(Y D O X D W L Q J D Q G V H W W L Q J X S D T 3 & 5 E\ K L J K U H V R O X W L R Q P
Leishmania species by targeting AAP 3 gene

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Leishmania as protozoan parasites causes major diseases of leishmaniasis in the people of tropical and subtropical regions. In di erent hosts including humans, clinical samples, rodents and/or other mammals as reservoir hosts and sand ies as vectors, mixed infections, co-infections and di erent hybrids of Leishmania parasite with di erent aneuploidy in chromosomes were observed. To di erentiate common old world parasite species and discriminate co-infection with di erent species the genetic variation analysis and SNP prediction was identi ed by using high resolution melting analysis as a powerful method. For each species, one standard sample was ampli ed and a recognized region was cloned. ree sets of primer were designed for nuclear gene of amino acid permeases (AAP3) gene and EvaGreen dye mechanism was used and the di erent temperature of HRM species was optimized. Temperature variation in HRM separated L. major and L. tropica co-infections and their sub-strains. e speci c and common primers were separate species and strains by melting temperature analysis. To compare with variety of mitochondrial and nuclear genes AAP3 gene is more sensitive and speci c than other genes for identi cation of Leishmania parasites. e setup HRM could separate common species of Leishmania parasite and useful in separations intra-stains. E ciency and regression coe cient reactions for genus and species of Leishmania were also validated.

Biography

Notes:

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Page 36