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Molecular epidemiology of leptospirosis in western and southern provinces in Sri Lanka

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Objective: The present study investigated the molecular epidemiology of leptospirosis in selected provinces in Sri Lanka

Methods: A prospective study was carried out between January 2013 to 2014. Adult patients with clinically suspected leptospirosis admitted to the medical wards at selected hospital were included. A whole blood sample was collected and DNA was extracted. leptospira IgM was detected using an immunochromatographic assay. PCR was done using fla B primers followed by RFLP using Hind III and Hae III. Nested PCR was performed using rrs primers which amplifies 16S rRNA gene. Amplicons resulting from rrs PCR were purified and subjected to bidirectional DNA sequencing and phylogenetic analyses were conducted.

Results: Out of the 168 clinically suspected leptospirosis cases 84 (50%) were IgM positive and 13 (7.7 %) were positive with Fla B PCR while 14 were rrs PCR positive. Based on sequence analysis, *Leptospira interrogans* (11/14, 79%) was the most common cause of disease followed by *Leptospira borgpetersenii* (2/14,14%) and *Leptospira kirschneri* (1/14,7%). Renal failure was the most common complication (4/11, 36%) associated with *L. interrogans* followed by myocarditis(2/11,18%). *Leptospira borgpetersenii* was associated with myocarditis and liver failure while *Leptospira kirschneri* was associated with acute renal failure. RFLP Hind 111 digestions could not differentiate between *L. interrogans* strains *Canicola*, *Icterohaemorrhiae* and *Pyrogenes* while Hae 111 digestion showed better discrimination.

Conclusions: *L. interrogans* was the predominant circulating strain in western and southern provinces in 2013 in Sri Lanka. The current data will contribute to determining molecular epidemiological diversity of circulating leptospira in Sri Lanka