Population genetics of the invasive honey locust (*Gleditsia triacanthos*) using AFLP’s

A comparison between native and invasive ranges

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What is an invasive species?

- an organism which colonises a new geographic location outside of its native range and disrupts local ecosystems
  - egs. blackberry, *Lantana*, rabbit
- why are some species capable of invading?
  - escape from enemies/competition
  - life history traits (high reproductive rates, good dispersal capabilities)
- plant specific traits
  - vegetative reproduction
  - generalist pollinator syndrome
  - tolerance of varying environmental conditions

Invasive species and evolution

- population genetic consequences
  - founder effects
  - genetic drift
  - gene flow – which arises from high dispersal of seeds and pollen.
- novel selective pressures (evolution of different traits)
  - the evolution of different traits
- Therefore, microevolutionary changes and macroevolutionary changes

Honey locust as an invader in Australia

- dioecious, leguminous tree native to the US
  - floating seed pods (dispersal)
  - edible seed pods (dispersal)
- ~30 seeds/pod, lots of pods
- short generation time (3-5 years)
- generalist pollination syndrome
- often utilised by people

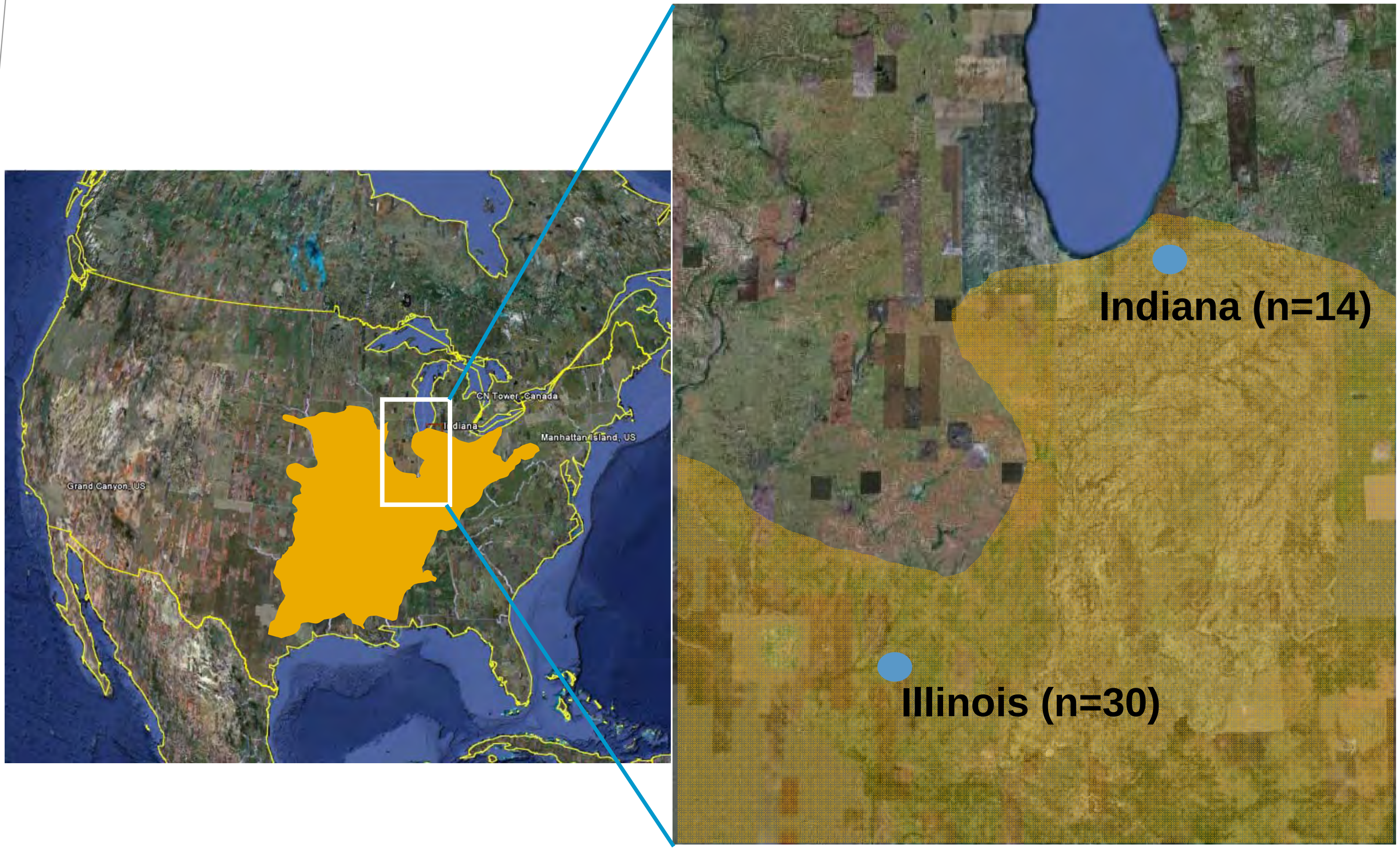
Honey locust as an invader in Australia

- Queensland
  - 1907 – first plantings by McConnel
  - 1955 – noticed as a pest in Esk Shire (“McConnel’s curse”)
  - 1993 – declared a noxious weed
  - 1994 – eradication begins
- NSW
  - mid-20th Century plantings in NSW (Camden Park)
  - no eradication program
- Canberra
  - planted as a street tree
  - new populations along Molongolo River

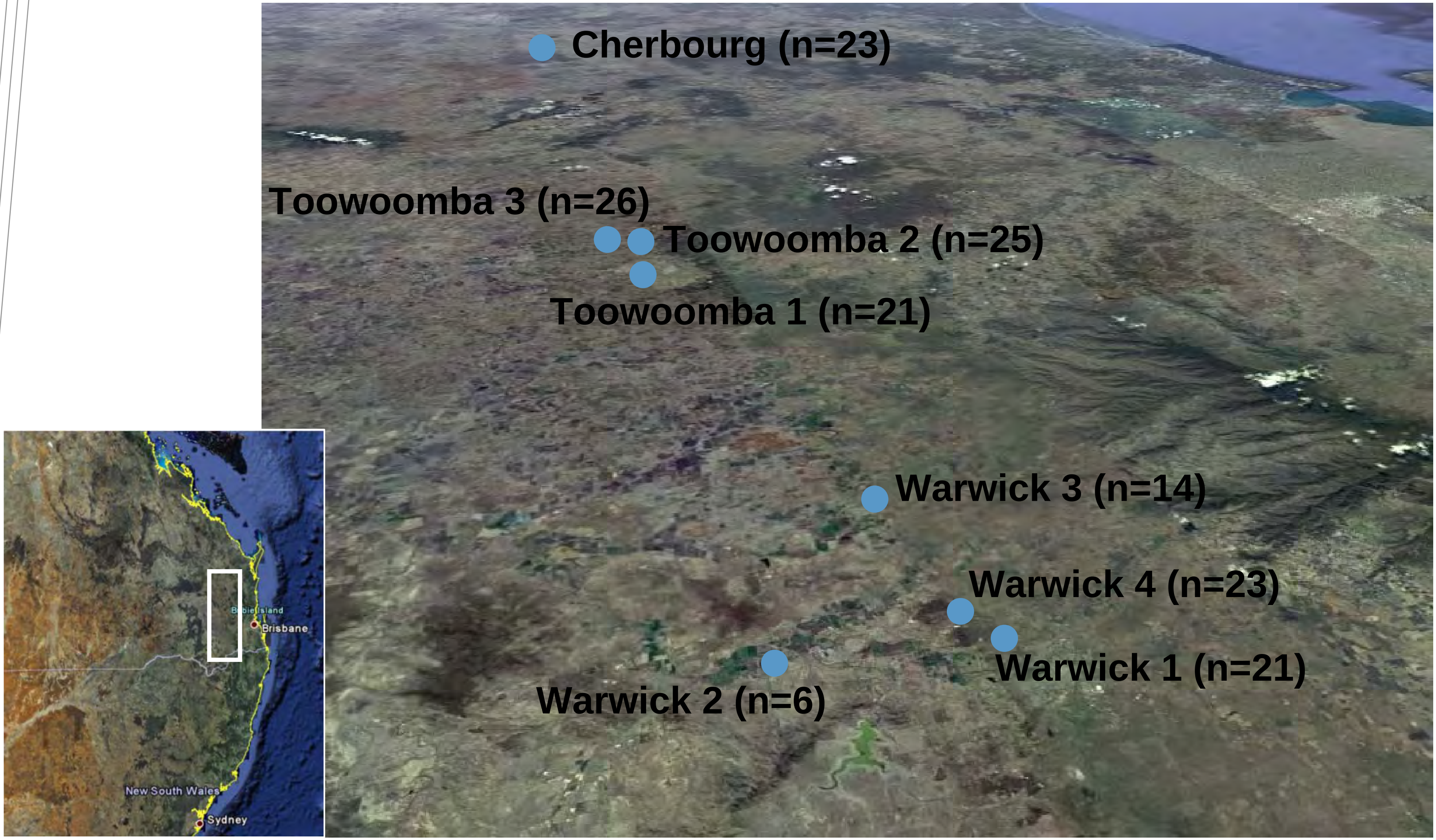
Predictions

- Why study the honey locust?
  - a successful invader with known history
  - clear population genetic predictions
- QLD populations will have lower genetic diversity than U.S populations
  - the founder effect
- QLD populations will be genetically similar to each other
  - gene flow between populations
- QLD populations will be genetically similar to US populations
  - limited time for changes to occur

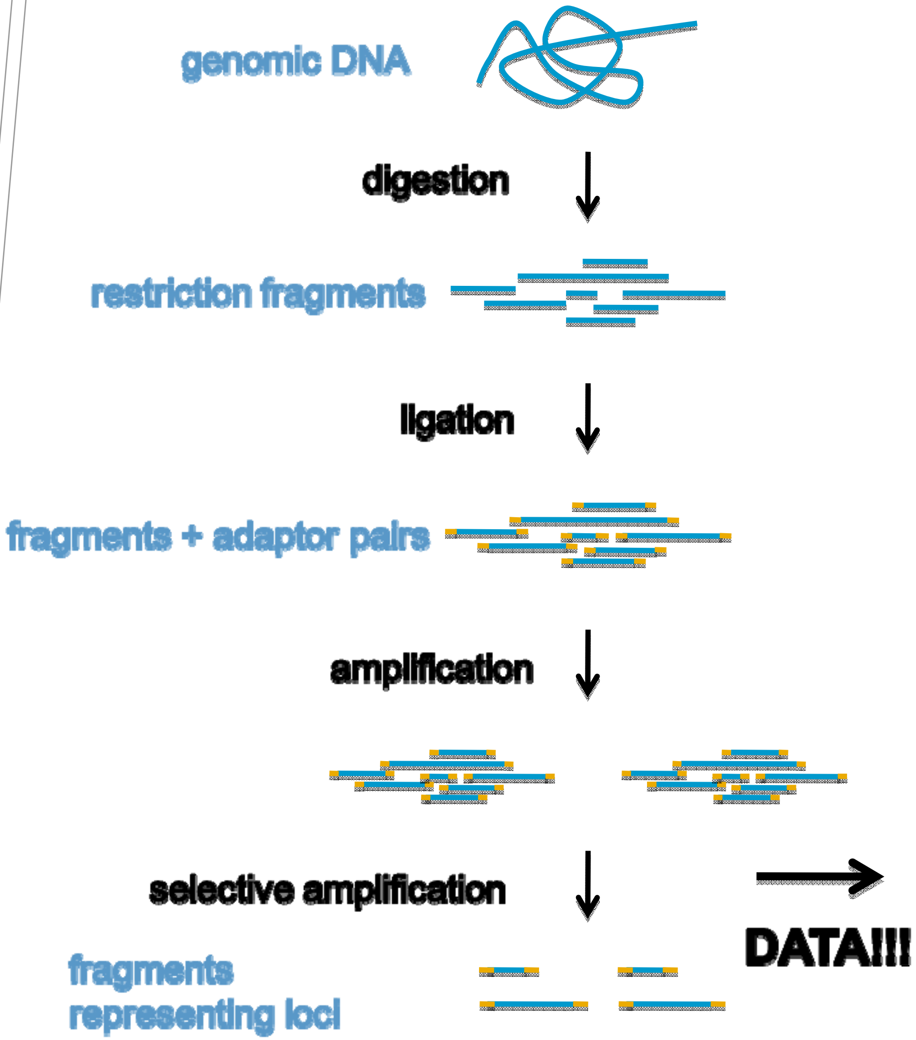
Distribution in the United States



South East Queensland



Amplified Fragment Length Polymorphism (AFLP)



genomic DNA

digestion

restriction fragments

ligation

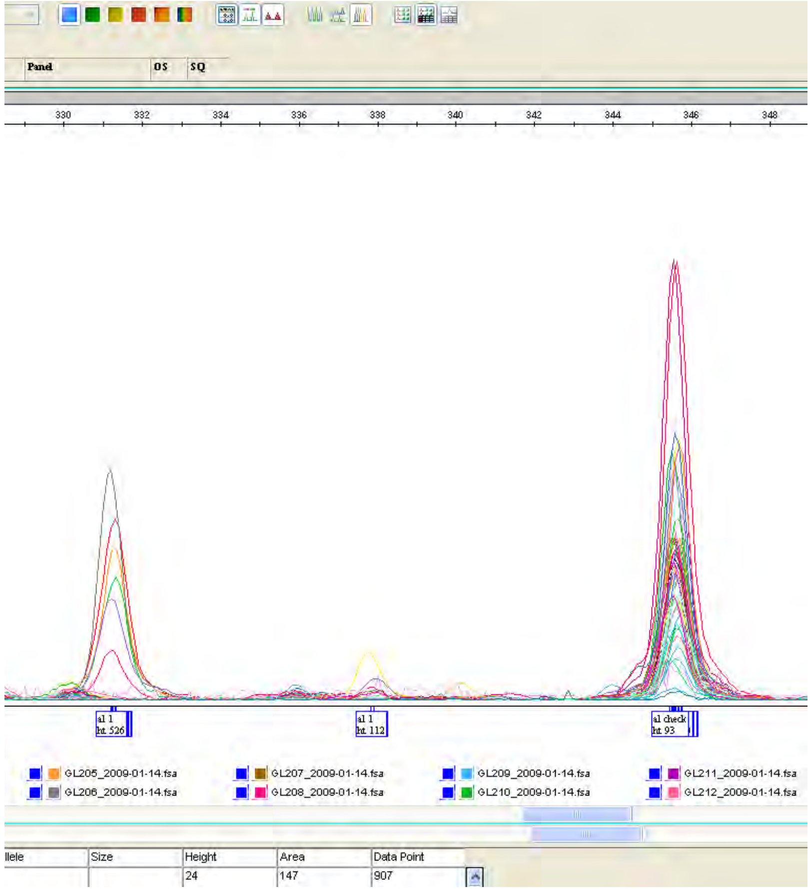
fragments + adaptor pairs

amplification

selective amplification

fragments
representing loci

DATA!!!



llele	Size	Height	Area	Data Point
		24	147	907

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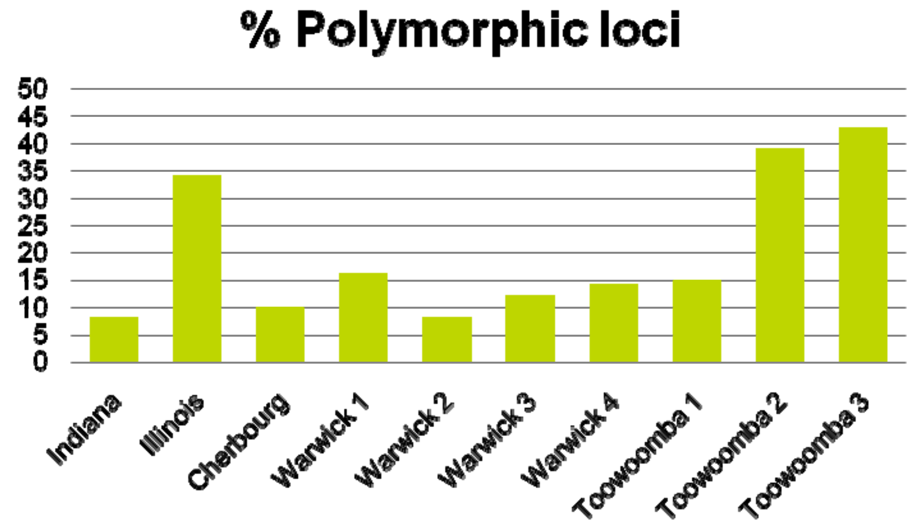
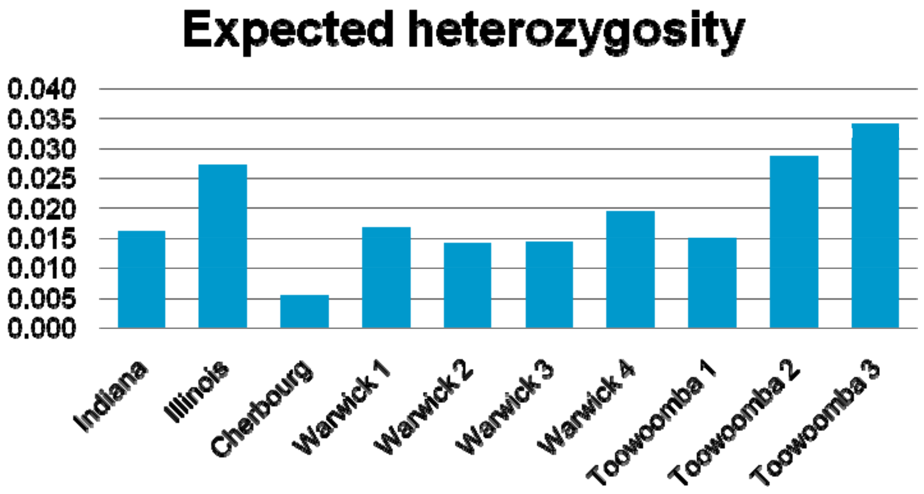
Genetic diversity within populations

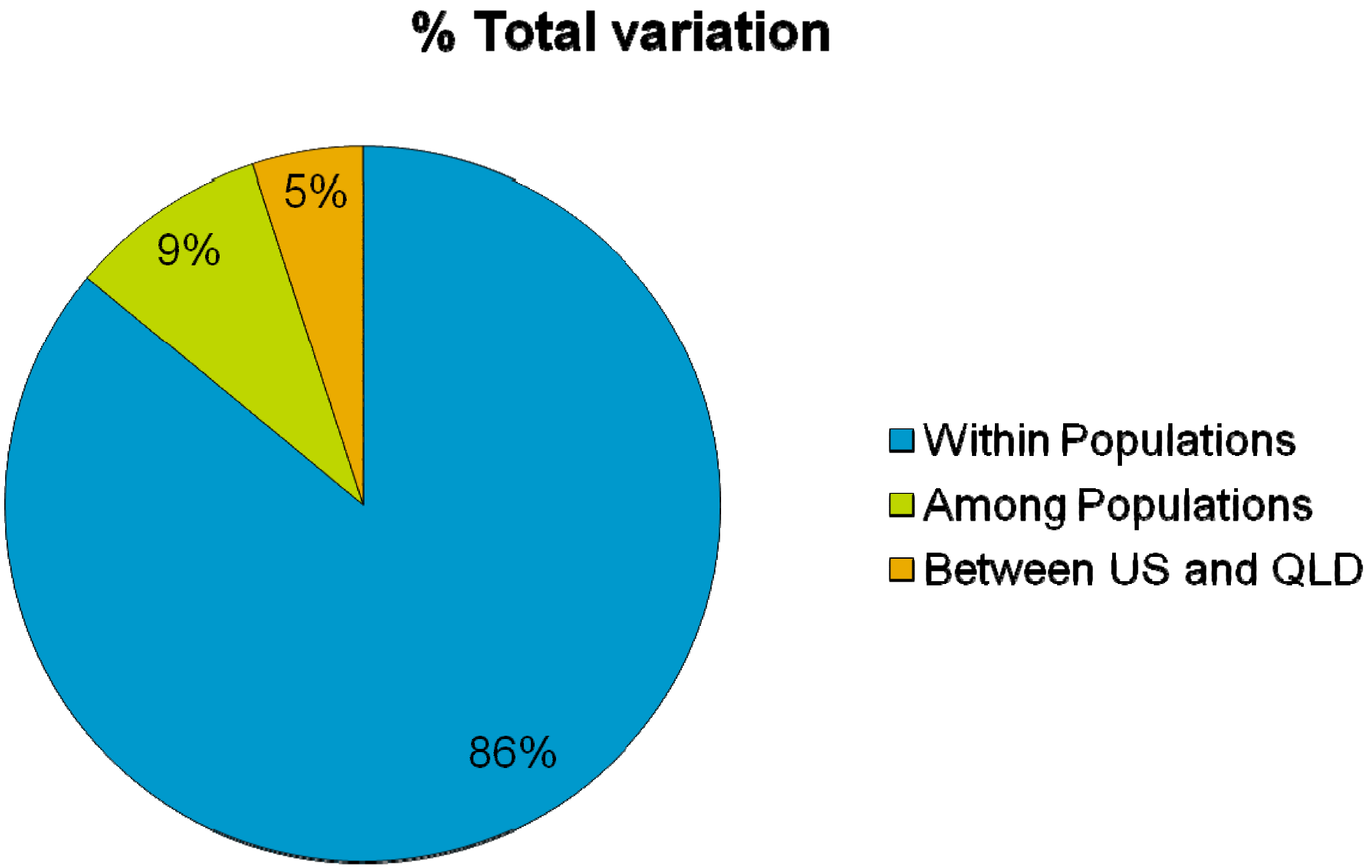


Allozyme estimate = 62%
(from native range)

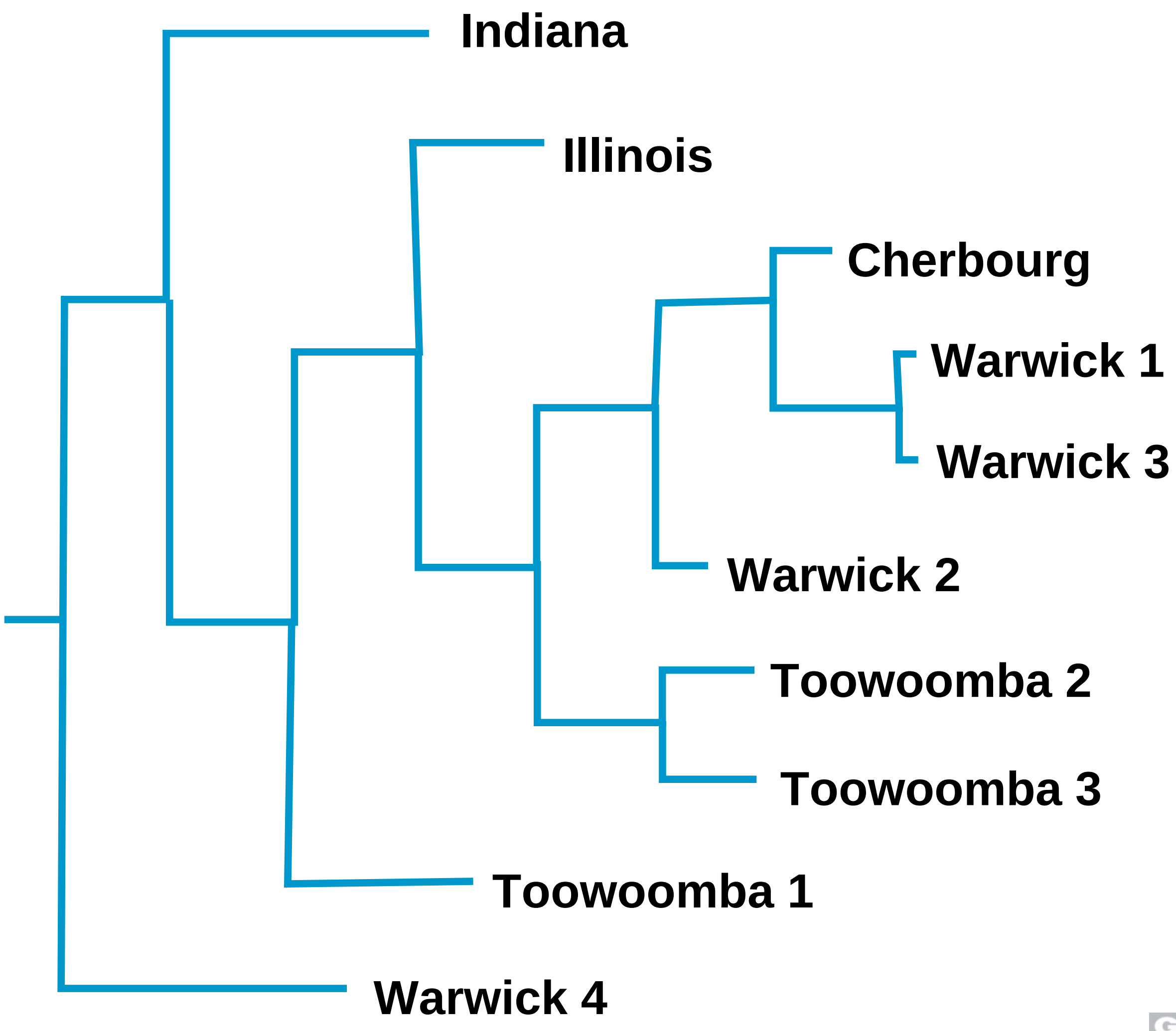


Allozyme estimate = 19.8%
(from native range)

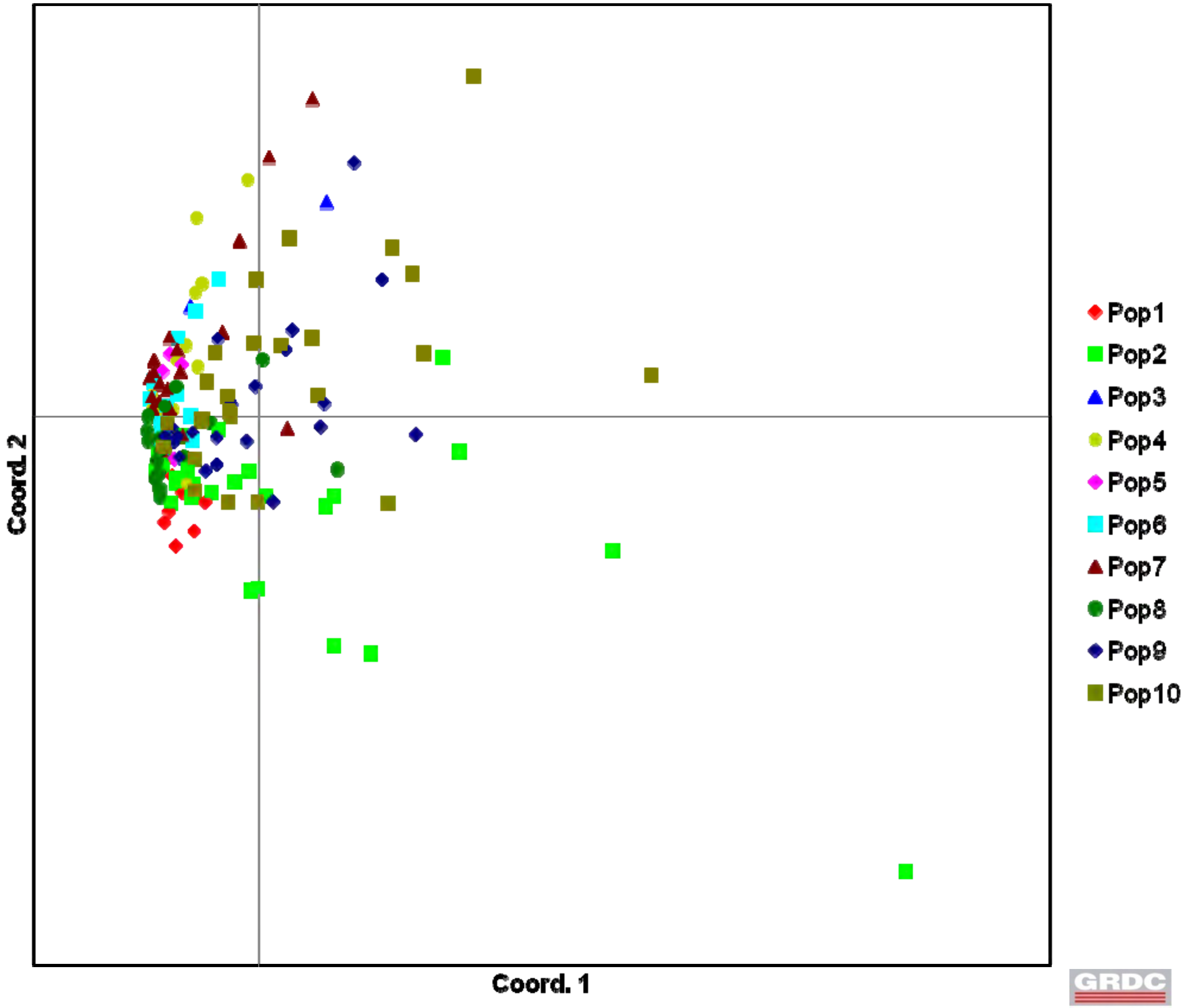
Analysis of Molecular Variance



UPGMA dendrogram



Principle Coordinates Analysis



Summary of results

- low levels of diversity in all populations
  - consistent with predictions of low genetic diversity in Australian populations
  - inconsistent with predictions for US populations
- QLD populations are genetically similar
- native and invasive populations are genetically similar
- Conculsion: little microevolutionary change in invading populations

Future Directions

- conduct analyses on more populations over a wider geographical area
  - more populations from the US
  - include NSW populations
- reanalyse loci, increase number of loci

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