Transposable elements are mobile DNA.

Transposable elements can drive genome evolution.

- Material for homologous recombination and genome reorganization
- Contribute protein-coding sequences to host
- Changing expression of nearby genes

Presentation Outline

- Transposable elements and species' histories
  - Transposable elements
  - Genomic effects of species' history
- Cardiocondyla obscurior
  - A model of an invasive organism
- C. obscurior contains TE islands
  - Depleted for conserved processes
  - Differentially expressed
- Two invasive and diverged lineages
  - TE islands are faster-evolving between lineages.
  - Interplay between TE-activity and life history.

TE accumulation can occur through reduced effective population size.

Presentation Outline

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  - Constraints on genetic diversity
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**Cardiocondyla obscurior**

- Small colonies
- Globally invasive
- Inbreeding and sexual selection within colonies.

**C. obscurior** is an invasive species

![Map of Cardiocondyla obscurior distribution](image)

Lukas Schrader

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**An Ideal Laboratory Model**

- Sequencing
  - 454 Titanium FLX from 100’s of diploid Brazilian females
  - 200 bp Illumina HiSeq2000 from five haploid Brazilian males
- Assembly
  - MSRA
  - 187.5 Mbp reference genome
  - N50 length: 2.8 Mbp
  - 11,094 scaffolds
- Annotation
  - 454 RNAseq from all castes and developmental stages
  - MAKER 2.0
  - 17,552 genes
- Quality Control
  - Filtered for prokaryotic scaffolds
  - Reduced to 1,854 scaffolds and 177.9 Mbp
  - No reduction in gene count

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**Cardiocondyla obscurior has the smallest genome assembly of any ant**

- 177.9 Mbp reference assembly
- Previous smallest
  - *Linepithema humiler*; 215 Mbp assembly

**Among ants, genome size is negatively correlated to exon content**

![Graph of genome size vs exon content](image)

- A. *S. invicta*
- B. *A. cephalotes*
- C. *A. echinatior*
- D. *H. saltator*
- E. *C. floridanus*
- F. *P. barbatus*
- G. *L. humiler*
- H. *C. obscurior*
But not intron content


C. obscurior has about the same proportion of TEs as other ants.

Among ants, genome size is positively correlated with simple repeat content

But not with class 1 or class 2 TE content.

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TEs are organized into TE islands.

**Low-density regions (LDRs) Low-density regions (LDRs)**

- 7.18% (12.78Mbp) of reference is TE islands which contain:
  - 27.54% (4.92Mbp) of TEs.

But it’s TEs are organized differently compared to other ants

- 7.18% (12.78Mbp) of reference is TE islands which contain:
  - 27.54% (4.92Mbp) of TEs.

The pattern of TE islands in *C. obscurior* is more similar to *Nasonia* than other ants.

Orange: TE islands
Blue: Low-density regions

TE island regions are depleted for conserved processes.

- 2-tailed GO analysis
  - 59 GO terms associated with conserved processes are under-represented in TE islands
    - Cytoskeleton organization, ATP binding, organ morphogenesis
  - 18 GO terms are over represented
    - 4 olfactory receptors
    - 12 TE-derived

How are TE island genes expressed?

- RNAseq of seven queen larvae (17 Gbp)
- RNAseq of seven queens (14 Gbp)
- Mean normalized expression with DESeq2
TE island genes are overexpressed in adult queens compared to larvae.

Brazilian and Japanese lineages differ in a number of phenotypes.

Both lineages have approximately the same number of workers per colony.

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Queens and workers from Japanese lineage are significantly larger than Brazilian queens and workers.

Japanese colonies have approximately twice the number of queens.
Brazilian colonies are more aggressive than Japanese colonies.

How do these phenotypically different lineages differ genomicsly?
- DNA Illumina resequencing
  - Brazilian and Japanese male pupae (haploid)
  - 60X pooled coverage for each population

Coverage differs most between lineages in TE island regions.
- Interplay between genome organization and life history and possibly adaptation.
  - *C. obscurior* is a successful invasive insect and model organism.
  - TEs in *C. obscurior* are organized in TE islands.
  - Genes important for development are excluded from TE islands.
  - TE island genes are preferentially expressed in adult queens.
  - Generated exonic variants between Japanese and Brazilian lineages.
Future Directions

• Tie differences in genomics to phenotypic differences in lineages.

• Which TEs are actively proliferating in *C. obscurior*?
  – How does this differ between the lab cultivated lineages?

• Are there TE islands in other insects?
  – *Nasonia vitripennis*
  – Beyond hymenopterans?

Questions?

Acknowledgments

• Jürgen Heinze lab
  – Jan Oettler
  – Antonia Klein
  – Lukas Schrader
  – Katharina Wyschetzki
  – Tobias Weichselgarner

• Johannes Stökl
• Eva Schultner
• Aleksey Zimin
• Mark Yandell lab
• Jay W. Kim
• Christopher D. Smith
• Carsten Kemena
• Yannick Wurm
• Jürgen Gadau

DFG grant Hu662/31