



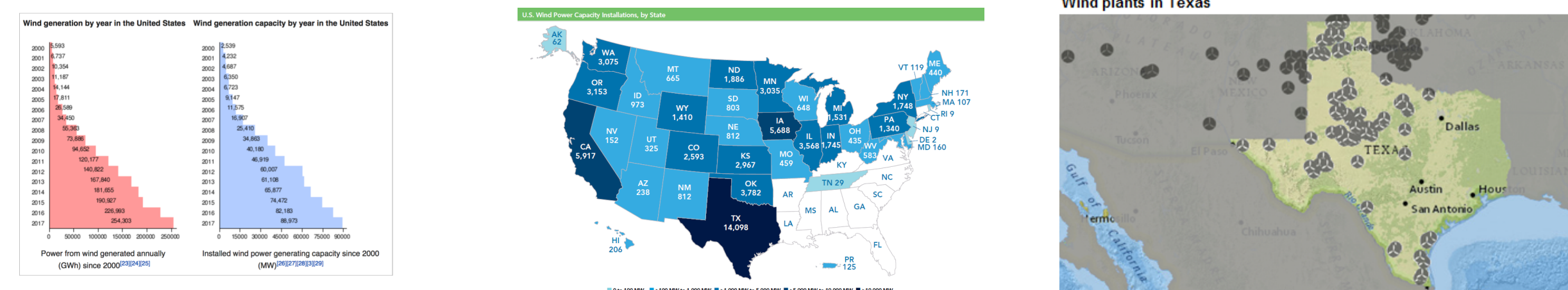
Yellow bat fatalities at wind farms – what can we learn using genetic approaches?



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Introduction

As the world seeks to move toward renewable sources of energy, Texas has been on the forefront of the growing use of wind power for energy. Texas has installed more wind capacity than any other state in the nation and is more than the amount of energy in Oklahoma, Iowa and California combined (the next 3 leaders of wind energy in the country). However the use of this energy comes with a cost.

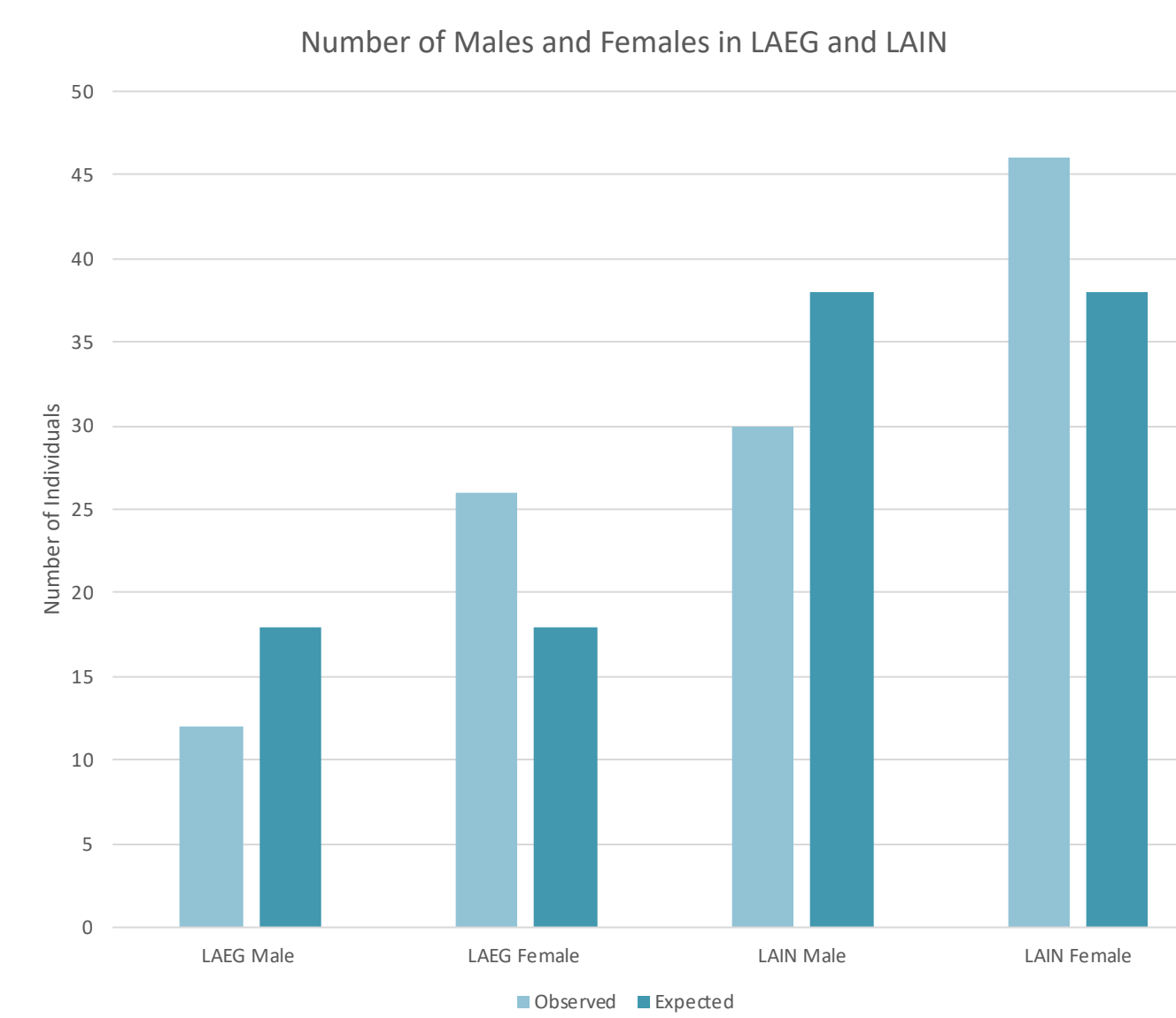


Many bat species are particularly harmed by wind turbines hypotheses as to why include random collisions, coincidental collisions, and collisions that result from attraction of bats to turbines. Fatalities are likely the result of either barotrauma or direct collision with the rotating blades. While the ultimate cause of fatalities remains unclear, we do know that the *Lasiurus* genus is of particular concern. Northern and Southern yellow bats (*L. intermedius* and *L. ega*) are being killed at these sites however there is much of these species that we do not know about. This project seeks to genetically identify carcasses found at these site as well as determine the sex to and compare the results to field identification. These efforts represent the first steps in a study to evaluate genetic diversity and population structure in two species of yellow bats that will likely be negatively impacted by wind energy development. (Cryan and Barclay 2009) (Arnett and Baerwald, 2013)

Methods

- 88 northern yellow bat carcasses and 64 southern were extracted from Windstarr and Hidalgo counties by teams at Texas State University
- DNA from tissues was extracted using methods from Koristan et.al 2013
- Regions of the X and Y chromosome were amplified using polymerase chain reaction (PCR) to sex the bats using methods from Koristan et.al 2013
- Small region of the mitochondrial cytochrome I gene was amplified with the dgLCO and dgHCO primers using BigDye Terminator Cycle Sequencing kit v. 3.1 (Applied Biosystems) –still working on exact methods
- Products were electrophoresed on an ABI 3130XL Genetic Analyzer.
- Sequences were trimmed and put into contigs using Sequencher v. 4.8 and then aligned in MEGA v.7

Results



Graph 1: Compares the observed numbers of male and female *L.ega* and *L.intermedius* to expected numbers. Chi square test was performed on each species. Chi square value for *L.ega* was 5.56 giving a p value of 0.01. Chi square value for *L.intermedius* was 3.30 giving a p value of 0.10. Ratios of *L.ega* are out of Hardy Weinberg and are statistically significant. *L.intermedius* is within expected ranges.

Conclusions

- Specific findings
- What this means
- What should be done next

Acknowledgments

References

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