GENETIC DIVERSITY OF PHLEBOTOMUS PAPATASI POPULATIONS IN TWO DIFFERENT GEOGRAPHICAL REGIONS IN EGYPT

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DEDICATION

This thesis is dedicated to my mother for her encouragement, inspiration and love devoted to me

To my dear Husband for sacrifices he made, continuous help and encouragement he offered, throughout my study period

Finally, to my lovely sons (Ali & Omar) for many hours they spend without their mother around

ABSTRACT

Phlebotomus papatasi (Scopoli) (Diptera: Psychodidae) is the main vector of *Leishmania major*; which is the cause of self-limiting cutaneous leishmaniasis in the Old World. This sand fly is found in houses, animal shelters, caves and rodent burrows. It has a large geographical range, which includes the Middle East and the Mediterranean regions. The internal transcribed spacer 2 (ITS 2) of rDNA and the cytocrome b (*cyt b*) gene of mtDNA were sequenced from two populations originating from Sinai and Alexandria. The query lengths of ITS2 was 455 bp in both populations with the proportion of AT greater than 69%. The ITS2 sequences reflect inter-specific variation which affected the geographical distribution and this can affect the infectivity status and the disease transmission by the sand flies and may be used as a base for better control of the disease, while the query lengths of *Cyt b* gene was 442 bp which was rich with AT content with the proportion of AT greater than 75%. The results observation reflect that *cyt b* not affected by the geographical distribution, this give clue that it has no role in the infectivity and transmission of the disease by the sand fly and it can be used as genetic marker in differentiation between different types of *Phlebotomus* species. A phylogenetic study was carried out on the same populations, ITS 2 showed little variations within populations according to different localities. This is actually the reason for poor geographical structuring in the NJ tree. No clear phylogeographical pattern was observed in *Cyt b* gene for the populations because shared haplotypes were present at the external nodes or at different nodes. These Methods might represent useful tools for a molecular large scale screening of Phlebotomine sand fly species caught in areas where leishmaniasis is endemic, in order to plan appropriate epidemiological surveillance programs for both Leishmania spp. and their vectors.

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LIST OF ABREVIATIONS

A	Adenosine
Alex	Alexandria
Bp	Base pair
C	Cymine
Cl	Cutaneous lieshmaniasis
cm	centimeter
COI	cytochrome *c* oxidase I
Cyt b	*Cytochrome b*
G	Guanine
L	*Lieshmania*
Lu	*Lutzomyia*
ITS2	Internal transcribed spacer 2
ML	maximum likelihood
Min	Minute (s)
Ml	millimeter
µl	Microliter
Mm	Millimeter
mt DNA	Mitochondrial DNA
NJ	neighbor- joining

P.	*Phlebotomus*
PCR	polymerase chain reaction
rDNA	Ribosomal DNA
RH	relative humidity
RTC	Research and Training Centre
T	Thymine
VL	visceral leishmaniasis
WHO	World Health Organization

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