







## Why Gap Analysis?

- Tool to assess crop and crop wild relative genetic and geographical diversity
- Allows detecting incomplete species collections as well as defining which species should be collected and where these collections should be focused
- Assesses the current extent at which the ex situ conservation system is correctly holding the genetic diversity of a particular genepool

# To know what you don't have, you first need to know what you do have

....and that's where things already get complex

### Welcome to database hell

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Andy Jarvis is about to talk about database hell. 11 minutes ago - Comment



Andrew Farrow is enthused by diffusion. about an hour ago - Comment

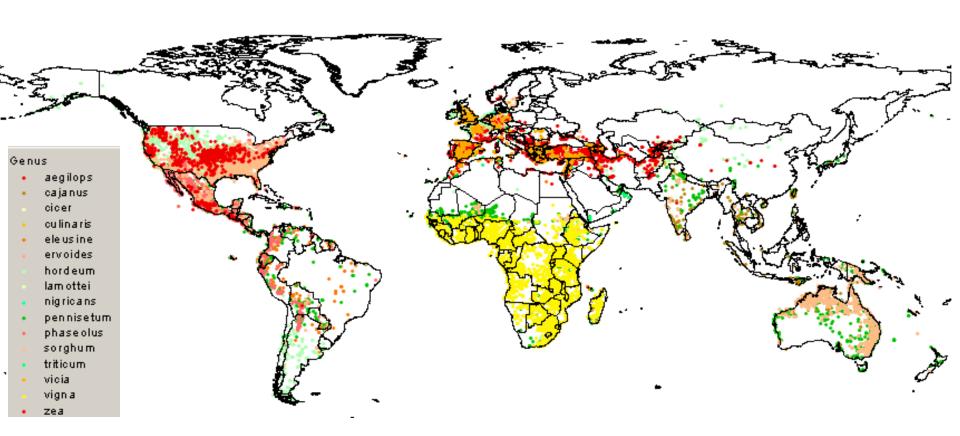


Luigi Guarino is in database hell. 4 hours ago - 1 Comment

- 1. Árboles de la Península de Yucatán, Flora del Distrito de Tehuantepec, Oaxaca y Familia Asteraceae en México (IBUNAM)
- 2. Arizona State University Vascular Plant Herbarium
- 3. Biodiversidad de Costa Rica
- 4. California State University, Chico
- 5. CIAT-Genetic Resources Unit
- 6. Colecciones de George Boole Hinton depositadas en el herbario de Kew: Familia Leguminosae
- 7. Daniel Debouck Cahiers de Phaséologie
- 8. DAO Herbarium Type Specimens
- 9. Ejemplares tipo de plantas vasculares del Herbario de la Escuela Nacional de Ciencias Biológicas, México (ENCB, IPN)
- 10. Fairchild Tropical Botanic Garden Virtual Herbarium Darwin Core format
- 11. Freytag and Debouck (2002)
- 12. GRIN
- 13. Harvard University Herbaria
- 14. Herbario de la Universidad de Arizona, EUA
- 15. Herbario del Instituto de Ecología, A.C., México (IE-BAJIO)
- 16. Herbarium (UNA)
- 17. Herbarium de Geo. B. Hinton, México
- 18. Herbier de la Guyane
- 19. Instituto de Ciencias Naturales
- 20. ITIS
- 21. Missouri Botanical Garden
- 22. National Botanic Garden of Belgium (NBGB)
- 23. National Vegetable Germplasm Bank, Mexico (BANGEV)
- 24. Native Seeds/SEARCH (NSS)
- 25. New York Botanical Garden (NYBG)
- 26. NMNH Botany Collections
- 27. Phanerogamie
- 28. Repatriación de datos del Herbario de Arizona (ARIZ)
- 29. Royal Botanic Gardens, Kew
- 30. The AAU Herbarium Database
- 31. The Deaver Herbarium, Northern Arizona University
- 32. United States National Plant Germplasm System Collection
- 33. USDA PLANTS Database
- 34. Vascular Plant Type Specimens



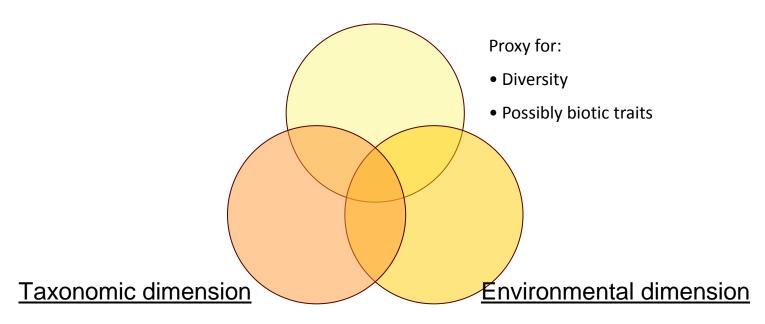
# The visible global system



## The Gap Analysis process

Identifying gaps

#### Geographic dimension

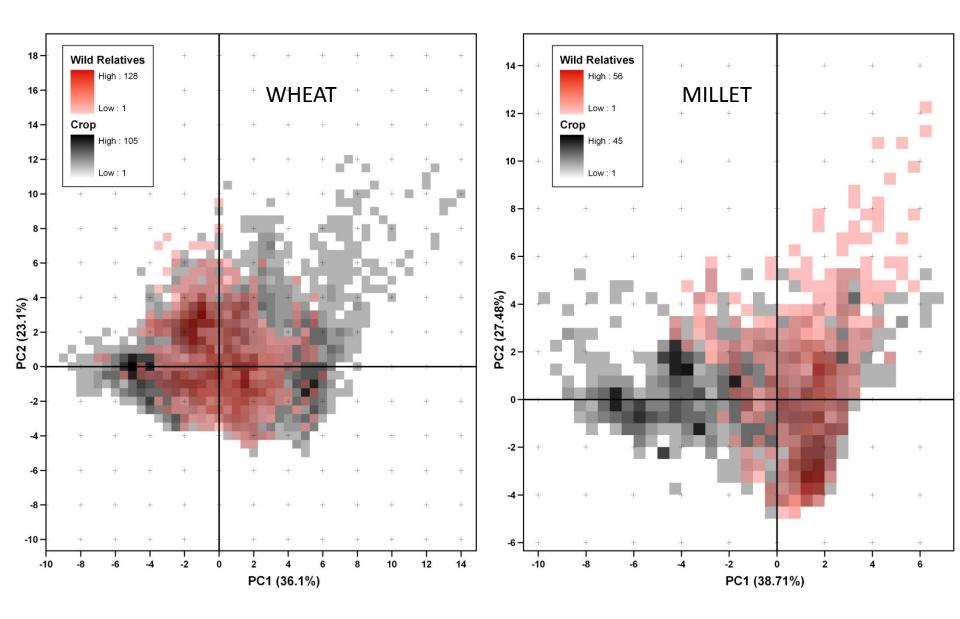


Proxy for:

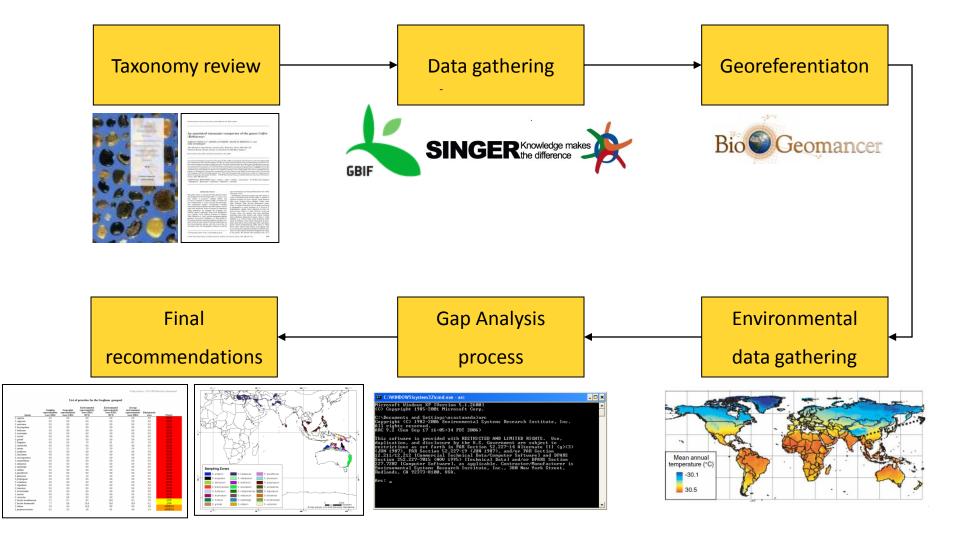
• Range of traits

Proxy for:

• Abiotic traits



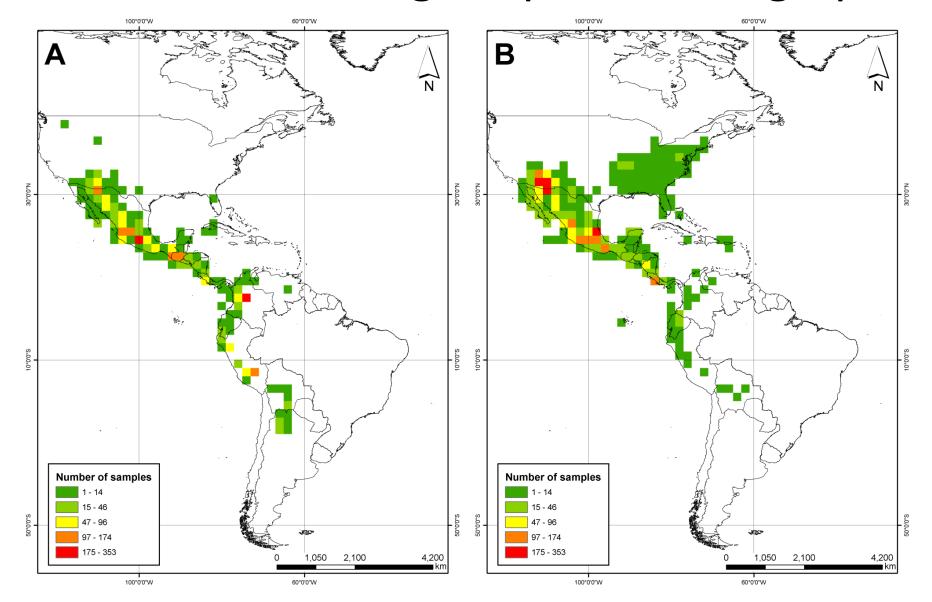
## The Gap Analysis pathway



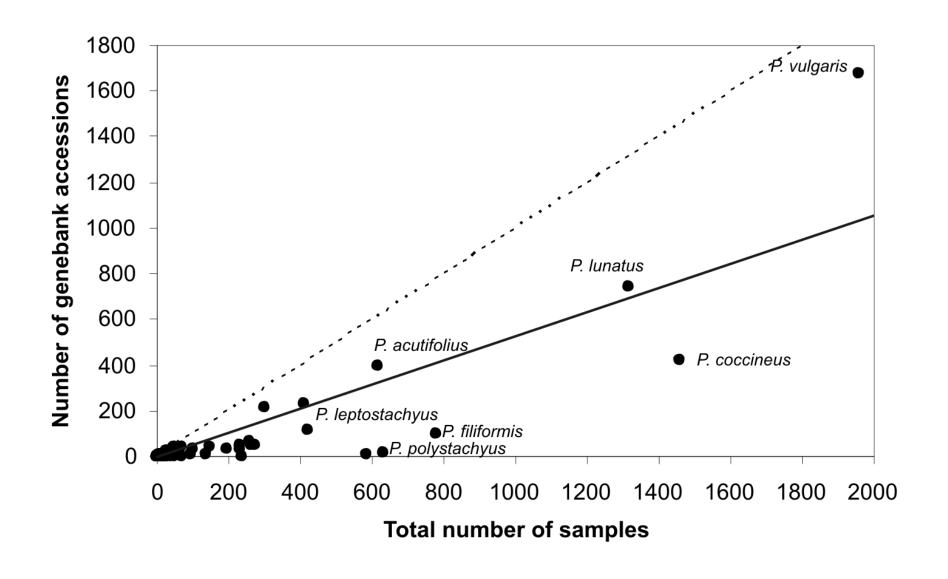
# An example in *Phaseolus*



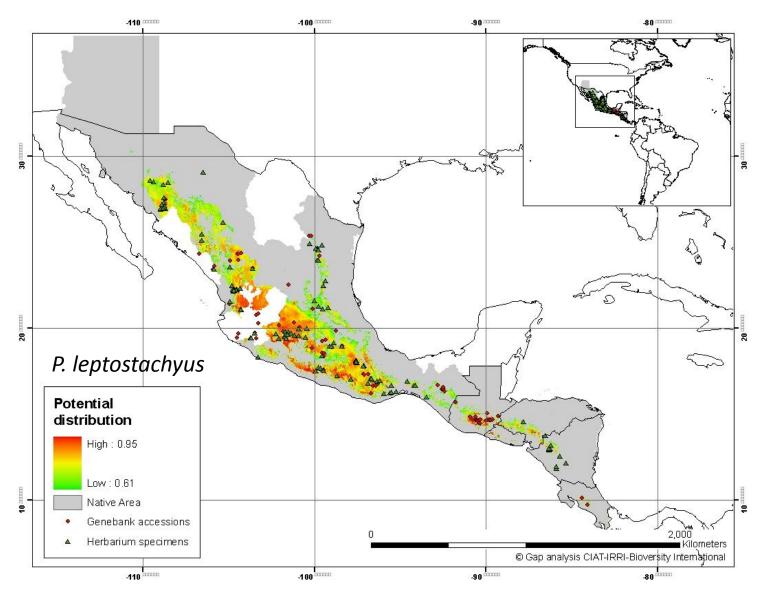
## Herbarium versus germplasm: Geographic



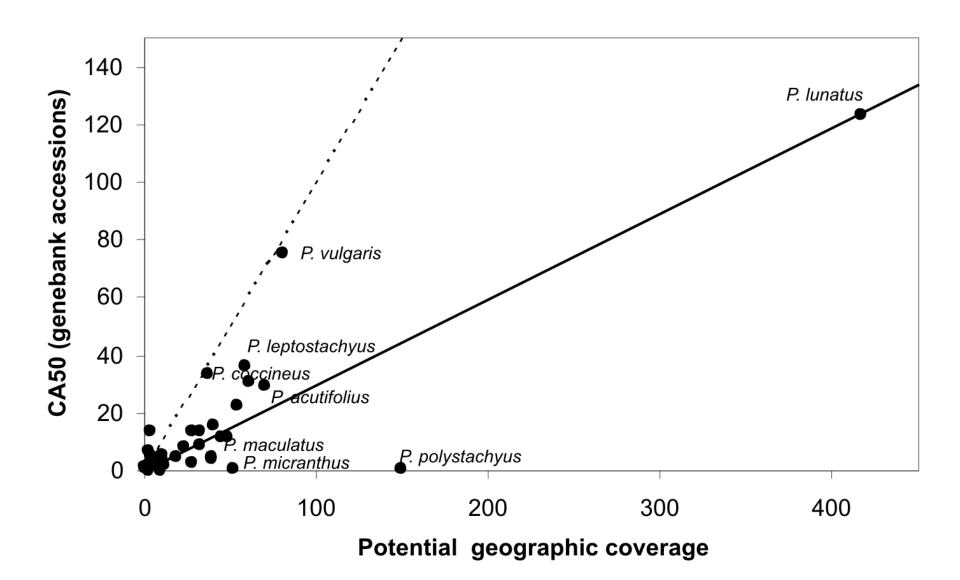
## Herbarium versus germplasm: Taxon



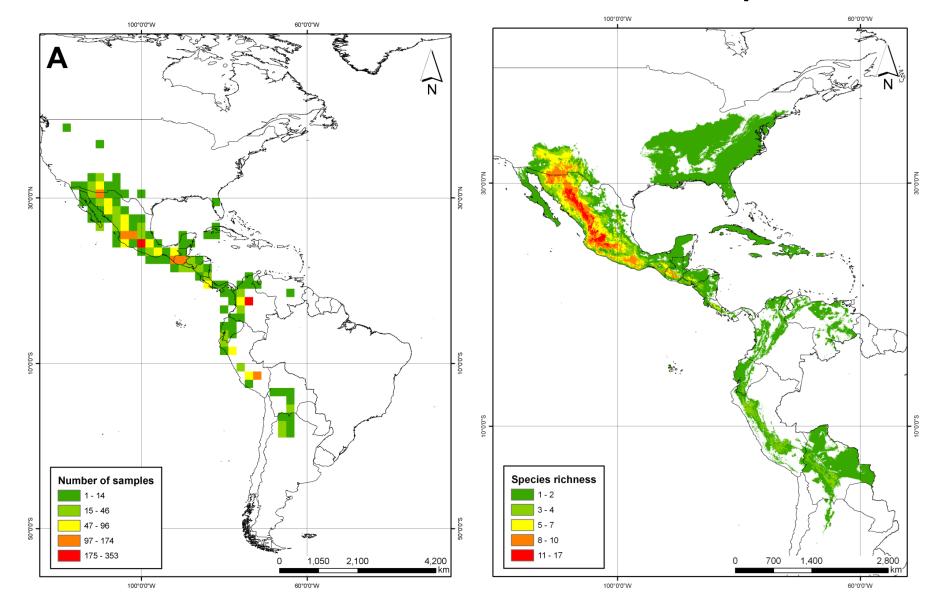
# Geographic coverage: Potential



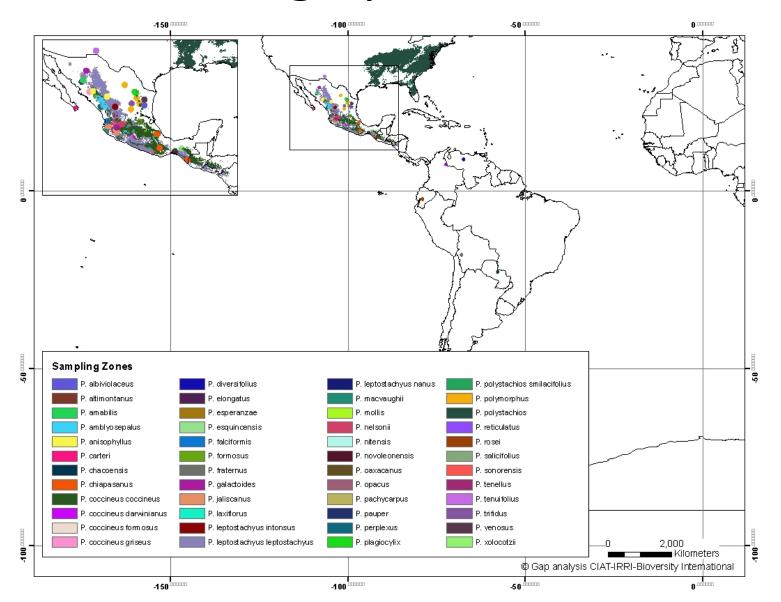
## Geographic coverage: Taxon priorities



## Conserved ex situ richness versus potential



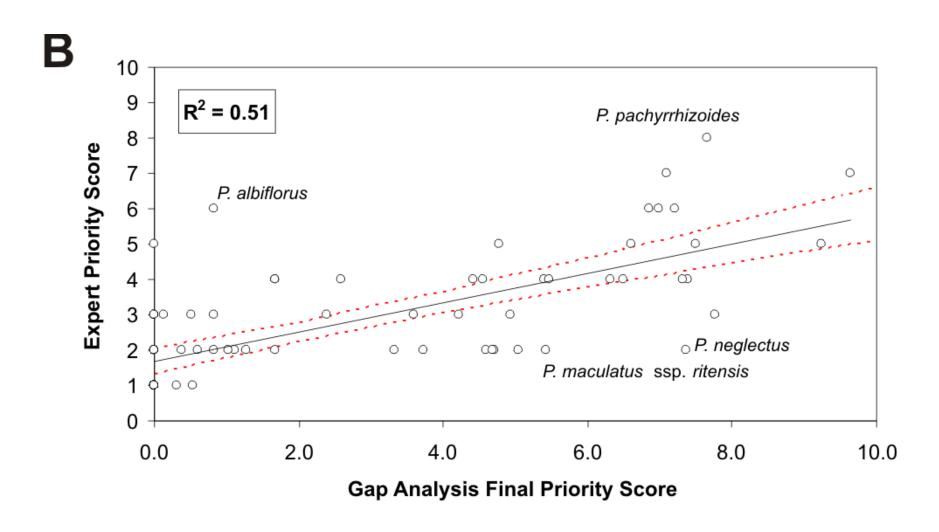
## Priorities: Geographic and taxonomic



### "Validation": The man versus the machine



## Model priorities versus expert priorities

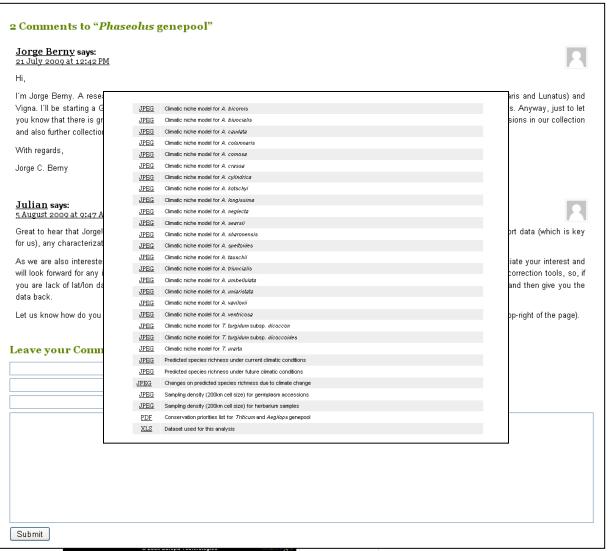


### **Gap Analysis**

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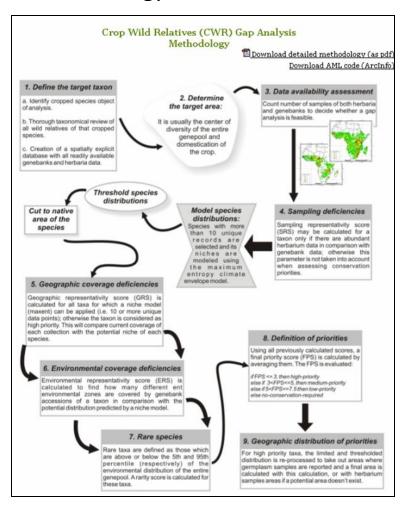
Search

#### **GapAnalysis**



## Methodology and code

#### Methodology

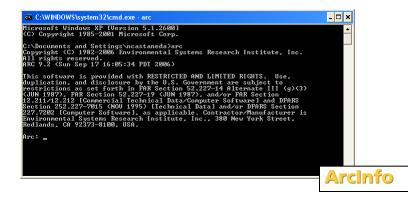


#### Code

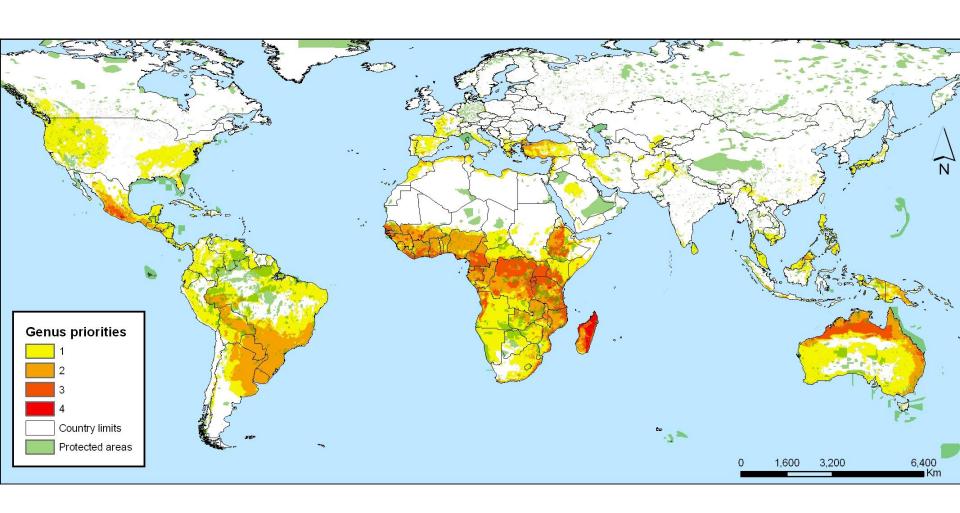
```
A This mai performs the whole may manipris procedure for a series of genegols. Too just need to change the path to the variable viscotdiry

/* and the mess of the genegols to which you want to perform the analyses, and run it under the ARC prompt.

**To you have been properly and the process of the performance of the genegols. The process of the performance of the perform
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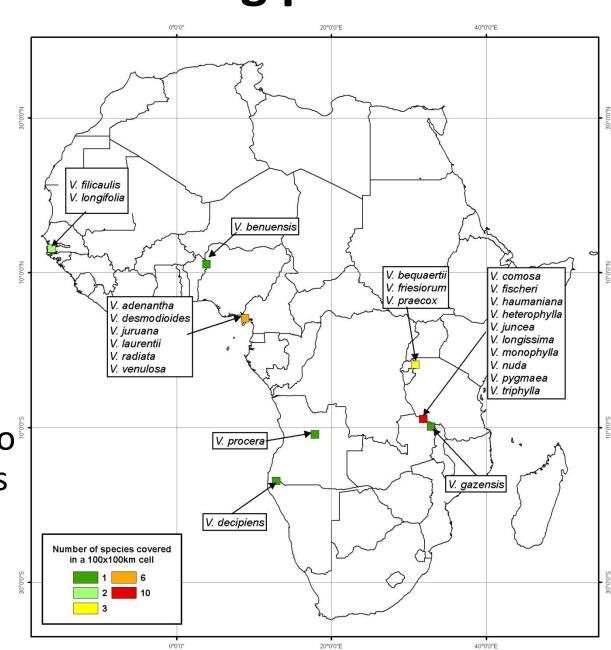


## Taxon-level and genepool level priorities



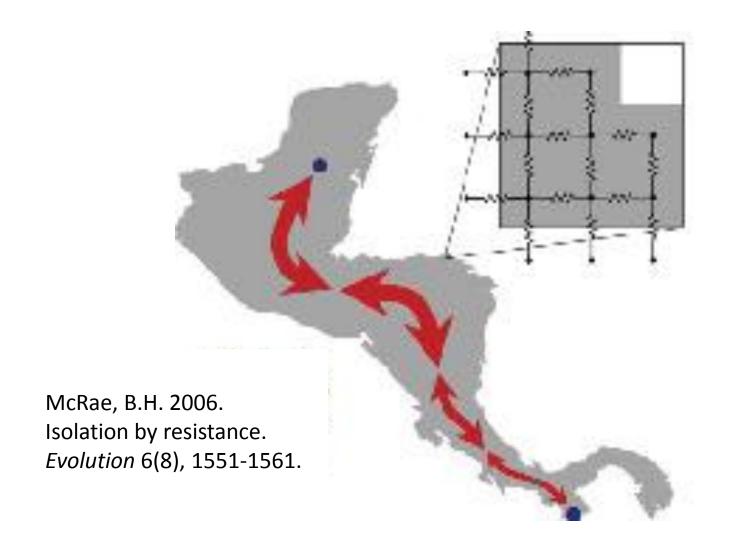
## Wild Vigna collecting priorities

- Spatial analysis on current conserved materials
- \*Gaps\* in current collections
- Definition and prioritisation of collecting areas
- 8 100x100km cells to complete collections of 23 wild Vigna priority species



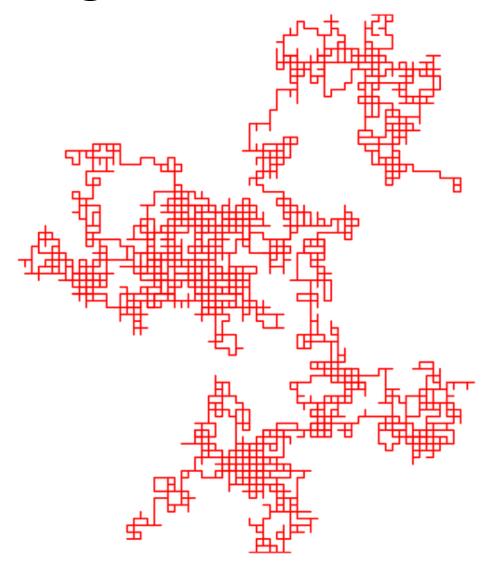


### Even better: resistance distance

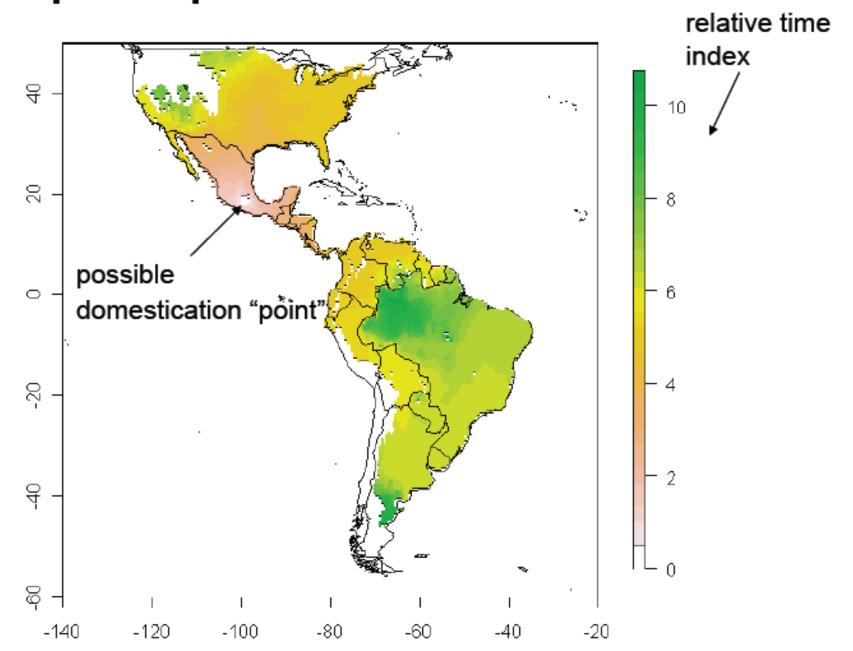


# Drunk genes



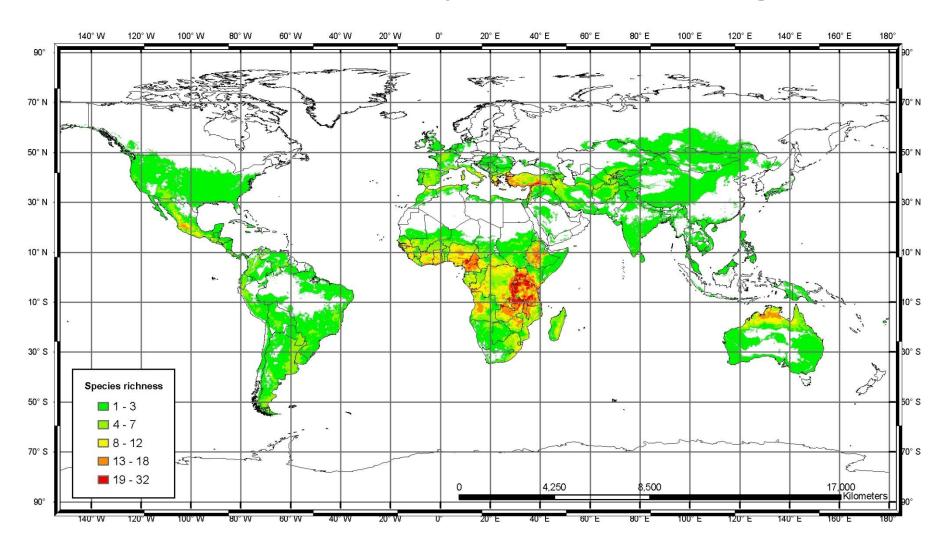


# Crop dispersal arrival time

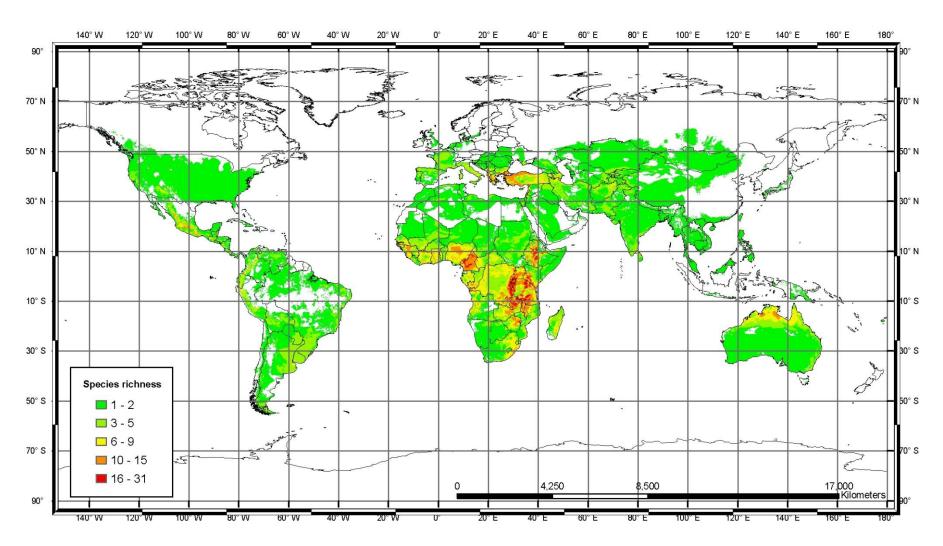




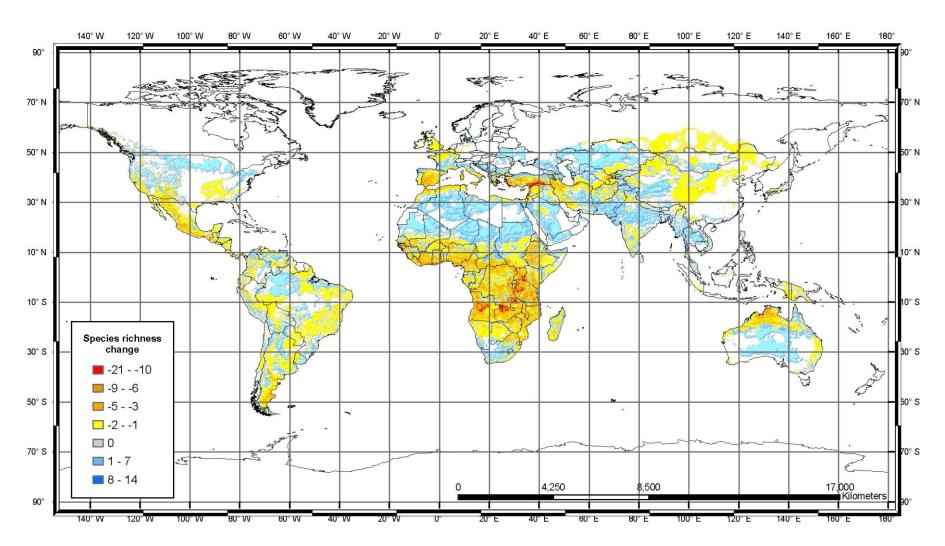
# CWR supporting adaptation but also threatened by climate change



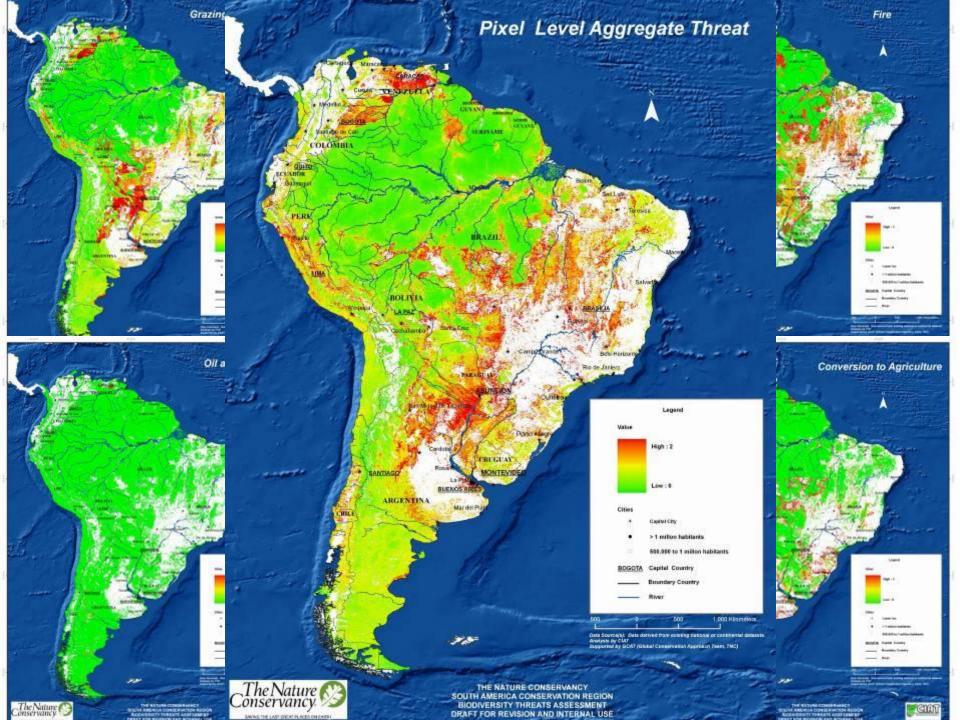
# CWR supporting adaptation but also threatened by climate change



# CWR supporting adaptation but also threatened by climate change



## More immediate threats....



## Conclusions and open-ended issues

- Gap analysis can focus priorities for collecting, and cost/benefit lies in collecting multiple genepools simultaneously
- But, analysis as good as input data
- If you can't see the data, is the collection valid?
- Multiple methods available
- Key question: what is a "complete" collection?