The Origins of Post-eruption Insect Populations on the Aleutian Island of Kasatochi

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Abstact

This project compares the dispersal and/or survival ability of insects on the recently erupted volcanic Aleutian Island of Kasatochi. The island erupted in 2008, two months after the island had been briefly surveyed for terrestrial arthropods. Having pre-eruption specimens provides biologists with a unique and rare perspective of island ecosystem assembly. We have analyzed the DNA of 47 pre- and post-eruption *Scathophaga* sp. specimens to determine the origins of post-eruption insect populations. This genetic work is especially important for the Aleutians arthropods because they are among the most understudied in the United States.

Introduction

When a catastrophic natural event such as the volcanic eruption on Kasatochi occurs in such an isolated area, it provides scientists with rare opportunities to see succession in action. Each year since the eruption scientists ranging from botanists to ornithologists have journeyed to Kasatochi Island to study the slow reassembly of the island's ecosystem (Sikes & Slowik 2010).

These studies on Kasatochi Island are of high significance when compared to similar studies performed after eruptions on Krakatau and Mount St. Helens, because we have knowledge of what organisms lived on Kasatochi Island prior to its eruption. This, along with the fact that Kasatochi Island is highly isolated, makes it an ideal subject for the study of succession. (see fig. 1)

The knowledge we gain from studying Kasatochi island could be a small window into how ecosystems all over the world have been altered or have had to adapt to the changes brought about by nature's forces of destruction, as well as improve our understanding of the changes taking place in Northern ecosystems due to global warming effects.

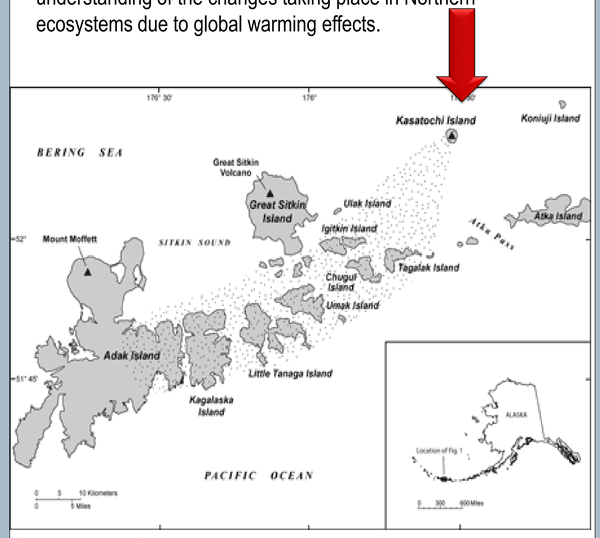


fig. 1 Location of Kasatochi Island in the Aleutian archipelago. alaska.usgs.gov/science/kasatochi/

Kasatochi Island prior to its Eruption

Kasatochi Island after its Eruption Aug, 7, 2008

Materials and Methods

Phase I – Specimen Processing

Before DNA lab work could begin, Kasatochi and other relevant specimens from the 2010 collecting season had to be processed and identified. Approximately 200 specimen lots were processed and data-based in the UAM entomology department. Diptera specimens were further identified by Steve Peek.

In addition, 2009 Kasatochi Diptera specimens returned from loan had their identifications updated in the database and integrated into the UAM insect collection. Other important specimens for this project include 2008 pre-eruption Kasatochi specimens and specimens from the nearby islands of Atka and Great Sitkin.

Phase II –Genetic data and analysis of results

To date, DNA extractions have been successfully completed on 132 pre- and post- eruption Kasatochi specimens using a QIAGEN DNeasy kit. DNA was pulled from two sources for these extractions; tissues (legs pulled from specimens and stored in 100% ETOH) and whole bodies (mounted dry on pins and re-mounted after extractions were completed).

These extractions were done using the University of Alaska Museum (UAM) molecular lab. Upon completion, the success of each extraction was analyzed using a nanodrop spectrophotometer provided by the core lab in the University of Alaska, Fairbanks (UAF) WRRB lab.

We found that whole body extractions yielded much higher ng/ul DNA concentrations (up to 335.8 ng/ul) while tissue extractions yield numbers going only as high as 35.5 ng/ul. Due to the significant differences between sources, DNA is now extracted from whole bodies whenever possible.

Materials and Methods cont.

Once extractions were successfully completed PCRs were performed using standard forward (L-C-1490) and reverse (H-CO-2198) primers. These primers are designed to amplify the CO1 mtDNA gene.

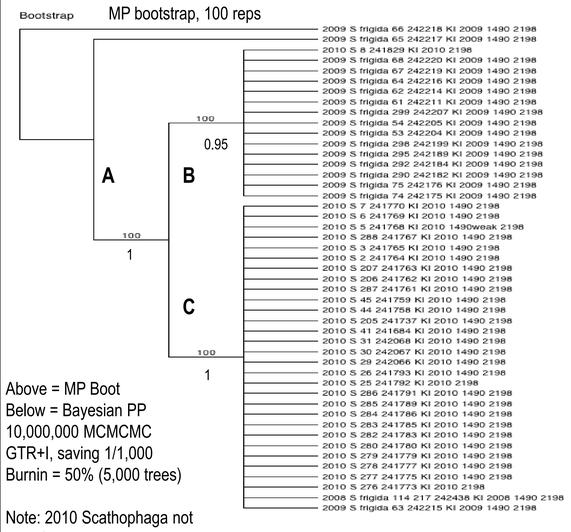
Once enough successfully amplified PCR results were completed to fill a 96 well plate they were sent to the High Throughput Genomics Unit at the University of Washington for rapid DNA sequencing. These sequenced specimens enabled us to complete a genetic comparison of specimens.

Bidirectional sequencing provided two reads of 688 bp for each specimen. These were aligned with each other manually. The software 4 Peaks was used to inspect chromatograms. A final alignment for all samples was prepared in MacClade and verified against its amino acid alignment. PAUP* 4b10 was used to perform Parsimony bootstrapping and MrBayes was used to perform Bayesian analyses. MrModeltest (AIC) chose the GTR+I model. Four independent runs of 10M steps were conducted saving one of every 1000 trees.

Results

Results obtained thus far include: identifications of the 2010 Kasatochi Island and 2009 Atka Island specimens by Steve Peek, the analysis of extraction success as measured using the nanodrop spectrophotometer, and the successful amplification of the mtDNA CO1 gene in 1 pre- eruption and 46 post- eruption (from 2009 and 2010) Kasatochi specimens.

There were large among group distances (4.8-9%) which suggests there are two to three species (A, B, C). The 2008 sample belongs to species rare in 2009 but common in 2010. In 2009 all three species were present, however only 2 species were present in 2010.



Above = MP Boot
Below = Bayesian PP
10,000,000 MCMCMC
GTR+I, saving 1/1,000
Burnin = 50% (5,000 trees)

Note: 2010 Scathophaga not identified to species

Fig. 2 Bootsrap comparison of CO1 gene sequences from 2008 (pre-eruption) , 2009 (1 year post eruption) and 2010 (2 years post eruption) *Scathophaga frigida* specimens from Kasatochi Island.

Conclusions cont.

With these results it is hard to say whether or not the post eruption populations are descended from the 2008 pre-eruption population as only one 2008 sample successfully amplified. Still this sample is 100% identical to most of the 2010 samples which *suggests* survivorship as the origin of post-eruption populations for this species.

Upon completion, this project will help determine how these two groups of insects factor into the re-growth of an ecosystem. The information interpreted in the project will help indicate what the origins of the current insect populations on Kasatochi Island are, and will be prepared as a paper for publication. By answering this question, this project will help other researchers study Kasatochi's new beginnings and better understand the origins of insects on other Aleutian Islands. This is important because it will help us determine the rate at which an ecosystem like the one on Kasatochi can begin reestablishing itself in our Alaskan climate.

In addition, all results of the DNA work and identifications performed during the span of the project will be made available to other scientists online via the UA Museum internet database, ARCTOS along with information about and descriptions of the actual specimens.

Both Phase I and Phase II are yet to be completed on the most recently collected specimens. These specimens were collected from Kasatochi and 10 nearby islands in the summer of 2011 with the help of the University of Alaska Museum and the USFWS.

Future work

The next step in our research will include processing 2011 specimens from 10 island nearby Kasatochi and extracting, amplifying, and sequencing their CO1 genes for analysis. We will amplify the CO2 gene in *Lyrosoma opacum* specimens. If successful these sequences will allow us to analyze pre- and post- eruption populations of a second, less mobile, organism.

Aknowledgements & Literature Cited

Sikes, D. S., Slowik, J. 2010. Terrestrial arthropods of pre- and posteruption Kasatochi Island, Alaska, 2008-2009: A shift from a plant-based to a necromass-based food web. Arctic, Antarctic and Alpine Research. 42: 297-305.

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Support from: Alaska EPSCoR NSF award #EPS-0701898 and the State of Alaska.

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