

Genomic Analysis of Whole Genome Sequencing of Leishmania Major

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Abstract : Leishmaniasis represents a major public health problem because of the number of cases recorded each year and the wide distribution of the disease. It is a parasitic disease of flagellated protozoa transmitted by the bite of certain species of sandfly, causing a spectrum of clinical pathology in humans ranging from disfiguring skin lesions to fatal visceral leishmaniasis. Cutaneous leishmaniasis due to *Leishmania major* is a polymorphic disease; in fact, the infection can be asymptomatic, localized, or disseminated. The objective of this work is to determine the genomic diversity that contributes to clinical variability by trying to identify the variation in chromosome number and to extract SNPs and SNPs and InDels; it is based on four sequences (WGS) of *Leishmania major* available on NCBI in Fastq form, from three countries: Tunisia, Algeria, and Israel, the analysis is set up from a pipeline to facilitate the discovery of genetic diversity, in particular SNP and chromosomal somy.

Keywords : Leshmania major, cutaneous Leishmania, NGS, genomic, somy, variant calling

Conference Title : ICAB 2023 : International Conference on Advances in Biology

Conference Location : New York, United States

Conference Dates : December 11-12, 2023