Evaluation of Insecticide Resistance in *Aedes aegypti* in the Northern Chihuahuan Desert

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Background

- *Aedes aegypti* is the vector of several arboviruses, such as Zika and dengue viruses, that are of global health concerns. Major efforts have been made to control this mosquito with insecticides being the most widely used method (1).
- The massive use of these insecticides has caused resistance to these compounds among *Ae. aegypti* populations (2).
- Studies have shown a direct relationship between resistance and mutations in the genomic regions where these substances bind in the mosquito.
- Point mutations in the *Vgsc* genes S989P, I1011M/V, F1269C, F1534C, and V1016G/I lead to insecticide resistance, being the ones at V1016G/1 and F1534C related to pyrethroid resistance (3)
- Several studies have shown that mutations in the G119S gene are responsible for organophosphate resistance and one study found mutations in the T506T location in organophosphate-resistant mosquito colonies (4).

Objective

Determine and compare insecticide resistance genes through genetic analysis in *Ae. aegypti* populations from El Paso, Texas, United States and Ciudad Juarez, Chihuahua, Mexico.

Sample Collection

- *Ae. aegypti* samples were collected from two areas alongside the U.S.-Mexico border; Anapra, CH, MX and Sparks, TX, U.S.
- Mosquito collection period was from June to December 2017 within and outside 71 houses in Sparks and 70 in Anapra.
- Gravid Traps were placed inside and outside the houses to collect the mosquitoes.
- Each community was subdivided into five groups (red, green, blue, pink, and yellow) with a range of 12-15 houses per group.
- The number of visits per house ranged between 1 and 3 times.
- 1,777 mosquitoes were gathered from Sparks and 436 from Anapra.
- 297 mosquitoes from both communities (140 from Anapra and 157 from Sparks) were chosen for genetic analysis.

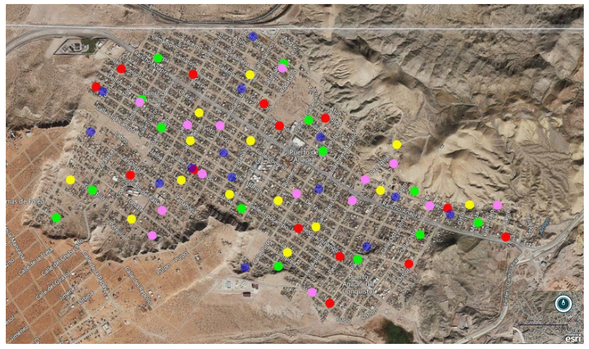

Figure 1: Aerial view of the community of Anapra, CH, Mexico. The colored dots represent the houses and their respective group classification.

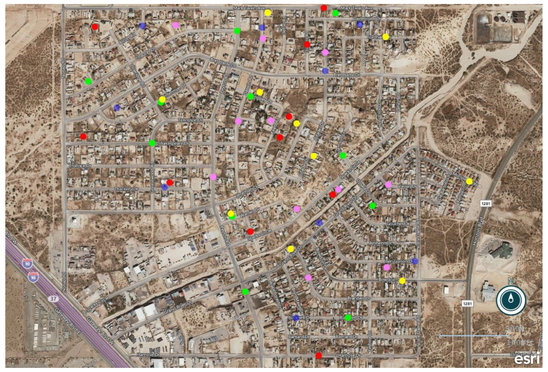

Figure 2: Aerial view of the community of Sparks, TX, United States. The colored dots represent the houses and their respective group classification.

Mosquito DNA Extraction

- The mosquito samples were labeled and categorized in a database according to the community and house where they were found and stored at -80°C.
- DNA analysis was performed to obtain representative samples from each community and house.

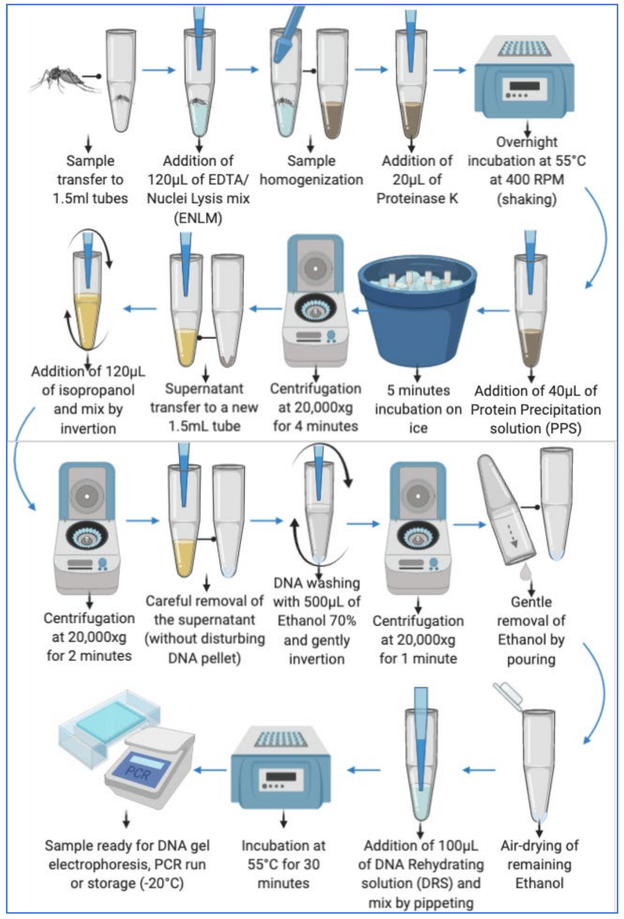

Figure 3: Diagram showing the methodology used to efficiently extract DNA from *Ae. Aegypti*). The last step shows the three possible outcomes for the DNA extraction.

Results

- We successfully extracted DNA from 18 out of 20 samples for a 90% success rate.
- The samples that did not have a satisfactory extraction were saved (Stored at -80°) for future DNA re-extraction.
- The Anapra samples included 17 samples collected from inside of participating houses and 123 outside.
- The Sparks samples included 18 samples collected inside of participating houses and 139 outside.
- DNA samples will be used to look for genes associated with insecticide resistance by analyzing the complete genome sequence.

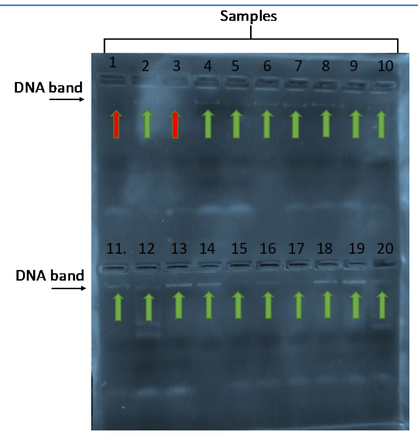

Figure 4: DNA electrophoresis gel showing 20 mosquito samples. The green arrows represent successful DNA extraction and the red arrows unsuccessful DNA extraction.

Future Work

- DNA extraction from the mosquitoes will be required to proceed with PCR (spell-out PCR) to generate more AND (spell-out AND). Until now we have extracted DNA from 18 samples out of 297 mosquitoes.
- After that, ddRAD sequencing will be performed on samples for population genetic analysis. Magnetic AMPure XP beads will be used to purify the amplified productions of genomic DNA.
- The highest quality reads will be mapped to identify BLAST hits. Finally, complete sequences will be sequenced to find and analyze the genes associated with insecticide resistance.

References

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Acknowledgments

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