

# Phylogeography of *Cactoblastis cactorum* (Lepidoptera: Pyralidae) in the southeastern USA based on fragments of the mitochondrial gene COI.



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# Background

From Zimmermann et al. (2000)  
and Hight et al. (2002)

- Introduced to the Caribbean (Nevis) in 1957 and other islands later.
- Recorded on Big Pine Key, Florida in 1989.
- Starting 1993 the moth spread quickly along the western and eastern coasts of Florida.

# Questions

- Where did *C. cactorum* come from?
- One or several introductions?
- Geographical pattern?

# Materials and methods

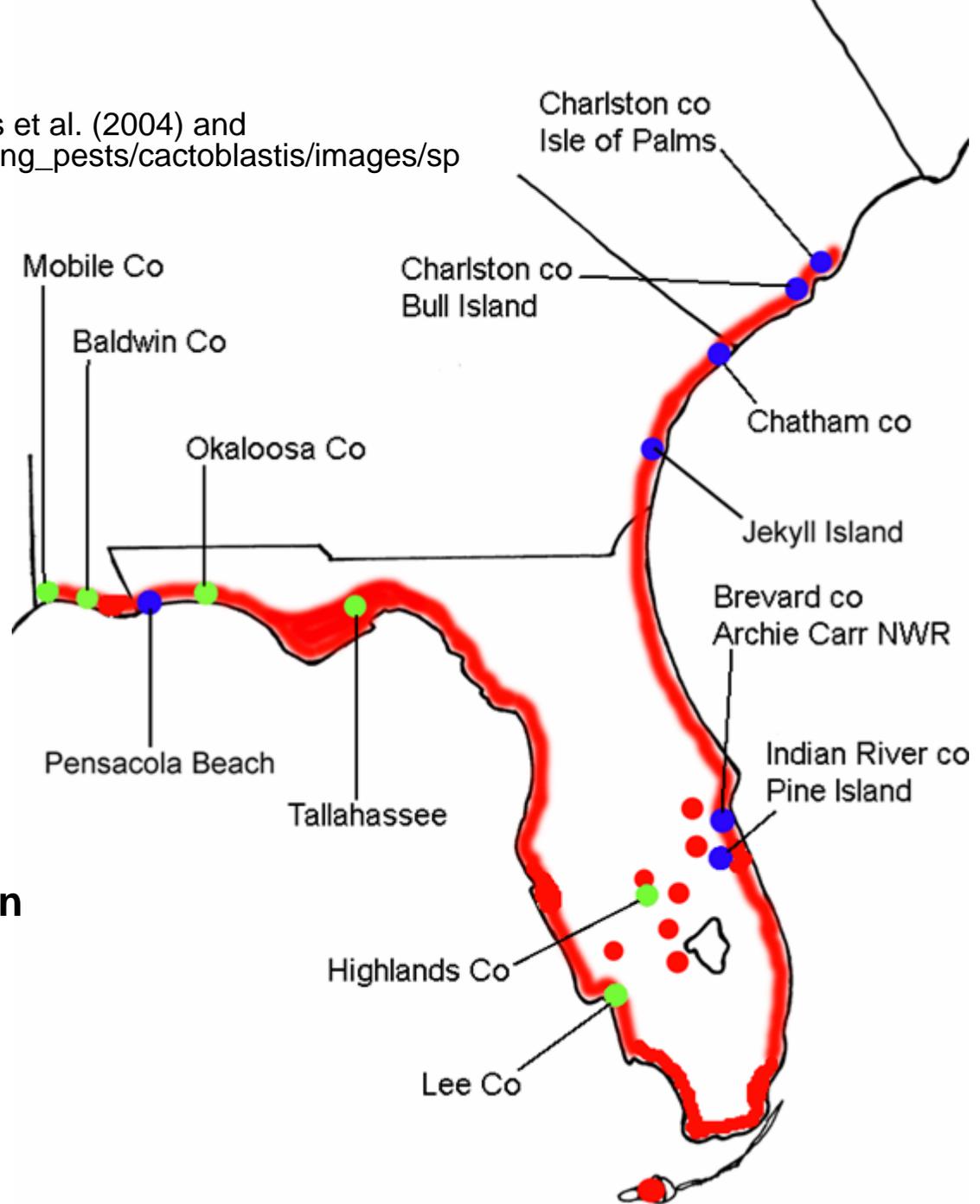
- 769 bp of COI were sequenced from 80 specimens from 20 localities:
  - Florida
    - Okaloosa Co
    - Sarasoto Co
    - Santa Rosa Co.
    - Tallahassee
    - Highlands Co.
    - Brevard Co
    - Indian River Co
  - Alabama
    - Baldwin Co.
    - Mobile Co.
  - Georgia
    - Chatham Co., Cockspur Isl.
    - Glynn Co. Jekyll Isl.
  - South Carolina
    - Charleston Co., Isle of Palms
    - Charleston Co., Cape Romain
  - Puerto Rico, 3 (2)
  - Dominican Republic, 1
  - South Africa, 1
  - Australia, 1
  - Mexico, Islas Mujeres
  - Hawaii
- Specimens were conserved in 95-100% ethanol or - in one case – in vodka!
- Parsimony based phylogeographical analyses were carried out in PAUP\* and NONA
- Nested clade analysis (Templeton et al. 1995, Templeton 1998, 2004) was carried out automatically after to Panchal (2007), on 731bp.

# Taxon sampling

Distribution, after Hight et al. (2002), Solis et al. (2004) and [http://www.aphis.usda.gov/ppq/ep/emerging\\_pests/cactoblastis/images/sp](http://www.aphis.usda.gov/ppq/ep/emerging_pests/cactoblastis/images/sp)

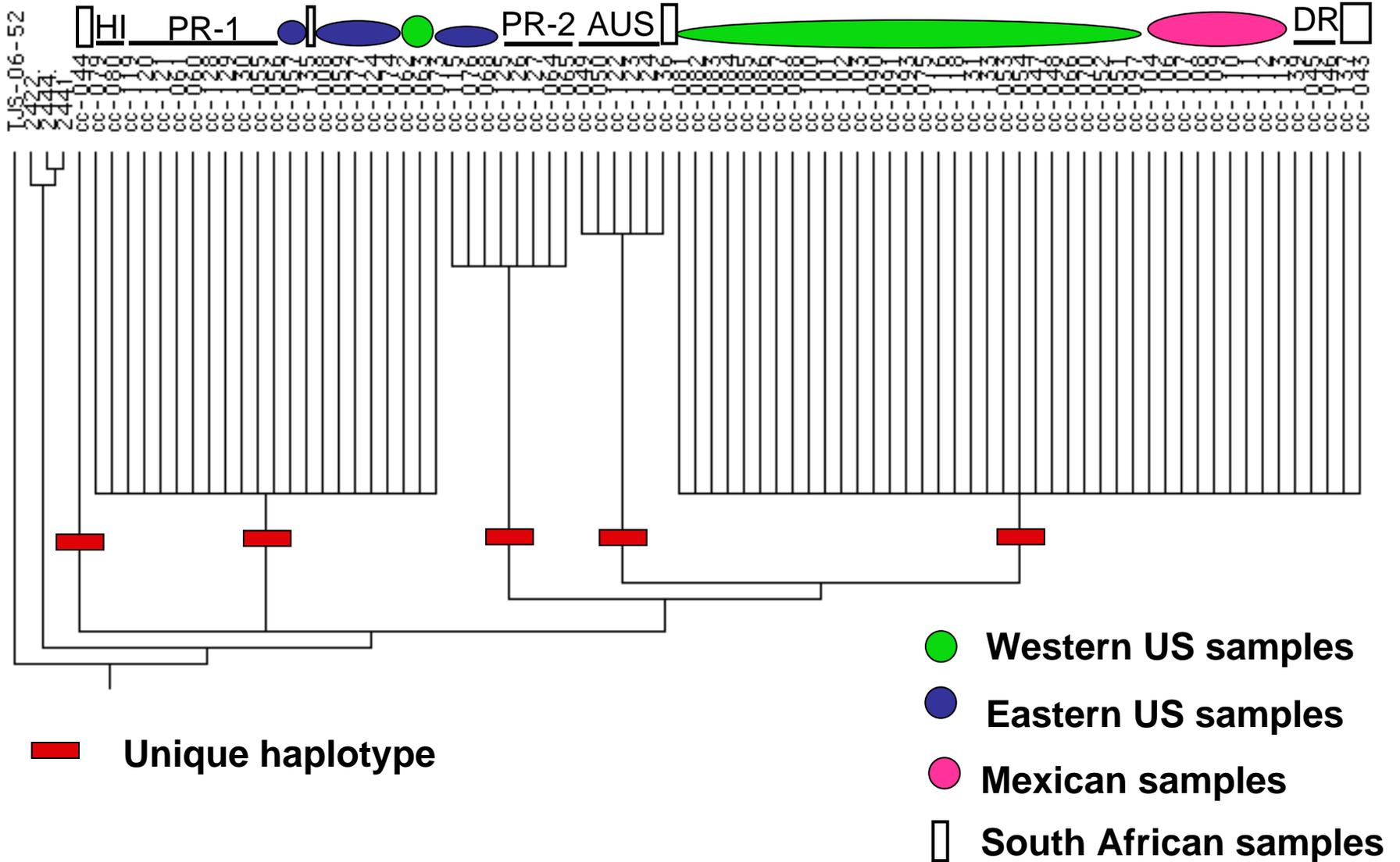
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- Approximate distribution
- Western haplotype
- Eastern haplotypes



# Results

Majority rule consensus three from six most parsimonious trees



# Results

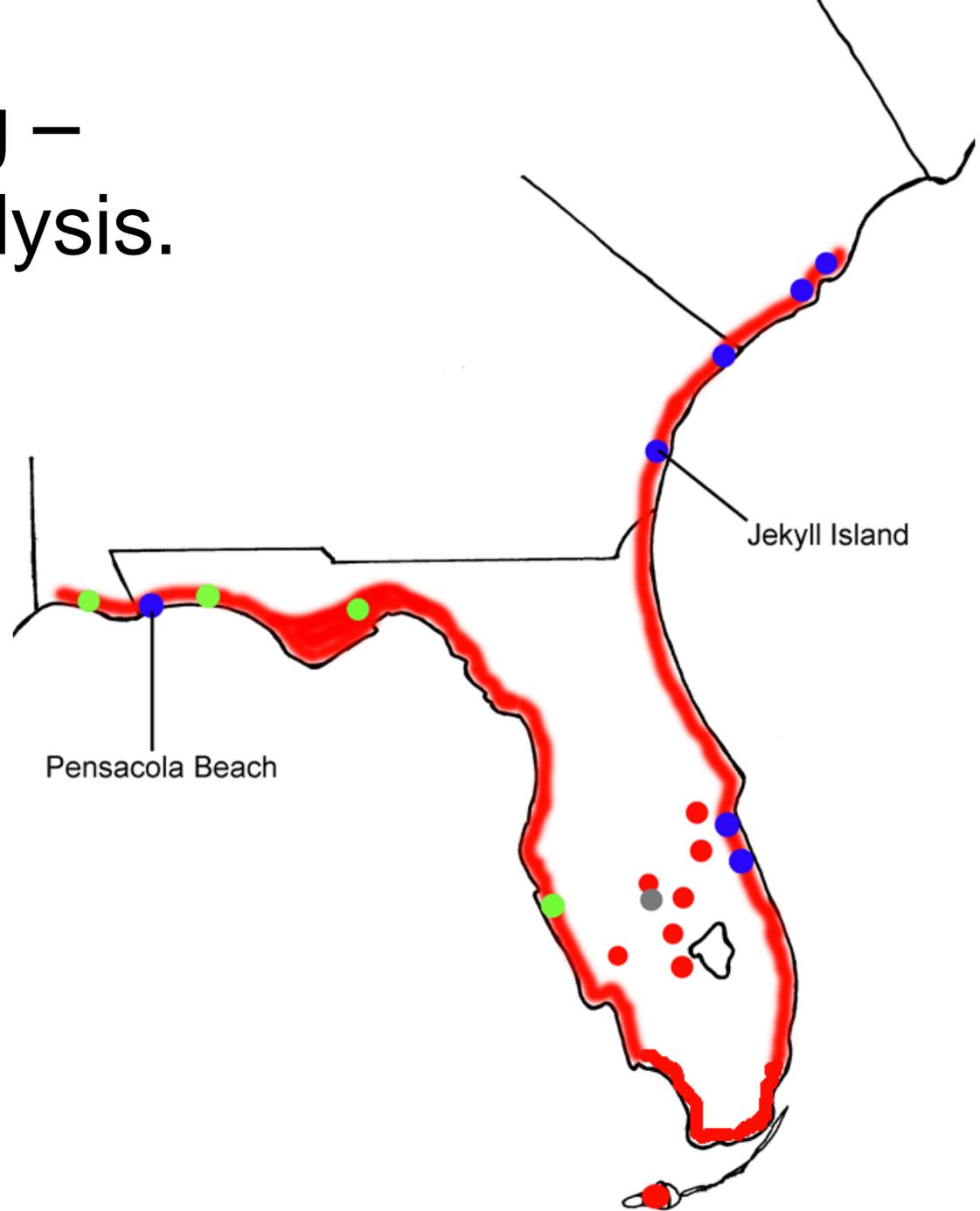
- Five distinct haplotypes were identified, displaying a clear geographical pattern.
- Mexican and most “western” US samples shared haplotype with samples from the Dominican Republic.
- The western group is closer to Australian samples than to “eastern” US samples.
- One western locality groups with eastern samples, being 0.5% different from other western samples.
- Are 769 bp sufficient data to resolve the patterns?

# Preliminary analysis

- 1080 bp of COI were sequenced from 31 specimens from 16 localities:
  - Florida, 6
  - Alabama, 1
  - Georgia, 2
  - South Carolina, 2
  - Puerto Rico, 2 (3)
  - Dominican Republic, 1
  - South Africa, 1
  - Australia, 1
- Parsimony based phylogeographical analyses were carried out in PAUP\* and NONA

# Taxon sampling – preliminary analysis.

- Western haplotype
- Eastern haplotypes
- Not sequenced

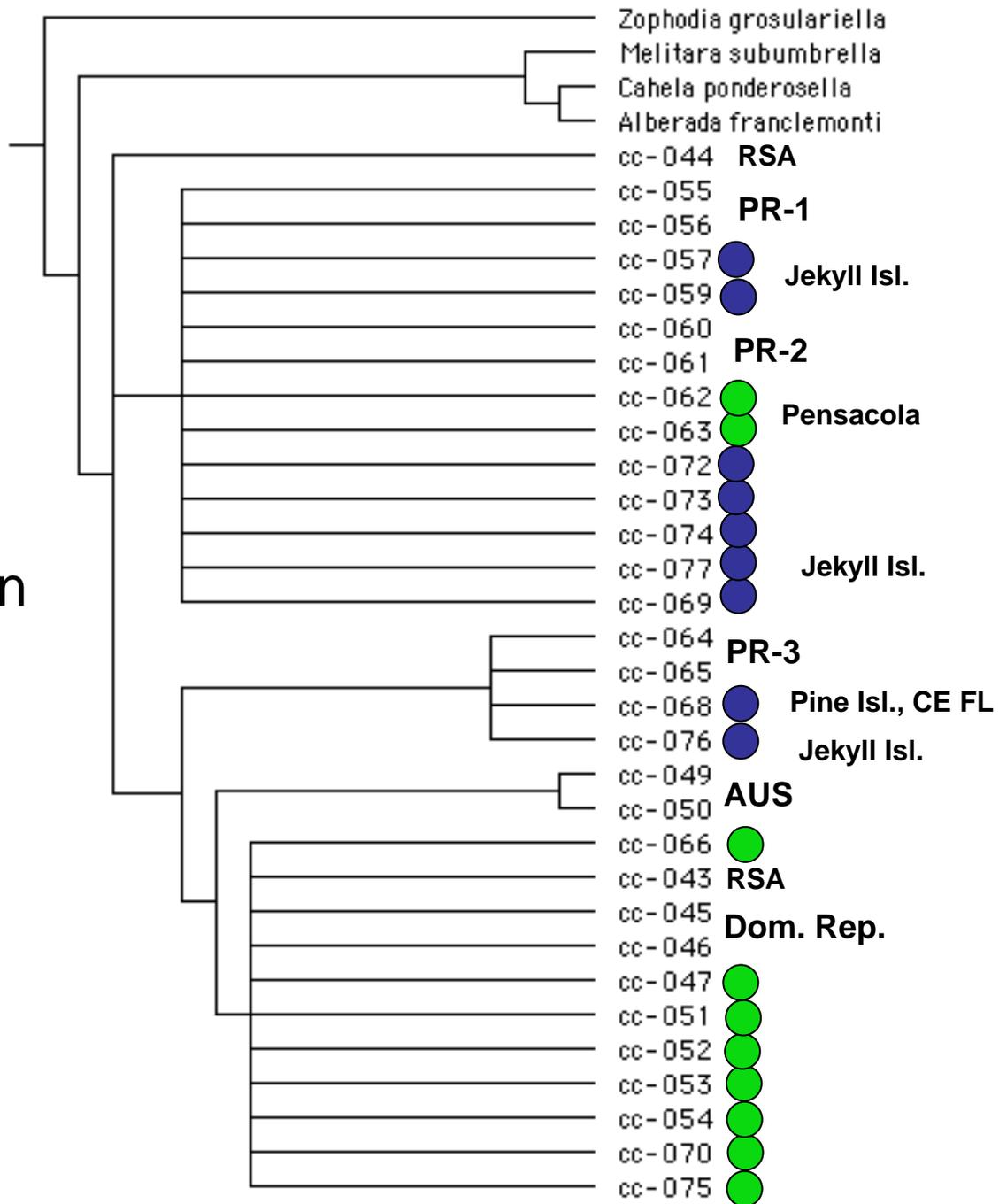


# Results

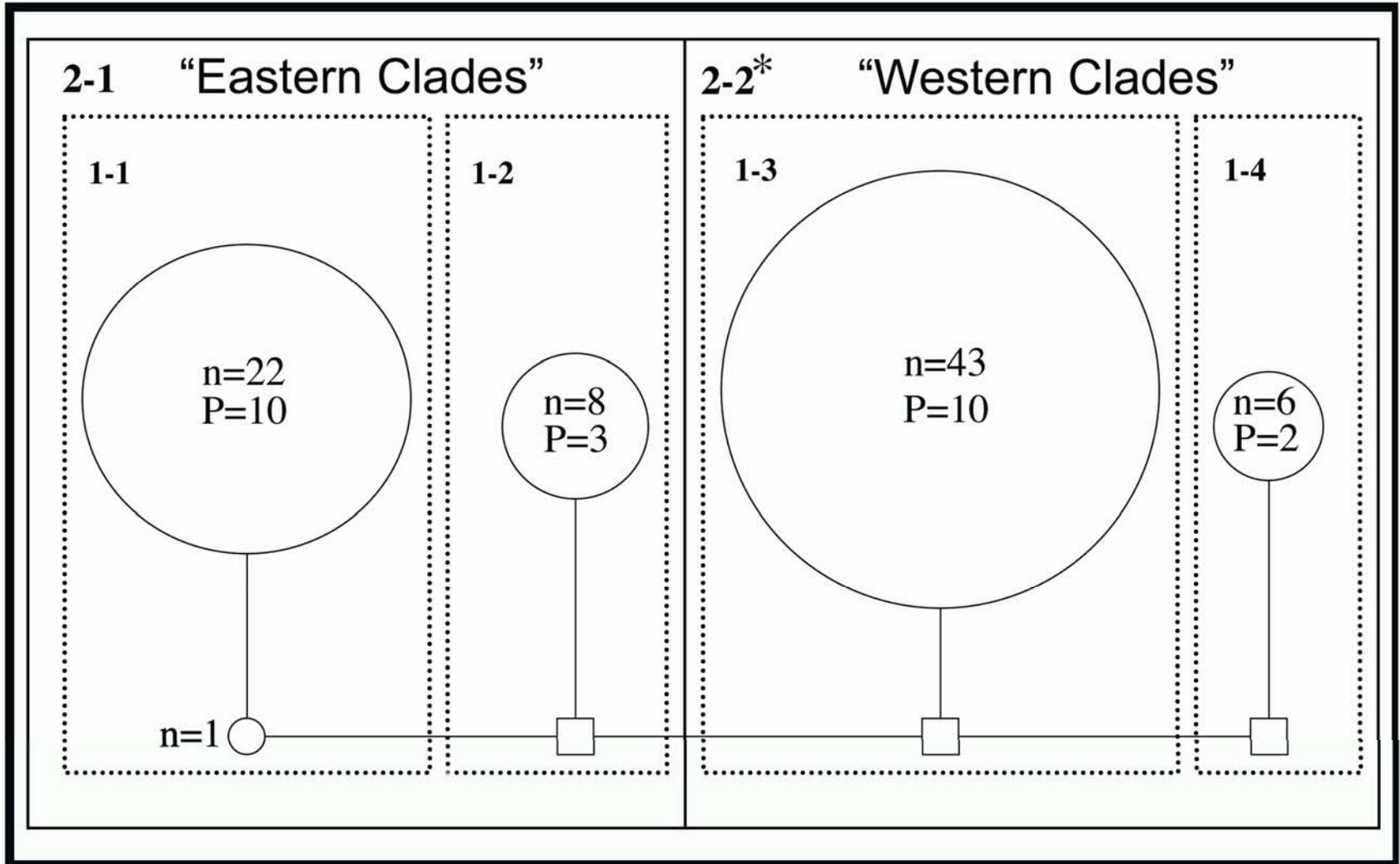
Majority rule consensus  
three from six most  
parsimonious trees

Basically the same pattern

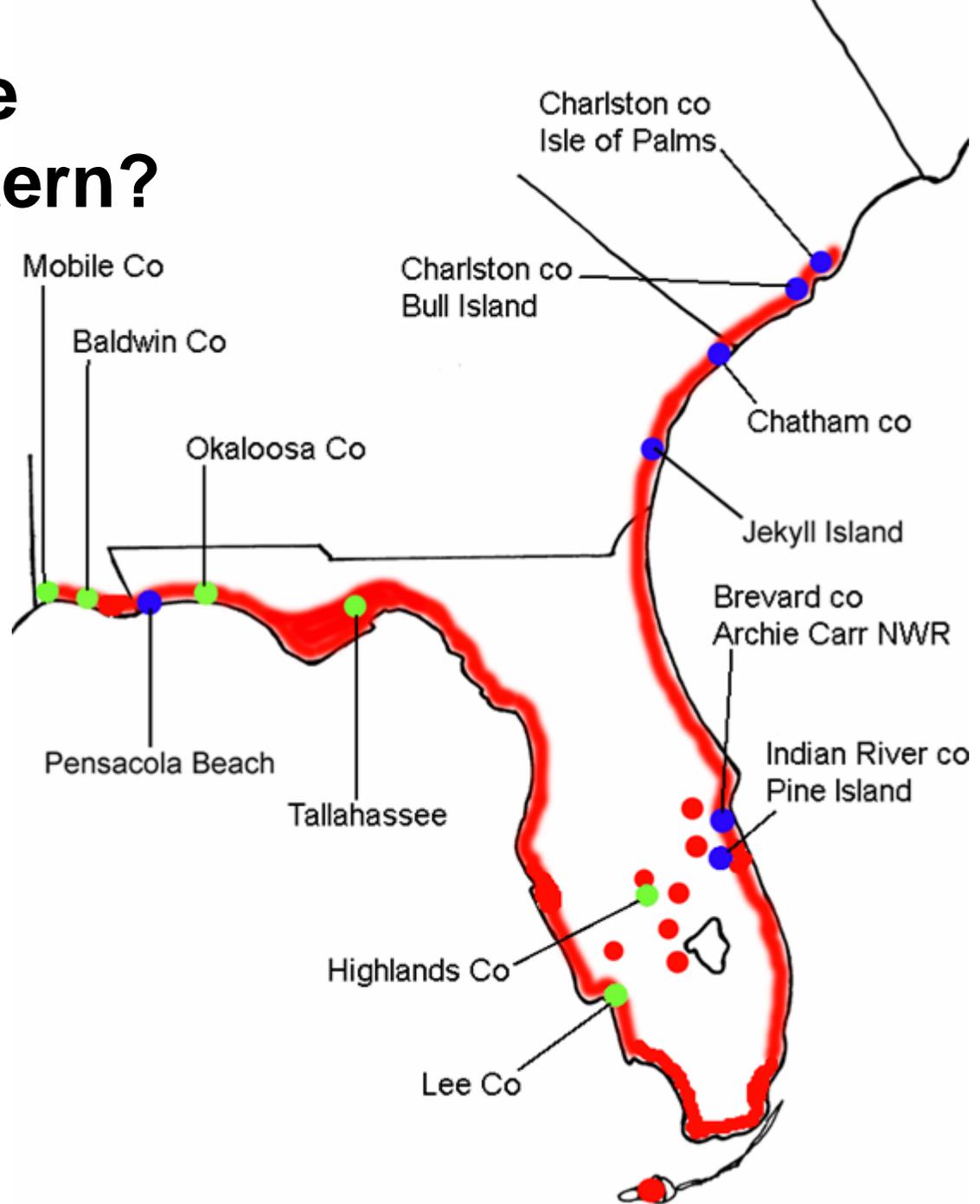
- Western samples
- Eastern samples



# Results – 2: Nested Clade Analysis

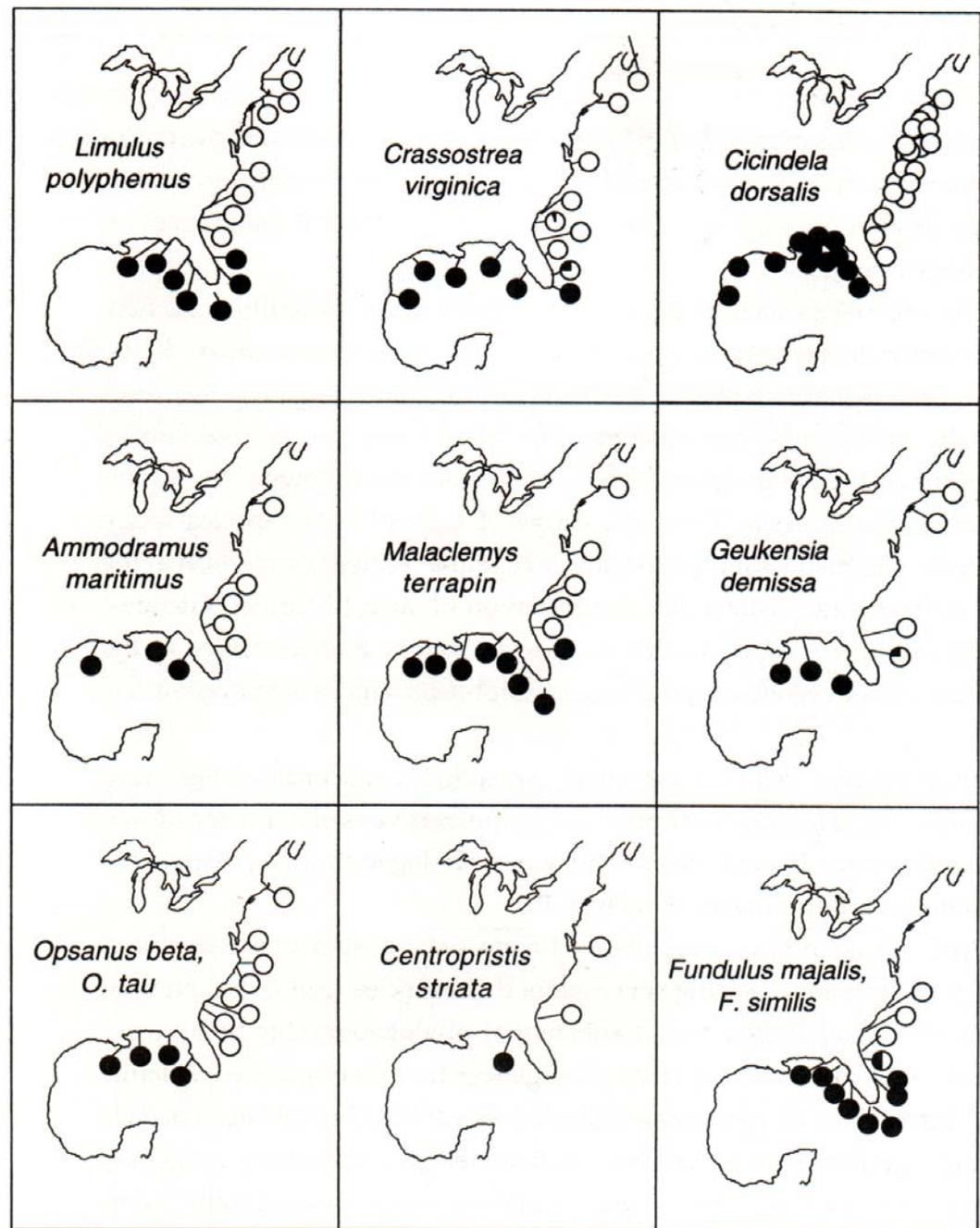


# OK – How do we explain this pattern?



# Avise (2000)

- Reviewed the phylogeography of a number of different taxa from south eastern USA.
- Found a clear east/west split.
- Patterns thought to result from geological history from late Oligocene to the last glaciation.
- This obviously cannot explain the distribution of *C. cactorum*!



# Other phylogeographic studies on invasive organisms - 1

- **Villablanca et al. (1998)**, studied intron variation in the med fly, *Ceratitis capitata*.
- High, but no phylogeographic population structure.
- Variation was highest in native (African) populations.

# Other phylogeographic studies on invasive organisms - 2

- **Slade & Moritz (1998)**, studied ND3 (468bp) variation in the marine toad, *Bufo marinus*, introduced from eastern South America to Puerto Rico (before 1844), to Hawaii (1920s) and Australia (1930s).
- Found 14 haplotypes in native range, but only one in introduced populations.

# Other phylogeographic studies on invasive organisms - 3

- **Scheffer & Grissel (2003)**, studied 800bp of COI in the seed feeding wasp *Megastigmus transvaalensis*.
- Found 25 haplotypes: 24 from Africa and one from the rest of the world (Reunion, Brazil, Hawaii, Florida, California).
- Concluded that the wasp probably was spread from Kenya to Reunion (where host plants are grown commercially) and then to the rest of the world.

# Other phylogeographic studies on invasive organisms - 4

- **Scheffer & Lewis (2005)**, studied 550bp of COI in *Liriomyza sativae* (a mining fly), native to North and South America.
- Found somewhat higher variation: 24 haplotypes, 11 of which were found outside the native range.
- All introduced haplotypes grouped together (with four native haplotypes) in a well supported clade.

# Other phylogeographic studies on invasive species - 5

- **Laffin et al. (2005a)** studied COI variation in the introduced weevil, *Ceutorhynchus obstrictus*, and compared the results to a similar study of the native North American weevil, *C. neglectus* (Laffin et al. 2005b).
- Found higher variation in the introduced species.
- *C. obstrictus* population in eastern and western North America were more similar to European population than they were to each other, concluding that *C. obstrictus* has been introduced to North America more than once.

# Conclusions

- *Cactoblastis cactorum* in the US can (roughly) be divided into two groups:
  - Genetically homogenous “western” group
  - Genetically heterogeneous “eastern” group
  - Both groups are closely related to groups outside the US
- *C. cactorum* has probably been introduced more than once to south eastern US
- The presence of “eastern” haplotypes in the west suggests that the moths are being transported passively
- Mexican population is closely related to the western group.

# Acknowledgements

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- Marie Djernæs.
- Sperling Lab.

# Literature

- Avise, J. C. (2000):** *Phylogeography. The history and formation of species*. Harvard University Press. 447 pp.
- Hight, S. D., J. E. Carpenter, K. A. Bloem, S. Bloem, R. W. Pemberton & P. Stiling (2002):** Expanding geographical range of *Cactoblastis cactorum* (Lepidoptera: Pyralidae) in North America. *Florida Entomologist*. 85. 527-529
- Laffin, R. D., L. M. Dossall & F. A. H. Sperling (2005a):** Population structure of the cabbage seedpod weevil, *Ceutorhynchus obstrictus* (Marsham) (Coleoptera Curculionidae): Origins of North American introductions. *Environmental Entomology*. 34. 504-510.
- Laffin R. D., L. M. Dossall & F. A. H. Sperling (2005):** Population structure and phylogenetic relationships of *Ceutorhynchus neglectus* (Coleoptera: Curculionidae). *Canadian Entomologist*. 137. 672-684.
- Panchal, M. (2007):** The automation of nested clade phylogeographic analysis. *Bioinformatics*. 23. 509-510.
- Scheffer, S. J. & E. E. Grissell (2003):** Tracing the geographic origin of *Megastigmus transvaalensis* (Hymenoptera: Torymidae): an African wasp feeding on a South American plant in North America. *Molecular Ecology*. 12. 405-414.
- Scheffer, S. J. & M. L. Lewis (2005):** Mitochondrial Phylogeography of Vegetable Pest *Liriomyza sativae* (Diptera: Agromyzidae): Divergent Clades and Invasive Populations. *Annals of the Entomological Society of America*. 98. 181-186.
- Slade, R. W. & C. Moritz (1998):** Phylogeography of *Bufo marinus* from its natural and introduced ranges. *Proceedings of the Royal Society of London. Series B*. 265. 769-777.
- Solis, M. A., S. D. Hight & D. R. Gordon (2004):** Tracking the Cactus Moth, *Cactoblastis cactorum* Berg., as it flies and eats its way westwards in the U.S. *News of the Lepidopterists' Society*. 46. 3-4, 7.
- Templeton, A. R. (1998):** Nested clade analysis of phylogeographic data: testing hypotheses about gene flow and population history. *Molecular Ecology*. 7. 381-397.
- Templeton, A. R. (2004):** Statistical phylogeography: methods of evaluating and minimizing inference errors. *Molecular Ecology*. 13. 789-809.
- Templeton, A. R., E. Routman & C. A. Phillips (1995):** Separating population structure from population history: a cladistic analysis of the geographical distribution of mitochondrial DNA haplotypes in the tiger salamander, *Ambystoma tigrinum*. *Genetics*. 140. 767-782.
- Villablanca, F. X., G. K. Roderick & S. R. Palumbi (1998):** Invasion genetics of the Mediterranean fruit fly: variation in multiple nuclear introns. *Molecular Ecology*. 7. 547-560.
- Zimmermann, H. G., V. C. Moran & J. H. Hoffmann (2000):** The renowned cactus moth, *Cactoblastis cactorum*: Its natural history and threat to native *Opuntia* floras in Mexico and United States of America. *Diversity and Distributions*. 6. 259-269.
- [http://www.aphis.usda.gov/ppq/ep/emerging\\_pests/cactoblastis/](http://www.aphis.usda.gov/ppq/ep/emerging_pests/cactoblastis/)

# Finally – a warning

Please take care when examining cactus!

