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
Hamarsheh, Omar; Presber, Wolfgang; Al-Jawabreh, Amer; Abdeen, Ziad; Amro, Ahmad; Schoenian, Gabriele (2009) Molecular markers for Phlebotomus papatasi (Diptera: Psychodidae) and their usefulness for population genetic analysis. Transactions of the Royal Society of Tropical Medicine and Hygiene 103:1085-1086

