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ABSTRACTS OF ORAL AND POSTER COMMUNICATIONS — OPEN ACCESS

Proceedings of the IX International Symposium on Phlebotomine Sandflies (ISOPS IX), Reims, France, June 28th–July 1st, 2016

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Molecular and biochemical characterization of insecticide resistance in *Phlebotomus* and *Lutzomyia* sand flies

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Identification of phenotypic traits associated with insecticide resistance in phlebotomine sand flies is an essential component of vector control programs. Chemical insecticides continue to be a critical tool of control programs in an effort to mitigate the spread of leishmaniasis. Sand flies have been exposed for decades to a variety of insecticide classes, which has increased evolutionary selective pressures of resistance. In many insects, resistance arises either from target-site insensitivity and/or metabolic detoxification. Target-site insensitivity involves single nucleotide polymorphisms (SNPs) in the paralytic (*para*) and acetylcholinesterase-1 (*ace-1*) genes, which have been implicated in conferring insensitivity to pyrethroids and organophosphates. Metabolic resistance involves changes in the expression of carboxylesterases, cytochrome P450's, and glutathione S-transferases that are capable of binding, sequestering, metabolizing, and conjugating insecticides. The primary objective of this research was to augment the understanding of target-site insensitivity and metabolic detoxification at the molecular level for pyrethroid and organophosphate resistance in *Phlebotomus papatasi* and *Lutzomyia longipalpis*. We are in the process of characterizing *para*, *ace-1*, and protein profiles in insecticide-susceptible and -resistant *Ph. papatasi* and *Lu. longipalpis* laboratory colonies. To do so, we initially determined the diagnostic doses and times for *Ph. papatasi* and *Lu. longipalpis* sand flies using the CDC bottle bioassay with 10 different insecticides covering four insecticide classes. Both species were determined to be highly susceptible to DDT and carbamates, whereas with other insecticides, these species varied substantially in their diagnostic dose and times. In addition, we have exposed separate *Ph. papatasi* and *Lu. longipalpis* colonies to permethrin (pyrethroid) and malathion (organophosphate) over multiple generations to induce resistance. At a 60% malathion lethal concentration exposure, F_7 generation *Ph. papatasi* are demonstrating 87.8% survival compared to a 58.7% survival in F_5 generation *Lu. longipalpis*. At a 60% permethrin lethal concentration exposure, F_{16} *Ph. papatasi* demonstrate 79.6% survival compared to a 77.1% survival in F_9 generation *Lu. longipalpis*. Baseline molecular and biochemical characterization have also been completed in the susceptible colonies. DNA sequence has been recovered surrounding *para* 1,014th (*kdr*), 918th super-*kdr* region, *ace-1* 119th codons, and upstream (5′) and downstream (3′) regions from these codons in the permethrin- and malathion-resistant-selected *Lu. longipalpis* and *Ph. papatasi* colonies. Initial sequence data from the F_3 generation of the *Lu. longipalpis* permethrin-resistant-selected colony and from the F_3 generation of the *Lu. longipalpis* malathion-selected colony has revealed no SNPs in the *para* and *ace-1* genes. Initial sequence data from the F_4 generation of the *Ph. papatasi* permethrin-resistant-selected colony and from the F_3 generation of the *Ph. papatasi* malathion-resistant-selected colony has revealed no SNPs in the *para* and *ace-1* genes. We have begun to conduct genotyping-by-sequencing, utilizing an Illumina sequencing platform, to identify genome-wide SNP markers associated with insecticide resistance in *Ph. papatasi* and *Lu. longipalpis*. Our working hypothesis is that insecticide resistance can potentially be more diverse than a single SNP or enzyme class and that resistance may be polygenic with many genes contributing to the resistance phenotype. Results from these analyses will provide significant insights into understanding the mechanisms of insecticide resistance in field-collected sand flies where leishmaniasis is a serious public health threat.

Evaluation of the spatial relationship between area of insecticide treatment and location of Leishmaniasis cases using geographical information systems in Adana, Turkey

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Insecticide spraying was conducted to control arthropod vector populations, especially sand flies and mosquitoes, in 103 districts in downtown Adana, after people had reported their mosquito and sand fly problems to the metropolitan municipality. People, from 103 locations telephoned the municipality 5,656 times in 2014. Leishmaniases are present in Turkey in two clinical forms; visceral and cutaneous, and show a tendency for spreading throughout the country. Numbers and distribution of cutaneous leishmaniasis cases in Adana province were obtained from the Turkish Ministry of Health. The aim of the present study was to compare the relationships between the locations of leishmaniasis patients and insecticide spraying area by using the data in selected study sites in Adana province. In this regard, city borders were drawn using ARCMAP10.0. Additionally the map was separated into different layers for querying each province independently. Altitude, leishmaniasis case numbers and insecticide application numbers of the selected locations were entered into the database and relationships between them were evaluated. Identification of the correlation levels of these data may provide useful information to better guide control program interventions.