Evolution and invasion in the Asteraceae

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Evolution and invasion

What type of evolutionary changes occur during invasion?

What is the molecular basis of these changes?
Evolution and invasion

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What is the molecular basis of these changes?

Are adaptations in introduced range from standing variation or new mutations?

Are parallel clines due to variation at the same loci?

Are the same mutations, loci or genomic regions involved across multiple invasion fronts or between species?
Evolution and invasion
Evolution and invasion

Trade-offs

Hybridization

Trade-offs vs. defence/abiotic tolerance
Common ragweed

wind pollinated, self-incompatible, monecious annual

native to North America

introduced in Europe, Asia and Australia

problematic weed (sunflower, soybean, corn)

severely allergenic (hay fever)
Introduced plants are larger than native.

Phenotypic differentiation

Maximum width (cm)

Leaf number

Introduced

Native

$P<0.001$

 Introduced

Native

range $P<0.001$

Reproductive biomass (g)

Control

Herbivory

Light

Nutrient

Hodgins & Rieseberg 2011
Phenotypic differentiation

Drought stressed introduced plants died more

Hodgins & Rieseberg 2011
Introduced plants grow larger and have greater reproductive success in benign and some stressful environments

Introduced plants have poor survival under drought conditions suggesting a trade-off

Similar patterns in other Asteraceae species (yellow starthistle, Canada thistle, diffuse knapweed, common sunflower)
Molecular basis of invasiveness

What is the molecular basis of these evolutionary changes?

Are there expression differences between native and introduced populations?
  - candidate genes
  - functional groups?

What genes show evidence of positive selection in introduced genotypes?
  - repeated changes among species

Is there evidence of higher genetic load in introductions?
Transcriptome resources

22 assemblies across 11 species

(Lai et al. 2012)
Gene expression

differential expression: range = 180; treatment*range=103

Hodgins et al. 2013 ME
Gene expression

secondary metabolism
stress response
detoxification
aromatic amino acid

phenylpropanoids
cinnamate 4-hydroxylase
terpenoids
(-)-a-terpineol synthase
sesquiterpenes
beta-caryophyllene synthase
sesquiterpene cyclase
amorphadiene synthase
flavonoids
flavonoid 3'-hydroxylase

Hodgins et al. 2013 ME
Comparisons of native and introduced transcriptomes

Most genes with high dN/dS between the native and introduced genotypes are unique to the species

Hodgins et al. 2015 ME
Genetic load estimated with Provean

No evidence of higher load in introduced vs native samples

Ambrosia artemisiifolia Ambrosia trifida Centaurea diffusa Centaurea solstitialis Cirsium arvense Helianthus annuus

Deleterious Tolerated

Hodgins et al. 2015 ME
Stucture of native and introduced common ragweed

948 GBS loci
281 individuals

Evidence of western and eastern North American cluster and admixture in the introduced range
Summary

Gene expression differences between native and introduced common ragweed
- few genes involved, secondary compounds, stress

Selection is variable among lineages and sites
- limited evidence for repeated genetic changes

No evidence of more deleterious substitutions in introductions
Current projects

Development of a reference genome
  - PE (40X), MP libraries (20x), MiSeq (8x), Dovetail Genomics
  - improved transcriptome, F1 genetic map

Genotype by sequencing
  - invasion history
  - candidate adaptive loci (climate)

Whole genome re-sequencing of native and introduced genotypes from Australia, NA and Europe
  - candidate “invasion” loci
Acknowledgements

Rieseberg lab
   - Alessia Guggisberg
   - Zhao Lai
   - Jie Huang
   - Nolan Kane
   - Rob Colautti
   - Qian Yu

Mike Martin

NSERC
Genome Canada

Levente Kiss
Francois Bretagnolle