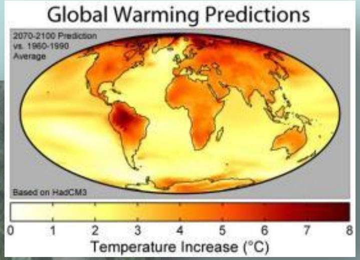
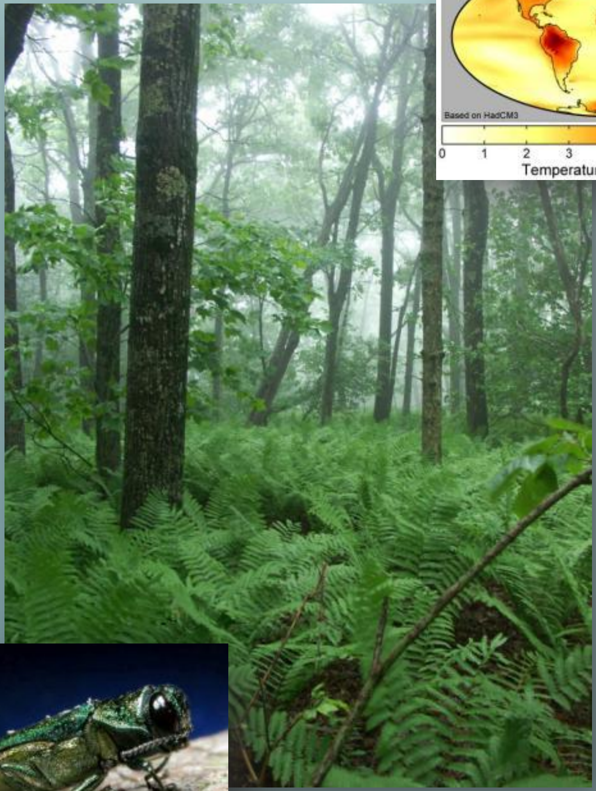
A Framework for Assessing the Relative Risk of Genetic Degradation to Forest Trees Affected by Climate Change and Other Threats





Kevin M. Potter

Barbara S. Crane

First Friday All Climate Change Talks

March 4, 2011

NC STATE UNIVERSITY

Road map for this talk

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

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

articles

A globally coherent fingerprint of climate change impacts across natural systems

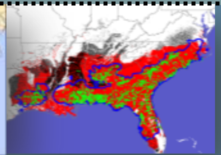
Camille Parmesan* & Gary Yohe†

* *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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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]

[a] USDA Forest Service, Northern Research Station, St. Paul, MN, United States
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[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."

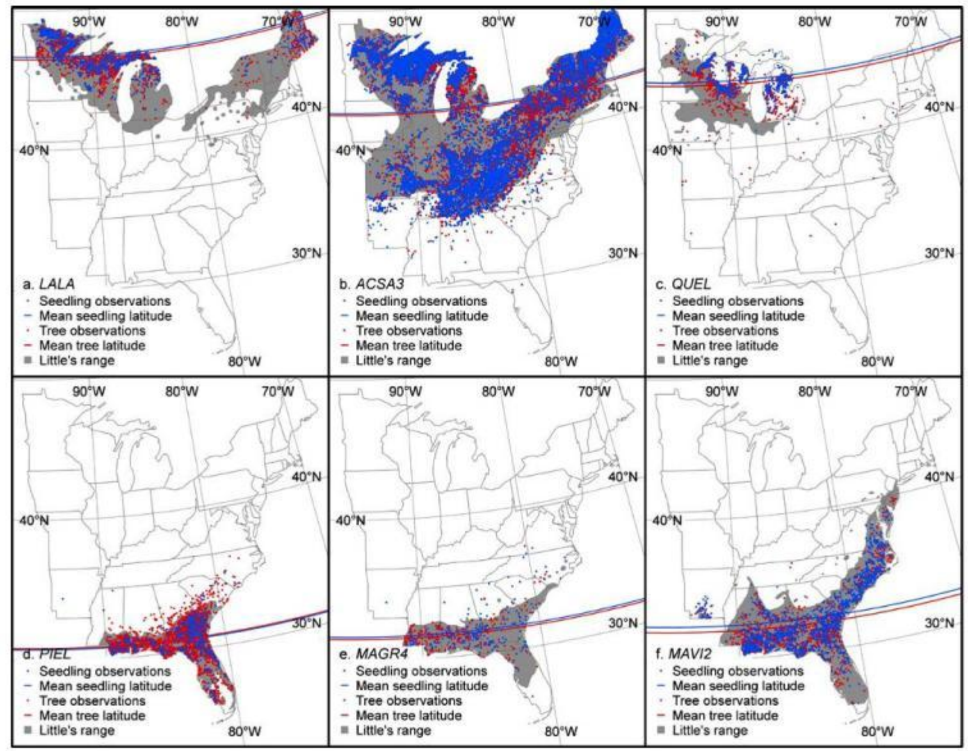
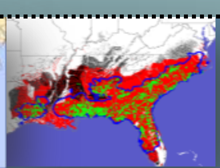


Fig. 2. Little's (1971) species ranges and plot locations for seedlings and tree biomass based on FIA data for selected species (a = tamarack, b = sugar maple, c = northern pin oak, d = shortleaf pine, e = southern magnolia, and f = sweetbay). Additionally, the mean latitude of tree seedlings and biomass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

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[10]*Department of Zoology, University of Stellenbosch, Private Bag X1, Stellenbosch 7602, South Africa*
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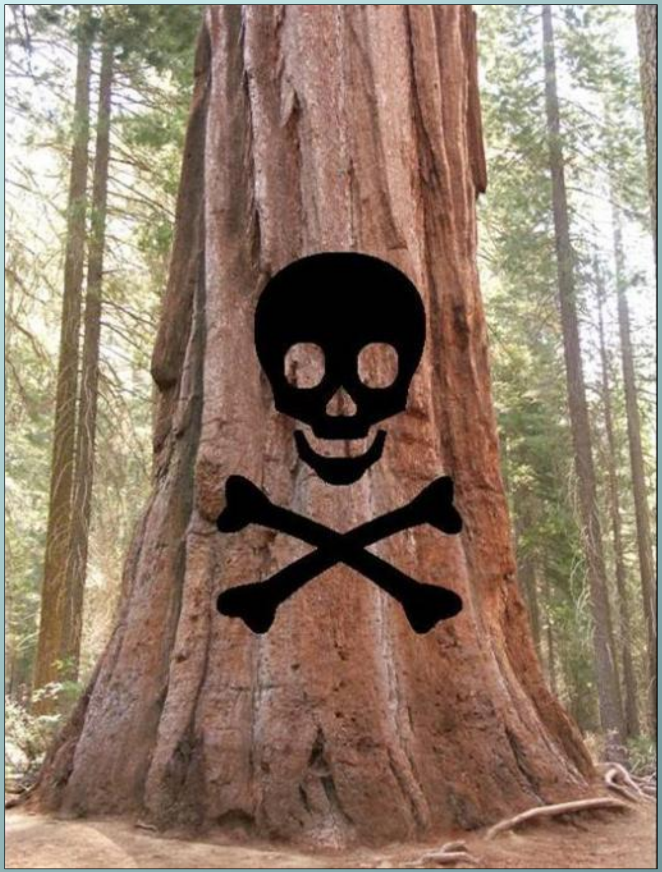
[13]*Natural History Museum and Biodiversity Research Center, University of Kansas, Lawrence, Kansas 66045 USA*

"[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**."

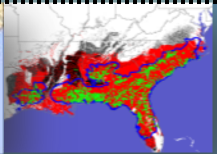
Tree responses to climate change

1) Toleration/adaptation
2) Shifting range
3) Population extirpation

All could have negative genetic consequences



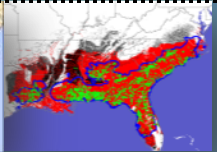




Potential genetic consequences

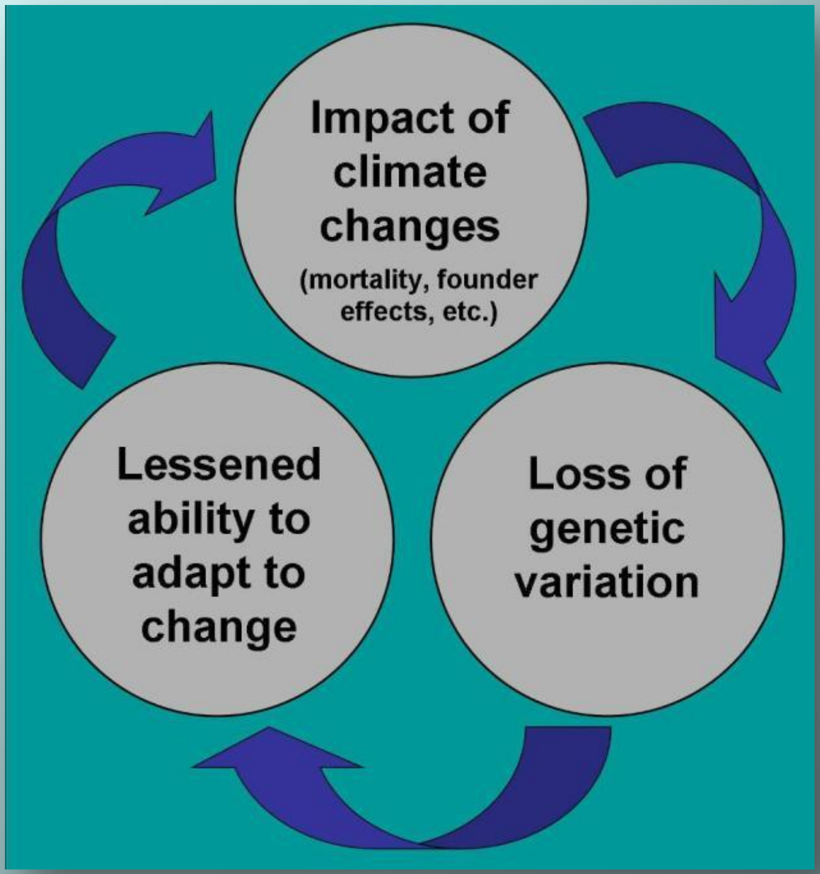
1) Toleration/adaptation
   - Strong selection could reduce genetic variation
2) Shifting range
   - Founder effects, loss of trailing edge populations
3) Population extirpation
   - Potential loss of unique genes and novel gene combinations





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.)

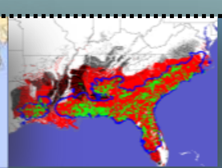


Why genetic risk assessment?

- Resources for conservation of forest tree species will be limited
- Climate change is not the only serious threat
- Traits and threats specific to species will result in wide variety of responses
- How do we decide where to invest?

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

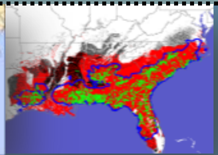




Forest Tree Genetic Risk Assessment System (ForGRAS)

- Framework usable for any medium to large region
- Accounts for a wide variety of species characteristics and multiple threats
- Allows users to choose which risk factors to include in the risk assessment, and how to weight
- User guide and assessment spreadsheet: **www.forestthreats.org/current-projects/project-summaries/genetic-risk-assessment-system**





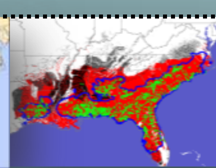
Southern Appalachian Mountains

- Highly diverse flora
  - More than 140 tree species
- Variety of distributions
  - High-elevation species
  - Endemics or near-endemics
  - Northern species with southern disjuncts
  - Common Southern species
  - Uncommon Eastern species







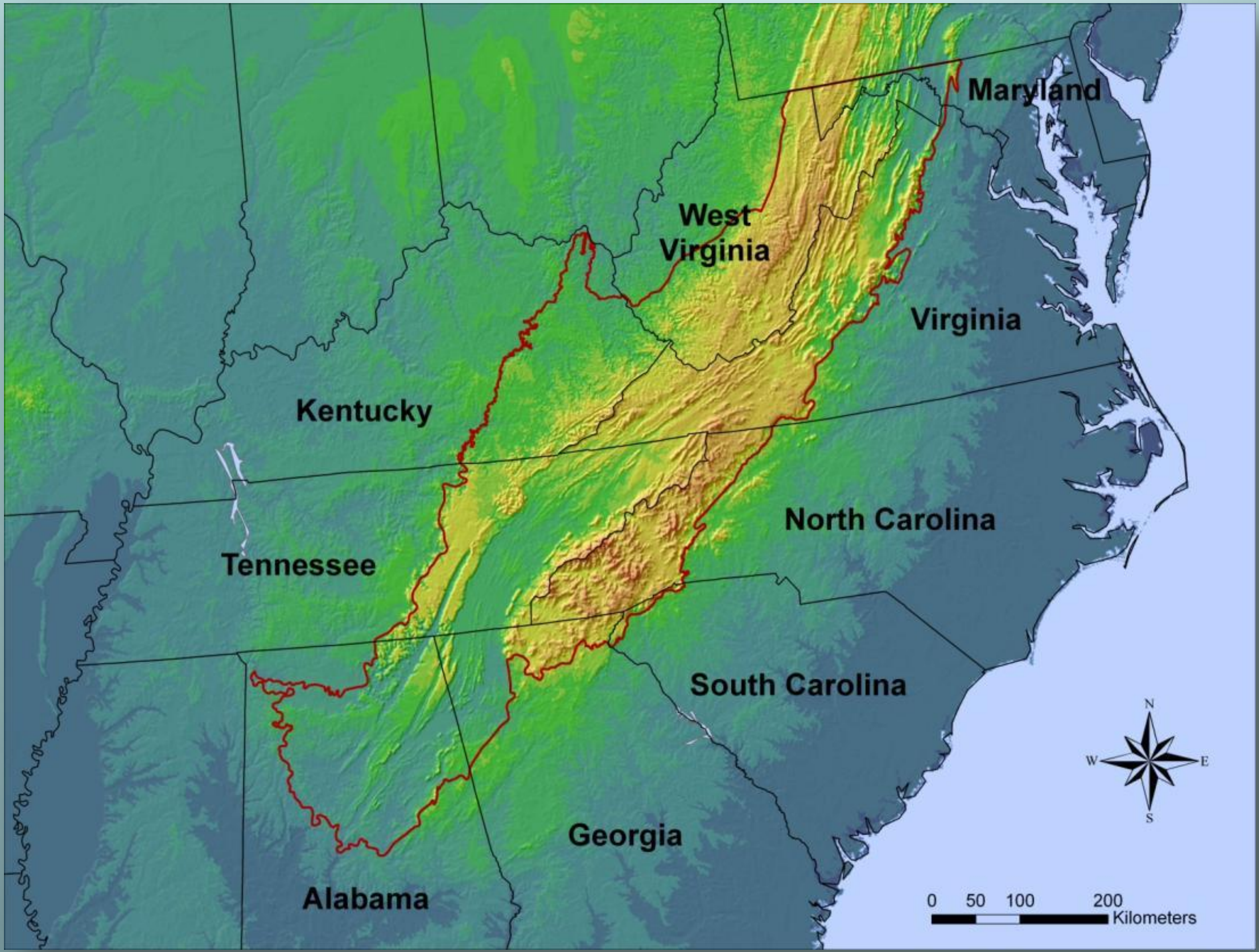


Southern Appalachian vulnerabilities

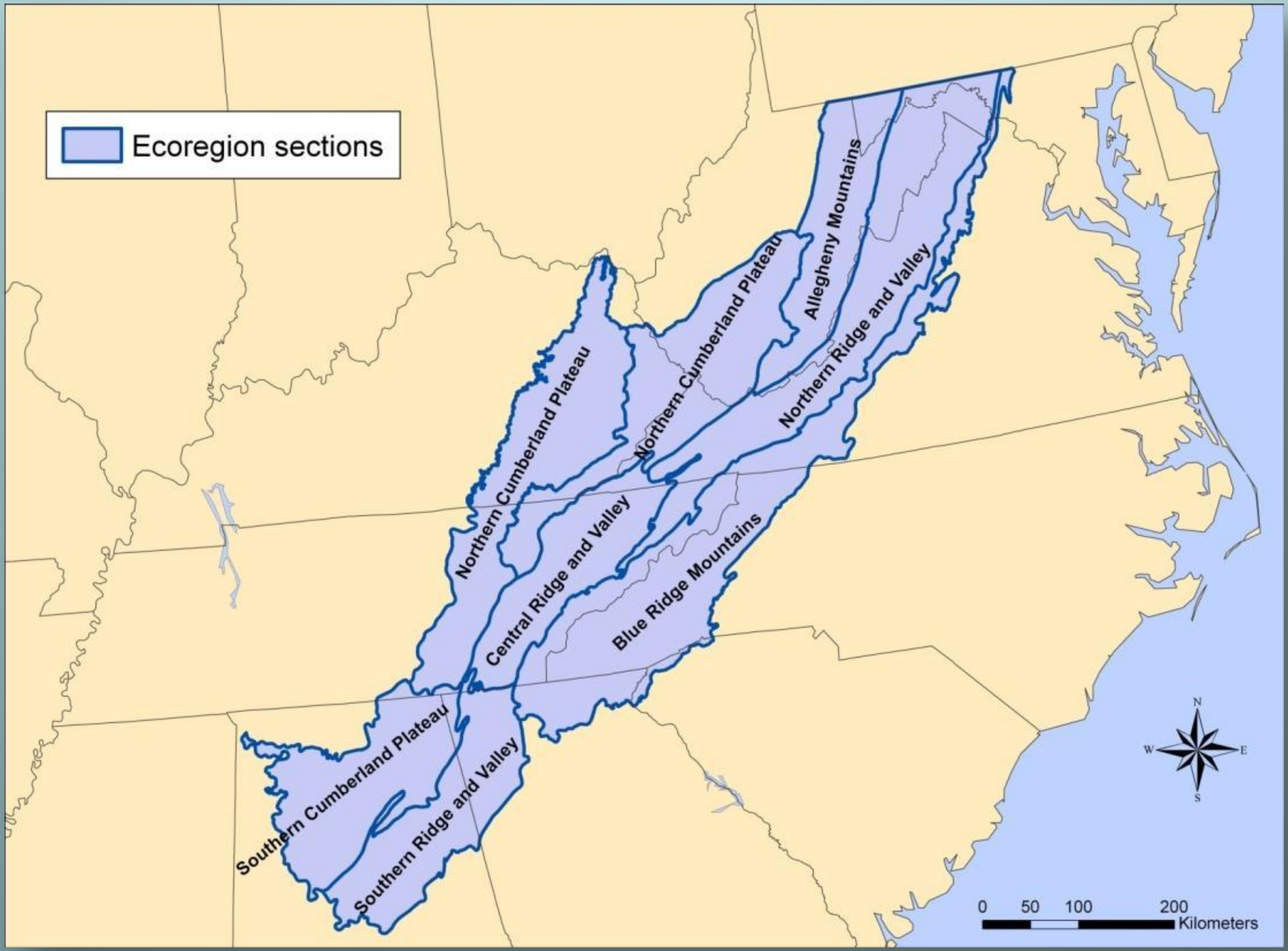
- Heavily forested, but impacted by several threats
  - Invasive pests and pathogens, fragmentation, air pollution
- Climate change may pose a particular problem
  - Tendency toward small and isolated populations (lower diversity and gene exchange)
  - Pressure may be to move uphill – running out of real estate

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

Southern Appalachian Mountains



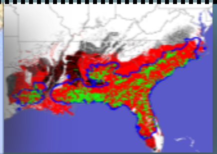
Southern Appalachian Mountains



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)

Pest and pathogen threats (*P*)

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

Climate change (*C*)

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

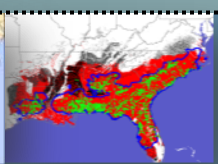
Predicted stability of current habitat (↓)
(Parmesan 2006)

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

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

Extrinsic risk factors





Endemism index (*E*)

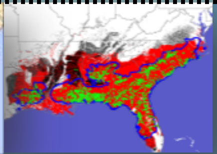
- **Degree to which species is identified with region of interest (↑)**

Conservation status (*L*)

- **IUCN listing(↑)**

Conservation modifiers



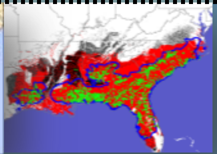


Data availability

- 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)

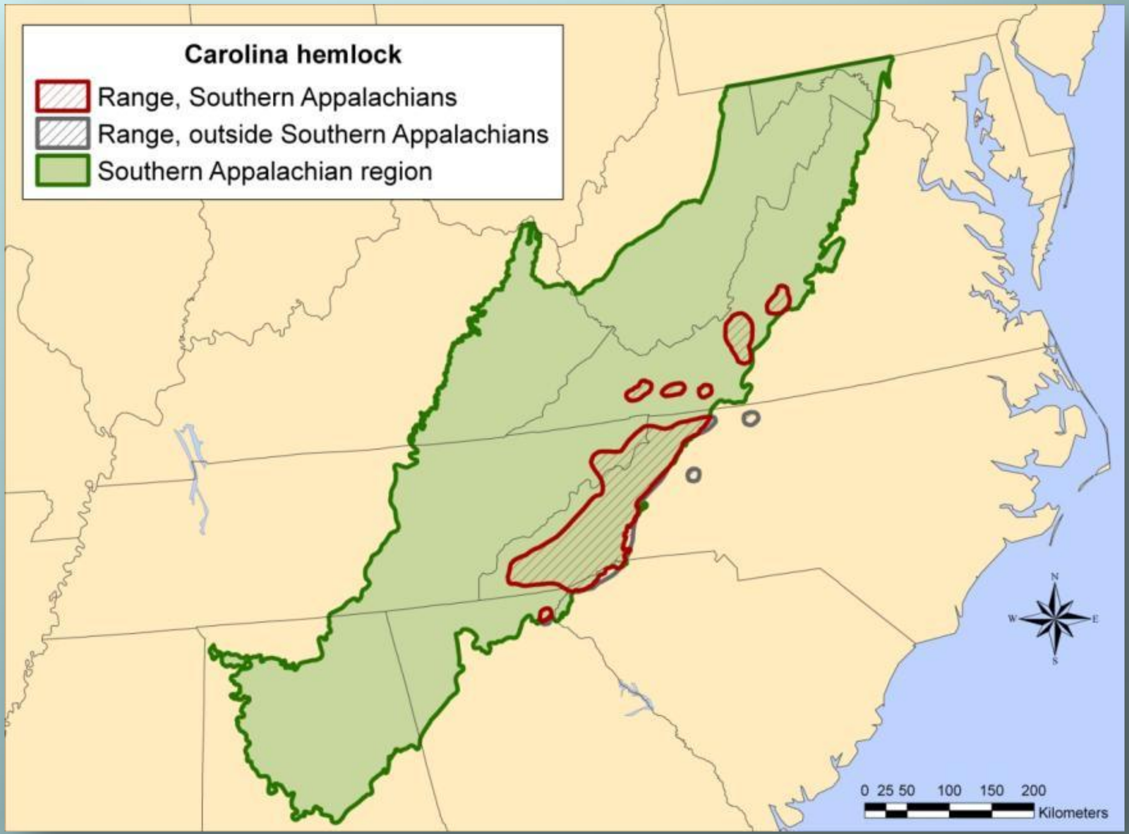
High-elevation hardwood forests, Shenandoah National Park, Virginia



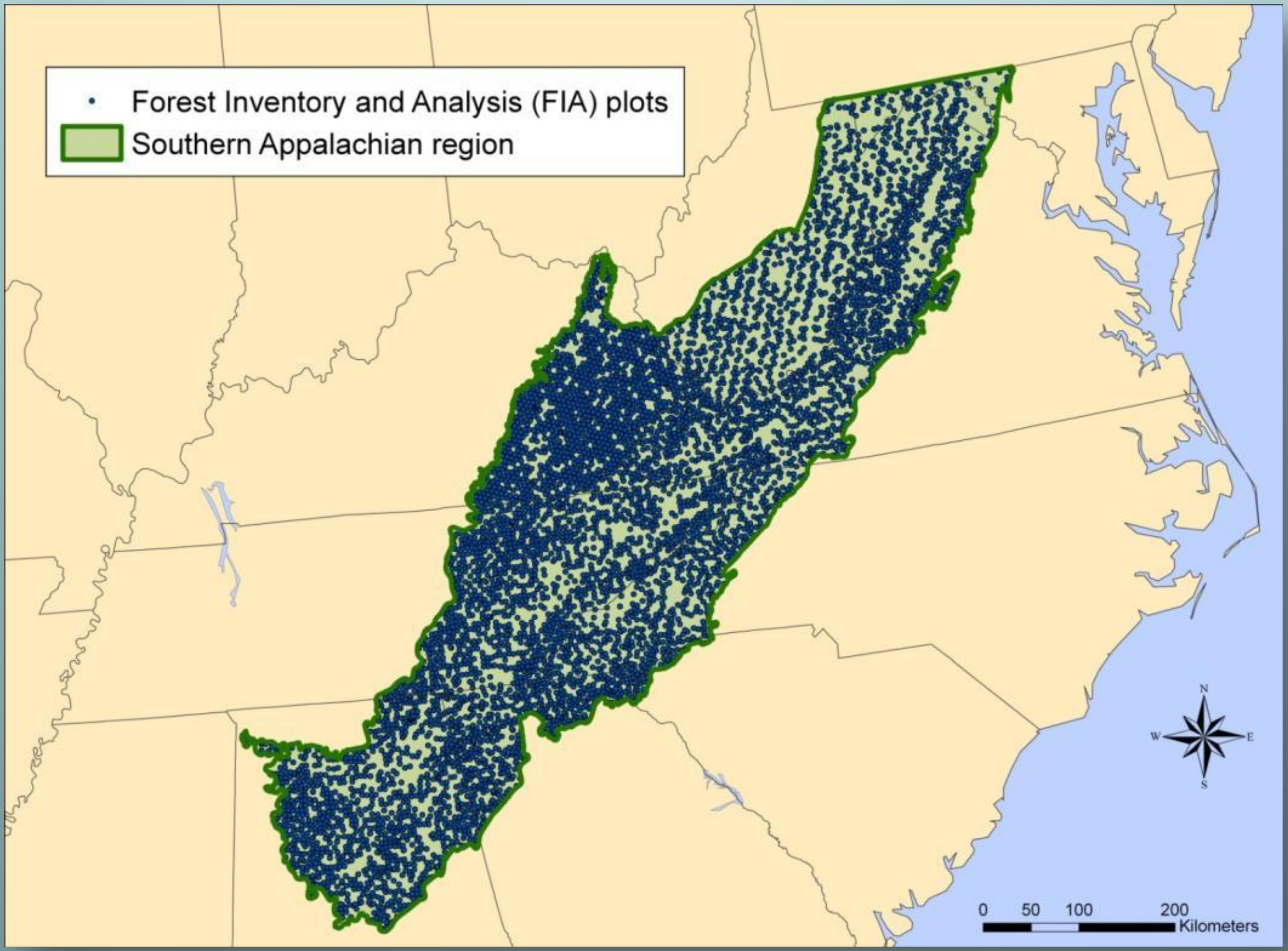


Tree distribution information

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

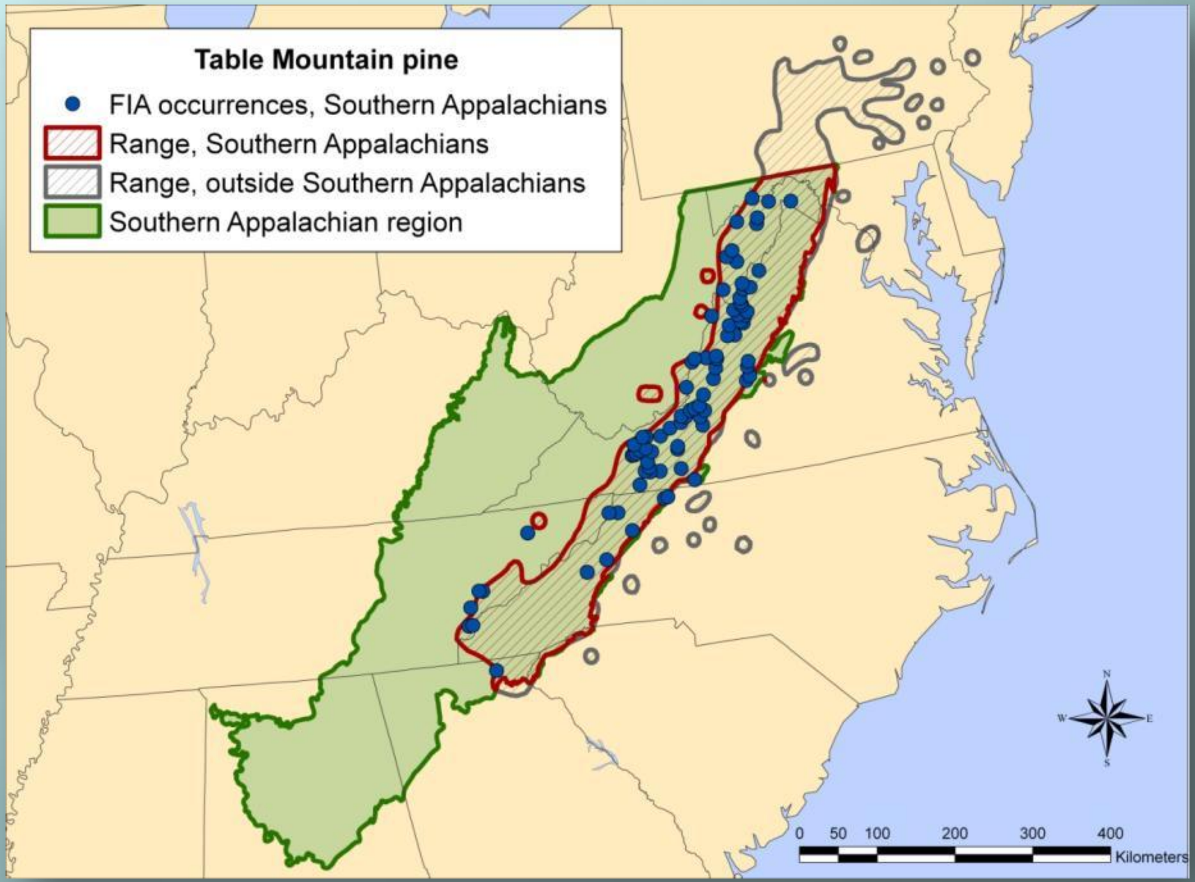


Forest Inventory and Analysis data



Forest Inventory and Analysis data

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



The **ForeCASTS** Project

Forecasts of Climate-Associated Shifts in Tree Species

- Habitat suitability maps generated for ~215 forest tree species so far (eventually ~300)
  - Two GCMs(Hadley and PCM), two emissions scenarios, two time points (2050 and 2100)
- Climate change pressure metrics compare current suitable habitat and 2050 suitable habitat under Hadley B1 scenario
- www.forestthreats.org/tools/ForeCASTS/

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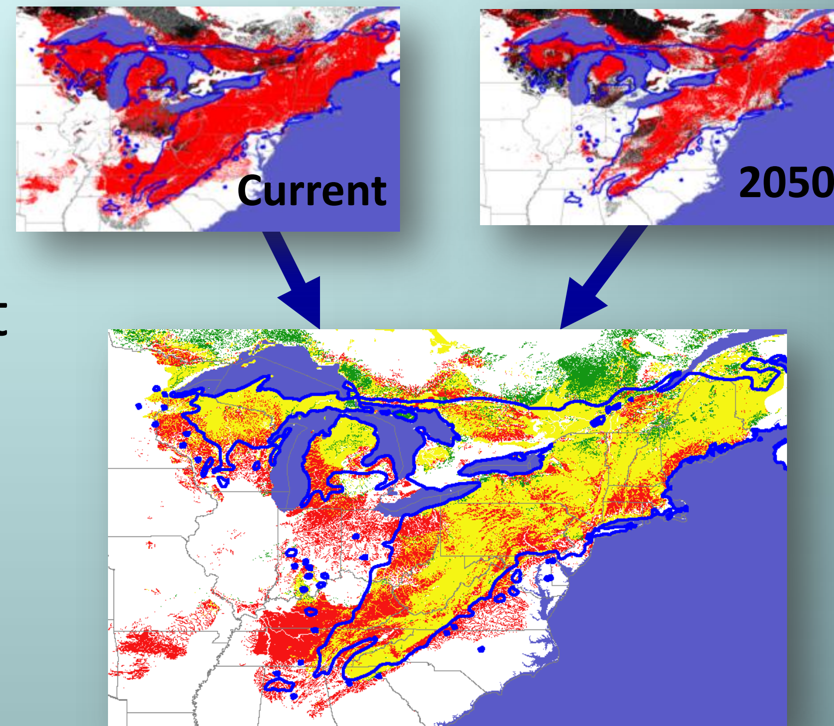
Metrics of climate change pressure

1) Decrease over time in area of suitable habitat
   - ***More = higher pressure/risk***

2) Percent of current habitat that remains suitable (stability)
   - ***Less = higher pressure/risk***

3) Mean distance from current habitat to nearest future habitat
   - ***Farther = higher pressure/risk***

Tsuga canadensis



New habitat in 2050

Habitat overlap, now and 2050

Current habitat gone in 2050

Weighting genetic risk factors

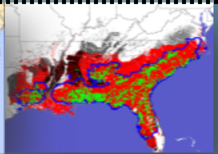
Intrinsic factors	Extrinsic factors
Population structure (*S*) (10%)	Pest/pathogen threat (*P*) (15%)
Density/rarity (*D*) (10%)	Climate pressure (*C*) (15%)
Regeneration capacity (*R*) (10%)	
Dispersal ability (*M*) (10%)	
Habitat affinities (*A*) (10%)	
Genetic variation (*G*) (10%)	

Conservation modifiers:

Endemism (*E*) (5%)

Conservation status (*L*) (5%)

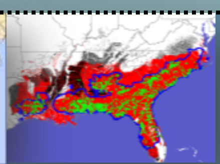




So. Appalachian species *most* at risk

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

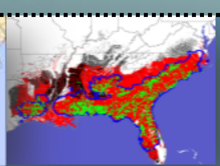




So. Appalachian species *least* at risk

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

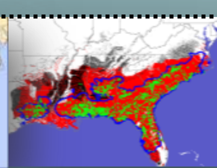




Western Washington State assessment

- Ranking genetic risk for species in National Forests and National Parks
- 36 species, sorted into three risk groups
- Tailored system to specific regional needs
- Used in NFS climate action plan

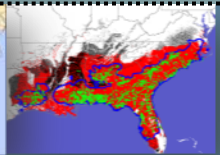




Summary

1) Climate change, in concert with other threats, may affect the genetic integrity of forest tree species
   - Risk varies based on attributes of species
2) Genetic risk assessment is necessary to efficiently and effectively use limited conservation resources
3) Forest Tree Genetic Risk Assessment System: framework for ranking the relative risk of genetic degradation
   - System flexible, applicable to different regions and scales
   - Used in Southern Appalachians and Western Washington

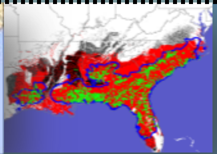


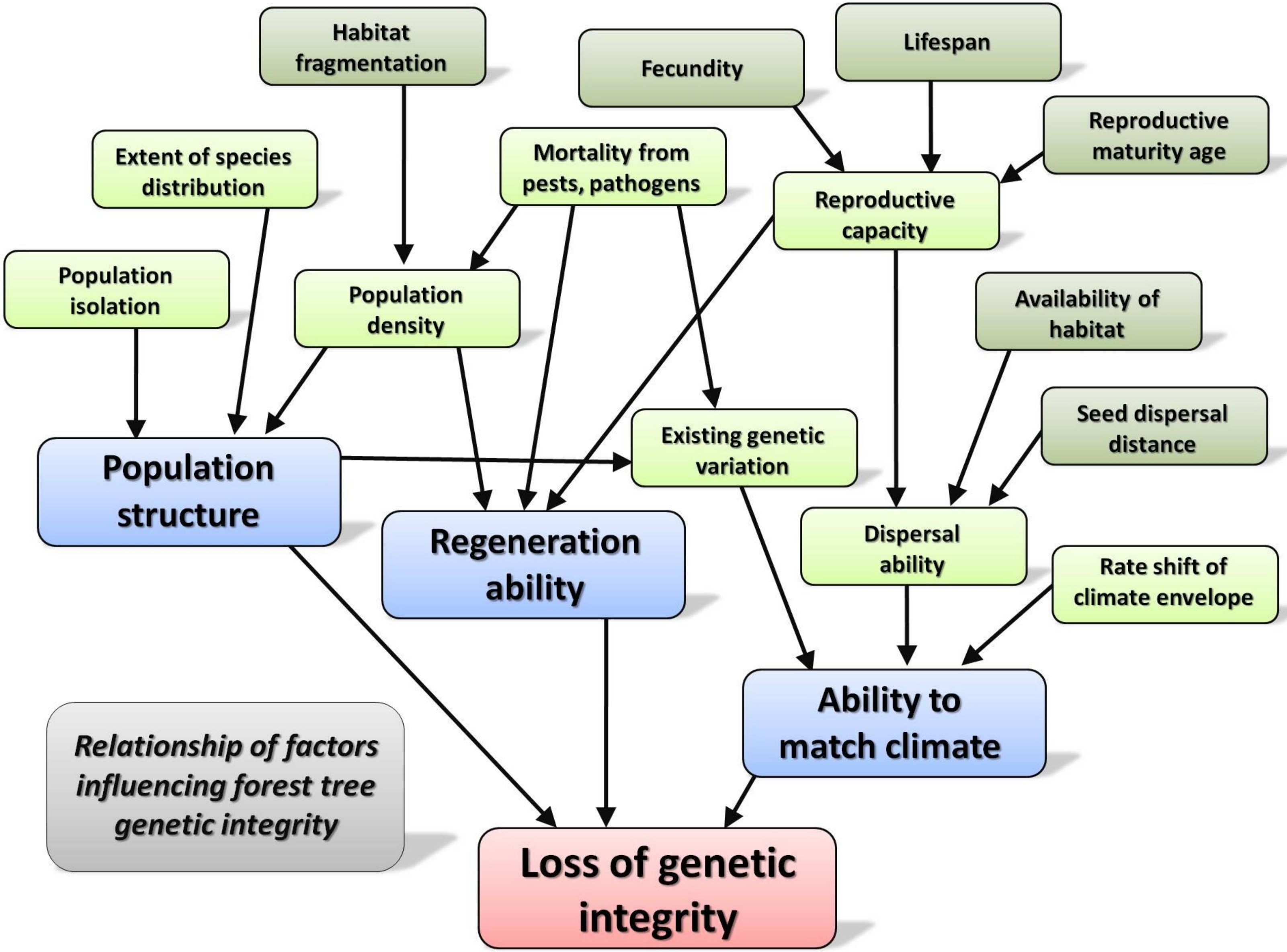


Next steps

1) Population-level risk assessments within species
   - In early stages for eastern hemlock
2) Database of risk factors for all North American forest tree species (~350)?
   - Web-accessible/searchable
3) Web interface for conducting custom genetic risk assessments?
4) An analysis of the relationships among the risk factors
   - Bayesian Belief Network approach incorporating expert opinion?







Relationship of factors influencing forest tree genetic integrity

ForGRAS Web site:

www.forestthreats.org/current-projects/project-summaries/genetic-risk-assessment-system

Canaan Valley State Park, West Virginia

Thanks to:

- Development of assessment methodology: Bill Hargrove, Carol Aubry
- Other assistance: Kurt Riitters, Danny Lee, Frank Koch, Barb Conkling, Fred Cubbage

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