Phylogenetic Study of the Great Hawaiian Dragonfly or Anax strenuus

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Introduction

There are around 5,462 endemic insect species in the Hawaiian Islands. This accounts for around 94% of all the insects found on this island chain. Twenty-seven of these represent the family Odonata which is made up of dragonflies and damselflies.

One such species is the Great Hawaiian Dragonfly or Anax strenuus. Arguably the largest dragonfly in the world with a wingspan of seven and a half inches, A. strenuus is a great Hawaiian mystery. Originally, this local giant was documented as a endemic cousin to Anax junius, an indigenous dragonfly found all over the world. The only data collected concerning A. strenuus comes from naturalists who conducted general insect studies.

Endemic dragonfly population biodiversity has been found to be on the decline in China, Korea, Japan, Sweden, Canada and the United States. Data collected from the Hawaiian Biological Survey, in comparison to the research done at the end of the nineteenth century, has shown that A. strenuus populations have been pushed higher into the mountains and suggest a possible waning in biodiversity.

The purpose of this study is to create a baseline genetic analysis of A. strenuus by generating a phylogeny of the Anax species found in the Hawaiian Islands. There are two main goals within this outline: to quantify the gene flow between the islands and to compare the genetic relationship between a. strenuus and A. junius.

Methods and Materials

Thirty-two specimens representing A. strenuus and A. junius were collected from thirteen populations across Maui, Oahu, Molokai and Kauai. The DNA from these specimens were extracted using standard Qiagen DNeasy protocol for animal tissues.

Molecular data was extracted for five genes: Tuba, 16S, 12S, H3, and COII using primers from Integrated DNA Technologies, Inc. Amplification of these genes was done using three step polymerase chain reaction (PCR) at forty cycles with annealing temperatures of 50°C. All genes were visualized using agarose gel electrophoresis. Purification was done using a montage PrepEase purification 96-well plate and cycled using BigDye Terminator chemistry, Brigham Young University’s DNA Sequencing Center, Provo, UT was used to generate sequences.

Geneious 6.1 was used to align sequences, ensure that gene ends were homologues and to create contigs. Final alignments were created in MAFFT.

Results

Assembly of the genes resulted in close similarities. Bp numbers varied from 387 to 690 but for all samples the genetic variability was around 99% (Appendix I, Table 3). When generating contigs, each gene resulted in a single contig with relatively high quality ranging from 85%-98%. There were no distinctions between populations or species. Two outliers were persistent in all analysis processes; ODS43 and ODS47. Both had bp numbers under 200, which may have resulted in their exclusion.

Due the nature of the outcome, phylogenetic analysis of the Hawaiian portion of Anax proved to be implausible and as such was not executed as originally planned.

Discussion

The inability to quantify gene flow may be a result of gene flow between populations. Gene flow between isolated populations has been found in even small groups of dragonflies. While research has shown dragonflies do have the ability to fly between islands, it must also be noted that a low number of individual interactions is needed to keep geographically separated populations genetically similar.

The speciation between A. strenuus and A. junius was originally inferred due to morphological differences. The relationship between these two species has never before been documented genetically and as such may be different than what was perceived.

Morphological differences between the two may result from the small genetic differences that were discovered. It is known that drastic genetic variation is not required for ranges in morphological differences. Environmental factors may also result in the morphological variations seen. The converse of Bergmann’s rule states that within insect species, size ratios may increase within areas of lower temperatures or higher elevations.

To gain a better understanding of the relationship between A. strenuus and A. junius, genetic tests focusing on faster genes, SNPs or haplotypes should be done.

Acknowledgements

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References


Table 1. The percent similarity for the genes amplified.

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