Endemic Hawaiian Bark Lice: Diverse, Abundant, and Undiscovered

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Why are there so many species on Hawaii?
Hawaii’s Endemic Species

GOALS:
Count & describe species
Document geographic distributions
Observe natural history & ecological interactions
Hawaii’s Endemic Species

GOALS:
Count & describe species
Document geographic distributions
Observe natural history & ecological interactions

→ Conserve species by identifying diversity hotspots & habitats
→ Draw conclusions about the evolutionary history of species
# Hawaii’s Endemic Species

<table>
<thead>
<tr>
<th>Endemic spp.</th>
<th>Single-island endemics</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Drosophila</em> flies</td>
<td>~700</td>
</tr>
<tr>
<td>Kaneshiro et al. 1995</td>
<td></td>
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<tr>
<td>Platynini beetles</td>
<td>128</td>
</tr>
<tr>
<td>Cryan et al. 2001</td>
<td></td>
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<tr>
<td><em>Tetragnatha</em> spiders</td>
<td>60</td>
</tr>
<tr>
<td>Gillespie et al. 1997</td>
<td></td>
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<tr>
<td><em>Laupala</em> crickets</td>
<td>37</td>
</tr>
<tr>
<td>Shaw 2002</td>
<td></td>
</tr>
<tr>
<td><em>Megalagrion</em> damselflies</td>
<td>23</td>
</tr>
<tr>
<td>Jordan et al. 2003</td>
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</tbody>
</table>

*Endemic spp.* indicates the number of endemic species. *Single-island endemics* indicates the percentage of species found only on one island.
Order Psocoptera

- Hemipteroid insects
- ~5000 described species worldwide
- Fungivores or Detritivores:
  Eat fungus & algae from plant surface and plant detritus
Discovery of species diversity

Lienhard & Smithers 2002
Psocids are psso pretty.
Bark Lice in Hawaii

I.W.B. Thornton (1926-2002)

Collected over 9800 psocid specimens in Hawaii.

Described majority of Hawaiian psocid species.
Bark Lice in Hawaii

• 2 endemic genera of Elipsocidae: 
  *Palistreptus*: 20 species 
  *Kilauella*: 7 spp. described, 100’s undescribed

• 1 genus of Psocidae: 
  *Ptycta*: 61 spp. Hawaiian endemics 
  ~170 spp. Worldwide

• Non-native bark lice: 20 genera, 50 species
Bark Lice in Hawaii

Ecological roles:

1. Primary consumers of fungus, algae, and lichen

2. Recyclers of dead plant material

3. FOOD FOR BIRDS
Studying Hawaiian Bark Lice

1. Collections & locality data
2. Morphological study
3. DNA extraction & sequencing
4. Molecular phylogenetics: build species trees
5. Describe a bunch of new species
Studying Hawaiian Bark Lice

1. Collections & locality data
2. Morphological study
3. DNA extraction & sequencing
4. Molecular phylogenetics: build species trees
5. Describe a bunch of new species
6. Think deep thoughts… what can bark lice can tell us about how evolution works?
Collecting: Where do *Ptycta* live?

**Forests** above 1000 ft.

- Koa or O’hia dominant
- Mesic to damp

**Trees & shrubs**

- with fungus or lichen on bark & leaves

And wherever else they feel like it!
METHODS
Morphological Study
METHODS
Phylogenetic Relationships

• Morphology: matrix of ~70 characters
• Mitochondrial genes: 12S, 16S, COI, ND5
• Nuclear genes: wingless, Ef1α

• Outgroups: Ptycta from outside Hawaii and closely related genera
RESULTS
Molecular phylogenetics

12S mtDNA
373 aligned basepairs
ML tree (GTR+I+G)
Bootstrap values: \( \frac{\text{ML}}{\text{parsimony}} \)
RESULTS

wingless nDNA + 12S mtDNA
694 aligned basepairs

ML parsimony
RESULTS

wingless nDNA + 12S mtDNA
694 aligned basepairs

ML parsimony

Ptycta colonized Hawaii twice
RESULTS

Back to Fiji
Rates of speciation

How quickly can new species evolve?

Number of endemic species on an island
age of the island
Rates of speciation

How quickly can new species evolve?

(Number of endemic species on an island)
(age of the island)

\[ \ln(\text{sp#}) \]
(age of island)

(McCune 1997)
### Rates of speciation

<table>
<thead>
<tr>
<th>Species</th>
<th>Number of Species</th>
<th>Rate of Speciation</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Drosophila</em> flies</td>
<td>~700</td>
<td>1.20 spp/my</td>
</tr>
<tr>
<td><em>Tetragnatha</em> spiders</td>
<td>60</td>
<td>0.82 spp/my</td>
</tr>
<tr>
<td><em>Laupala</em> crickets</td>
<td>6 (Big Island only)</td>
<td>4.17 spp/my</td>
</tr>
<tr>
<td><em>Hyleaus</em> bees</td>
<td>60</td>
<td>9.23 spp/my</td>
</tr>
<tr>
<td><em>Ptycta</em> barklice</td>
<td>&gt;100</td>
<td>~9 spp/my (2 lineages)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>&gt;11 spp/my (1 lineage)</td>
</tr>
</tbody>
</table>

Reference:
Coyne & Orr 2004
Gillespie et al. 1997
Mendelson & Shaw 2006
Magnacca & Danforth 2006
Results Summary

1. Hawaiian Ptycta are more diverse than currently described.
2. Ptycta may have colonized Hawaii twice.
3. Ptycta may have colonized the youngest island first.
4. Speciation rates of Ptycta may be exceptionally high.
How can you help?

• Collecting continues!
  – Seeking collecting sites on the Big Island and Oahu
  – Keep an eye out for bark lice. Let me know if you see some nice ones.

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A boatload of thanks…

DOFAW & NARS
Betsy Gange
John Cumming
Lisa Hadway
Steve Bergfeld

HAWAII STATE PARKS
Michelle Hookano
Holly McEldowney
Wayne Souza
Galen Kawakami

THE NATURE CONSERVANCY
Stefanie Loo Jefts
Lynette Williams
Russell Kallstrom
Couldn’t do it without…

NATIONAL PARKS
Guy Hughes
Patti Welton
Rhonda Loh

BISHOP MUSEUM
Keith Arakaki
Shep Myers
Dan Polhemus
Hunter Polhemus
Diana Crow
Paul Krushelyntcyk
Dan Rubinoff
Becca Carter
Diana Percy
Neil Miller
Luc LeBlanc
Mary Merello, Missouri Botanical Garden

Kevin Johnson, Illinois Natural History Survey
Ed Mockford, Illinois State Univ.
at Haleakala Summit
Bob, Phil, Marcos & Ambrose
TNC Lanai
Pat Bily, TNC Maui
Jill, Chris, Allison, and John
West Maui Mountains Watershed Partnership
More thanks to…

Kazunori Yoshizawa, Hokkaido U
Chris Dietrich, INHS
Jim Whitfield, UIUC
Andrew Suarez, UIUC
Stephen Cameron, CSIRO
Courtenay Smithers, AM
David Britton, AM

Funding:
National Science Foundation EAPSI & DDIG programs
Japan Society for the Promotion of Science
Australian Academy of Science
Society of Systematic Biologists
Illinois State Academy of Science
University of Illinois School of Integrative Biology
University of Illinois Graduate School
Australian Museum Postgraduate Award
Coxal organ morphology
HYPOTHESIS
Stepping-stone pattern
HYPOTHESIS
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HYPOTHESIS
Stepping-stone pattern
Does Ptycta follow the stepping stone pattern?
Endemicity in Hawaii

>9000 endemic species
~6000 endemic arthropods
Descended from ~250 ancestral immigrants
Geologic Isolation

- Niihau: 5.1 my
- Kauai: 5.1 my
- Oahu: 3.7 my
- Molokai: 1.8 my
- Lanai: 1.3 my
- Maui: 1.3 my
- Kahoolawe: 1.0 my
- Hawaii: 0.4 my
Order Psocoptera

- Hemipteroid insects
- ~5000 described species worldwide

Bark Lice in Hawaii

2 endemic genera (7 spp. & 20 spp.)
1 native genus: **Ptycta**
   - 61 spp. in Hawaii
   - 170 spp. worldwide
   - Center of diversity Pacific Islands
Rates of speciation

How quickly can new species evolve?
Morphology vs Molecules

12S mtDNA, 373 aligned basepairs
ML tree (GTR+I+G)
Bootstrap values: ML parsimony

0.01 substitutions/site
Morphology vs Molecules

12S mtDNA, 373 aligned basepairs
ML tree (GTR+I+G)
Bootstrap values: ML parsimony

Msp #4
Msp #5

K  O  M  H

Copostigma sp., French Polynesia
Ptycta sp., Australia (r)
P. johnsoni, Japan
P. polluta, Illinois
Ptycta sp., Australia (t)
Copostigma sp., Australia (u)
Oreopsocus buholzeri, Switzerland

BIG ISLAND

WIDESPREAD CLADE

Ptycta sp. 1
Ptycta sp. 2
Ptycta sp. 3
Ptycta sp. 4
Ptycta sp. 5
Ptycta sp. 6
Ptycta sp. 7
Ptycta sp. 8
Ptycta sp. 9
Ptycta sp. 10
Ptycta sp. 11
Ptycta sp. 12
Ptycta sp. 13
Ptycta sp. 14
Ptycta sp. 15
Ptycta sp. 16
Ptycta sp. 17
Ptycta sp. 18
Ptycta sp. 19

0.01 substitutions/site
Cryptic species

12S mtDNA, 373 aligned basepairs
ML tree (GTR+I+G)
Bootstrap values: $\frac{ML}{parsimony}$