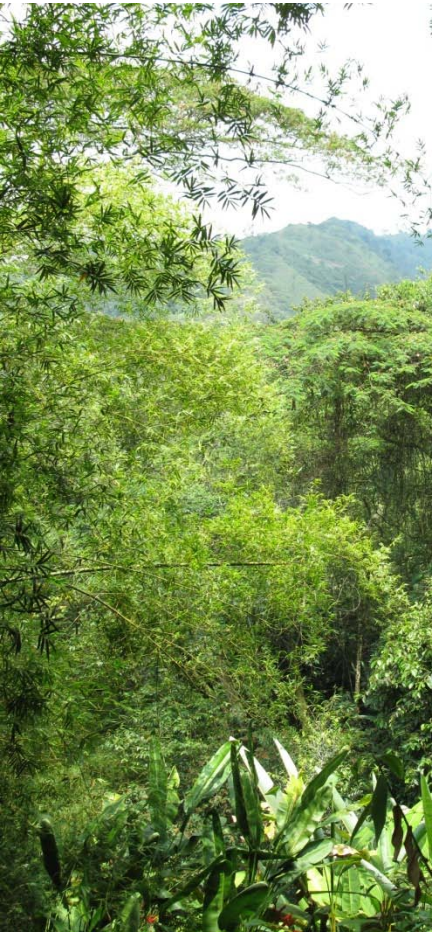
Understanding, tracking and documenting genetic resources of forest trees to improve management practices



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Setting the Stage

The problem:

Loss and degradation of forest ecosystems

→ loss of populations and associated adaptive potential of forest tree species.

- Too many important tree species to study each in detail (~60,000 species, 7000 threatened, several thousand useful)
- In spite of advances and decreasing costs of genetic technology, resources are not available to carry out genetic analyses on all
- Result: genetic aspects are usually ignored in management plans and practices, for lack of specific genetic information

- Conservation through use in a managed system – necessary but rarely sufficient solution.
- Sustainable forest management at ecosystem or landscape scale is not enough to ensure conservation of FGR

Question: what can we infer about genetic resources and how can we manage them without genetic analyses?

Forest genetic resources (FGR):

genetic variability that is of actual or potential value for human well-being.

- source for improvement of traits of commercial, subsistence or other importance
- source of raw material for adaptation to environmental change
- source of resistance/tolerance to insects, diseases, climatic extremes


Latin America

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Key characteristics:

- High species diversity
- Recent or current high rate of deforestation and site degradation
- Many species of interest/value to rural populations
- People/governments are poor
- Very little information about most species, ecosystems; nothing known about genetics of most species
- High predicted impacts of climate change

Three key questions

1) What do forest managers need to know to make informed decisions about conservation and sustainable use of FGR?

2) How can available information be used and interpreted to predict status and threats to FGR?

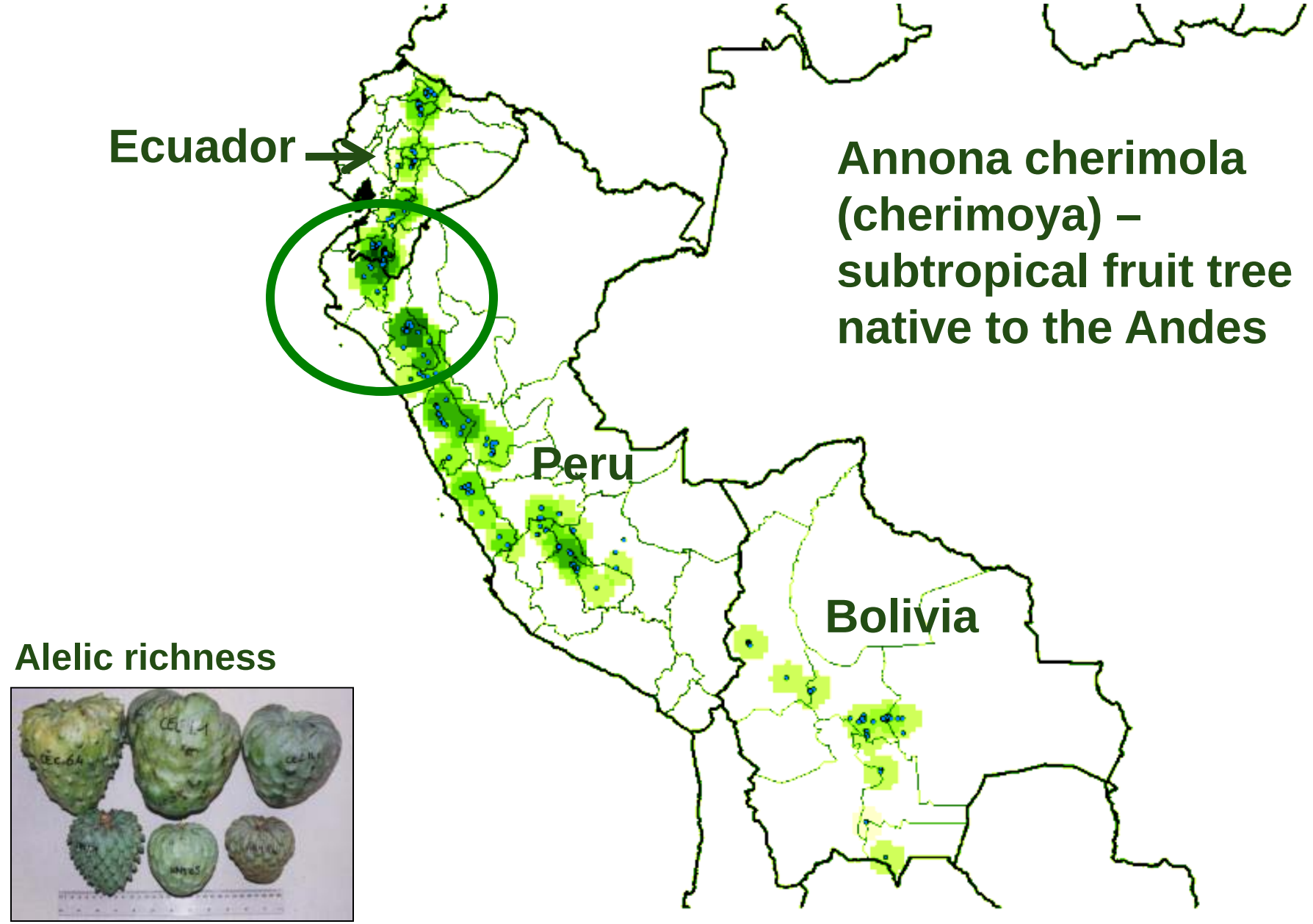
3) How can such information be made available and useful for forest and park managers?

What do forest managers need to know to make informed decisions about conservation and sustainable use of FGR?

Ideal:

- Population distribution and sizes
  - Changes, trends
- Distribution of genetic diversity
- Ecological requirements, life history traits of tree species
- Level and location of “useful” genetic variation (quantitative knowledge of variation in adaptive traits, useful characteristics)
- *In situ*, *ex situ* conservation status and potential
- Threats
  - Type
  - Intensity

Geo-referenced microsatellite diversity



Annona cherimola (cherimoya) – subtropical fruit tree native to the Andes

Alelic richness

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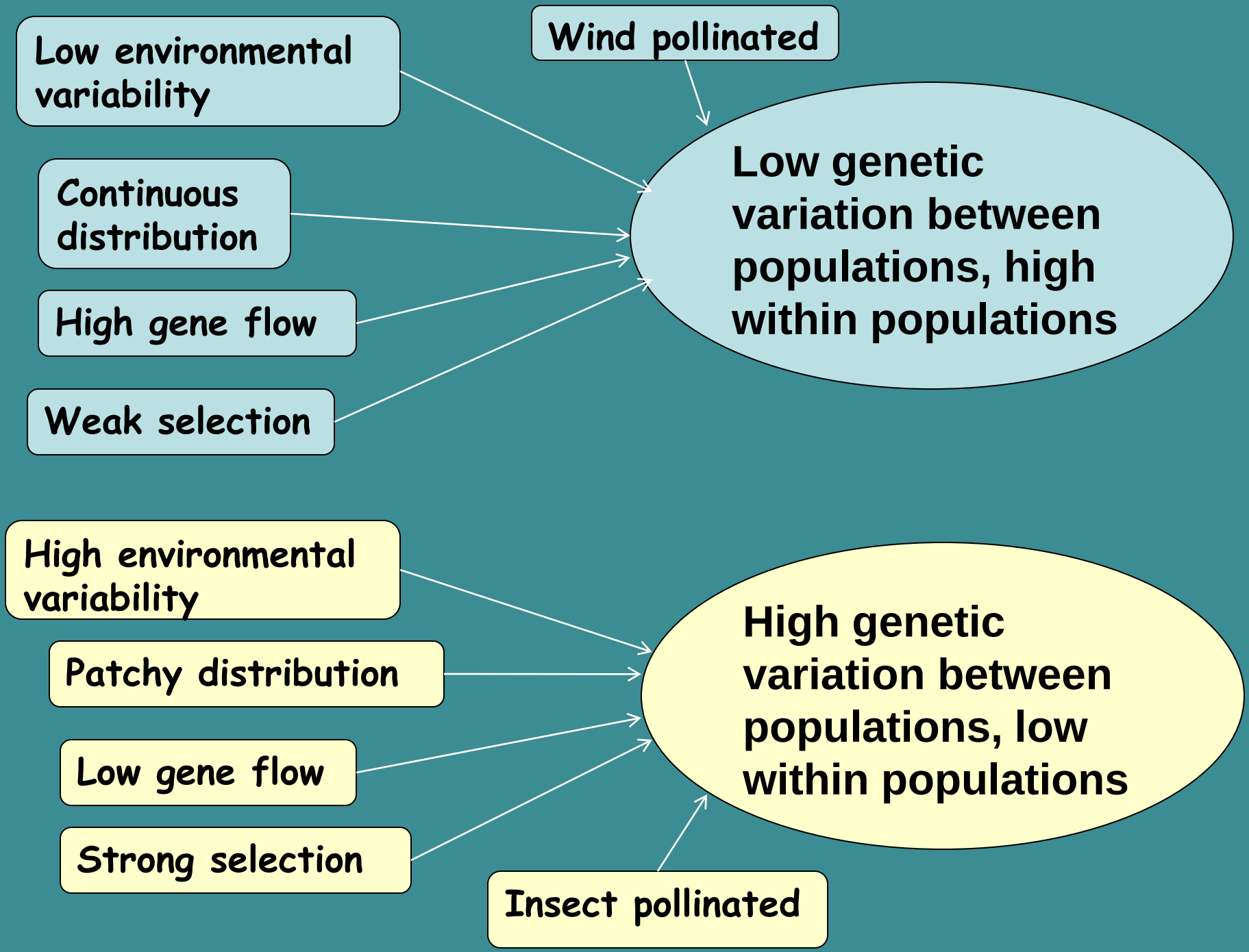
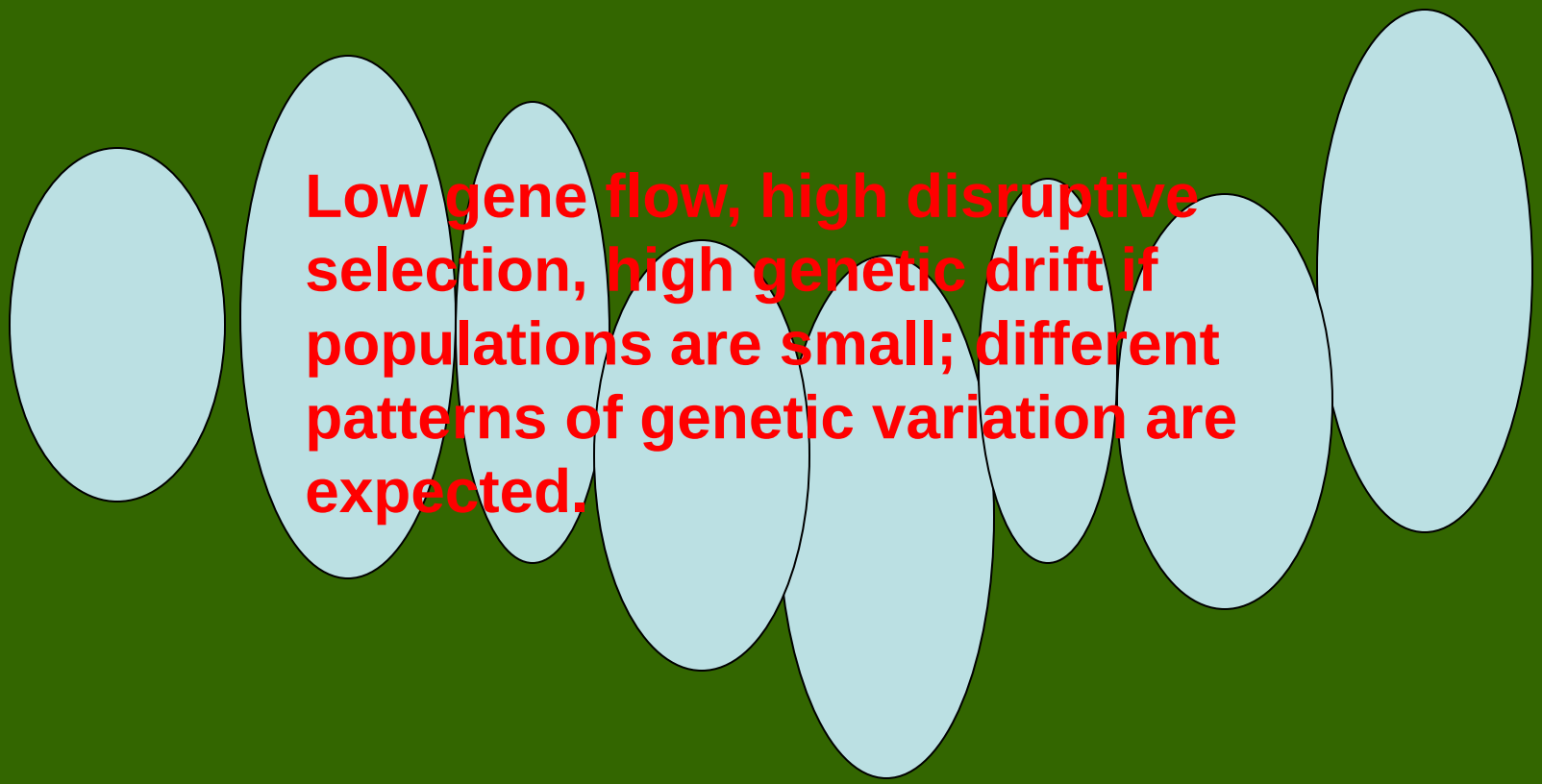
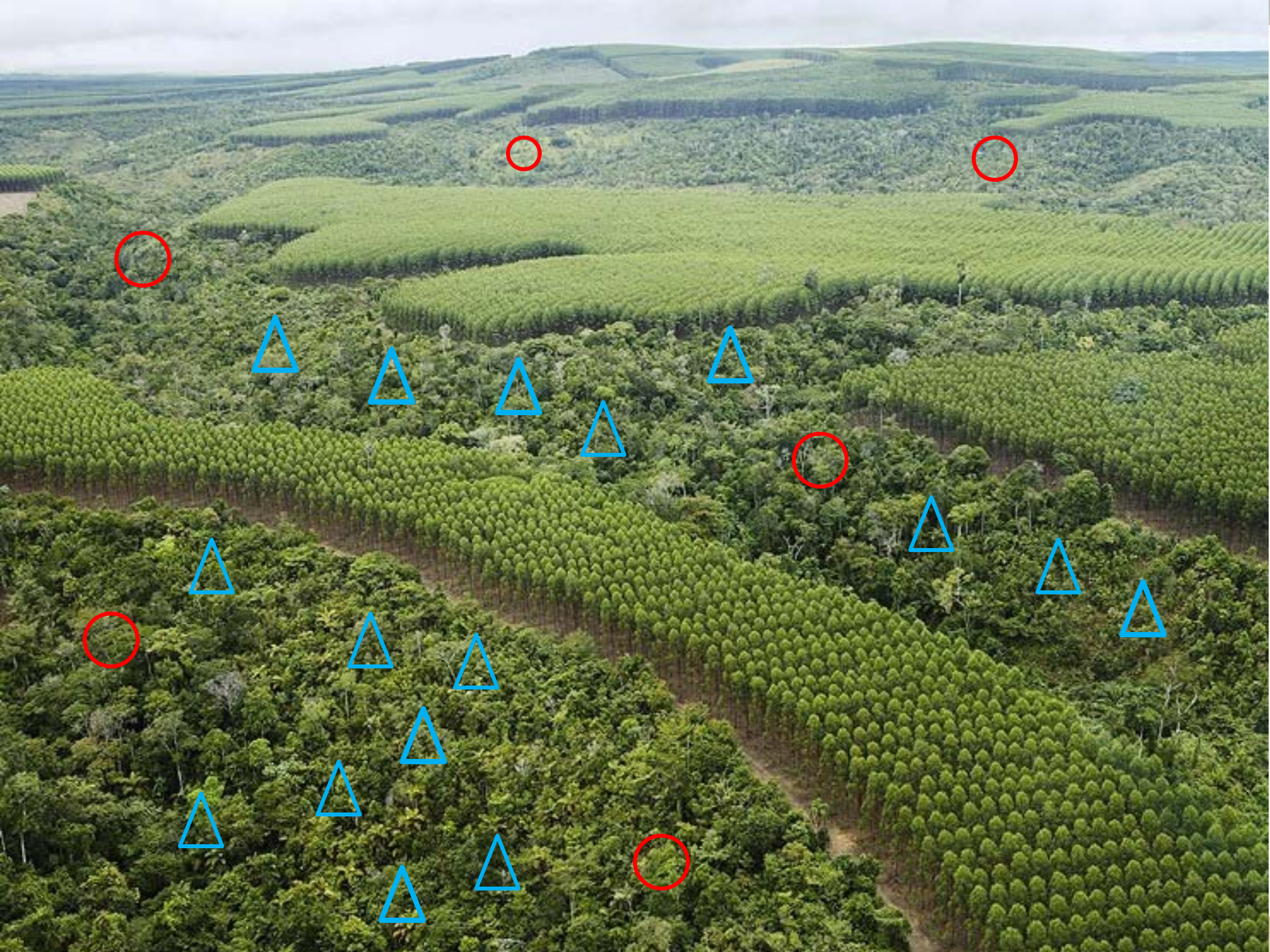
Without genetic analysis:

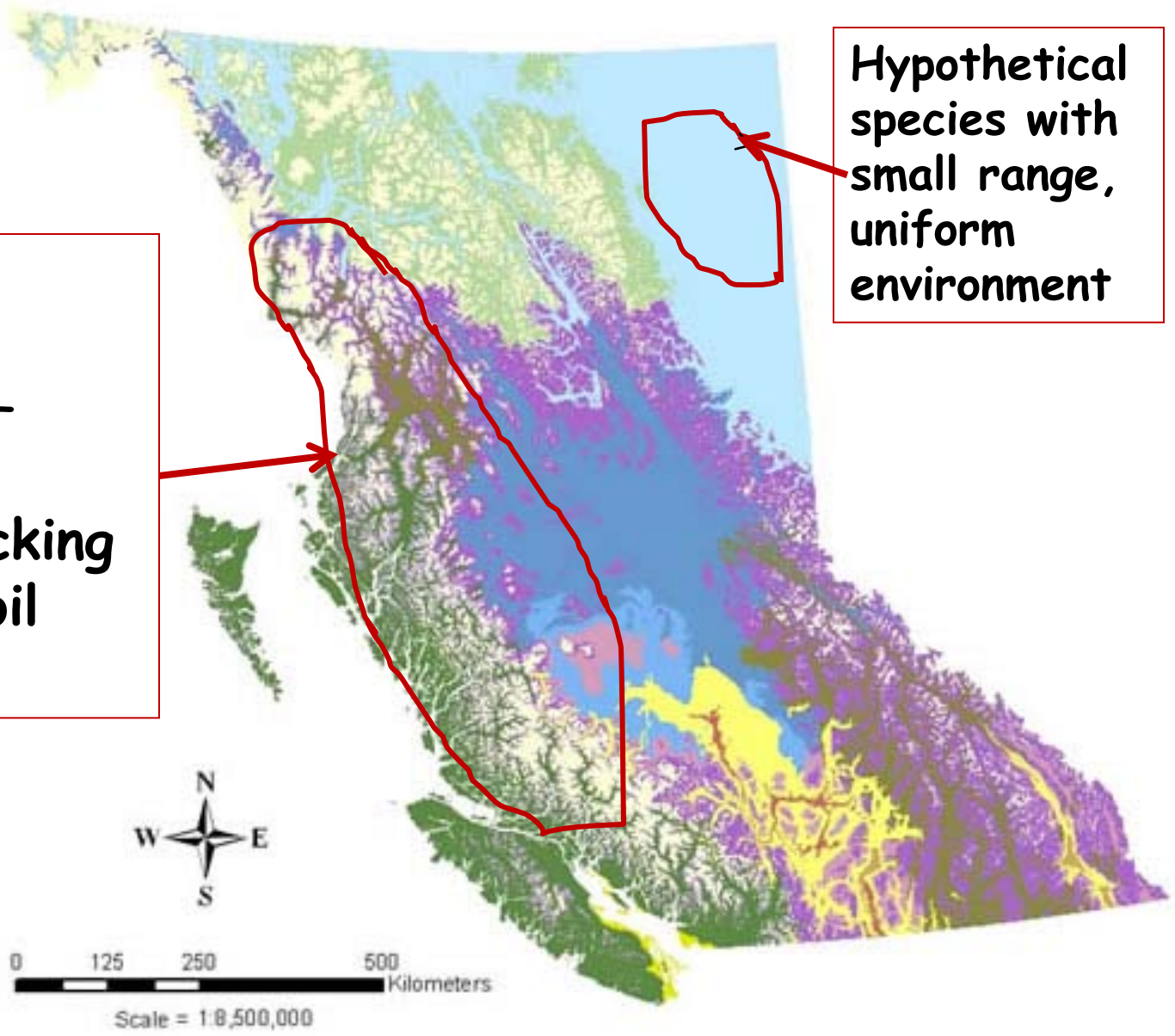
- Species natural (or naturalised) distribution, frequency, and trends; succession status
- Environmental uniformity or variability
- Ecological limits (frost, drought)
- Mating system (out-crossing, selfing or mixed)
- Pollination mechanism; likely effects of fragmentation
- Regeneration success
- *In situ*, *ex situ* conservation, threats


Low environmental variability
Wind pollinated
Continuous distribution
Low genetic variation between populations, high within populations
High gene flow
Weak selection
High environmental variability
Patchy distribution
High genetic variation between populations, low within populations
Low gene flow
Strong selection
Insect pollinated


Low gene flow, high disruptive selection, high genetic drift if populations are small; different patterns of genetic variation are expected.



Biogeoclimatic zones of British Columbia, Canada



Hypothetical species with small range, uniform environment

Wide-ranging species span several zones – expect genetic variability tracking climatic and soil conditions.

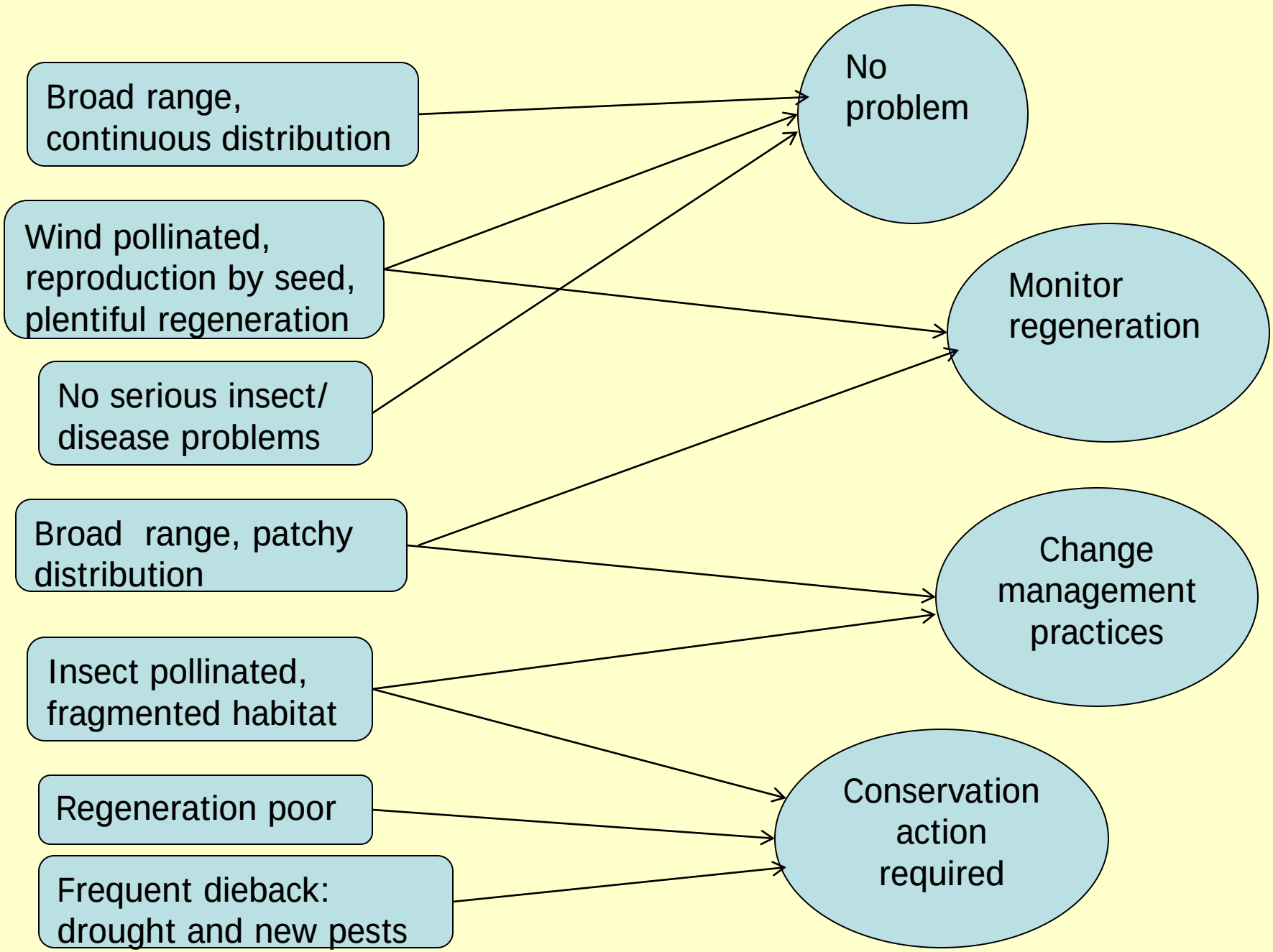
How can available information be used and interpreted to predict status and threats to FGR?

Prioritise:

- **Species of actual or potential value to people**

- **Which ones have limited/shrinking distribution and/or are widely scattered?**
- **Which ones are insect pollinated and subject to fragmented habitat?**
- **Which are vegetatively propagated or are self-pollinated?**
- **Which are susceptible to climatic fluctuations, introduced insects or diseases?**

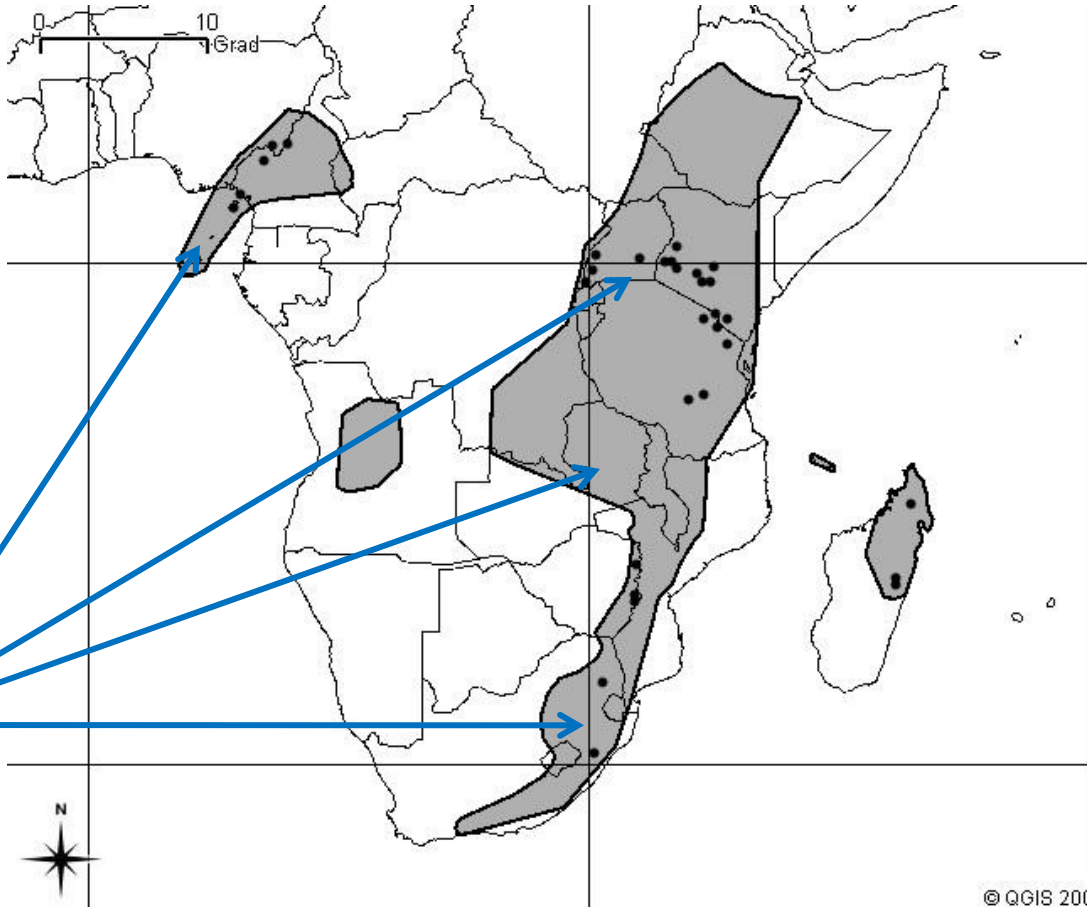
Decision support system can guide management and conservation actions


Broad range, continuous distribution
Wind pollinated, reproduction by seed, plentiful regeneration
No serious insect/ disease problems
Broad range, patchy distribution
Insect pollinated, fragmented habitat
Regeneration poor
Frequent dieback: drought and new pests
No problem
Monitor regeneration
Change management practices
Conservation action required

Assessing security of genetic resource

A genetic resource gap analysis examines the present adequacy of in situ conservation for genetic diversity of native tree species.

Location of protected areas?



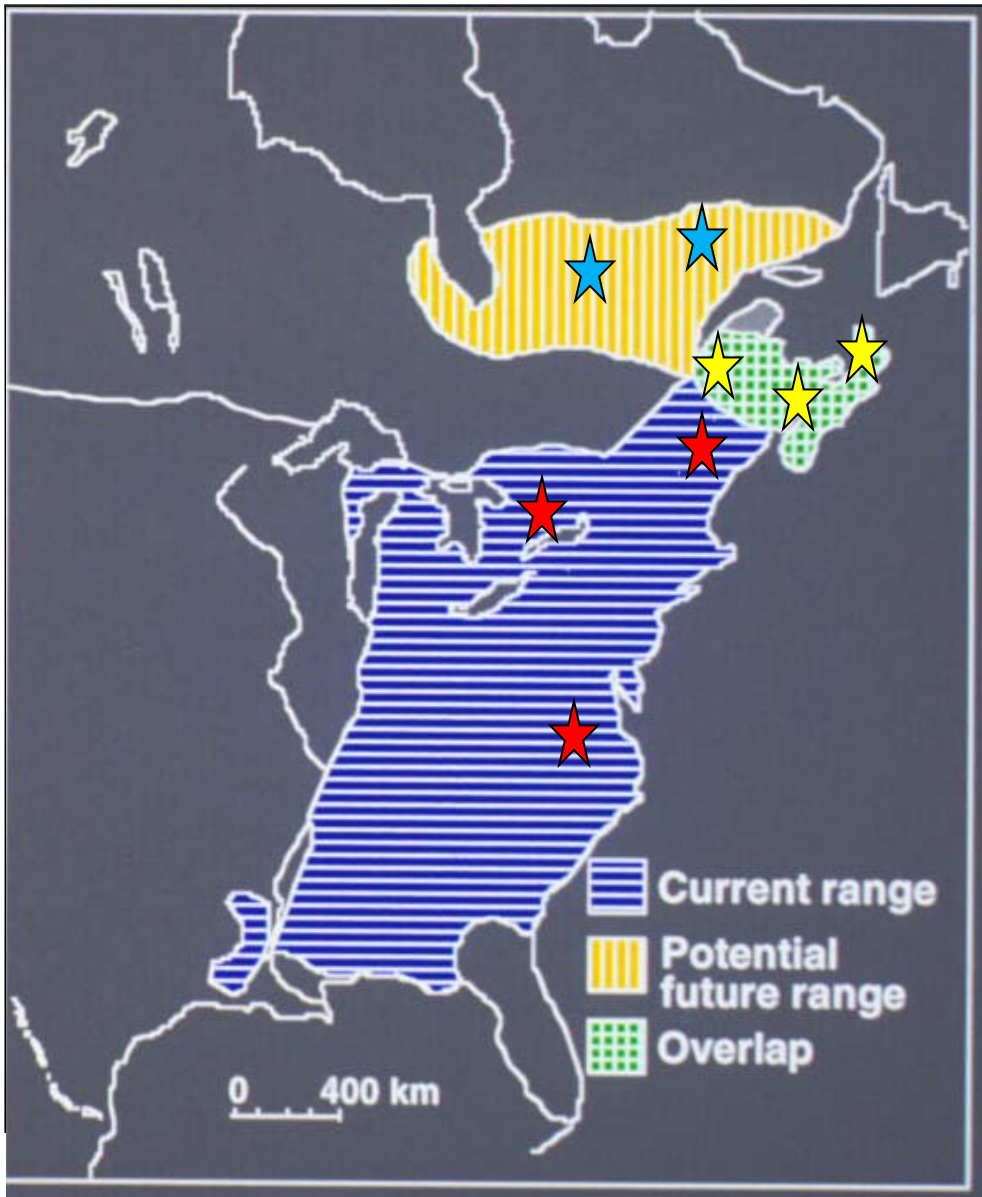
Prunus africana range and sampled populations

Adequacy of *in situ* protection in future can predicted with climate change models

Fagus grandifolia current distribution: blue striped and green hatched; predicted climatic suitability in 2100: yellow striped and green hatched.

Protected areas 100 years from now:

- Secure
- No viable populations
- Suitable climate, no trees



How can such information be made available and useful for forest and park managers?

A good accessible information management system is vital.

Components: Map layers – species distribution, ecological land classification, protected areas, sources of *ex situ* collections, ...

Non-spatial: species description, including reproductive biology, ecological reguirements, threats, ...

On-line facility for adding information.

Concluding remarks

- When possible it is important to base management and conservation on genetic data, but genetic resources should not be ignored when genetic data are lacking.
- Management and conservation of forest resources can and should include genetic considerations for all important tree species even if genetic analyses have not been carried out.
- To understand variation in adaptive and other important quantitative traits, field tests are important, and should be carried out if possible, but until it is possible, we must assume that variation tracks environmental variability.
- Genomic tools are becoming sufficiently sophisticated to test efficacy of ecological surrogates and this should be a research priority.
- A decision support tool can be developed using available biological, silvics and ecological information to guide management and conservation of forest genetic resources and the tool will be improved as genetic information becomes available.

Thank you!

Understanding and Managing Biodiversity

Conservation and Sustainable Use of Forests and Other Wild Plants

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