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Molecular characterization and genetic diversity of cutaneous leishmaniasis from North Eastern Pakistan

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The genetic diversity of Leishmania spp. in North Eastern Pakistan remains undetermined despite increase cases of Cutaneous leishmaniasis (CL). This study was designed to decipher the molecular characterization and genetic diversity of Leishmania spp. in North Eastern Pakistan. Out of 13761 microscopically suspected CL cases, 567 cases were confirmed with Leishmania spp. by internal transcribed spacer (ITS) gene amplification through PCR- RFLP technique. Further, isolates were directly sequenced to conduct phylogenetic analysis for genetic diversity. Among suspected CL cases, Mirpur showed the highest proportion of 4.85% (118/2431) CL infection while Neelum district showed the lowest 3.29% (9/273). The slide positivity rate, annual blood examination rate, and annual parasitic incidence rate were 3.84, 0.27, and 0.01% respectively and the incidence of CL in the age group 1-20 was higher in males 50.92% than females 25.75%. The RFLP analysis and sequencing confirmed the occurrence of L. tropica, L. major, and L. infantum. The L. tropica (p=0.02) confirmed significant nucleotides variation than L. major (p=0.05). Current findings confirmed the prior assumption that anthroponotic CL is the primary CL present in AJK. Moreover, this is the first report based on molecular identification of L. major, and L. infantum from North Eastern Pakistan. The Leishmania spp. with remarkable heterogeneity is the leading cause of treatment failure and emergence of new haplotypes. Therefore, more extensive investigations are recommended from all geographical regions of North Eastern Pakistan, a using large sample size.

Biography

Nargis Shaheen has completed her M.phil from Quaid-i-Azam University, Islamabad Pakistan in Parasitology. She has submitted her PHD thesis in Quaid-i-Azam University, Islamabad Pakistan in Parasitology. Currently, she is working as a short term visiting scholar in the Department of Pathology and Microbiology of Ohio State University Columbus, USA. She has published more than 10 papers in reputed journals. Her research field is Parasitology and Entomology with focus on vector borne diseases. Her engrossment is on epidemiology, molecular diversity, and drug formulation from plant. She has also experienced in identifying the drugs targets by computational studies and genetic variation in hereditary disease.

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