blood samples were collected from 182 febrile patients in Mymensingh Medical College hospital, located in north-central Bangladesh, between April and December 2019. The enrolled patients had fever (temperature >38.5°C) for more than 5 days with headache, myalgia and general prostration associated with additional symptoms (e.g. jaundice) (Supplementary Table S1). *Leptospira*-specific IgM was detected in 60 samples (33.0%) by an enzyme-linked immunosorbent assay (ELISA) kit (DRG International, Springfield Township, NJ, USA), and the leptospiral 16S ribosomal RNA (rRNA) gene was identified in 65 samples (35.7%) by the nested PCR method [6]. A total of 89 samples (48.9%) tested positive for *Leptospira* by ELISA, PCR or both, while 24 and 29 samples were positive by solely ELISA or PCR respectively. Among the 89 positive cases, 65 occurred in male subjects, and 67 occurred in patients who lived in rural areas. Although positive cases were found in any month during the study period, more cases occurred in July, September and October. The overall detection rate of *Leptospira* was higher than that in our previous study in Bangladesh [5] but was comparable to that in Malaysia [7]. All patients were cured by administration of doxycycline and ceftriaxone for a 7- to 10-day period along with treatment of symptoms.

Nucleotide sequences of partial 16S rRNA gene were directly determined with PCR products of 29 samples. Phylogenetic analysis revealed that 27 samples (93%) clustered with *L. wolffii*, while one sample each was assigned to *L. borgpetersenii* (pathogenic group) and *L. meyeri* (nonpathogenic group) (Fig. 1). Nucleotide sequences were deposited in GenBank under accession numbers MT611935 to MT611940.

Our previous study in 2018 demonstrated the dominance of *L. interrogans*, while *L. wolffii* was identified in only a single sample [5]. In contrast, in the present study, *L. wolffii* was predominant and we found no *L. interrogans*. *L. wolffii* was detected sporadically from April to November, which may suggest that this species is persistently transmitted among the local population. *L. wolffii* has been classified as an intermediate species and is found in a wide area from South-East Asia to the Middle East as a minor pathogen of human leptospirosis which is also detected in animals and the environment [7–11]. Our study is the first to note the predominance of this species in human infection.

By whole genome-based phylogenetic analysis of *Leptospira*, the formerly described ‘intermediate group’ was classified into subclade P2, one of the pathogenic clades, as well as P1, representing the former ‘pathogenic group’ [12]. Such genetic evidence may also underscore the importance of *L. wolffii* as a

cause of human leptospirosis. *L. wolffii* has been reported to be a dominant species in dogs in Iran, suggesting its putative transmission to humans [10]. Further surveillance is necessary to monitor the prevalence and species of *Leptospira* in Bangladesh, particularly to determine the epidemiologic trend of *L. wolffii* and its prevalence in dogs as a potential reservoir.

Conflict of interest

None declared.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.nmni.2020.100765>.

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