IDENTIFICATION OF PATHOGENIC LEPTOSPIRA SEROVARS IN SRI LANKA USING POLYMERASE CHAIN REACTION

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R.A. PRAHARSHINIE RUPASINGHE

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ABSTRACT

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Praharshinie Rupasinghe

Post Graduate Institute of Science

University of Peradeniya

Peradeniya

Sri Lanka

Leptospirosis is a cosmopolitan public health problem. In humid tropical and subtropical areas, where most developing countries are found, it is a major issue compared to temperate climate. The magnitude of the problem in tropical and subtropical regions can be largely attributed to climatic and environmental conditions but also to the great likelihood of contact with a leptospira-contaminated environment caused by, for example, local agricultural practices and poor housing and waste disposal, all of which give rise to many sources of infection. In countries with temperate climates, in addition to locally acquired leptospirosis, the disease may also be acquired by travelers abroad, and particularly by those visiting the tropics.

Leptospirosis is a potentially serious but treatable disease. Its symptoms may mimic those of a number of other unrelated infections such as influenza, meningitis, hepatitis, dengue or viral hemorrhagic fevers. Some of these infections, in particular dengue, may give rise to large epidemics, and cases of leptospirosis that occur during such epidemics may be overlooked. For this reason, it is important to distinguish leptospirosis from dengue and viral hemorrhagic fevers, etc. in patients acquiring infections in countries where these diseases are endemic. At present, this is still difficult, but new developments may reduce the technical problems in the near future. It is necessary, therefore, to increase awareness and knowledge of leptospirosis as a public health threat.

Polymerase chain reaction was developed for the rapid detection of leptospirosis. The PCR amplification of *Leptospira spp* using primers of *flaB* gene gave products of 732bp. In this study, a PCR method for the clinical diagnosis of leptospires was evaluated. Further the DNA extracts which gave positive PCR results were sent to Japan for DNA sequencing. DNA sequences were analyzed in http://www.ncbi.nlm.nih.gov/BLASt/ and phylogenetic analysis was done using MEGA4 (11).

A total of 50 human serum samples were analyzed and *Leptospira fla*B gene was detected in 9 samples (18%). They were subjected to DNA sequencing and leptospires were identified up to serotype level, and their possible reservoirs. Sample no 47 was identified as *Leptospira interrogans* Akiyami B, which comes under Genus *Leptospira*, species *interrogans*, serogroup Hebdmadis and strain Akiyami B for which pigs have been identified as reservoirs. Sample no 46 was identified as *Leptospira* Moskva V, which comes under Genus *Leptospira*, species *kirschneri*, serogroup Grippotyphosa, serovar Gryppotyphosa and strain Moskva V for which wild boars have been identified as reservoirs. Sample no 47 was identified as *Leptospira* serovar Lai strain 607, which comes under Genus *Leptospira*, species *interrogans*, serogroup Icterohaemorrhagiae, serovar Lai and strain 607 for which pigs, dogs, cattle, rats and horses have been identified as reservoirs.