

# **Application of Bioinformatics in molecular data analysis for *Leishmania major* vector *Phlebotomus papatasi* sand fly.**

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## **Abstract**

Three molecular typing tools: multi-locus microsatellite typing, *cytochrome b* and internal transcribed spacer II sequence analysis, have been evaluated using bioinformatics application for their usefulness to infer population structure of *P. papatasi* sand flies. Microsatellite markers showed high resolution power for differentiating globally distributed *P. papatasi* populations, whereas analysis of *cytochrome. b* sequences provided insight into relationships of closely related populations from the Mediterranean. Population structure, differentiation, and demographic history among *P. papatasi* populations are important to understand patterns of dispersal in this species and for planning appropriate control measures.

## **References**

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