conferenceseries.com

12th International Conference on

Pediatric Pathology & Laboratory Medicine

March 15-16, 2017 London, UK

Analyses of five nuclear and mitochondrial genes for the identification the old and new world *Leishmania* parasites

Parviz Parvizi and Reza Fotouhi-Ardakani Pasteur Institute of Iran, Iran

Background: The polymorphism and genetic diversity of *Leishmania* genus have status under discussion depending on many items from clinical samples, reservoir hosts and vectors.

Objectives: The objectives are to compare genetic changes and the role of each two enzymatic and mitochondrial genes (COII and *Cyt b*) or housekeeping and nuclear genes (*nagt*, ITS-rDNA and *HSP70*) for accurate identification of *Leishmania* parasites.

Methods: After DNA extractions, PCR products were sequenced and evaluation of genetic proximity and phylogenetic analysis were performed using MEGA6 and DnaSP5 software.

Results: Of the 72 sequences, 54 new haplotypes from five *Leishmania* species were submitted to GenBank. The number of polymorphic sites was significantly lower as compared to the monomorphic sites.

Conclusions: The highest and lowest levels of haplotype diversity were observed in *L. tropica* (81.35%) and *L. major* (28.38%). Tajima's D index analyses showed that Cyt *b* gene in *L. tropica* species was significantly negative, while COII and *nagt* genes were produced through evolutionary processes for both *L. tropica* and *L. major*.

Biography

Parviz Parvizi has completed his PhD from the London School of Hygiene and Tropical Medicine (London University) and Natural History Museum (London) in 2004. He was a Full Professor since 2015 and has been appointed as the Head of Parasitology department and also as the Director of Parasitology, Immunology and Mycology Research Group at Pasteur Institute of Iran. He has published more than 60 papers in reputed journals.

parp@pasteur.ac.ir

Notes: