

The First Isolation of *Leptospira weilii* in Sri Lanka and Comparative Genomic Analysis of RAST Subsystems

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Abstract

Leptospirosis is caused by spirochetes and is considered a reemerging infectious disease worldwide. *Leptospira* isolation and whole-genome sequencing are two key concepts that enable us to understand the poorly defined pathophysiology of this disease. *L. interrogans*, *L. borgpetersenii*, and *L. kirchneri* were isolated from Sri Lanka two to three decades back. Even though Agampodi *et al.* has reported that *L. weilii* was causing disease, it was not isolated from Sri Lanka. This study was planned to identify *L. weilii* as an etiological agent causing human leptospirosis. Culture isolation of *Leptospira* from febrile patients was done using EMJH media and log phase from the growing culture was used for DNA extraction. In 25 isolated *Leptospira*, whole genomic sequencing was done to define the species. Extracted DNA was used for Pac-Bio sequencing. Data generated from sequencing were assembled using Canu 2.1. The average guanine-cytosine (GC) content of *Leptospira* lies between 34 and 41%: the highest was observed in *L. weilii*. Subsystem analysis by RAST annotation revealed that proteins linked to amino acids and derivatives, protein metabolism, cofactors, vitamins, prosthetic groups, pigments, carbohydrates, motility and chemotaxis were found in all species in roughly equal numbers. There was a slight variation in genome features even within the same species. In-depth comparative genomic analysis is required for further understanding.

Keywords: *Leptospira weilii*, leptospirosis, Sri Lanka, comparative genomics, RAST subsy

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