

Genetic improvement of oaks

“Genetics, ecology, and management of oaks”
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Introduction



How to improve oaks?

Does it work?

Where are we today in the U.S.?



Introduction

Q: How to improve oaks??

A: It all depends on the word “What”

What species, what part of the species’ range, what traits to improve (timber vs. wildlife)



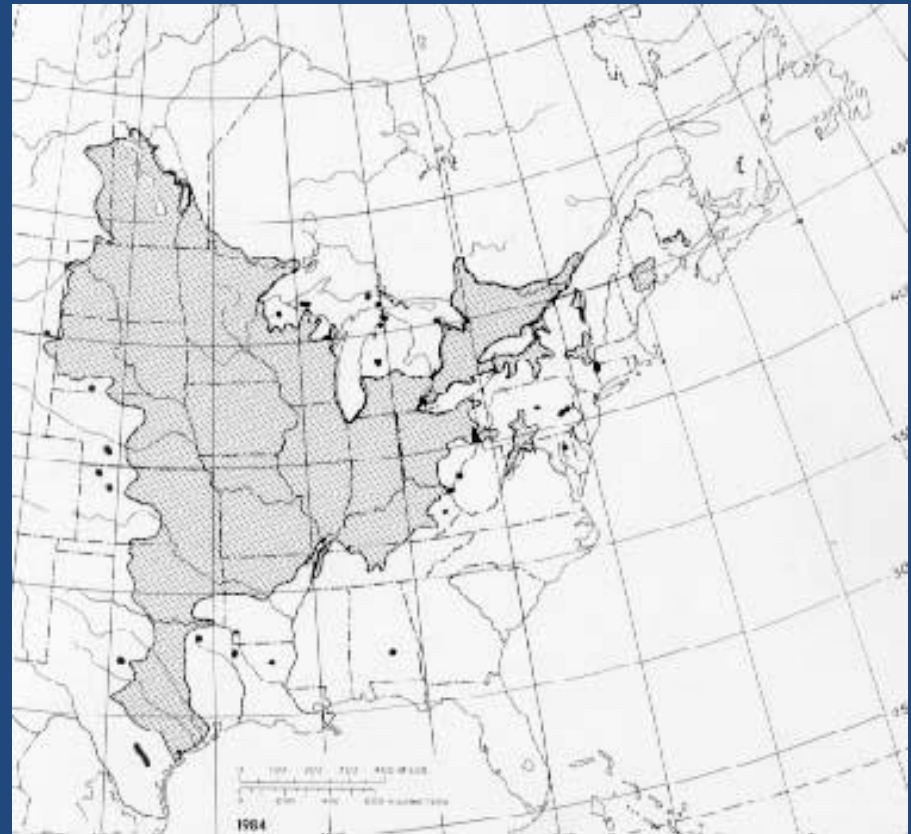
Provenance Testing



Provenance: refers to the source of the seeds used in reforestation. It is the geographic location of the mother tree(s) from which seed was collected.

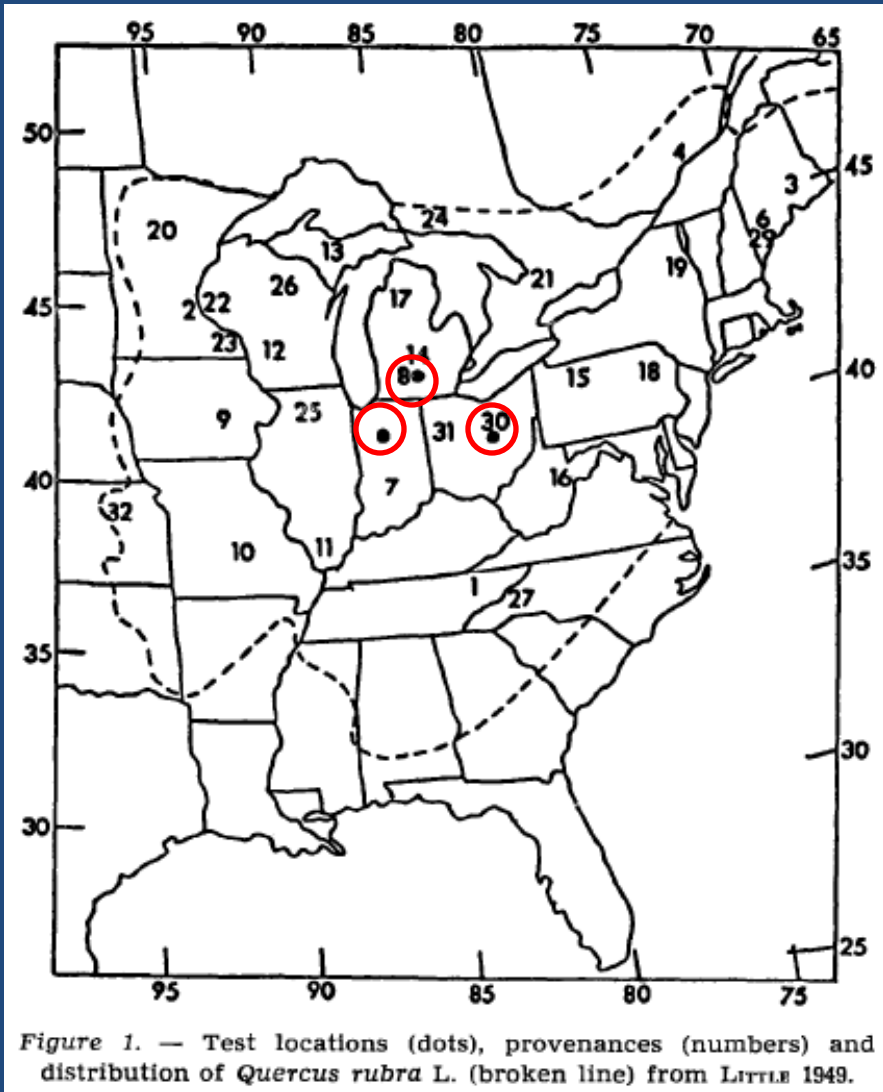
Most provenance tests are established for the practical breeding objective of determining the best performing provenances to use in the general vicinity of the test site.

The only way to maximize gains in forest tree improvement programs is to use the “best” provenances.



Quercus macrocarpa native range

1962-4 Northern Red Oak Provenance Test



47 year old planting in Indiana

Cherrybark oak (*Q. pagoda*) provenance testing

A limited range, provenance/progeny test was established in southern IN, 60 miles north of the species' range.

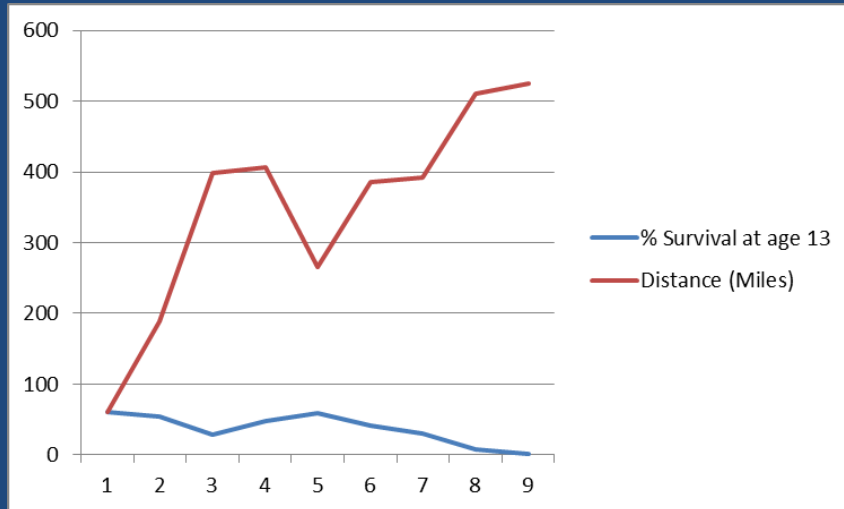
Thirty seedlots representing 16 stands in 6 states were planted in April 1983.

Winter hardiness was problematic for the LA and MS provenances.

At age 30, mean total height = 87' (96') and mean dbh = 16.1" (23.6")



Cherrybark oak (*Q. pagoda*) provenance testing



By age 13, survival ranged from 1 to 67%.

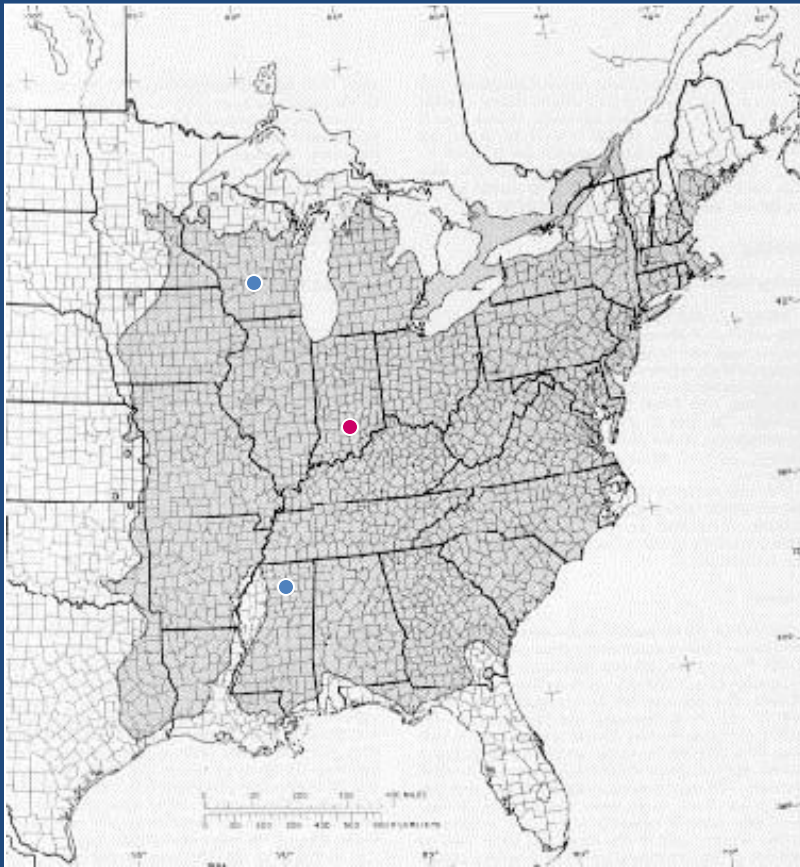
Provenances ranged from 60 to 525 miles south of the planting site.



Planted 1983, photo 2010, age 27

White oak (*Q. alba*) provenance testing

A small “common garden” white oak test was established in Indiana in 1982. Are the two largest trees from Wisconsin or Mississippi?



Planted 1982, photo 2008, age 26

Provenance Testing Results



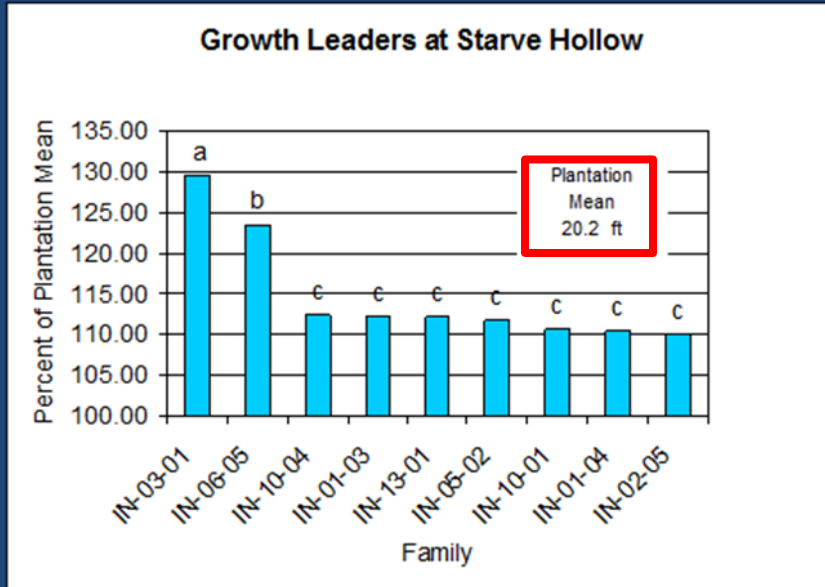
Planted 1982, photo 2008, age 26

Adaptive variation patterns of growth-related traits (height increment, bud break, hardiness) are primarily shaped by the thermoperiod.

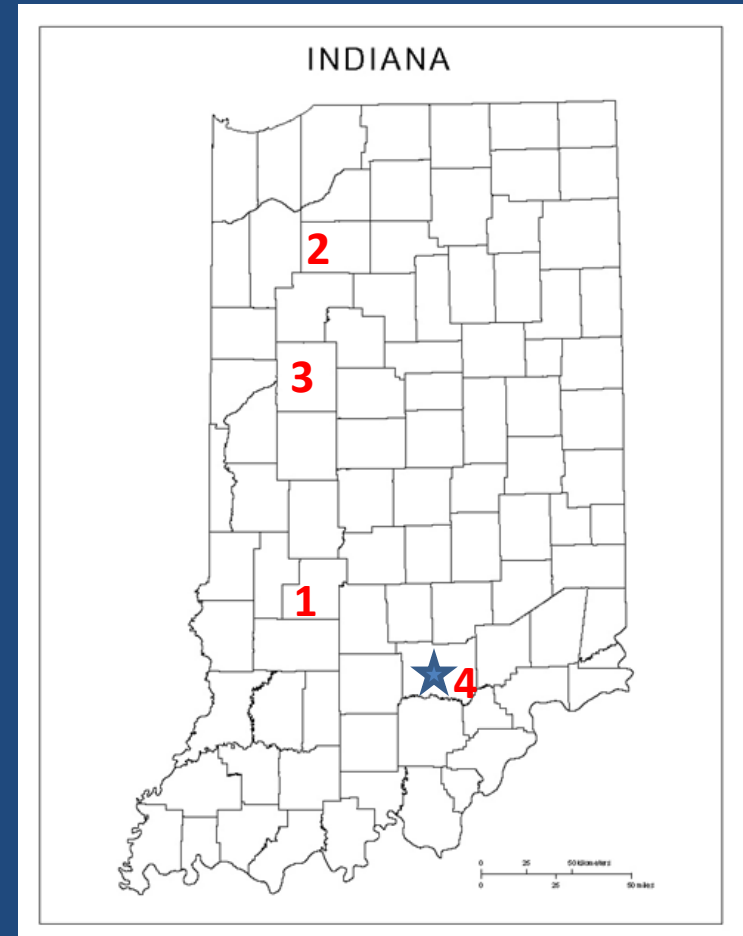
Growth and phenology data for provenances is best correlated with thermal parameters such as: mean/max/min temperature and heat sum.

Photoperiod effects are strongly confounded with thermal conditions.

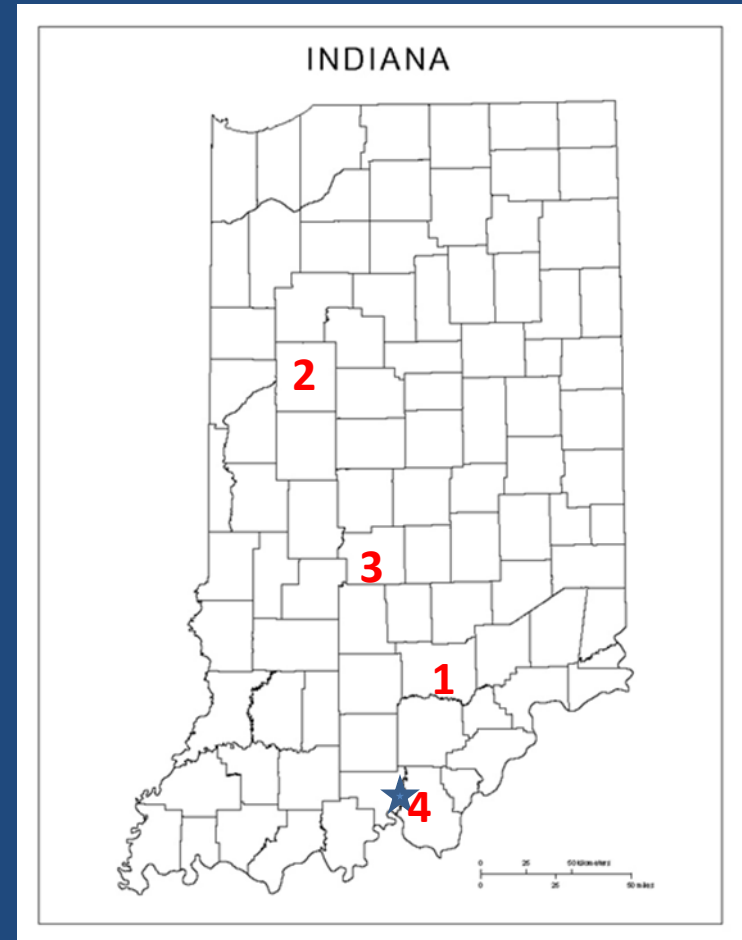
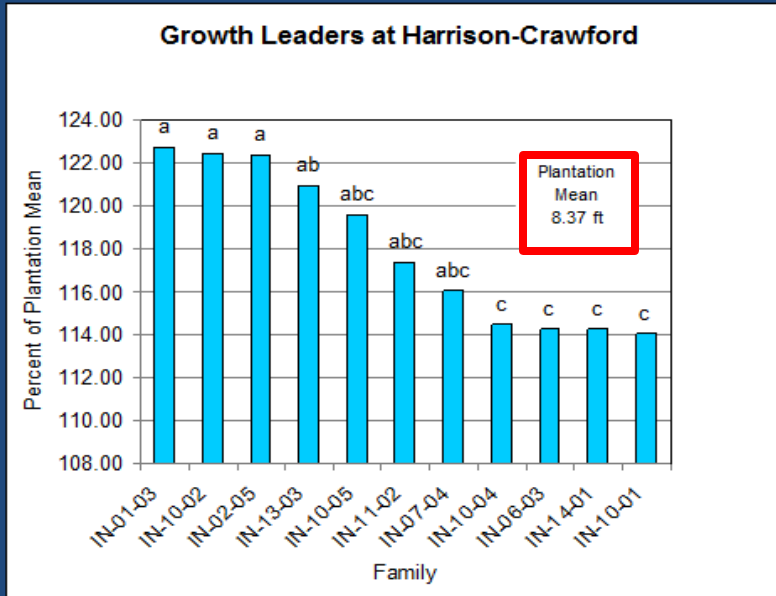
1984 Indiana white oak provenance/progeny test: ht age 15



Planted 1984, photo 2007, age 23

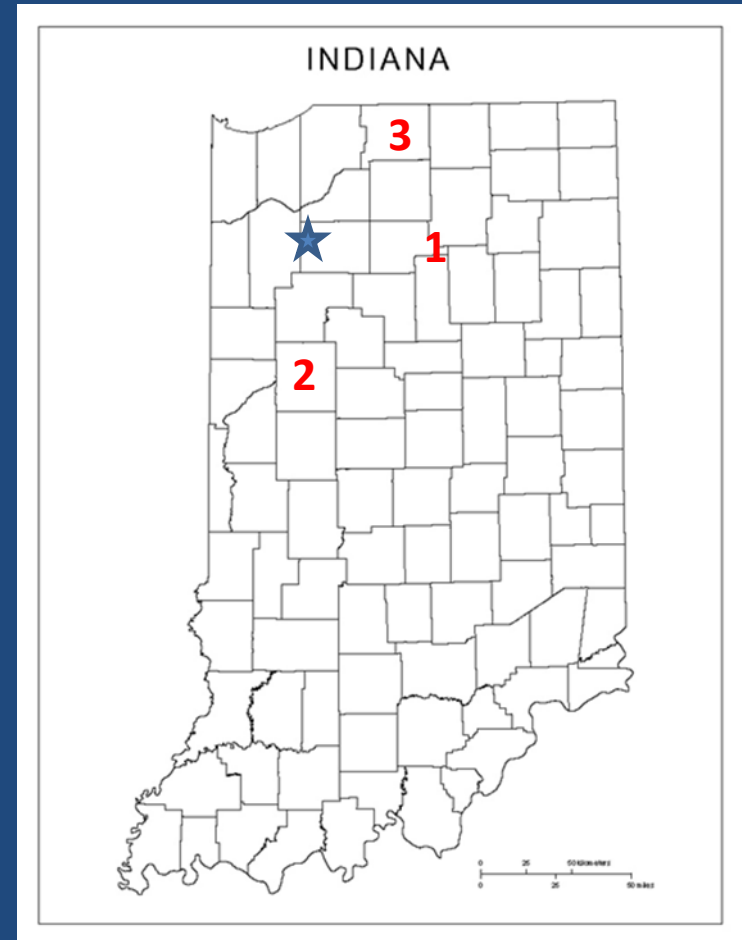
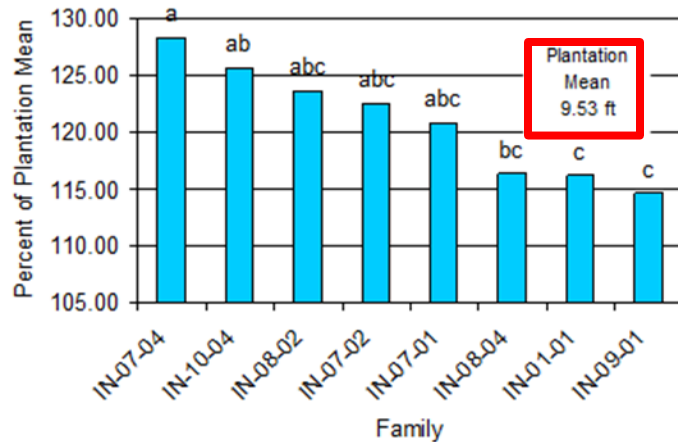


1984 Indiana white oak provenance/progeny test: ht age 15

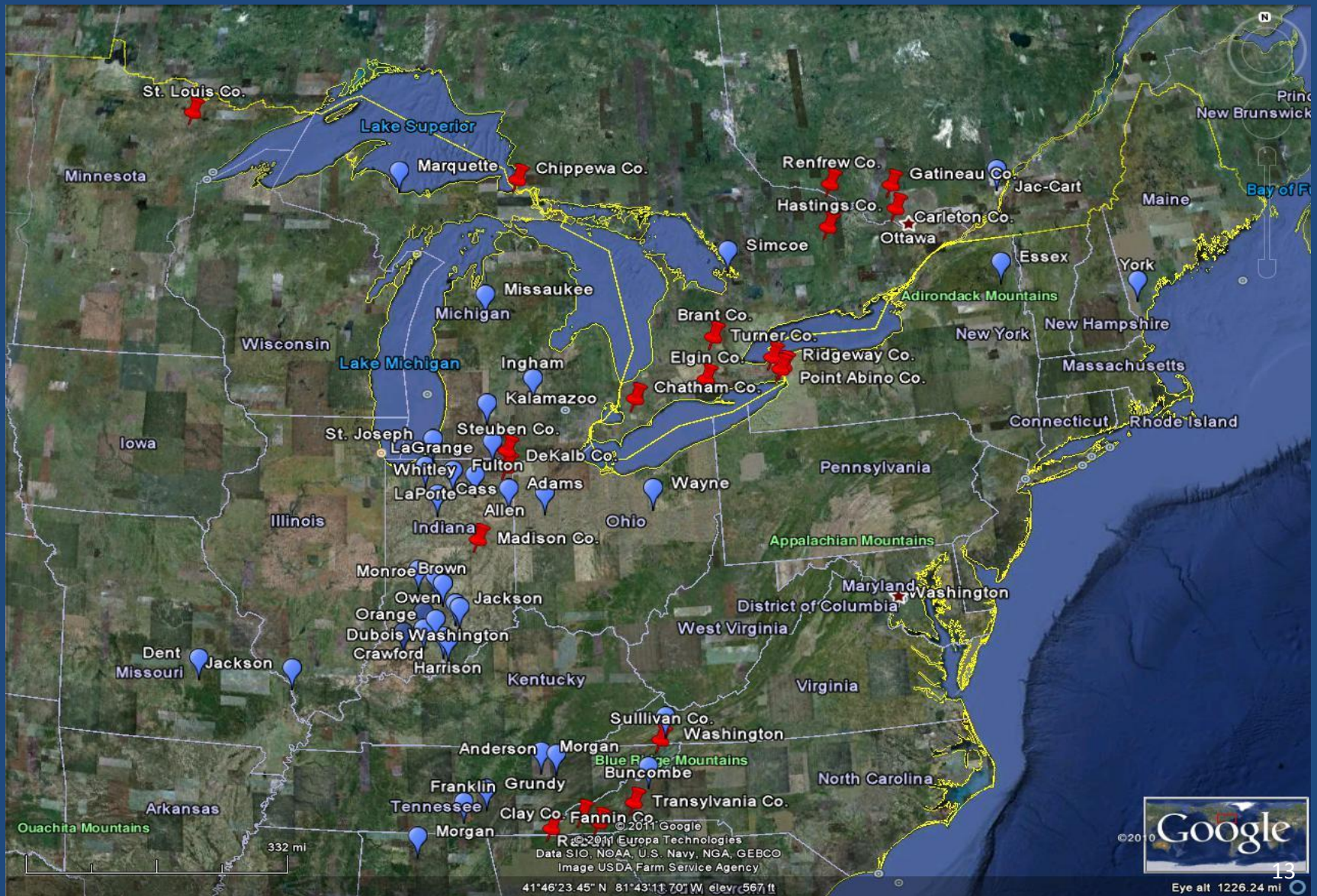


1984 Indiana white oak provenance/progeny test: ht age 15

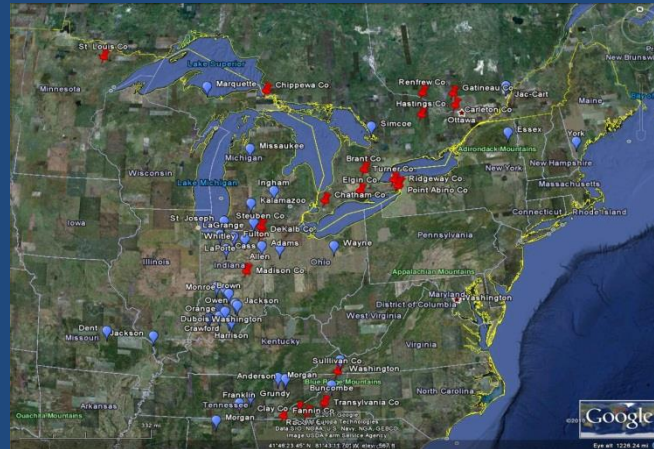
Growth Leaders at Jasper-Pulaski



Northern red oak (*Q. rubra*) genetic improvement



Genetic improvement of northern red oak (*Q. rubra*): two approaches



Grafted 1985, photos 2005, age 20

Planted 1992, photo 2009, age 17

Neighborhood Size

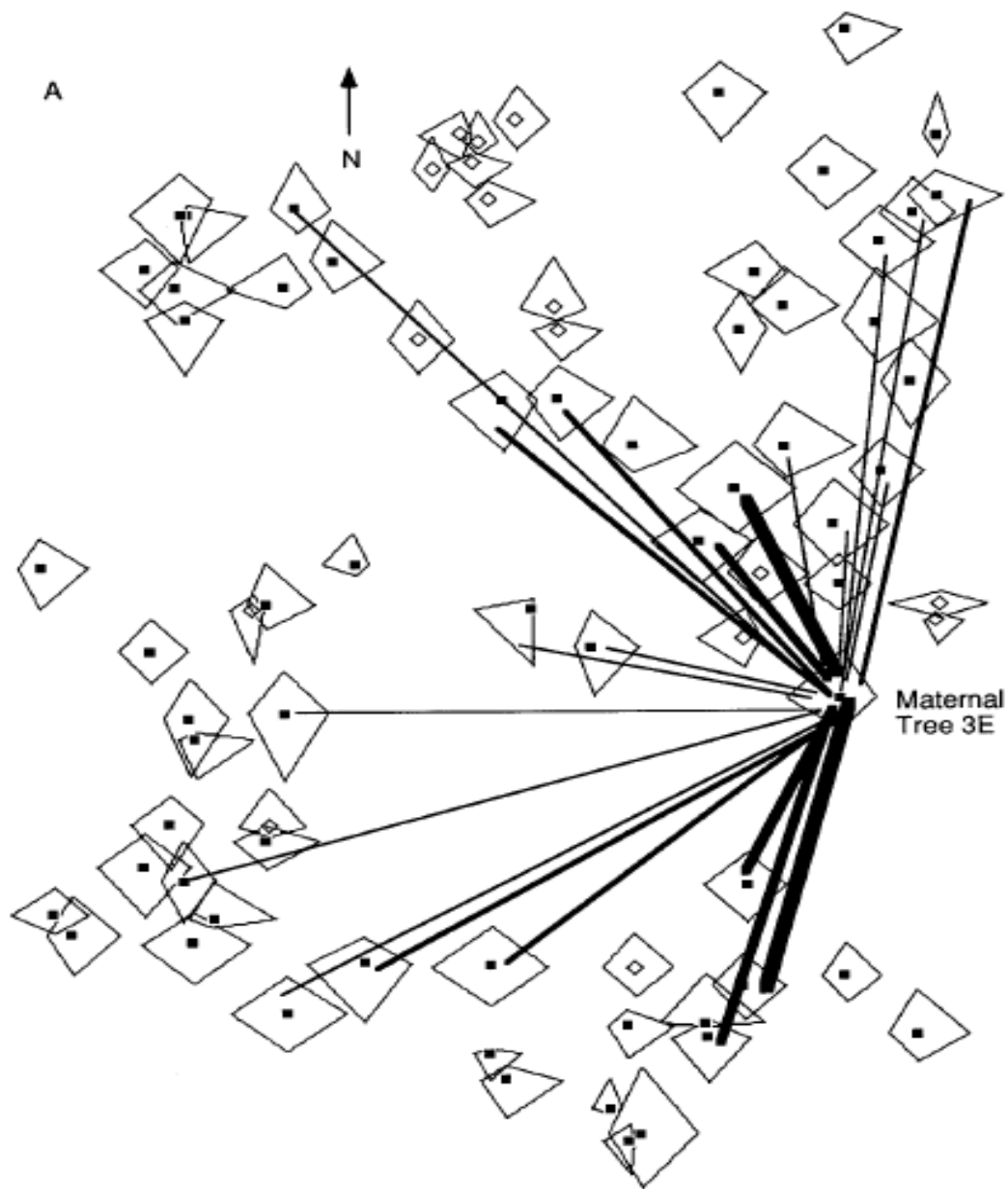


Figure 2. Locations of pollen donors for three seed parents: (A) tree 3E, (B) tree 17M, and (C) tree 33W. Filled squares represent bur oak trunks, open diamonds represent red oak trunks, and polygons represent approximate crown size. Width of line indicates number of pollinations from 1 (thinnest line) to 9 (thickest line).



Source: Dow and Ashley 1996. Microsatellite analysis of seed dispersal and parentage of saplings in bur oak *Quercus macrocarpa*. Mol. Ecol. 5:615-627.

Practical Implications of Within-Population Genetic Diversity

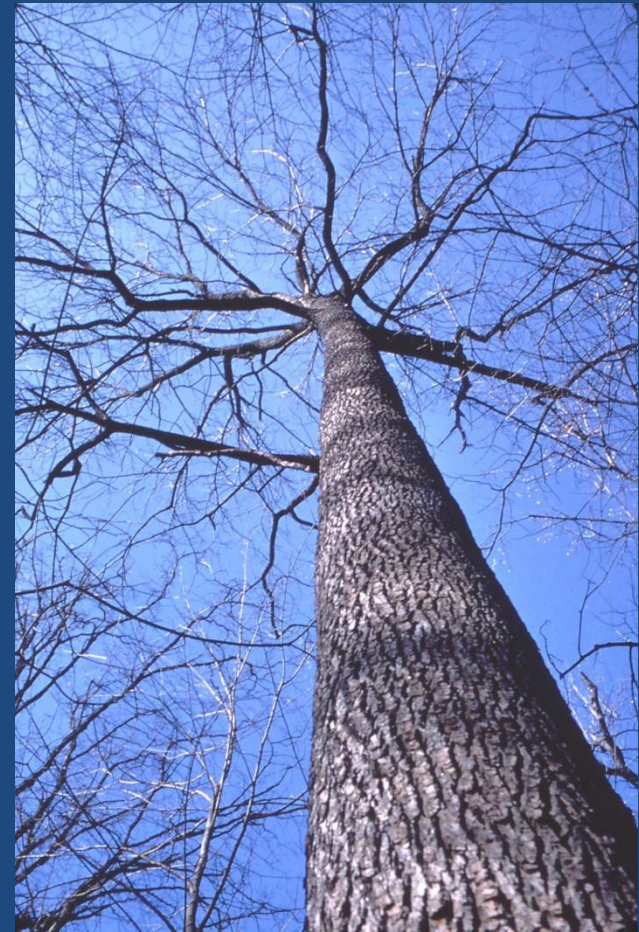
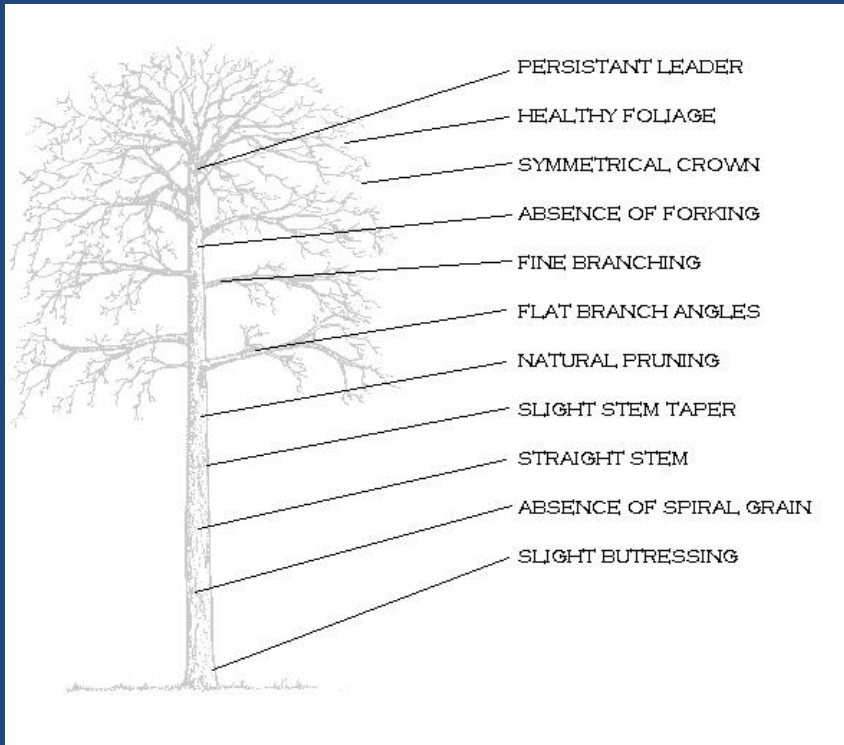
High levels of within-population (or within stand) genetic diversity are common in many forest tree species.

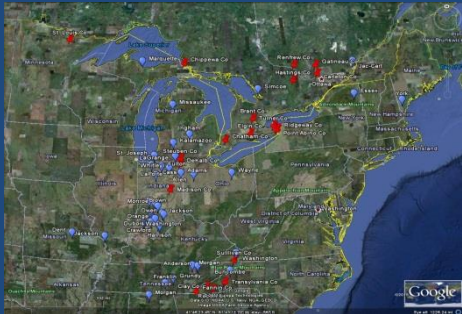
This type of genetic diversity is associated with a series of commercially important traits (e.g. stem form, wood quality, disease resistance, drought hardiness and flood tolerance).

So, large improvements can be made selecting the “best” genotypes to be the parents of seedling offspring that possess desirable characteristics.



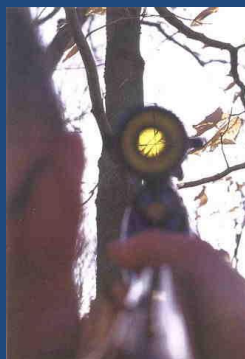
Example of a hardwood ideotype





Northern Red Oak Plus Trees

Red Oak #92:
Washington Co., IN
75 ft., no forks
2 crooks
10.2 in dbh
.22 in/yr





Northern Red Oak Subline E

Clone	Location	State	Latitude
92	Washington	IN	38 40
93	Washington	IN	38 40
96	Allen	IN	41 15
97	Allen	IN	41 14
100	Whitley	IN	41 05
101	Whitley	IN	41 07
104	St. Joseph	IN	41 43
105	St. Joseph	IN	41 43
108	Marion	IN	39 45
109	Henderson	TN	35 43
112	Franklin	TN	35 14
113	Washington	VA	36 42
116	Morgan	TN	36 08
117	Anderson	TN	36 05
119	Washington	IN	38 43

Clone	Location	State	Latitude
120	Putnam	IN	39 31
121	Putnam	IN	39 33
122	Putnam	IN	39 33
123	Jackson	IN	38 52
124	Athens	OH	38 26
125	Athens	OH	38 26
126	Athens	OH	38 26
127	Athens	OH	38 26
128	Athens	OH	38 26
129	Athens	OH	38 26
130	Athens	OH	38 26
131	Franklin	OH	40 05
149	Whitley	IN	41 10
151	Whitley	IN	41 10
151	Whitley	IN	41 10

Northern red oak subline breeding program

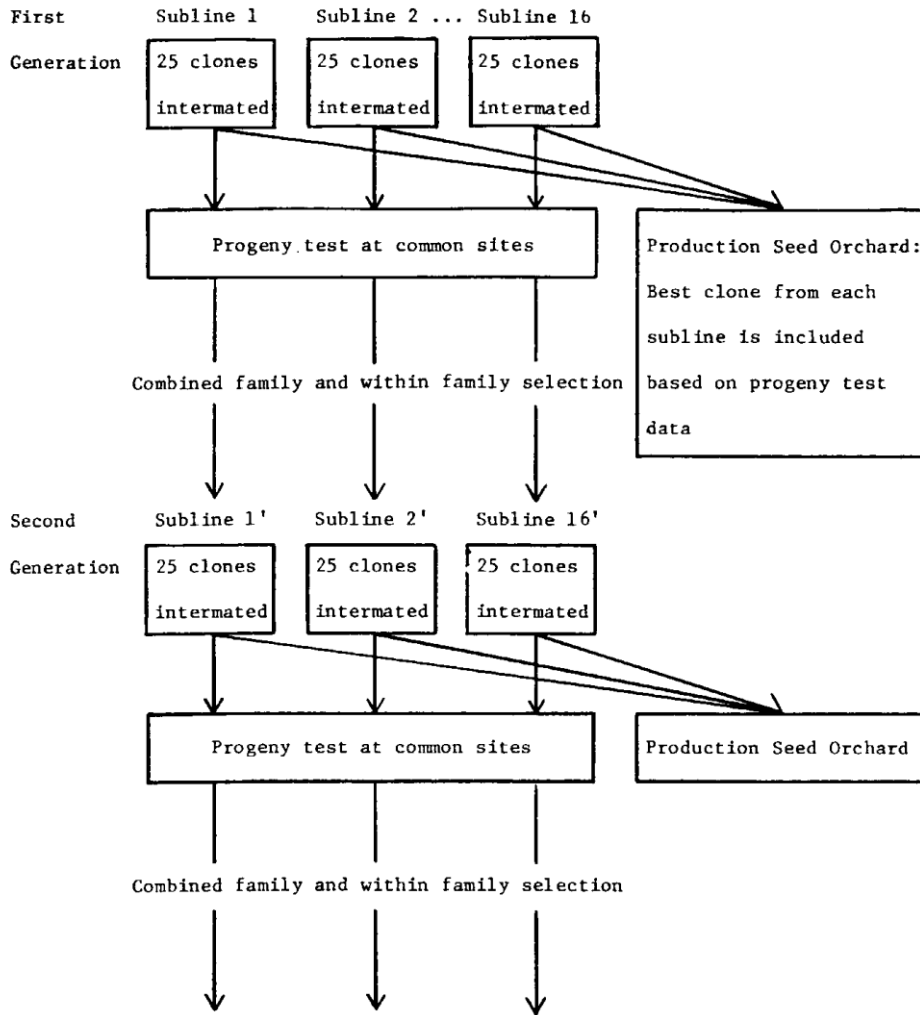
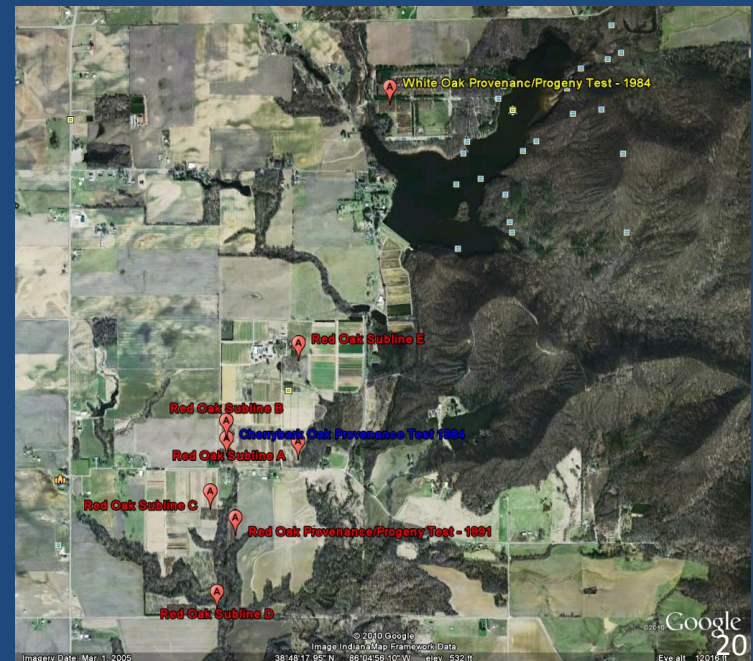
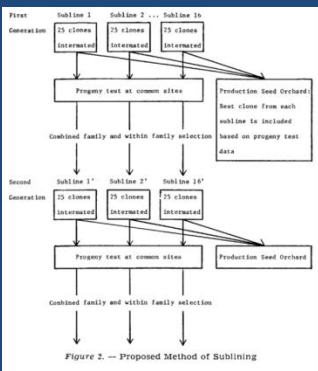


Figure 2. -- Proposed Method of Sublining





Northern red oak subline breeding program

A total of 184 NRO clones, propagated from 1984 to 1988 were deployed to 6 sublines (30 clones, 8 ramets).

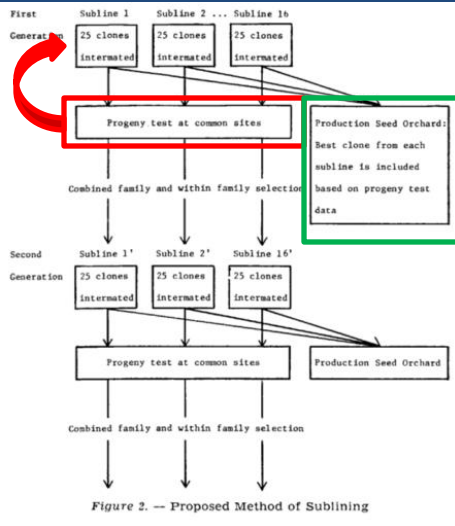
Worthen (unpublished) genotyped 367 ramets and 456 offspring @ 11 SSR loci over 3 years.

A total of 46% of the 456 offspring could be assigned to known staminate parent (@ 95% LOD), or 90% (@ 80% LOD).

By far, the majority of the pollinations occurred within the 6 sublines.



Northern red oak subline breeding program

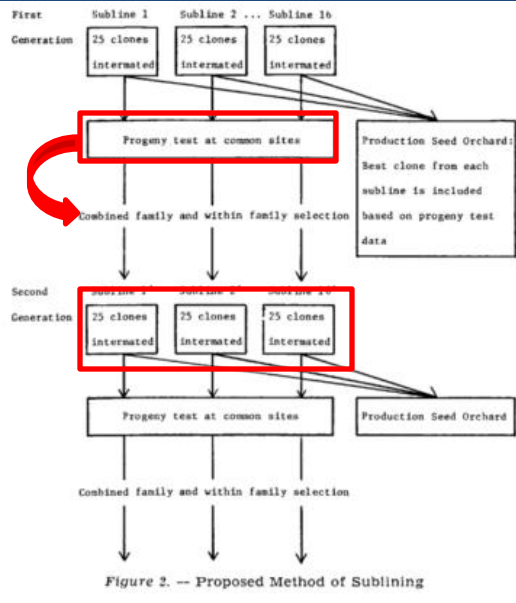


Planted 2007, photo 2013, age 7

To date, 90 open pollinated seedling families have been established in a series of progeny tests in IN and MI over multiple years.

Backward Selection: Progeny test growth data used to identify “best” individual parent clone in each subline.

Clonal Seed Orchard: This “best” clone in each subline is *re-propagated* and established in a new seed orchard. In the IN program, this would equal a six clone orchard.

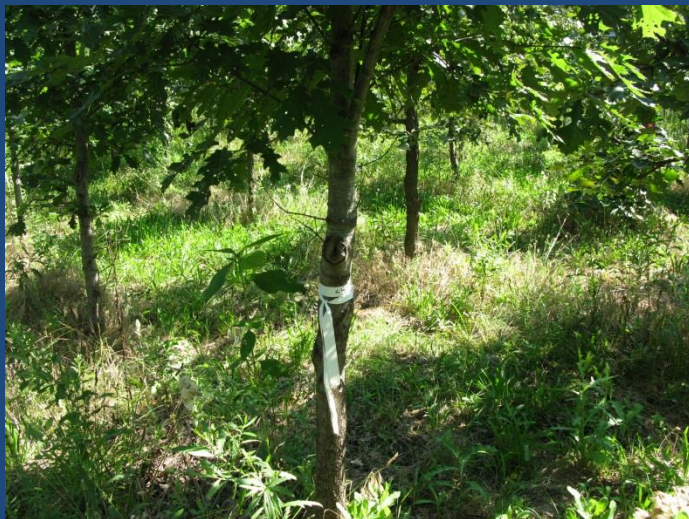
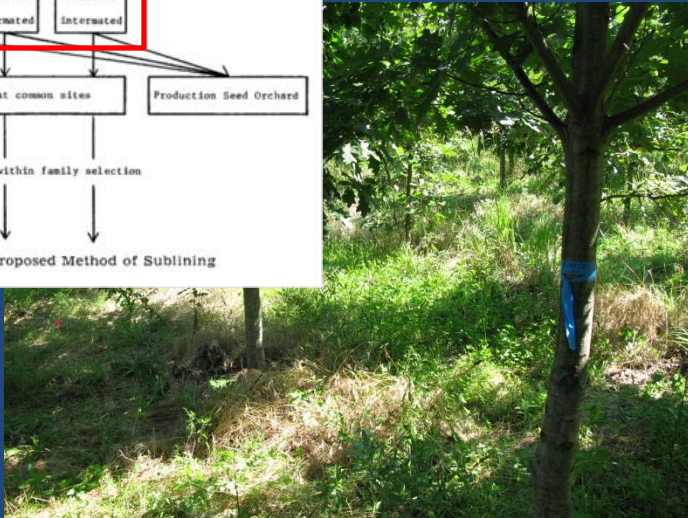


Northern red oak subline breeding program

Forward Selection: Combined family and within family

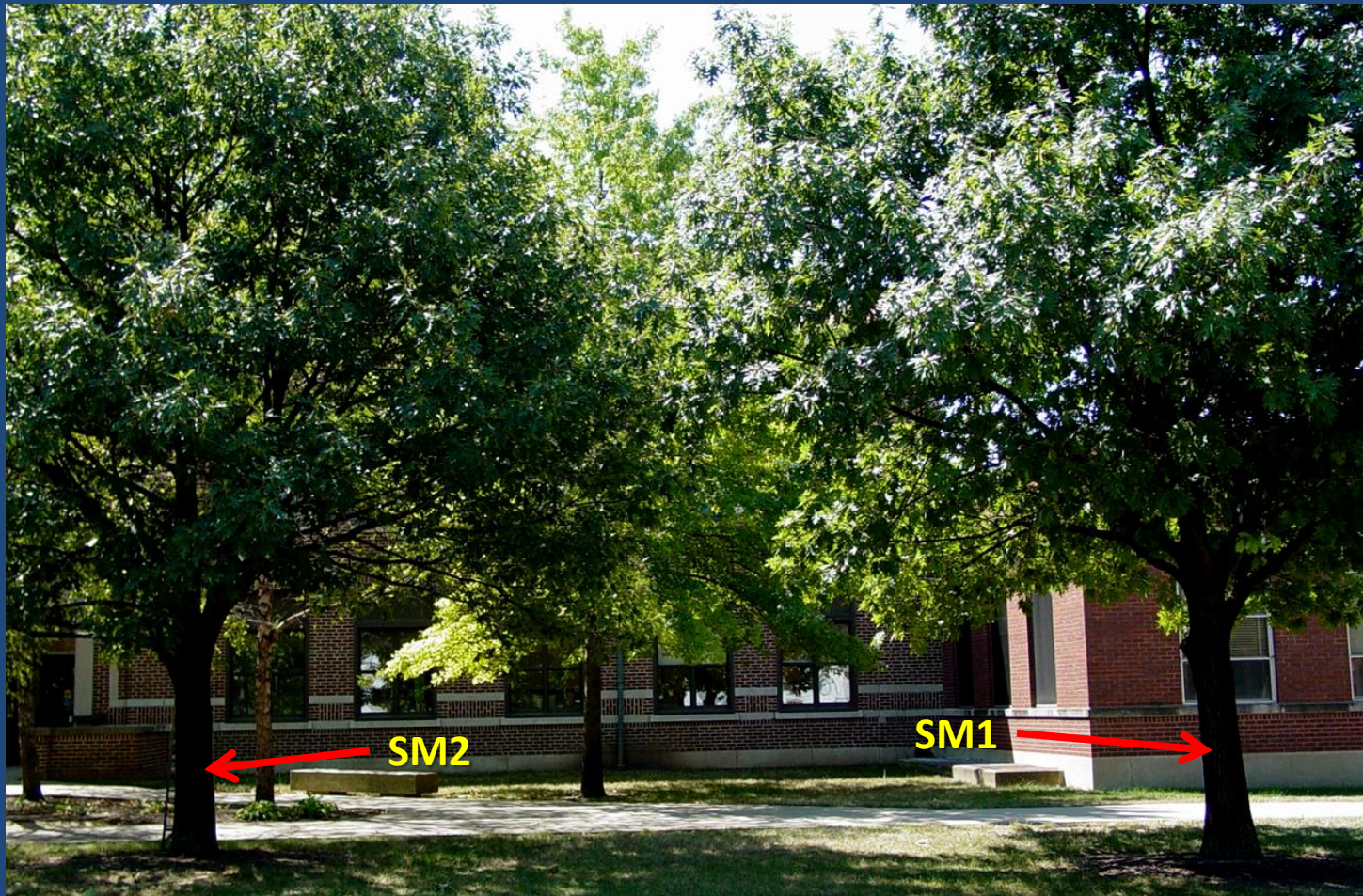
selection: The “best” individual families and/or trees are selected, propagated and established in a new, geographically distinct subline series.

Each new subline is composed of 30 different clones, as in the previous (parent) generation. However, some of the original parents may not be represented by their offspring in the new subline.





Northern red oak (*Q. rubra*) mapping parents





Northern red oak mapping population

A total of 509 full sibs derived from crossing SM1 and SM2 at Purdue University.

Open pollinated seeds collected in 2001, 2003, 2007 and 2010.

Full sibs identified using paternity exclusion (PE).

Full sibs established at Purdue and at UT in western TN.





Northern red oak mapping population

In 2013, we started to graft all of the 509 NRO full sibs in Missouri.

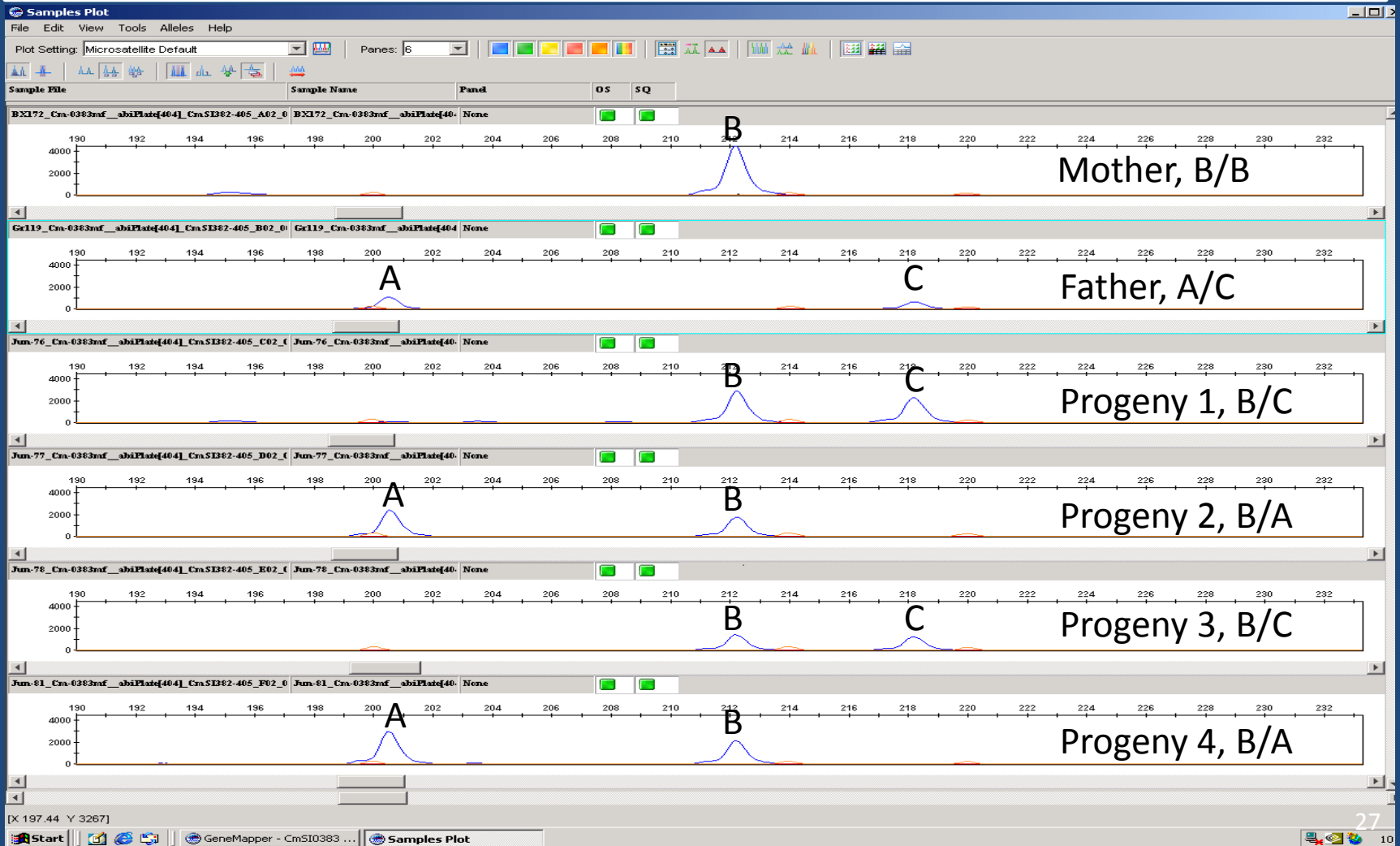
This clonal population will serve as a “back-up” to seedlings populations previously established and allow for additional characterization of these full sib individuals for the purpose of developing the first genetic linkage map for the species.





SSR marker inheritance

Inheritance of a polymorphic SSR marker in a full-sib cross





Quantitative Trait Loci (QTL) mapping in oaks

Basic idea: associate different phenotypes with the presence of genetic markers (QTLs)

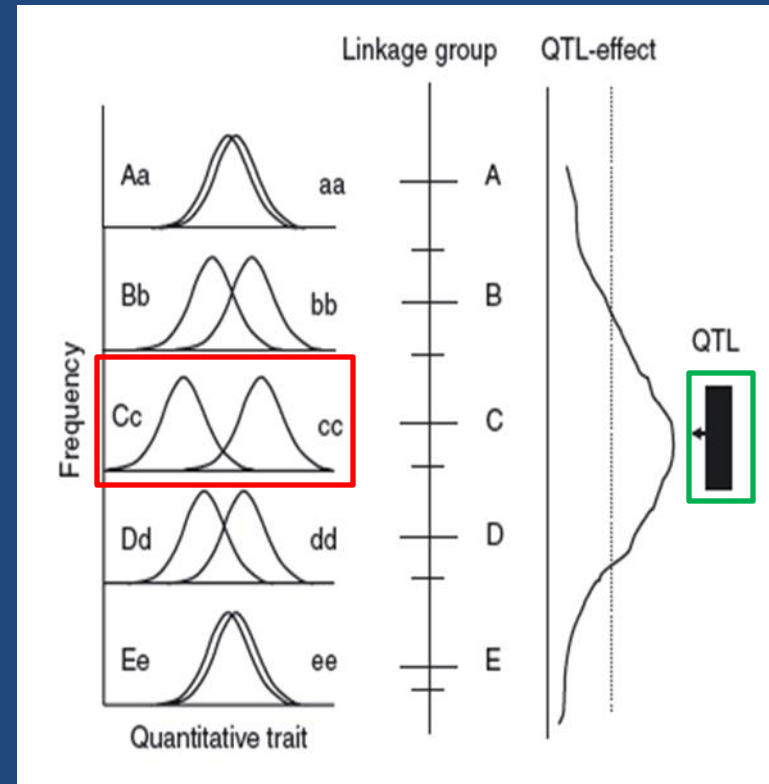
Steps:

Create an F_1 mapping population using paternity exclusion

Evaluate phenotypes

Determine marker genotypes

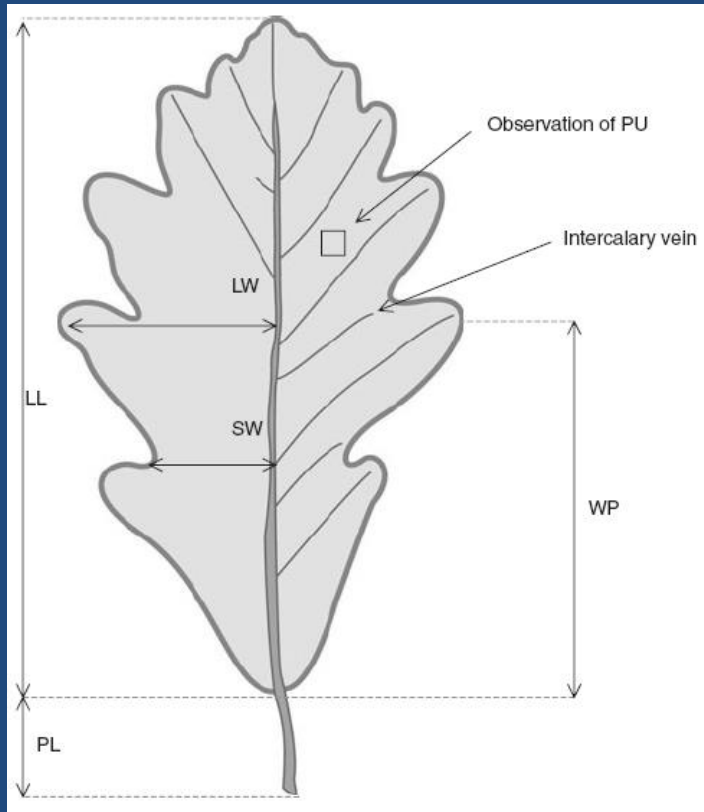
If phenotypic means vary among the genotypic groups, then a QTL resides in the vicinity of the marker.



The ultimate objective is to develop a genetic linkage map populated by many QTLs (blocks of genes) that are located at a specific region of the genome that affect phenotypic traits of interest.



Oak leaf morphology: QTL mapping



Lamina shape or obversity (OB): $OB = 100 \times WP / LL$

Petiole ratio (PR): $PR = 100 \times PL / (LL + PL)$

Lobe depth ratio (LDR): $LDR = 100 \times (LW - SW) / LW$

Percentage venation (PV): $PV = 100 \times NV / NL$

Lobe width ratio (LWR): $LWR = 100 \times LW / LL$

Figure 1. (a) Description of the dimensional leaf morphological traits in *Quercus petraea* and *Q. robur*. LL: lamina length; PL: petiole length; LW: lobe width; SW: sinus width; WP: length of lamina from base to widest point; PU: abaxial laminar pubescence. (b) Scoring of the basal shape of the lamina (BS) of *Quercus petraea* and *Q. robur*.



Oak leaf morphology: QTL mapping in *Quercus robur*

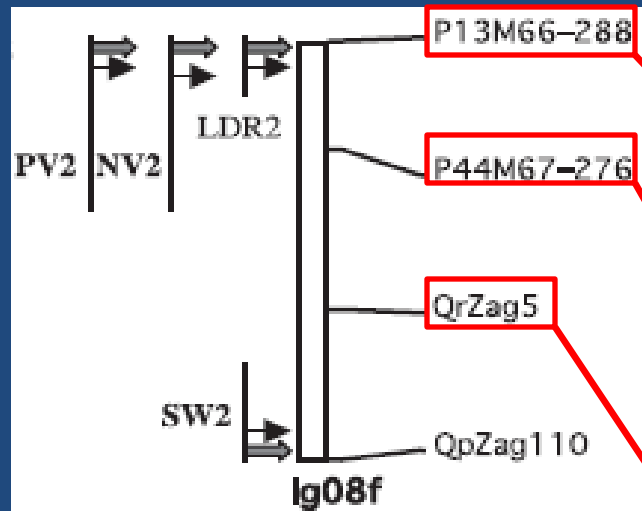
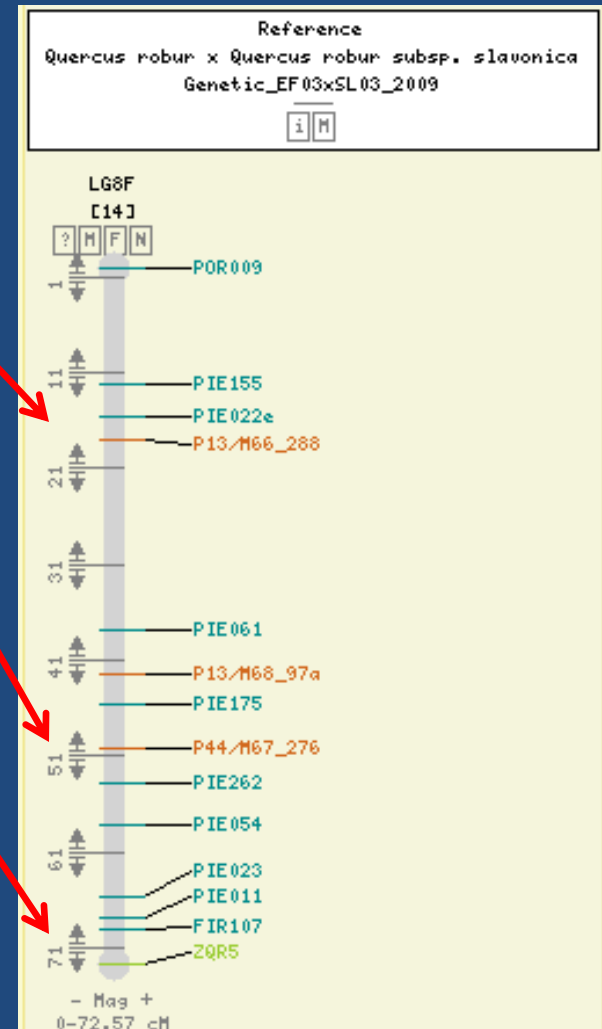


Table 1. Trait descriptions.

LDR	lobe depth ratio, $LDR = 100 \times [(LW - SW)/LW]$
LL	lamina length
LW	lobe width
LWR	lobe width ratio, $LWR = 100 \times LW/LL$
NL	number of lobes
NV	number of intercalary veins
OB	lamina shape or obversity, $OB = 100 \times WP/LL$
PV	percentage venation, $PV = 100 \times NV/NL$
SW	sinus width
WP	length of lamina at largest width

The scoring was performed according to Kremer *et al.* (2002).





Oak leaf morphology: QTL mapping in *Q. rubra*

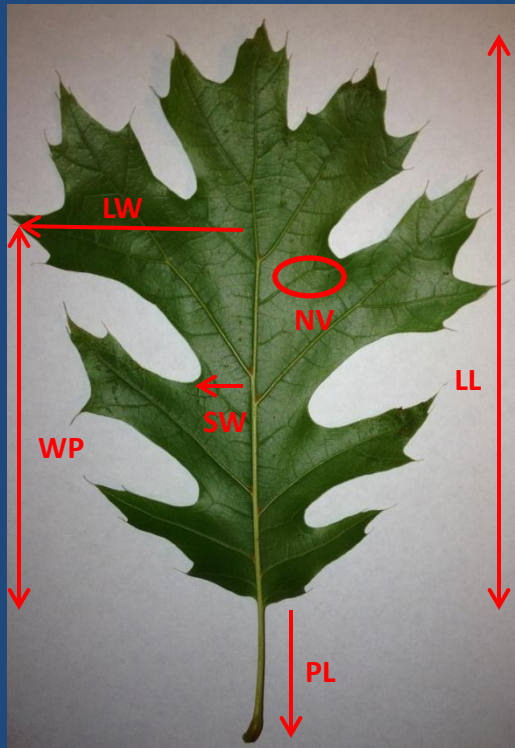


Table 1. Trait descriptions.

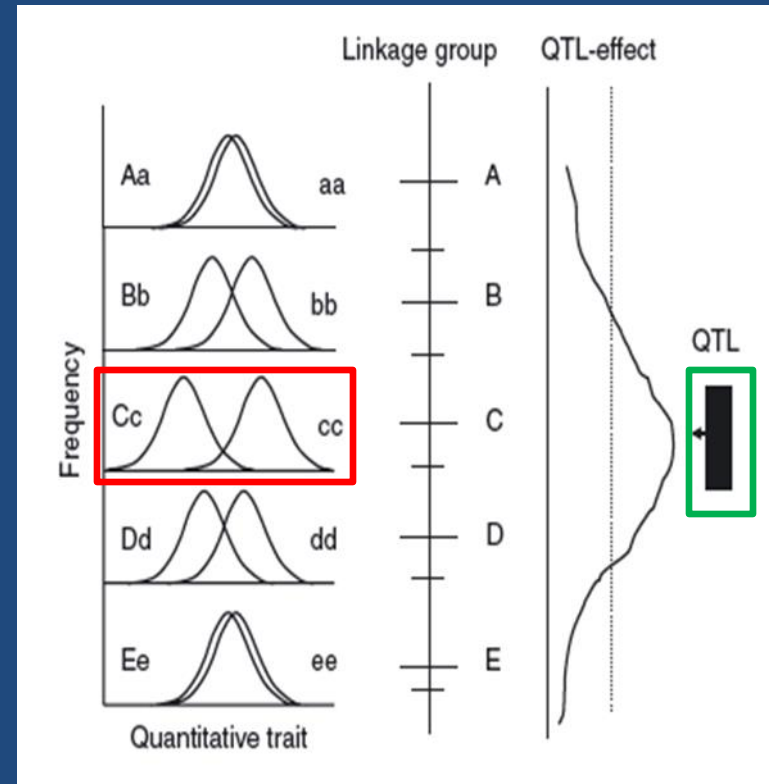
LDR	lobe depth ratio, $LDR = 100 \times [(LW - SW)/LW]$
LL	lamina length
LW	lobe width
LWR	lobe width ratio, $LWR = 100 \times LW/LL$
NL	number of lobes
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OB	lamina shape or obversity, $OB = 100 \times WP/LL$
PV	percentage venation, $PV = 100 \times NV/NL$
SW	sinus width
WP	length of lamina at largest width

The scoring was performed according to Kremer *et al.* (2002).

In 2013, we re-propagated 265 *Q. rubra* full sibs, plus both parents. For each tree, we measured six different leaf morphology traits, using two mature, first flush leaves from three grafted ramets. This dataset will allow us to map QTLs associated with leaf morphology traits in *Q. rubra* for the first time.

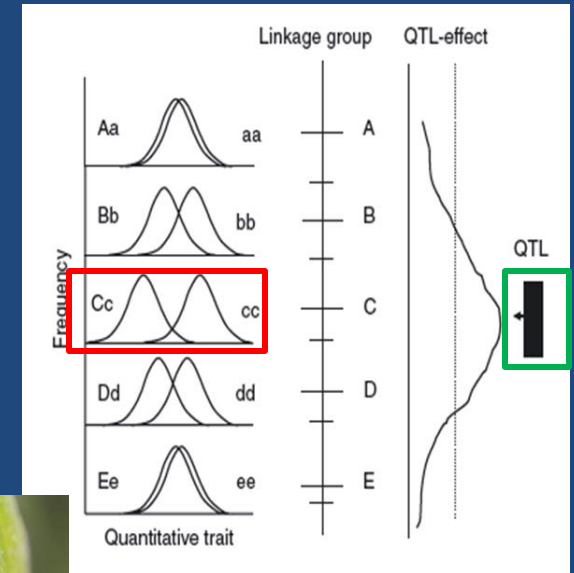
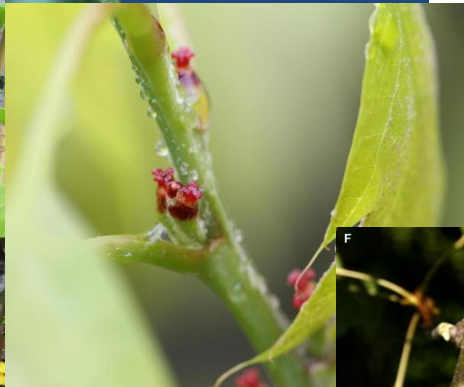


Oak leaf morphology: QTL mapping in *Q. rubra*





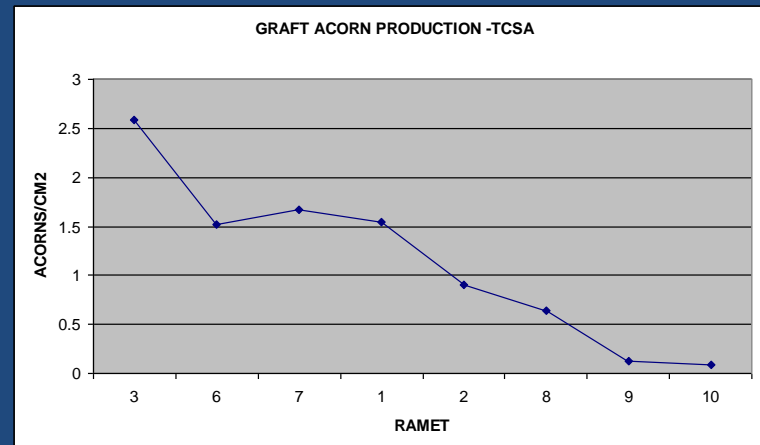
Oak flowering: QTL mapping in *Q. rubra*



Swamp white oak (*Q. bicolor*) acorn production study

We found a strong, positive relationship between the number of acorns produced per graft trunk cross sectional area (TCSA) at age 4 and the cumulative acorn production of the ortets over six years for 7 of the 8 trees used in this study.

Rootstock x scion interaction for acorn production was non-significant.



Swamp white oak (*Q. bicolor*) acorn production study

Seedling progeny derived from precocious clones can produce acorns by age 4.

Widespread flowering and fruiting was observed by age 5 (55 %).



Jack Daniels white oak seed orchard



Planted 2001, photo 2012, age 12



Acorn production 2008-2012:
 $h^2 = 0.121 (0.151) - 0.611 (0.233)$

Tree height 2001-2010:
 $h^2 = 0.434 (0.154) - 0.781 (0.254)$

Tree dbh 2003-2010:
 $h^2 = 0.315 (0.186) - 0.404 (0.149)$

Watauga, TN northern red oak seed orchard



Seedling seed orchard est. by USFS in 1973, now managed by UT. Acorn production documented annually from 1985 thru 1997 by family.



Acorn production rated on 1-4 scale. Acorn $h^2 = 0.311$ (s.e. 0.034)

Acorn production rated as Y/N :
Acorn $h^2 = 0.363$ (s.e. 0.038)

Oak Flood Tolerance Studies

We have been assessing the flood tolerance of 8 different oak species in the Flood Tolerance Laboratory (FTL) since 2003.

The FTL allows researchers to flood tree seedlings in a natural setting, using flowing or stagnant water in any season.

To date, intra-specific patterns of genetic variation for flood tolerance have been found for all species.



Oak Flood Tolerance Studies

The amount of genetic variation attributed to family vs. stand:

2.9:1 (leaf area)

3.0:1 (branch number)

3.2:1 (leaf number)

4.0:1 (shoot length).

Genetic differences in response to flooding were detected among seedling families of both bur oak (*Q. macrocarpa*) and swamp white oak (*Q. bicolor*) over multiple years.

No significant gains in flood tolerance were achieved using acorns derived from specific seed sources (or stands) collected along a hydrologic gradient.



Identification of oak seed sources for use in riparian buffer plantings



Development of a *Q. bicolor* seedling seed orchard population in Missouri: 1. parent tree selection; 2. nursery progeny testing; 3. flood tolerance evaluation; 4. seedlings representing most flood tolerant families to serve as source of improved seed for future riparian buffer restoration.

Where are we today in the U.S.?

			Progeny	Seedling	Mapping Population	Mapping Population
Section	Species	State	Testing	Seed Orchard	in Nursery	in Field
Quercus	<i>Q. alba</i>	TN	X	X	X	X ¹
	<i>Q. alba</i>	MO				X ²
	<i>Q. bicolor</i>	MO	X	X	X	
	<i>Q. lyrata</i>	TN	X		X	
	<i>Q. macrocarpa</i>	TN	X			
	<i>Q. macrocarpa</i>	MO	X	X		
	<i>Q. michauxii</i>	TN	X		X	
	<i>Q. montana</i>	TN	X	X		
	<i>Q. stellata</i>	TN	X			
	<i>Q. falcata</i>	TN	X			
Lobatae	<i>Q. nuttallii</i>	TN	X			
	<i>Q. pagoda</i>	TN	X			
	<i>Q. palustris</i>	TN		X		
	<i>Q. phellos</i>	TN	X			
	<i>Q. nigra</i>	TN	X			
	<i>Q. rubra</i>	TN	X	X		X ³
	<i>Q. shumardii</i>	TN	X			
	<i>Q. velutina</i>	TN	X			

¹ Progeny exclusion (PE) for this population of 976 half sibs underway in the John Carlson lab at the Penn State.

² A second *Q. alba* mapping population (n = 330) will be established in MO, in spring 2014

³ The Romero-Severson lab has completed progeny exclusion for this *Q. rubra* mapping population (n = 532 full



Questions ??