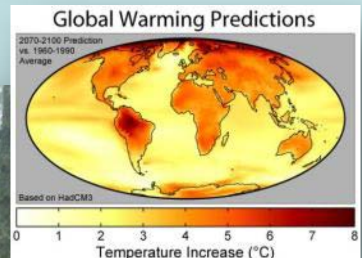
Assessing Forest Tree Genetic Risk across the Southern Appalachians: A Tool for Conservation Decision-Making in Changing Times



Kevin M. Potter
Barbara S. Crane

IUFRO Landscape Ecology Working Group International Conference

Bragança, Portugal

September 23, 2010

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Outline

1) Overview of potential genetic effects of climate change on forest trees

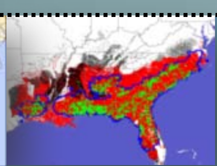
2) Need for regional genetic risk assessments of multiple forest tree species

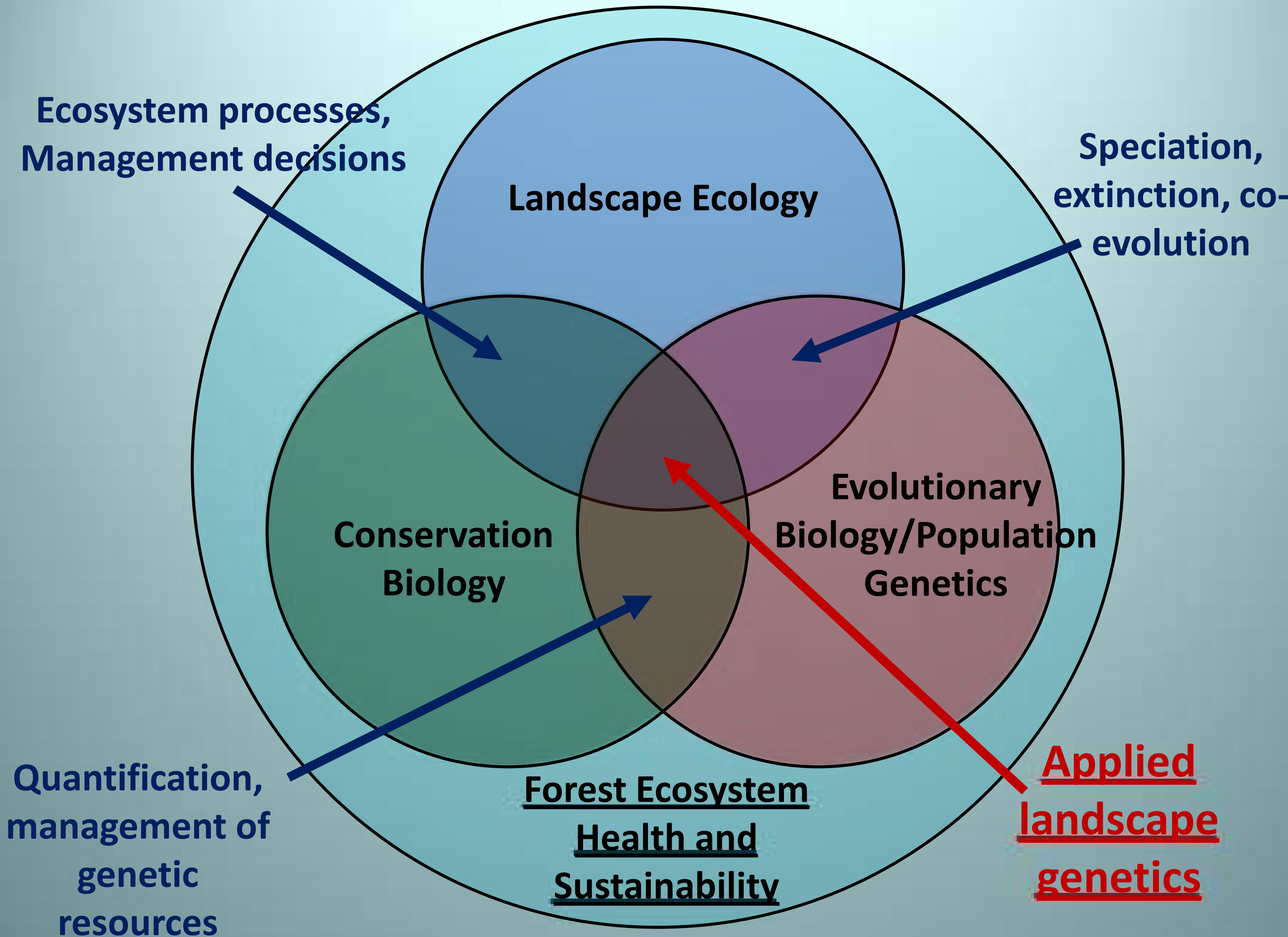
3) Description of the study region: Southern Appalachian Mountains of the Southeastern United States

4) Description of the genetic risk assessment and the risk factors included

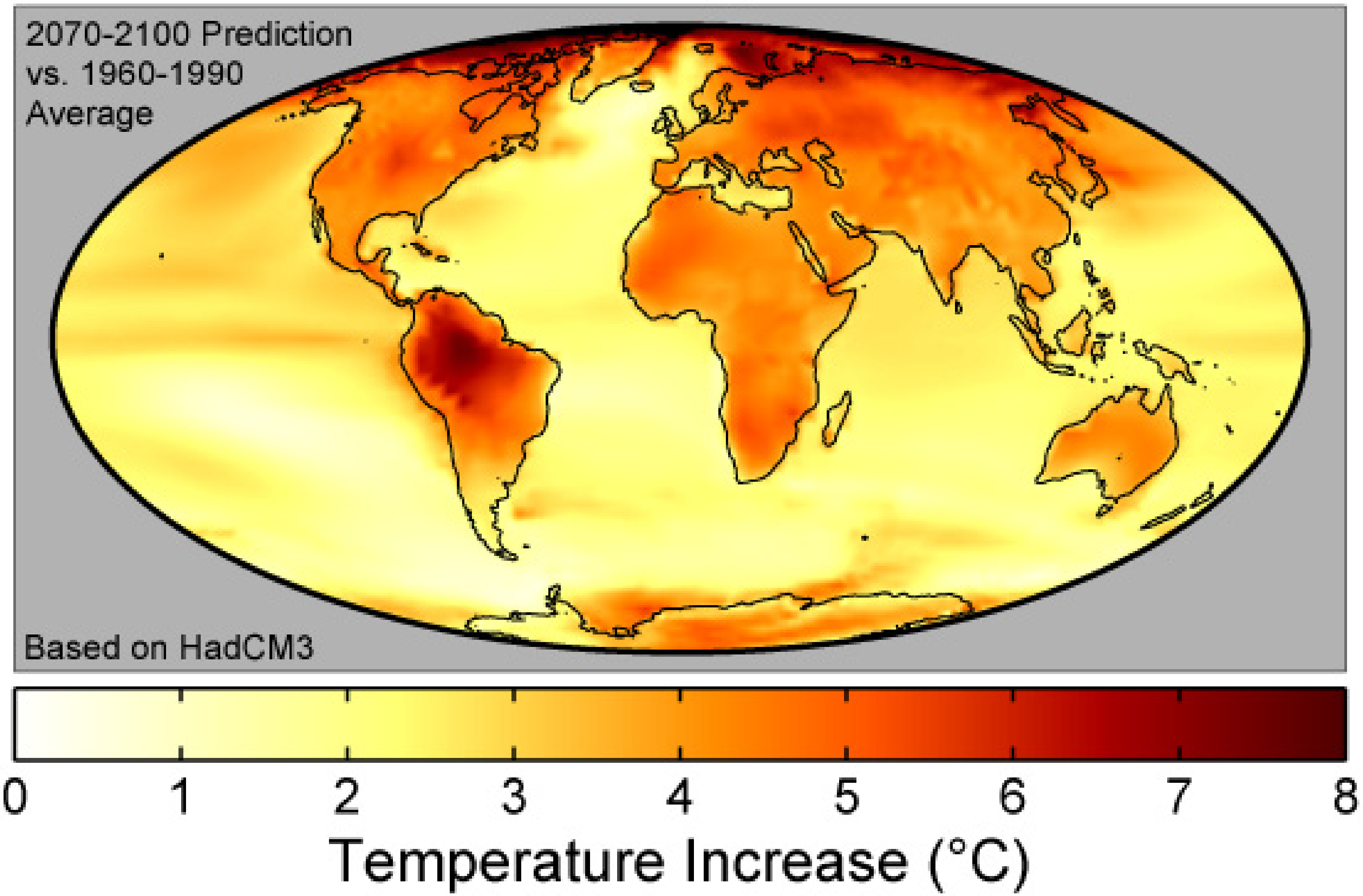
5) Assessment results and next steps






Ecosystem processes, Management decisions
Landscape Ecology
Speciation, extinction, co-evolution
Conservation Biology
Evolutionary Biology/Population Genetics
Quantification, management of genetic resources
Forest Ecosystem Health and Sustainability
Applied landscape genetics

Global Warming Predictions



Robert A. Rohde (http://en.wikipedia.org/wiki/Instrumental_temperature_record)

NATURE | VOL 421 | 2 JANUARY 2003 | www.nature.com/nature

articles

A globally coherent fingerprint of climate change impacts across natural systems

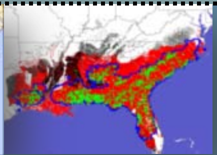
Camille Parmesan* & Gary Yohe†

* *Integrative Biology, Patterson Laboratories 141, University of Texas, Austin, Texas 78712, USA*
† *John E. Andrus Professor of Economics, Wesleyan University, 238 Public Affairs Center, Middletown, Connecticut 06459, USA*

"Global meta-analyses documented **significant range shifts** averaging 6.1 km per decade toward the poles (or meters per decade upward), and **significant mean advancement of spring events** by 2.3 days per decade. …

"This suite of analyses generates **very high confidence** … that **climate change is already affecting living systems**."





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Forest Ecology and Management 257 (2009) 1434–1444

Contents lists available at ScienceDirect

Forest Ecology and Management

journal homepage: www.elsevier.com/locate/foreco

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An indicator of tree migration in forests of the eastern United States

C.W. Woodall[a,*], C.M. Oswalt[b], J.A. Westfall[c], C.H. Perry[a], M.D. Nelson[a], A.O. Finley[d]

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[c] USDA Forest Service, Northern Research Station, Newtown Square, PA, United States
[d] Michigan State University, East Lansing, MI, United States

"[T]he process of **northward tree migration** in the eastern United States **is currently underway** with rates approaching 100 km/century for many species."

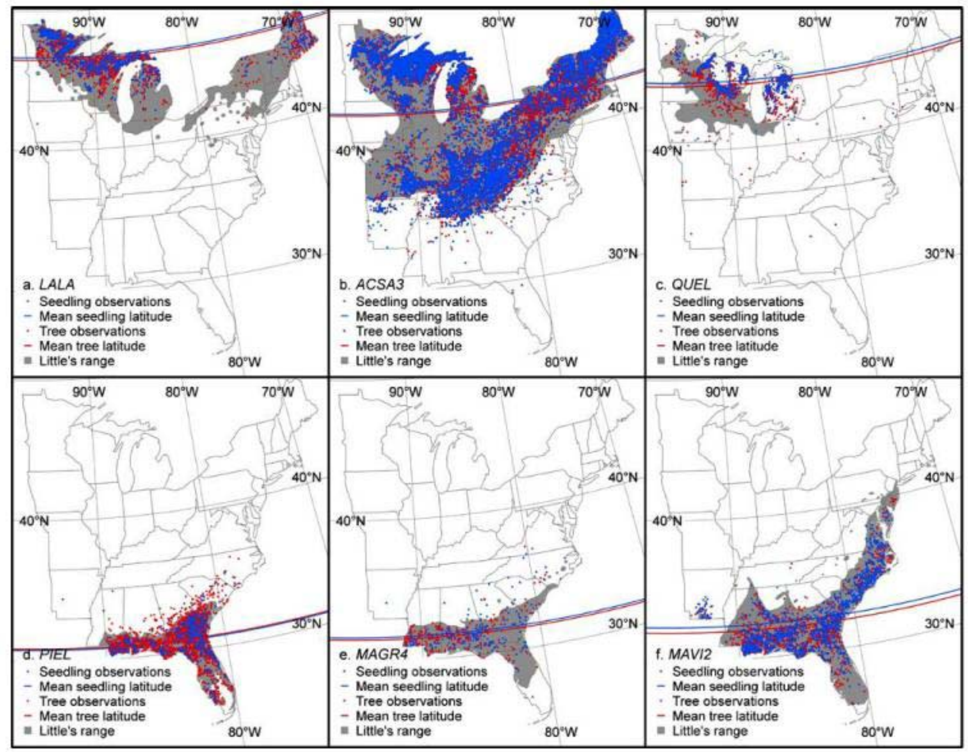
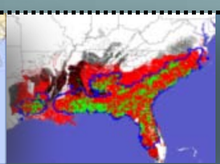


Fig. 2. Little's (1971) species ranges and plot locations for seedlings and tree biomass based on FIA data for selected species (a = tamarack, b = sugar maple, c = northern pin oak, d = shortleaf pine, e = southern magnolia, and f = sweetbay). Additionally, the mean latitude of tree seedlings and biomass based on FIA data are depicted.



NATURE | VOL 427 | 8 JANUARY 2004 | www.nature.com/nature

Extinction risk from climate change

Chris D. Thomas[1], Alison Cameron[1], Rhys E. Green[2], Michel Bakkenes[3], Linda J. Beaumont[4], Yvonne C. Collingham[5], Barend F. N. Erasmus[6], Marinez Ferreira de Siqueira[7], Alan Grainger[8], Lee Hannah[9], Lesley Hughes[4], Brian Huntley[5], Albert S. van Jaarsveld[10], Guy F. Midgley[11], Lera Miles[8*], Miguel A. Ortega-Huerta[12], A. Townsend Peterson[13], Oliver L. Phillips[8] & Stephen E. Williams[14]

[1]*Centre for Biodiversity and Conservation, School of Biology, University of Leeds, Leeds LS2 9JT, UK*
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[3]*National Institute of Public Health and Environment, P.O. Box 1, 3720 BA Bilthoven, The Netherlands*
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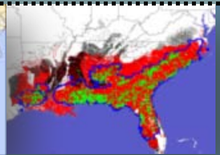
[8]*School of Geography, University of Leeds, Leeds LS2 9JT, UK*
[9]*Center for Applied Biodiversity Science, Conservation International, 1919 M Street NW, Washington, DC 20036, USA*
[10]*Department of Zoology, University of Stellenbosch, Private Bag X1, Stellenbosch 7602, South Africa*
[11]*Climate Change Research Group, Kirstenbosch Research Centre, National Botanical Institute, Private Bag x7, Claremont 7735, Cape Town, South Africa*
[12]*Unidad Occidente, Instituto de Biología, Universidad Nacional Autónoma de México, México, D.F. 04510 México*
[13]*Natural History Museum and Biodiversity Research Center, University of Kansas, Lawrence, Kansas 66045 USA*

"[W]e predict, on the basis of mid-range climate-warming scenarios for 2050, that **15-37% of species** in our samples of regions and taxa will be **committed to exctinction**."





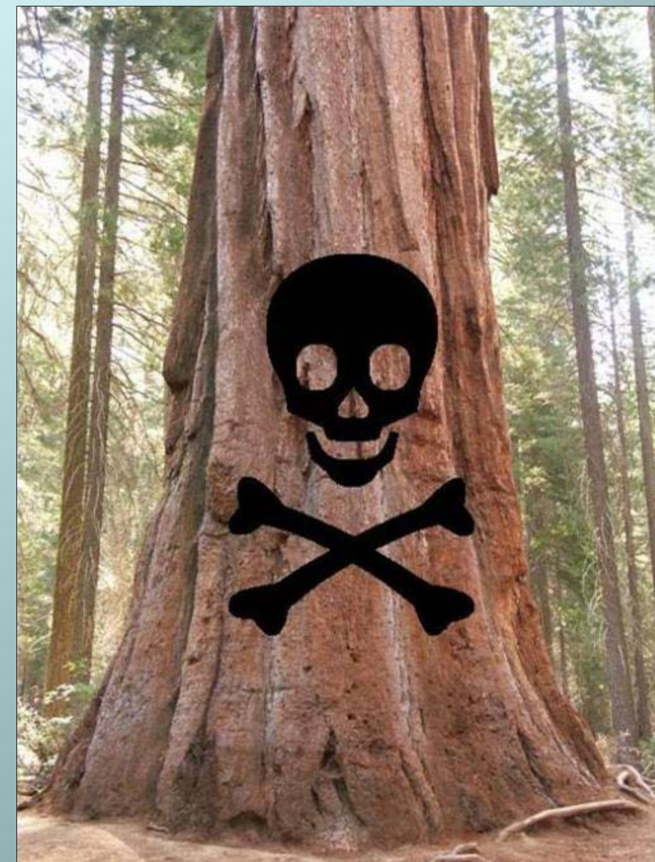
Tree responses to climate change

1) Toleration/adaptation

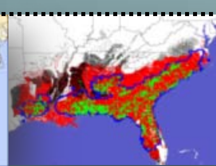
2) Shifting range

3) Population extirpation

<u>**All could have negative genetic consequences**</u>



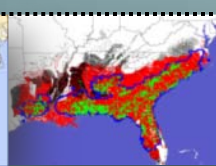




Potential genetic consequences

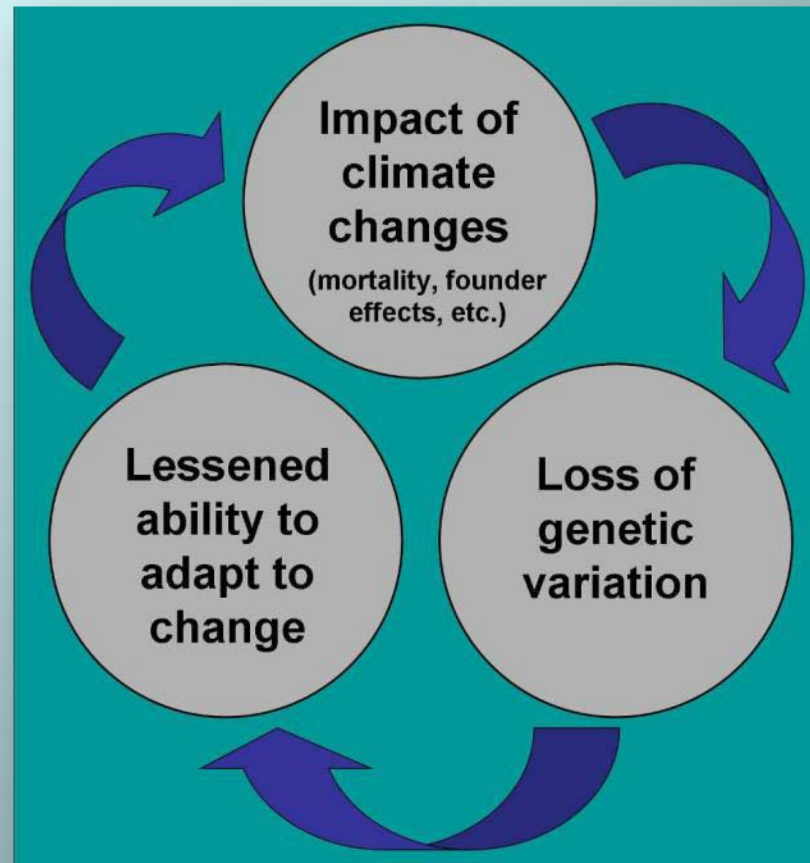
1) Toleration/adaptation
   - Strong selection could reduce genetic variation
2) Shifting range
   - Founder effects, loss of trailing edge populations
3) Population extirpation
   - Potential loss of unique genes and novel gene combinations



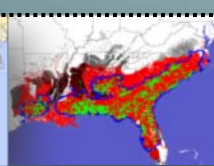


Why do we care about genetics?

- Genetic variation = evolutionary potential to adapt to change
  - Genetic degradation may increase susceptibility to other stressors (pests, pathogens, changing climate, etc.)

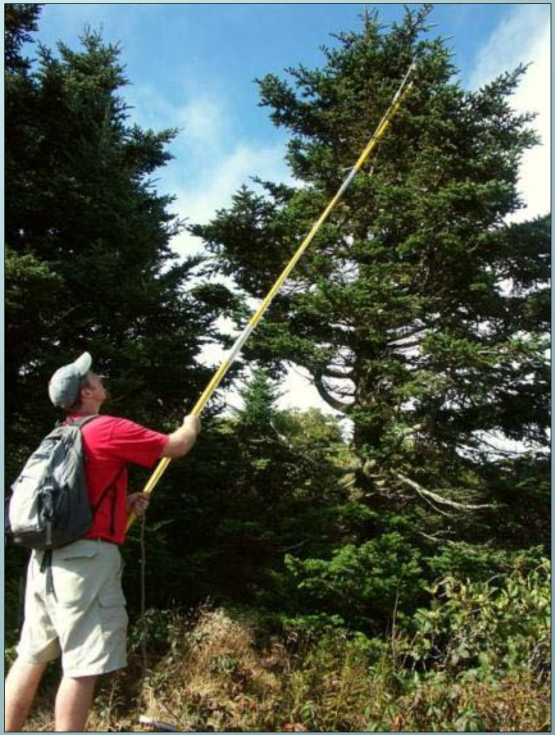






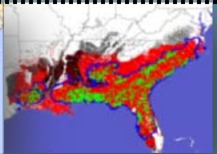
Why genetic risk assessment?

- Resources for conservation of forest tree species will be limited
  - Funding
  - People power
  - Time
- Climate change is not the only serious threat
- How do we decide where to invest?



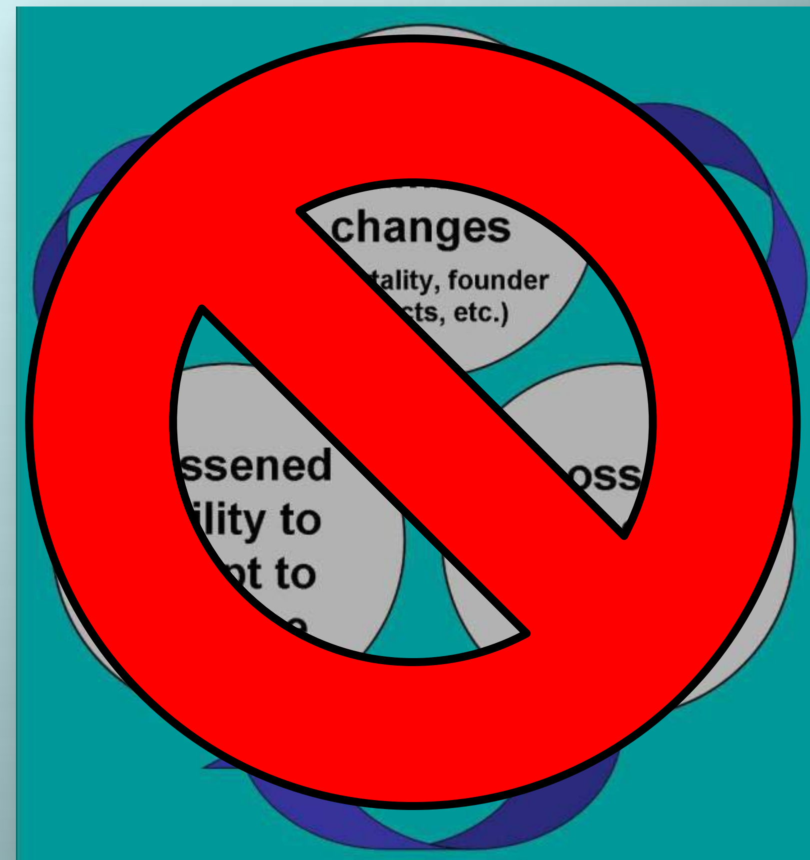
Collecting Fraser fir cones at Mount Rogers, Virginia, for *ex situ* gene conservation



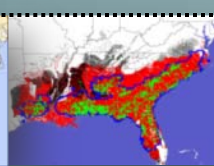


Regional multi-species assessment

- Needed: tool to prioritize species most at risk of genetic degradation
  - <u>Goal:</u> Conserve existing adaptedness and create conditions that allow for future evolution
  - Traits and threats specific to species will result in wide variety of responses





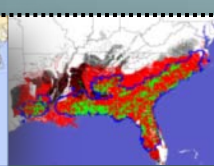


Southern Appalachian Mountains

- Highly diverse flora
  - More than 140 tree species
- Heavily forested, but impacted by several threats
  - Invasive pests and pathogens, fragmentation, air pollution
- Climate change may pose a particular problem

High-elevation hardwood forests, Shenandoah National Park, Virginia



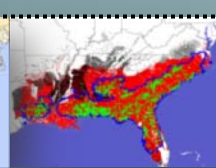


Risk for high-elevation species

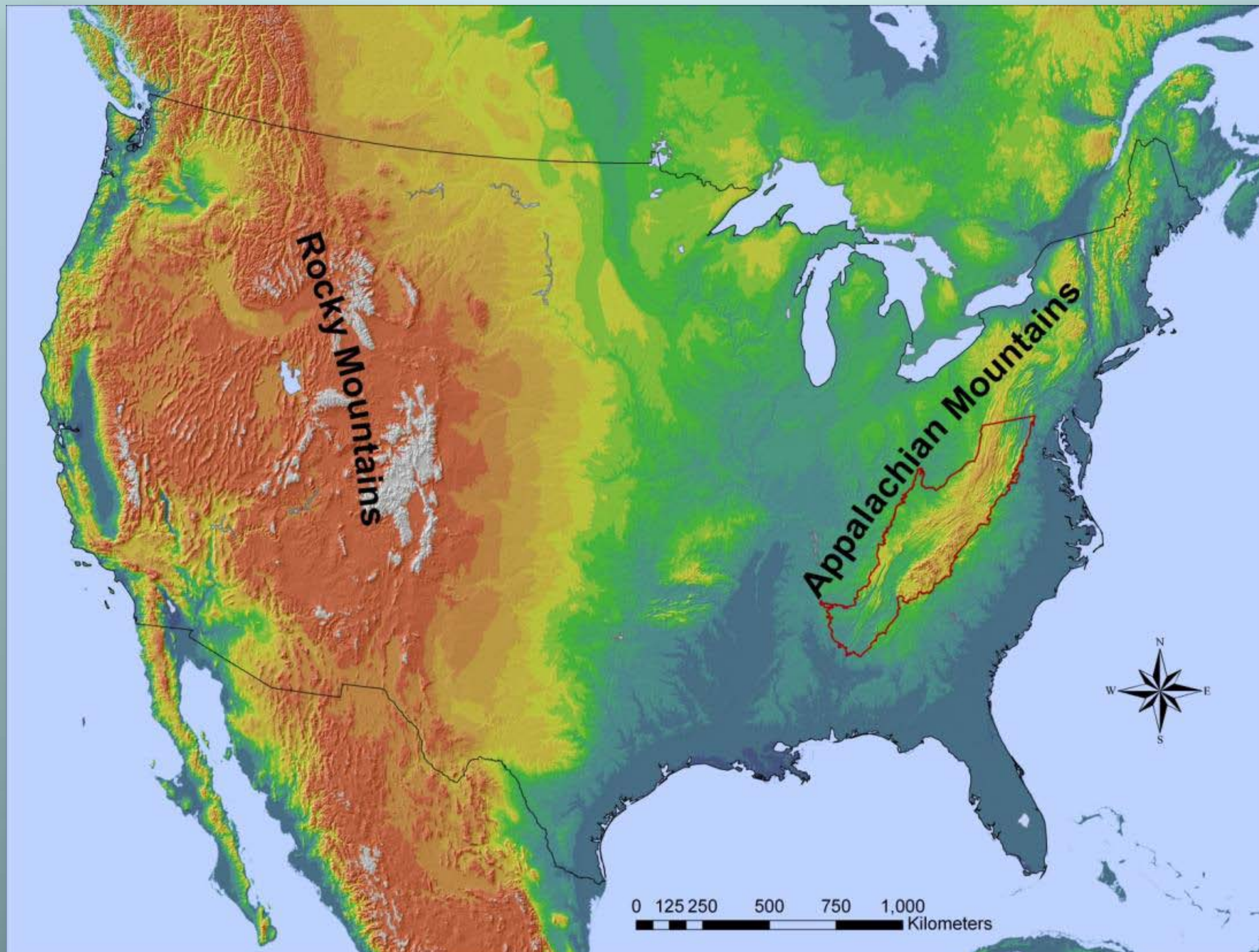
- Tendency toward naturally small, isolated and fragmented populations
  - Lower genetic diversity and interpopulation gene exchange
- Lack of suitable habitat
  - Only option may be uphill migration, but…
  - Could run out of real estate at the highest elevations

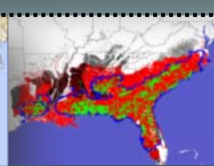
Red spruce-Fraser fir forest, Grandfather Mountain, North Carolina





Southern Appalachian Mountains





Eastern Forest Threat Assessment Center,
Research Triangle Park, N.C.

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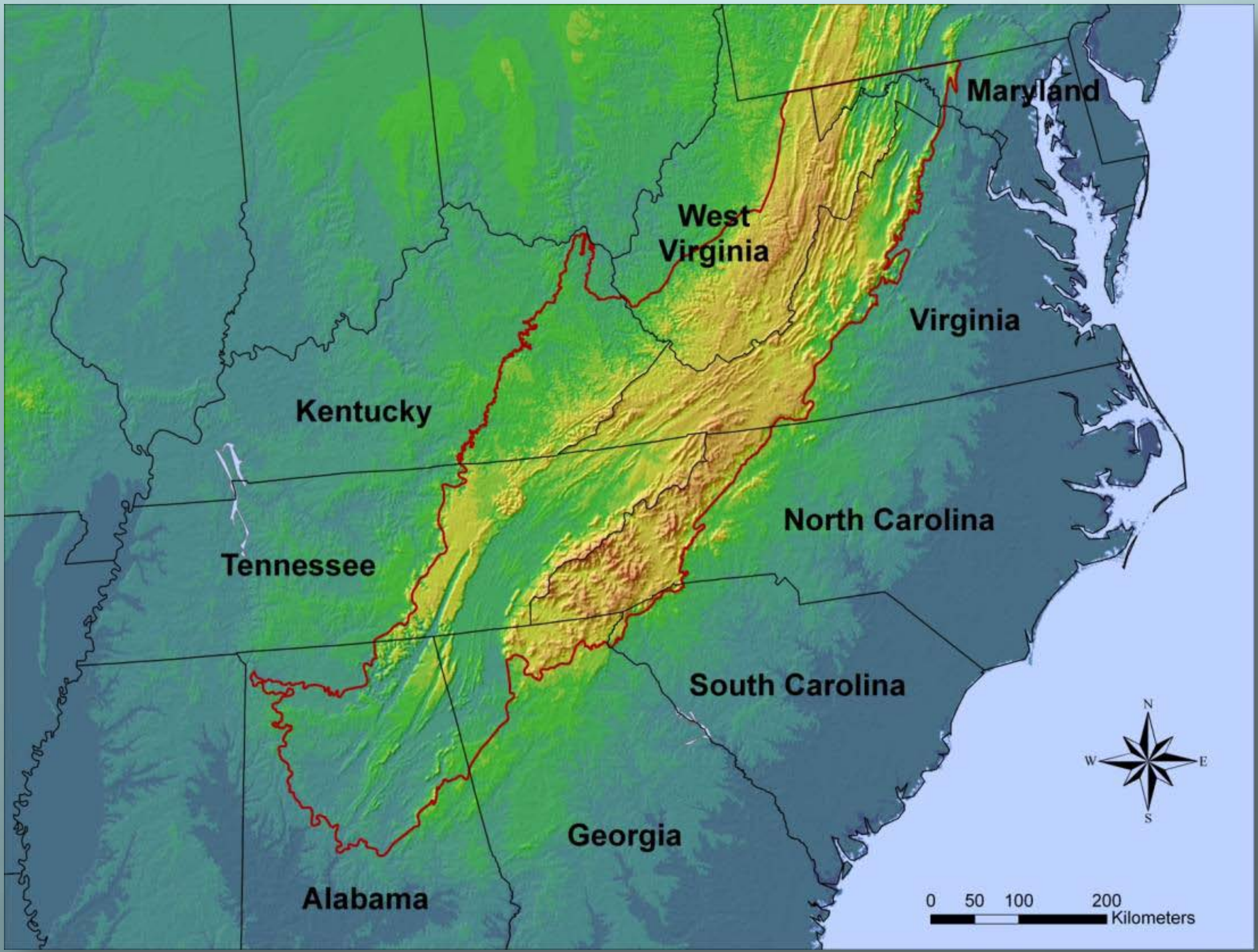
Southern Appalachian Mountains



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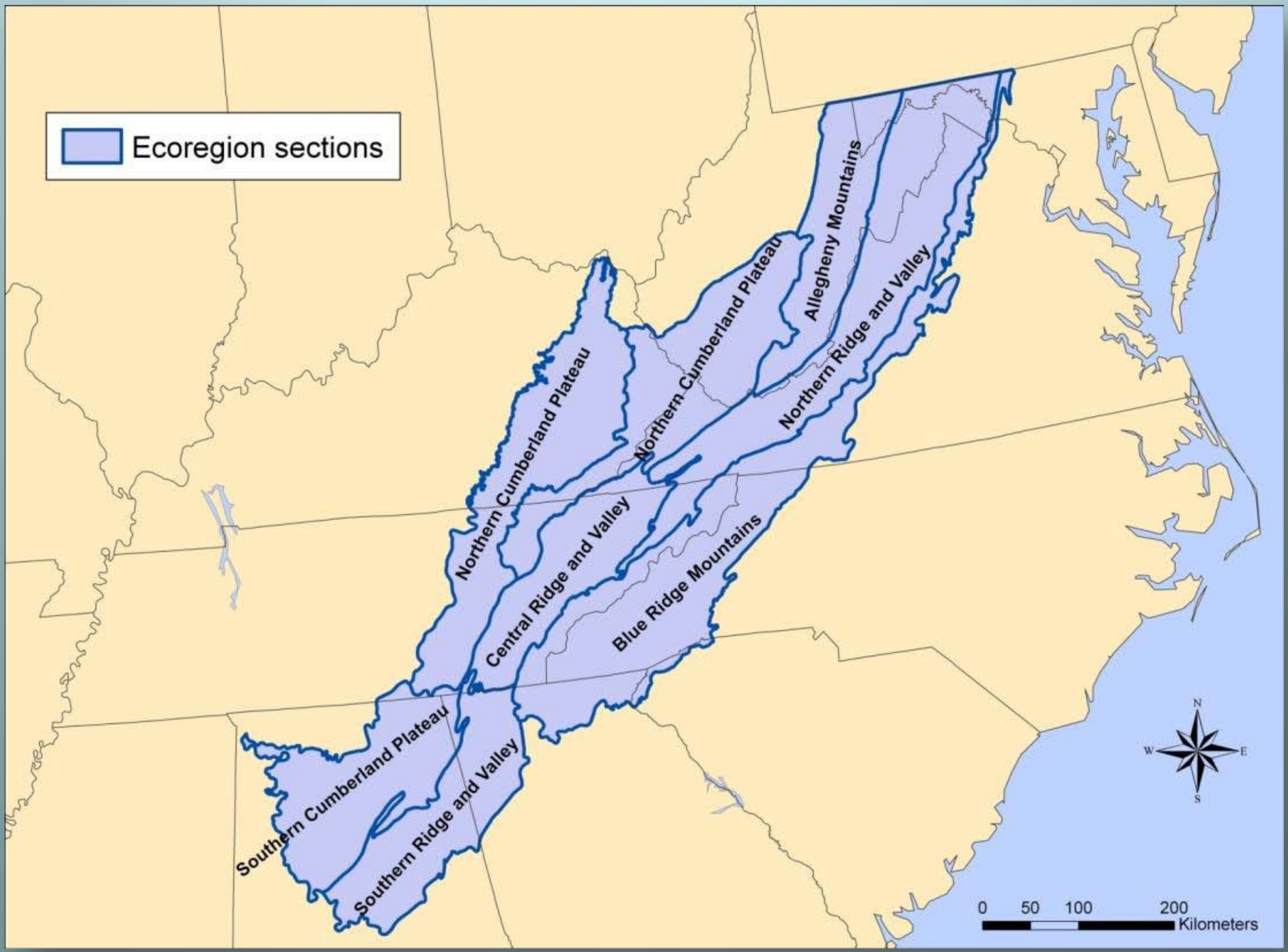
Southern Appalachian Mountains



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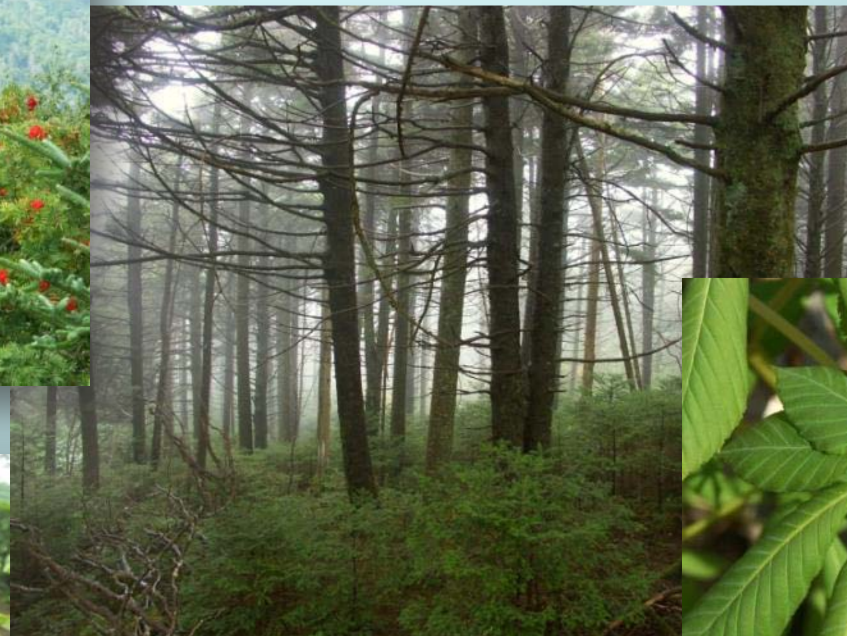
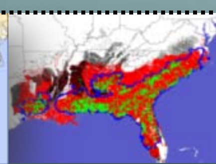
High-elevation species



Endemics or near-endemics



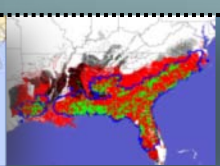
Northern species with Southern disjuncts

Common Southern species

Uncommon Eastern species

Genetic risk assessment methods

1) Literature review to determine attributes predisposing species to genetic risk
2) Identification of relevant data sources
3) Collection of data for 131 Southern Appalachian species
4) Calculation of relative risk across species
   - Six intrinsic risk factors, two extrinsic risk factors, and two conservation modifiers
   - Scored on a scale of 0 to 100 for each species



Intrinsic risk factors

Population structure (*S*)

- **Area of range (↓)** (Petit *et al.* 2008)
- **Number of populations (↓)** (Boyce *et al.* 2002)
- **Mean population area (↓)** (Willi *et al.* 2006)
- **Number of disjuncts (↑)** (McLaughlin *et al.* 2002)

Density and rarity (*D*)

- **Rarity of plot occurrences (↑)** (Jump & Penuelas 2005)
- **Density (↓)** (Stork *et al.* 2009)

Regeneration capacity (*R*)

- **Demographic structure** (fewer young trees = ↓) (Hamrick 2004)
- **Large seed crop frequency (↓)** (Brook *et al.* 2008)
- **Reproductive maturity age (↑)** (Stork *et al.* 2009)
- **Sexual + clonal reproduction (↓)** (Steinger *et al.* 1996)
- **Lifespan (↑)** (Jump & Penuelas 2005)
- **Dioecy (↑)** (Vamosi & Vamosi 2005)

Dispersal ability (*M*)

- **Seed dispersal distance (↓)** (Walther *et al.* 2002)

Genetic variation (*G*)

- **Genetic differentiation (↑)** (Hamrick 2004)
- **Mating system** (outcrossing = ↓) (Hamrick 2004)
- **Pollination vector (wind = ↓)** (Myking 2006)

Habitat affinities (*A*)

- **Mean elevation (↑)** (Hamann & Wang 2006)
- **Niche breadth (↓)** (Stork *et al.* 2009)
- **Successional stage** (later = ↑) (Myking 2002)
- **Site affinities** (generalist = ↓) (Myking 2006)

Extrinsic risk factors

Pest and pathogen threats (*P*)

Threats from pests and pathogens (↑)
(Logan *et al.* 2003)

Climate change (*C*)

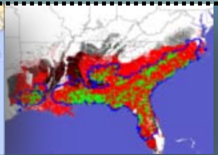
Predicted decrease in suitable habitat (↑)
(Parmesan 2006)

Predicted stability of current habitat (↓)
(Parmesan 2006)

Predicted distance to future suitable habitat (↑)
(Parmesan 2006)

Forest fragmentation (↑)
(Thomas *et al.* 2004)





Endemism index (*E*)

Degree to which species is identified with region of interest (↑)

Conservation status (*L*)

IUCN listing(↑)

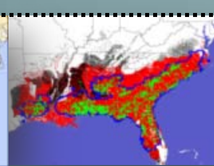
Conservation modifiers

Data availability

- Tree range maps for distributional information
- Forest Inventory and Analysis (FIA) data for rarity and density information
- Widely available publications for species life-history traits
  - *Silvics of North America* (Burns and Honakala 1990)
  - *Woody Seed Plant Manual* (Bonner and Karrfalt 2008)
  - *Fire Effects Information System* (Brown and Smith 2000)

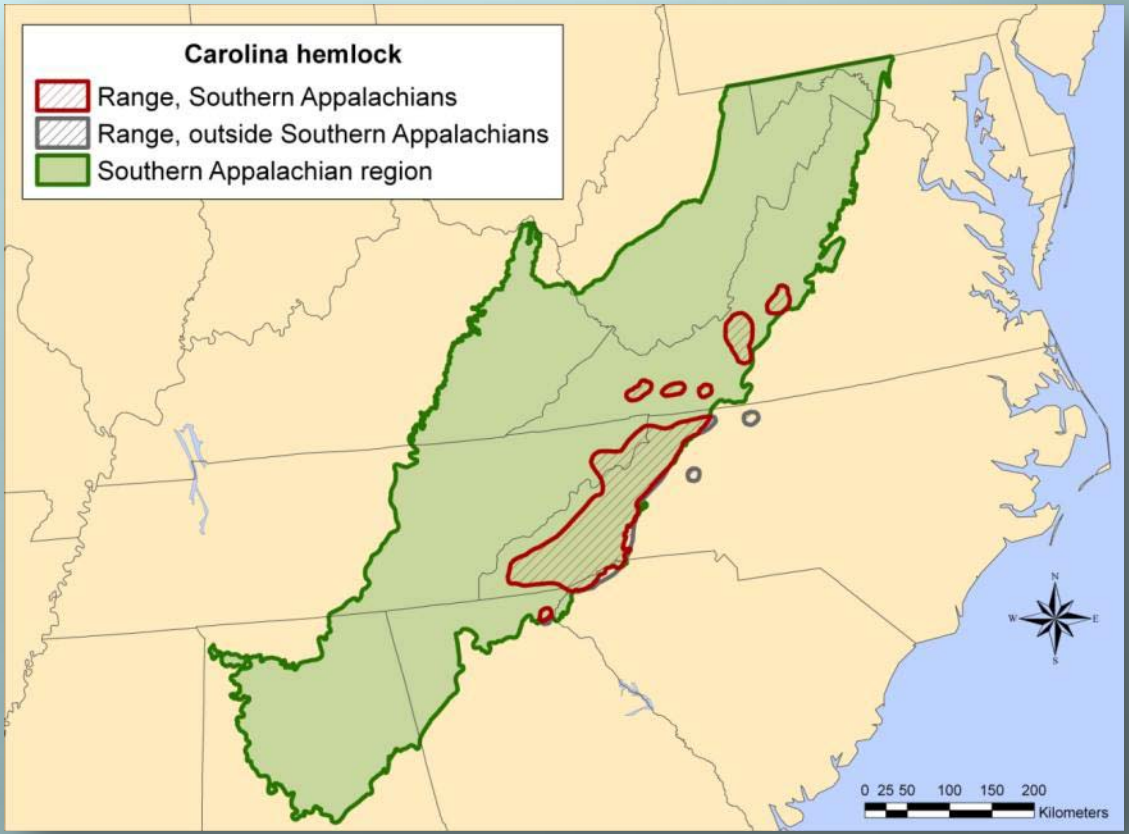
Eastern hemlock-white pine forest, Linville Gorge, North Carolina



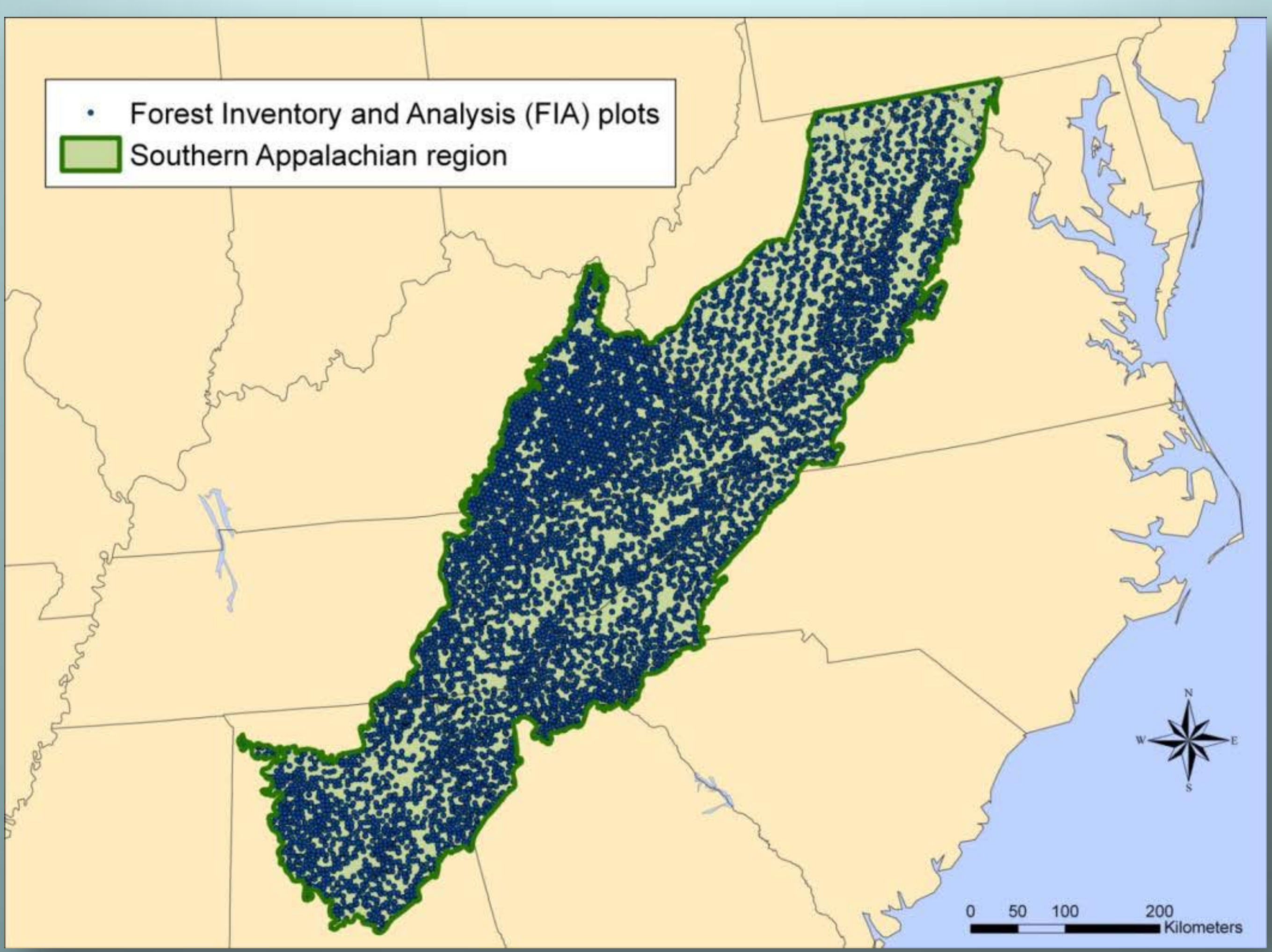


Tree distribution information

Carolina hemlock (*Tsuga caroliniana*), Linville Falls, North Carolina

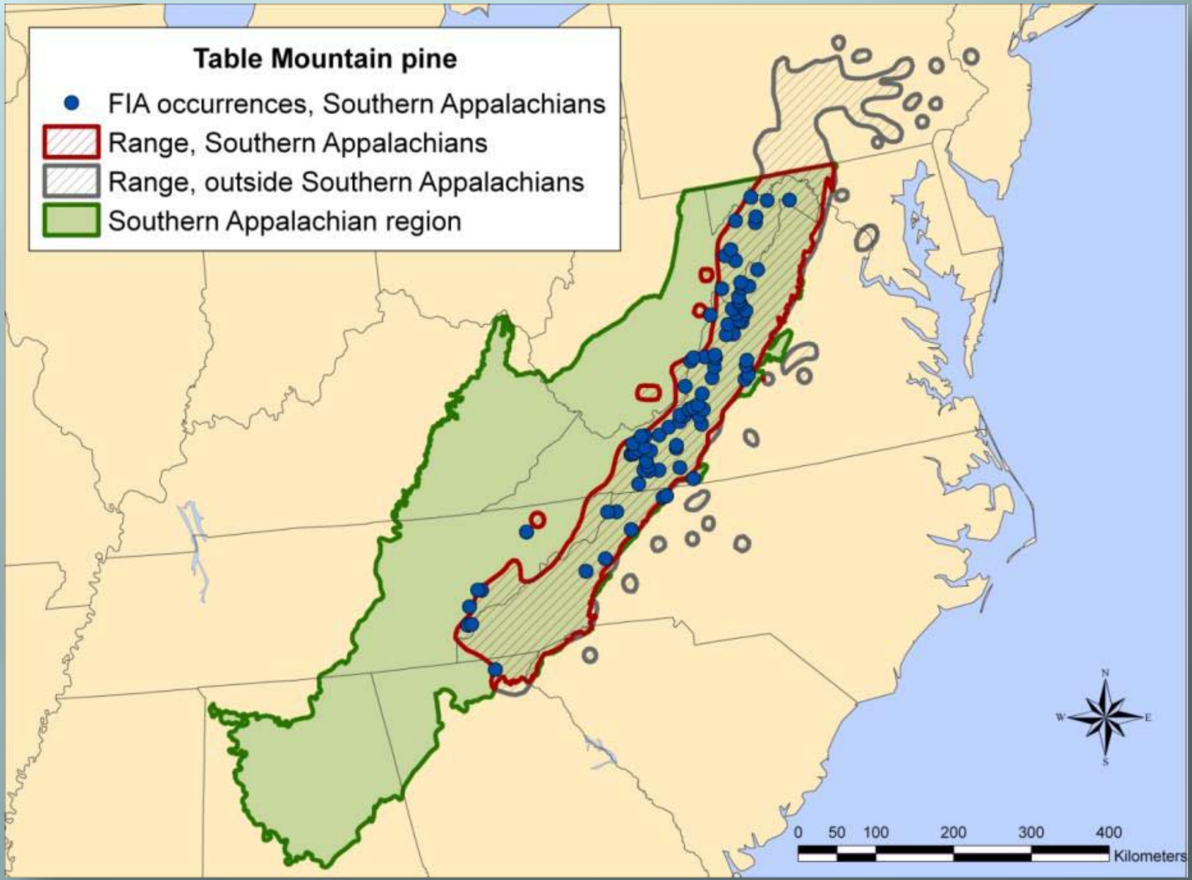


Forest Inventory and Analysis data

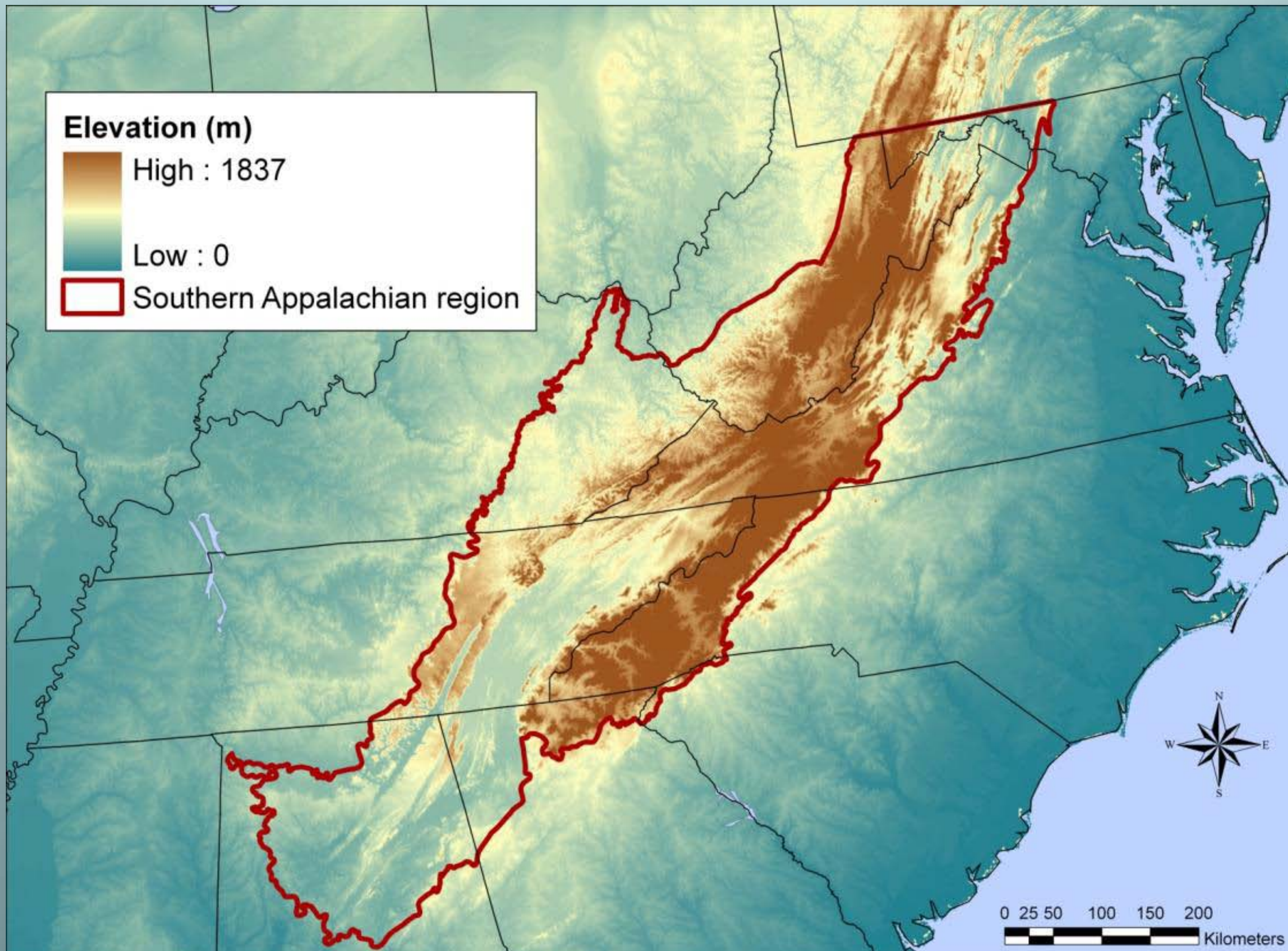


Forest Inventory and Analysis data

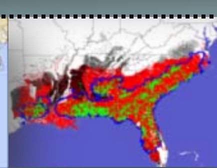
Table Mountain pine (*Pinus pungens*), Blue Ridge Parkway, North Carolina



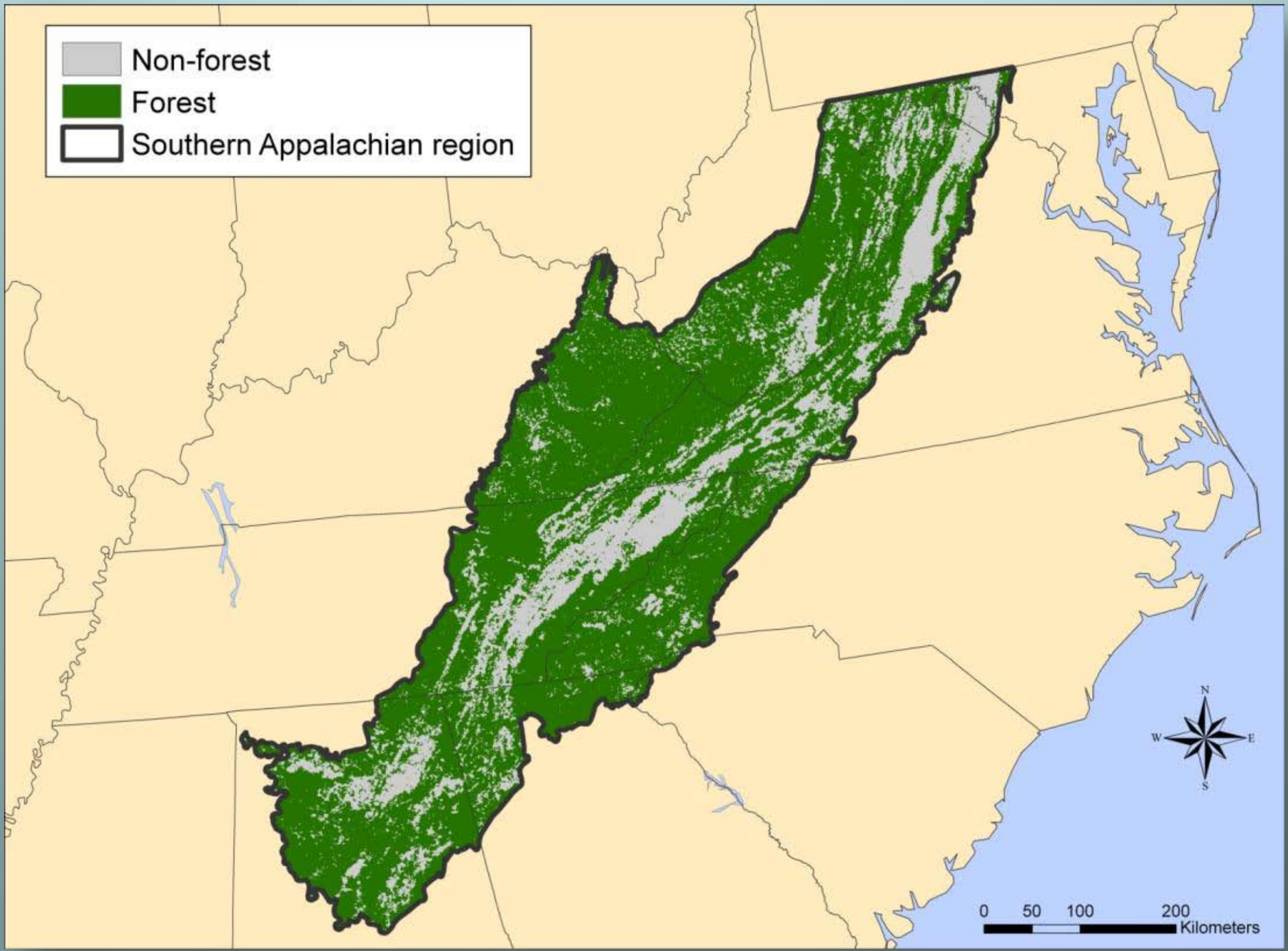
Digital elevation model







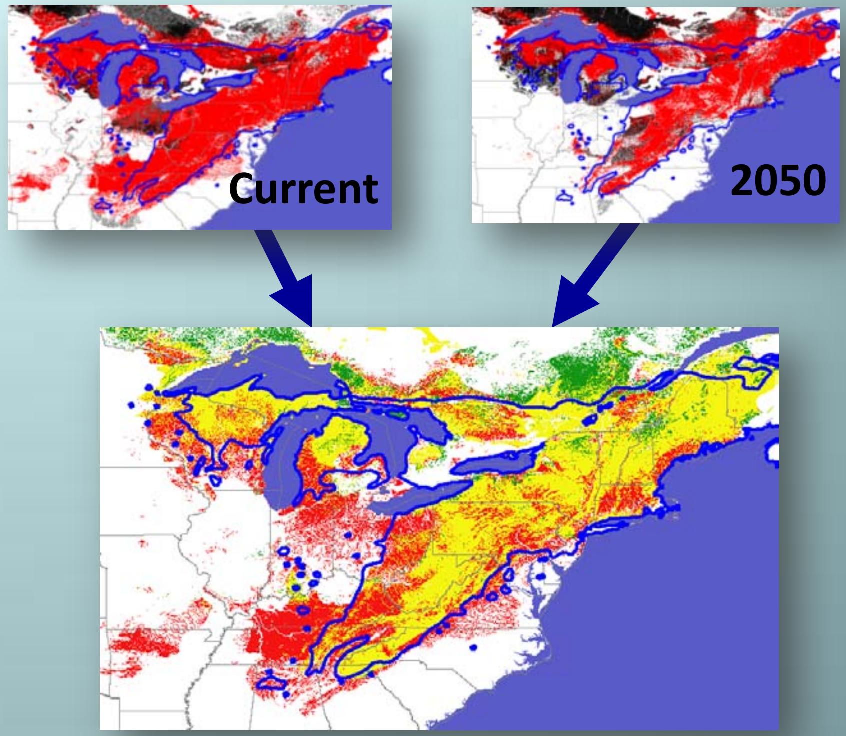
Fragmentation (forest land cover)



Climate change pressure

1) Change over time in area of suitable habitat (Hadley B1, 2050)
   - ***More = higher risk***
2) Percent of current habitat that remains suitable
   - ***Less = higher risk***
3) Mean distance from current habitat to nearest future habitat
   - ***Farther = higher risk***

Tsuga canadensis



New habitat in 2050

Habitat overlap, now and 2050

Current habitat gone in 2050

Species genetic risk (score 0-100)

$$\textbf{Risk} = (w_S S + w_D D + w_R R + w_M M + w_A A + w_G G)$$

$$+$$

$$(w_P P + w_C C)$$

$$+$$

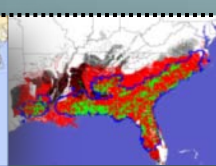
$$(w_E E + w_L L)$$

S, D, R, M, A, G = intrinsic risk factors
P, C = extrinsic risk factors
E, L = conservation modifiers

Relativized from 0 to 100, with 100 the highest risk

w_x = weights of factors and modifiers (must sum to 1)





Weighting genetic risk factors

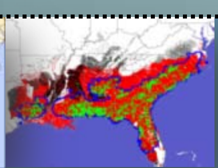
Intrinsic factors	Extrinsic factors
Population structure (*S*) (10%)	Pest/pathogen threat (*P*) (15%)
Density/rarity (*D*) (10%)	Climate pressure (*C*) (15%)
Regeneration capacity (*R*) (10%)	
Dispersal ability (*M*) (10%)	
Habitat affinities (*A*) (10%)	
Genetic variation (*G*) (10%)	

Conservation modifiers:

Endemism (*E*) (5%)

Conservation status (*L*) (5%)

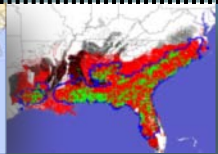




So. Appalachian species ***most*** at risk

Rank	Species	Risk Score
1	Carolina hemlock (*Tsuga caroliniana*)	63.14
2	September elm (*Ulmus serotina*)	62.53
3	Fraser fir (*Abies fraseri*)	54.97
4	Blue ash (*Fraxinus quadrangulata)*	54.61
5	Butternut (*Juglans cinerea*)	54.53
6	Shumard oak (*Quercus shumardii*)	53.84
7	Table Mountain pine (*Pinus pungens*)	52.77
8	Carolina silverbell (*Halesia carolina*)	52.59
9	American chestnut (*Castanea dentata*)	52.49
10	Black ash (*Fraxinus nigra*)	52.21

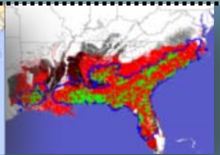




So. Appalachian species *least* at risk

Rank	Species	Risk Score
122	Common serviceberry (*Amelanchier arborea*)	27.46
123	Northern red oak (*Quercus rubra*)	27.29
124	American holly (*Ilex opaca*)	26.49
125	Black cherry (*Prunus serotina)*	26.43
126	Black oak (*Quercus velutina*)	26.39
127	Eastern redcedar (*Juniperus virginiana*)	26.24
128	Red maple (*Acer rubrum*)	25.94
129	American hophornbeam (*Ostrya virginiana*)	25.57
130	Black gum (*Nyssa sylvatica)*	24.50
131	Musclewood (*Carpinus caroliniana*)	23.70

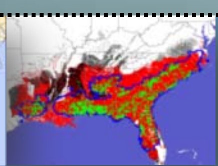




Western Washington State assessment

- Ranking genetic risk for National Forests and National Parks
- 36 species, sorted into three conservation risk groups
  - Ranking risk of species in top group
- Tailored system to specific regional needs

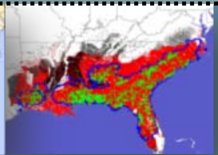




Conclusions

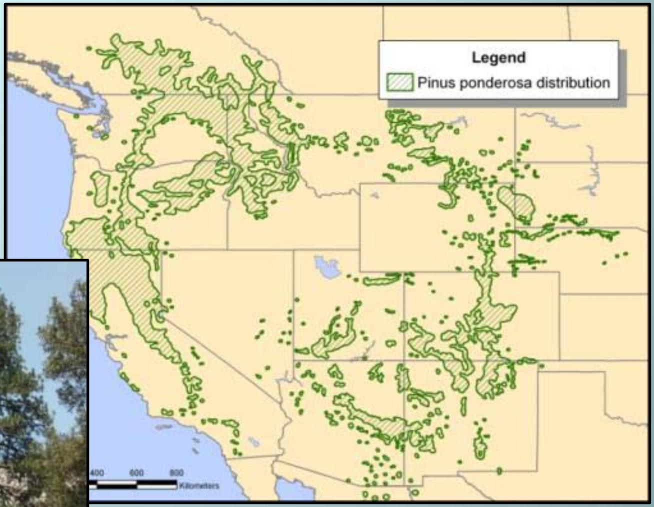
1) Climate change, in concert with other threats poses a threat to genetic integrity of forest tree species
   - Risk varies based on attributes of species
2) Genetic risk assessment is necessary to efficiently and effectively use conservation resources
3) A risk assessment system for the Southern Appalachians ranks the relative risk of genetic degradation
   - System flexible, applicable to different regions and scales
4) Next: population-level assessments within species
   - Account for interaction among threats, attributes

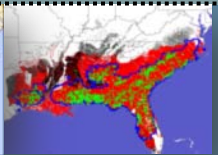


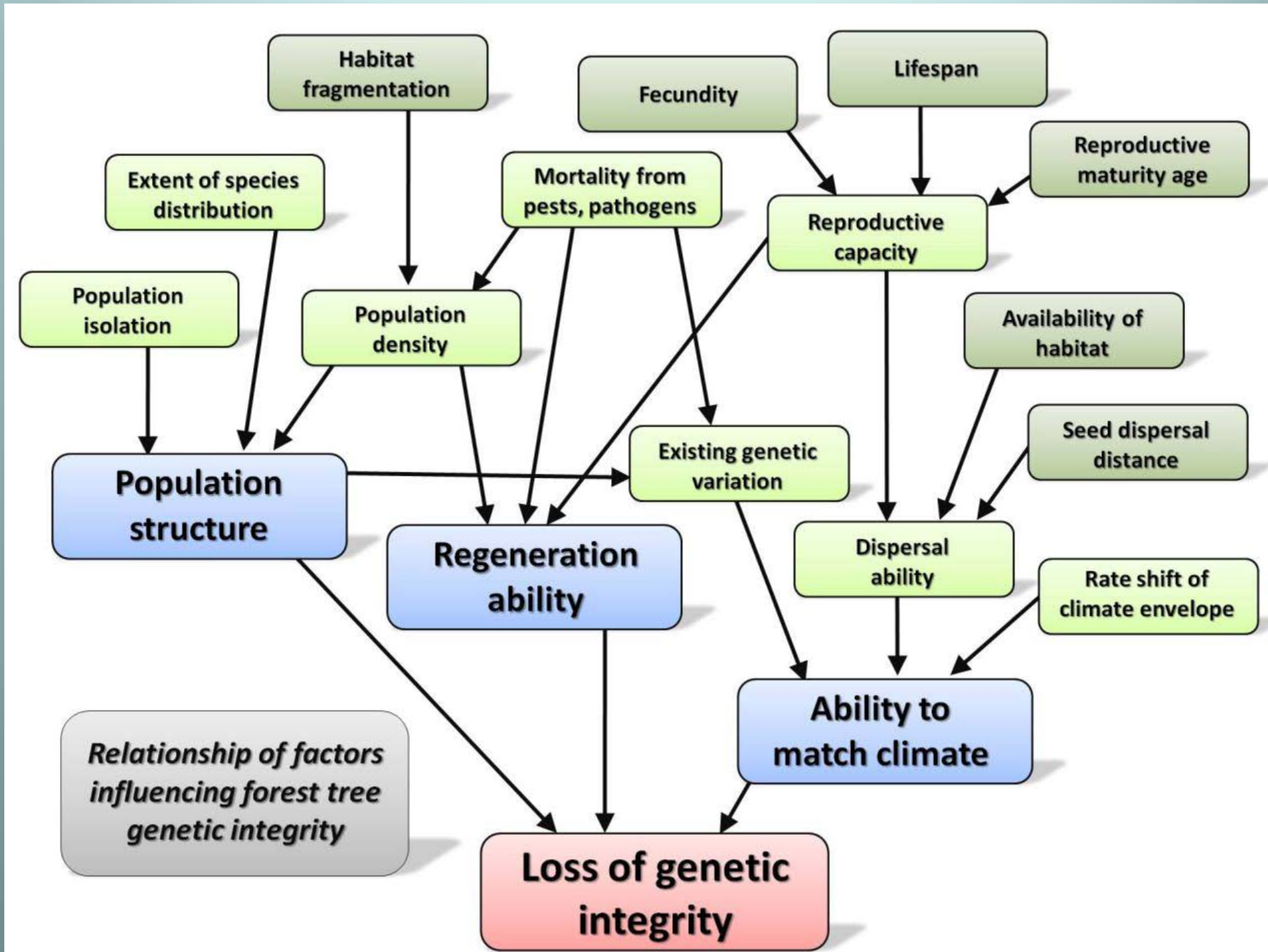


Population-level risk assessment

- Ponderosa pine (*Pinus ponderosa*), Eastern hemlock (*Tsuga canadensis*)
- Species-wide genetic variation using molecular markers
- Will compile as much population-level data as possible
- Interactions of threats and species attributes
  - Bayesian Belief Network approach incorporating expert opinion






Habitat fragmentation
Fecundity
Lifespan
Reproductive maturity age
Extent of species distribution
Mortality from pests, pathogens
Reproductive capacity
Population isolation
Population density
Availability of habitat
Seed dispersal distance
Population structure
Existing genetic variation
Regeneration ability
Dispersal ability
Rate shift of climate envelope
Ability to match climate
Relationship of factors influencing forest tree genetic integrity
Loss of genetic integrity

Thoughts? Please contact me:

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Canaan Valley State Park, West Virginia

Thanks to:

- Funding: U.S. Forest Service Forest Health Monitoring Program
- Development of assessment methodology: Bill Hargrove, Carol Aubry
- Other assistance: Kurt Riitters, Danny Lee, Frank Koch, Barb Conkling, Fred Cubbage
- FIA field crews