Conifer Translational Genomics Network Coordinated Agricultural Project

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Genomics in Tree Breeding and Forest Ecosystem Management

Module 5 – Introduction to Tree Breeding and Provenance Trials

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Basic principles of forest tree breeding

- Three primary goals
 - Improve economic traits (genetic gain)
 - Maintain or improve adaptability
 - Maintain genetic diversity for future improvement and evolution
- Tradeoff between genetic gain and diversity
 - To get genetic gain, genetic variation must be reduced
 - (What is the appropriate balance?)
- Most tree breeding relies on population improvement
 - A few breeding programs rely on clonal development



Tree improvement definitions

- Tree improvement goal: Increase the value of land ownership (timberlands) through genetics
- Tree breeding objective: A carefully defined array of traits for improvement with priorities given to their relative importance
- Tree breeding strategy: A detailed document specifying the design, timing, and implementation logistics of all components of the tree improvement process



Image Credit: Nicholas Wheeler, Oregon State University



A tree breeder's considerations

- Most tree species are out-crossing; inbred lines do not exist; and pedigree tracking is critical
- Traits of interest are typically controlled by many genes and have low heritabilities
- Most tree species possess a lot of genetic variability for most traits of interest
 - Improved varieties must be widely adapted and retain a lot of diversity
- Trees require a lot of land and time to breed and test, and desirable traits are not always easily measured
- Trees must be bred to survive over decades in highly heterogeneous environments
- Are trees good candidates for marker-assisted selection and breeding applications?



Provenance trials: A good start

A logical first step in tree improvement is the provenance trial

- This is a common garden study that contrasts progeny of trees from many geographic origins in a uniform environment(s)
- Patterns of genetic variation associated with patterns of geographic variation are often observed (e.g. trees from latitudes 1-3 degrees closer to the equator or from a lower altitude than the intended planting site tend to grow better than local trees)
- Often such tests will be designed to simultaneously test families within provenances
- The goal: Selecting the right provenances within which selections for a tree improvement program may begin



Genetic diversity in pine provenances and families



Image Credit: Michael Carlson, British Columbia Ministry of Forests

Traditional tree breeding: The tree breeding cycle

- Tree improvement incorporates one or more cycles of some or all of the following processes
 - Selection
 - Breeding
 - Testing
 - Production
- Most tree breeding programs adhere to a process called "recurrent selection" in which repeated cycles of selection, breeding, and testing are performed to improve a population

Populations

- Base or foundation population: An initial group of trees available for improvement through recurrent breeding, testing, and selection; typically a natural population (or provenance trial)
- Selection population: A group of trees selected from all possible trees in the base population (e.g. mass selection in 1st cycle; combined selection in advanced cycles)
- Breeding population: Generally a subset(s) of the selection population that are inter-mated
- Production population: A finite number (subset of the breeding population) of trees used to create propagules for deployment

The tree breeding cycle: Selection

- The selection process drives tree improvement. Successful selection is dependent on genetic variability in the trait of interest and the ability to identify superior genotypes
- In genetic terms, the goal of selection is to increase the frequency of favorable alleles in loci that control the traits being selected
- Ideally, we would like to select based on a tree's genotype. Historically, this has not been possible. Consequently, selection has been performed exclusively on phenotypic traits of either the candidate tree alone (mass selection) or of the candidate tree and its relatives (genetic selection). Markers offer a way to select based on both phenotype and genotype

The goal of selection

a) Seedling Forestry (h² = 0.20)

b) Clonal Forestry ($H^2 = 0.40$)

Figure Credit: White, T. L, W. T. Adams, and D. B. Neale. 2007. Forest genetics. CAB International, Wallingford, United Kingdom. Used with permission.

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Stages of selection

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SP = Selection Population

BP = Base Population

Early/Indirect selection is the norm in forest trees

- Imagine a breeding objective as follows
 - At rotation age (35 years), maximize volume growth while keeping wood density >0.400
- The breeding strategy can be either to
 - Maximize gain per rotation
 - Maximize gain per year through indirect selection
- Indirect selection is practiced when selection is made on the basis of juvenile traits in order to improve mature traits
- Selection efficiency depends on
 - Heritablilities of both the juvenile and mature traits
 - Age-age correlations

The tree breeding cycle: Breeding

- Tree breeders strive to
 - Increase the frequency of favorable alleles at select loci
 - Retain or enhance genetic diversity at all other loci
 - Keep inbreeding in the deployment population to a minimum

Open-pollinated family (may include selfs & sib-matings) Image: A sib-matings) Ima

Equal pollen from many trees

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Image Credit: Nicholas Wheeler, Oregon State University Figure Credit: Glenn Howe, Oregon State University

Mating designs: Incomplete pedigree

- Open-pollinated (OP) designs: Seeds are collected from cones pollinated by wind-borne pollen. One genetic entry for each tree from which seed is collected goes into the genetic test
- Polymix (PMX) designs: Trees are control pollinated using a mixture of pollen from many male parents. As above, genetic entries in tests equal the number of female trees pollinated
- What might be pros and cons of these methods?

Mating designs: Complete pedigree

- Complete pedigree designs use "full-sib" families created from controlled crosses between two known parents
 - Single pair matings
 - Factorial mating designs
 - Nested mating designs
 - Diallel mating designs
- These are best described by illustration

Disconnected diallele mating design

Figure Credits: White, T. L, W. T. Adams, and D. B. Neale. 2007. Forest genetics. CAB International, Wallingford, United Kingdom. Used with permission.

The tree breeding cycle: Genetic testing

Figure Credit: White, T. L, W. T. Adams, and D. B. Neale. 2007. Forest genetics. CAB International, Wallingford, United Kingdom. Used with permission.

Reasons for genetic tests

- Define genetic architecture (information)
- Evaluate parents (information)
- Produce advanced-generation populations (genetic materials)
- Quantify realized gains (information)

Image Credit: Steve McKeand, North Carolina State University

Genetic architecture

- Tree improvement program can be optimized by having precise estimates of many different genetic parameters including
 - Variance components for genetic and environmental factors, by trait
 - Heritability for each trait
 - Magnitude of G x E interaction
 - Juvenile-mature correlations for each trait
 - Genetic correlations between pairs of traits

Image Credit: John Anthony, Weyerhaeuser Co

Data analysis directs the next cycle of selection

- There are two primary objectives of data analysis of genetic test information
 - Estimating genetic parameters
 - Predicting genetic values (breeding values)
- Today, tree breeders use relatively complex mixed model (MM) methods, often incorporating BLUP (best linear unbiased prediction), to calculate variance components and estimate breeding values

Mixed models

- By definition, a mixed statistical model is one that contains both fixed and random effects. In modern genetic analysis of trees, family effects, breeding values, and interactions containing those effects are considered random
 - A factor is considered fixed if the statistical interest centers on the level of the factor (blocks, sites, year, irrigation, density)
 - A factor is considered random if the statistical inference is for a population, not the specific sample being tested (families, clones)

Phenotyic = Fixed + Random + Interaction + Residual

Value Effects Effects Effects Error

The tree breeding cycle: Production population

Capturing value from tree improvement

- Genetic gain created in the tree breeding cycle is captured in the propagation (or production) population (PP)
- The PP is composed of a relatively few (10 70), highly selected individuals. Consequently, there is considerably less genetic diversity in the PP than in the breeding (100's) or selection (1000's) populations
- The management objective of the propagation population is to produce mass quantities of high-quality plants at the lowest possible cost

Seed orchards

- Clonal seed orchards
 - Rooted cuttings/grafts
 - Roguing
- Actual deployment is in mixed seedlots or in half-sib families

Image Credit: Steve McKeand, North Carolina State University

Full-sib family forestry

- Large-scale deployment of superior full-sib families in operational plantations.
 Families may be mixed or kept separate in the field
- Seed are produced via large-scale mass or controlled pollination methods
- Trees may be deployed as seedlings or plantlets produced via subsequent vegetative multiplication (rooted cuttings, tissue culture)

Image Credit: White, T. L, W. T. Adams, and D. B. Neale. 2007. Forest genetics. CAB International, Wallingford, United Kingdom. Used with permission. Photos courtesy of Tim White

Clonal forestry: Hybrid poplar in E. Oregon

Effect of deployment options on genetic diversity

- Consider the hypothetical situation
 - To be planted: 2,500 acres with 400 trees/acre = 1M trees
- We have 20 selected parents in production population
 - Seedling forestry: 20 ½-sib fam x 50K trees/fam = 1M genotypes
 - Family forestry: 5 full-sib fam x 400 seed/fam x 500 ramets/seed = 2,000 genotypes (clones)
 - Clonal forestry: 10 fam x 2 clones/fam x 50K ramets/clone = 20 genotypes (clones)

Tree Improvement Cycle

PRODUCTION

Coastal Douglas-fir genetic trial

- The testing program alone represents millions of dollars of investment
- Annual maintenance expenditures are on the order of \$350 K/yr
- Substantial challenges in database management, documentation, and security
- Currently > 3.5 million trees with 'pedigree' information

Image Credits: Alvin Yanchuk, British Columbia Ministry of Forests

↓	Association Population	Mainline Population					Production Population			↓
Time (years)	Discovery/Validation	Polymix Crosses		Pedigree Crosses			Orchard	Rooted	SE	Time (years)
0		Measure	ML1	Measure		ML1				0
1	Collect Seed	Select and Graft	ML2	Select and Graft		ML2	Established			1
2	Grow Seedlings	Polymix Cross		Pedigree Cross			2nd Cycle			2
3	Root Cuttings	Polymix Cross		Pedigree Cross						3
4	Root Cuttings	Collect Seed		Collect Seed	 Mother Stock 	SE Cultures				4
5	Root Cuttings	Collect Seed		Collect Seed	Mother Stock	SE Cultures				5
6	Establish Field Tests	Plant PMX Tests		Plant Pedigree Plots	Root Cuttings	Select & Grow				6
7	Age 1	Age 1		🚆 Age 1	Root Cuttings	Select & Grow				7
8	Age 2	Age 2		Age 2	Plant MIB 5	Plant				8
9	Age 3	Age 3		🚡 Age 3	Age 1	Age 1				9
10	Age 4	Age 4		Age 4	Age 2	Age 2				10
11	Association Tests	MIB 1		Age 5	Age 3	Age 3				11
12	Conduct Yearly	MIB 2A / MIB 2B		MIB 4A / MIB 4B	Age 4	Age 4	MIB 8			12
13	Age 7	Select and Graft	ML3	Pedigree Cross		ML3	Srd Cycle			13
14	Age 8	Polymix Cross		Pedigree Cross			or Cull	MIB 9	MIB 9	14
15	Age 9	Polymix Cross		Collect Seed & Genotype			2110 Cycle	Production	Production	15
16	Age 10	Collect Seed		Collect Seed & Genotype						16
17	Age 11	Collect Seed		MIB 6						17
18	Age 12	MIB 3		Select and Graft	2	ML4				18
19	Age 13	Plant PMX Tests		Grow	0 Z					19
20	Age 14	Age 1		Pedigree Cross						20
21	Age 15	Age 2		Pedigree Cross	Mother Stock	SE Cultures				21
22		Age 3		🚆 Collect Seed	Mother Stock	SE Cultures				22
23		Age 4		5 Collect Seed	Root Cuttings	Select & Grow				23
24				MIB 7	Root Cuttings	Select & Grow				24
25		Select and Graft	ML4	Plant Pedigree Plots	Plant	Plant				25
26		Polymix Cross		Age 1	Age 1	Age 1				26
	Α	В			С			D		

Figure Credit: Nicholas Wheeler, Oregon State University

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References cited

White, T. L, W. T. Adams, and D. B. Neale. 2007. Forest genetics. CAB International, Wallingford, United Kingdom. Available online at: http://bookshop.cabi.org/?page=2633&pid=2043&site=1 91 (verified 31 May 2011).

Thank You.

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