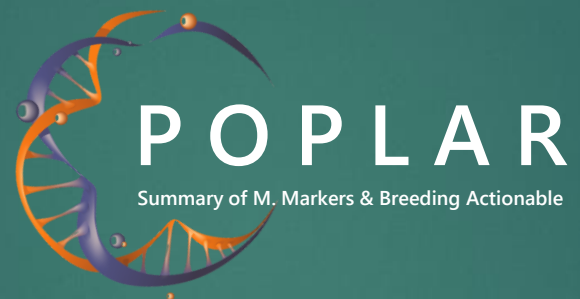




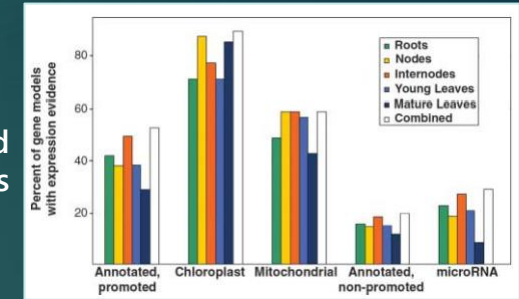
The Blueprint for Growth



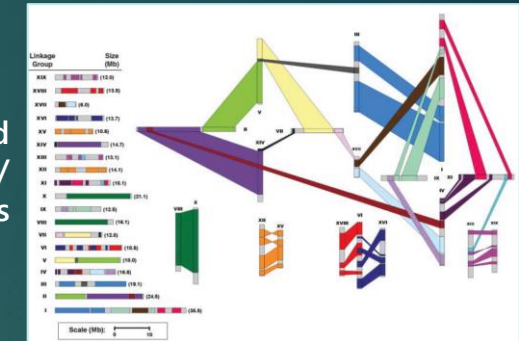
A MODEL SYSTEM FOR PLANT BIOLOGY

- Dioecious
- Anemophilic pollination
- Crossable with available species
- Genome size: ~500mb
- Ploidy: $2n = 2x = 38$ (Earlier 4x)
- Rich Genomics / functional genomics tools
- Availability of high-density genetic map.
- Availability of sufficient SSRs & SNPs for genome scan

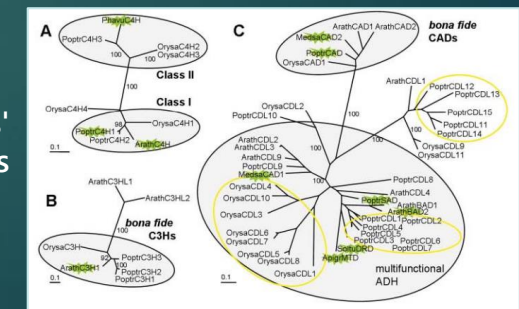
Well annotated
45K genes



Well established
orthologues /
paralogues



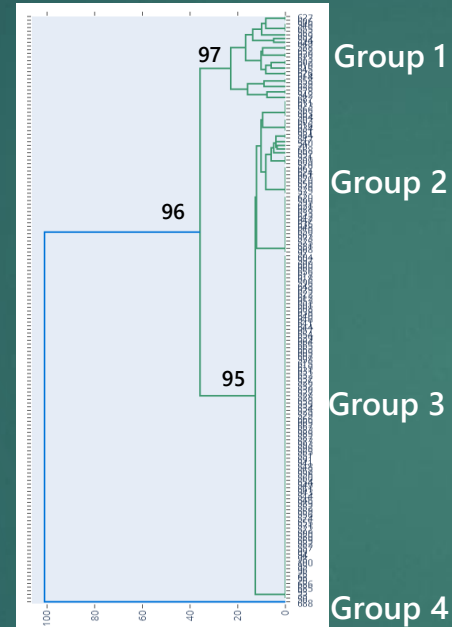
Gene families' classifications



GERMPLASM

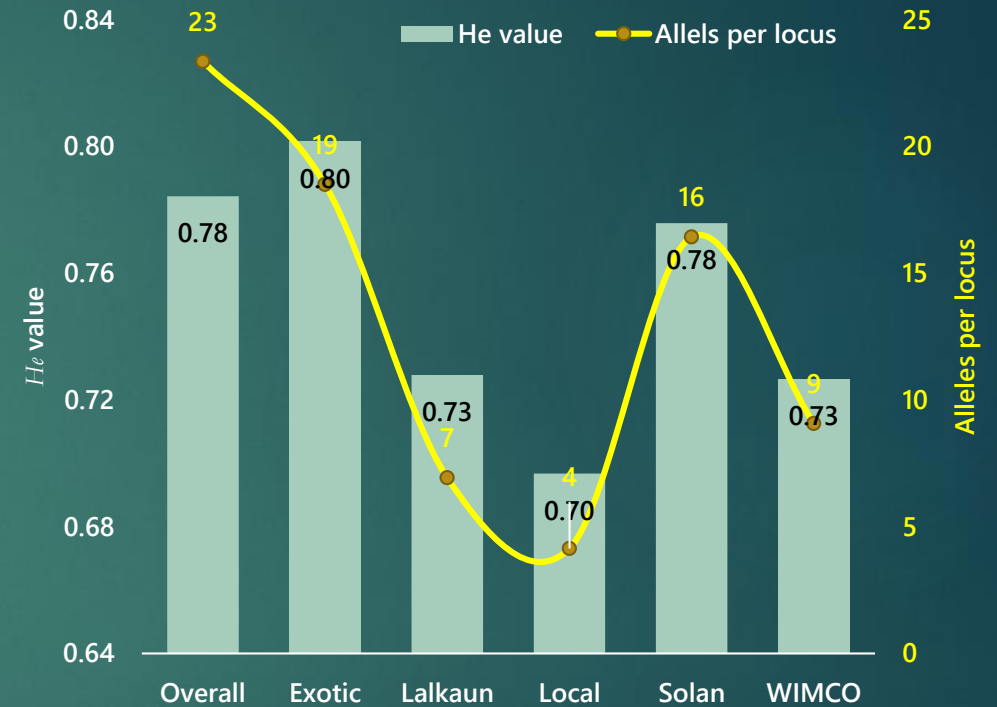
Group	GTs
Wimco collection	18
Lalkuan collection	11
Exotic collection	70
Solan collection	56
<i>Populus gamblei</i>	1
Total	156

GROUPS



3 distinct groups based
SSR Genomic sampling

POPULATION STATUS



$$H_e = 1 - \sum_{i=1}^n p_i^2$$

$H_e > H_o$: Inbreeding

$H_e < H_o$: High heterozygotes

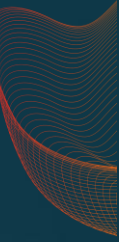
$H_e > 0.5$: great for improvement

- Very high potential for segregants with high trait diversity
- High potential for hybrids
- Current lower Trait diversity NOT NECESSARILY be the indicator potential improvement

KEY METRICS	STATUS	BREEDING ACTIONABLE
Overall GD & AMOVA	○ $H_e = 0.64$ vs $H_o = 0.79$ Allelic diversity, Highly heterozygous, Not inbred, excess of heterozygotes ○ Within populations – High (99%) ○ Pop differentiation among W, S & G) – Low (1%) ○ Private alleles (range 1.07 to 1.64)	○ Highly heterozygous, Not inbred, excess of heterozygotes ○ Genetically almost identical, heavily shared germplasm pool. ○ Individual groups hold unique alleles, beneficial for selective breeding.
PCoA	Three clusters ○ Cluster1 - Distinct Wimco (Wimco – 39, 83, 108 & 109) ○ Intermediate cluster (Intermix of all series) ○ Cluster3 – Highly distinct (G3, G48 from Australia & Bhinmal)	○ Genetically distinct from central cluster ○ Relatively similar ○ Most valuable source of genetic divergence.

Tree Breeding Program Architecture Metrics

Selection Framework: Detailing Provenance Testing, Full-Sib Recurrent Selection, Half-Sib Progeny Testing, and Clonal Archiving.



3 Paths

Integrated Selection Lines

Combines clonal trials, controlled full-sib breeding, and open-pollinated half-sib evaluation for maximum yield and diversity.

200–300

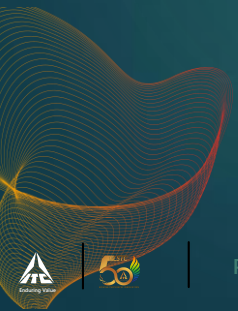
Preserved Clonal Lines

Elite ortets and parental clones maintained long-term in the central Archive Plantation for ongoing genetic conservation.

20–30

Elite Commercial Clones

Selected for final deployment in Steckling Seed Orchards, delivering high volume timber and pulpwood gain to plantations.



Tree Improvement Master Flowchart

COMPLETE PROCESS ARCHITECTURE

■ Clonal Pathway ■ Full-Sib Cycle ■ Half-Sib Cycle ■ Archive

NATURAL STAND

→ **SELECTED PHENOTYPES** MASS SELECTION OR PLUS TREES

PATHWAY A: PROVENANCE

CLONAL PROVENANCE TRIAL

↓ EVALUATE

STECKLING SEED ORCHARD

↓

COMMERCIAL PLANTATIONS

PATHWAY B: FULL-SIB CONTROLLED BREEDING

FULL-SIB FAMILIES (TOP CROSS / POLY-CROSS)

↓

PROGENY TESTS

↓

BEST SELECTED TREES CLONED (200 - 300 Clones)

CLONAL TESTS

ARCHIVE PLANTATION

↓ RECURRENT CYCLE

2nd GEN FULL-SIB FAMILIES & PROGENY

PATHWAY C: HALF-SIB LINE

HALF-SIB FAMILIES

↓

PROGENY TEST

↓

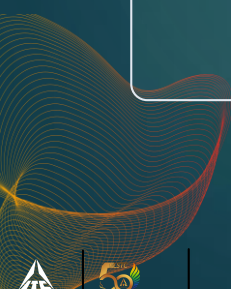
BEST SELECTED ORTETS CLONED (200 - 300 Clones)

↓

MULTI-LOCATIONAL CLONAL TESTS

↓

STECKLING SEED ORCHARD & PLANTATIONS



Phenotypic Selection & Source Identification

STAGE 1 FOUNDATION



Natural Stand Selection

Wild populations provide foundational genetic diversity. Phenotypes are screened visually for superior growth, stem straightness, and pest resistance.



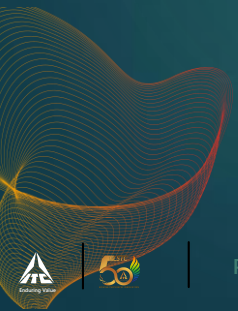
Plus Tree Identification

Mass selection screens thousands of candidate stems to isolate elite "Plus Trees" representing top 1% genetic superiority.



Breeding Branching

Selected material is directed into three concurrent pathways: Direct Clonal Trials, Controlled Full-Sib Crosses, and Open-Pollinated Half-Sib Lines.



Full-Sib Crossing & Recurrent Selection

1. TOP CROSS / POLYCROSS



2. FULL-SIB PROGENY TESTS



3. CLONE BEST 200–300 TREES



4. RECURRENT BREEDING FAMILIES

Controlled Breeding Control

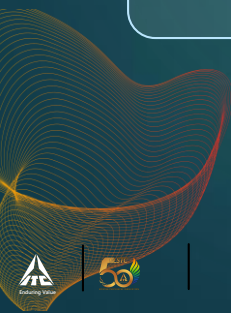
Both parentages (maternal and paternal) are strictly known. Controlled crosses maximize specific combining ability and genetic gain.

Rigorous Progeny Testing

Offspring performance is evaluated across site trials to verify additive genetic variance and remove inferior genotypes early.

Recurrent Breeding Loop

The top 200–300 individuals are cloned for secondary evaluation, forming the baseline for next-generation breeding cycles.



Half-Sib Line & MLT

COMMERCIAL DEPLOYMENT

Half-Sib Family Testing

Open-pollinated seeds from plus trees evaluate general combining ability (GCA) with reduced initial crossing costs.

Ortet Selection (200–300 Clones)

Superior individual trees (ortets) within elite progeny rows are vegetatively propagated into distinct clonal lines.

Multi-Locational Environmental Screening

Clones are deployed across diverse soil and climatic zones to test genotype-by-environment (G×E) interaction and stability.

1. HALF-SIB FAMILIES



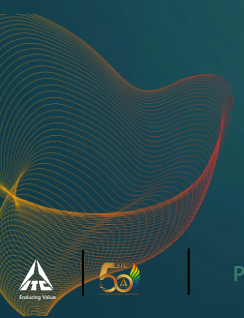
2. PROGENY TEST



3. ORTETS CLONED (200–300)



4. MULTI-SITE CLONAL TESTS



Germplasm & Mass Production Integration

PRESERVATION & SCALING

CENTRAL HUB

Archive Plantation

Serves as a safe gene bank storing all top-performing clones from both Full-Sib and Half-Sib lines. Protects long-term genetic gain against catastrophic losses.

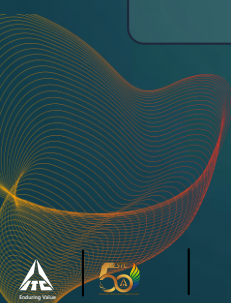
- Preserves top 200–300 elite clones
- Provides material for future breeding cycles
- Prevents genetic erosion over generations

MASS PROPAGATION

Steckling Seed Orchards

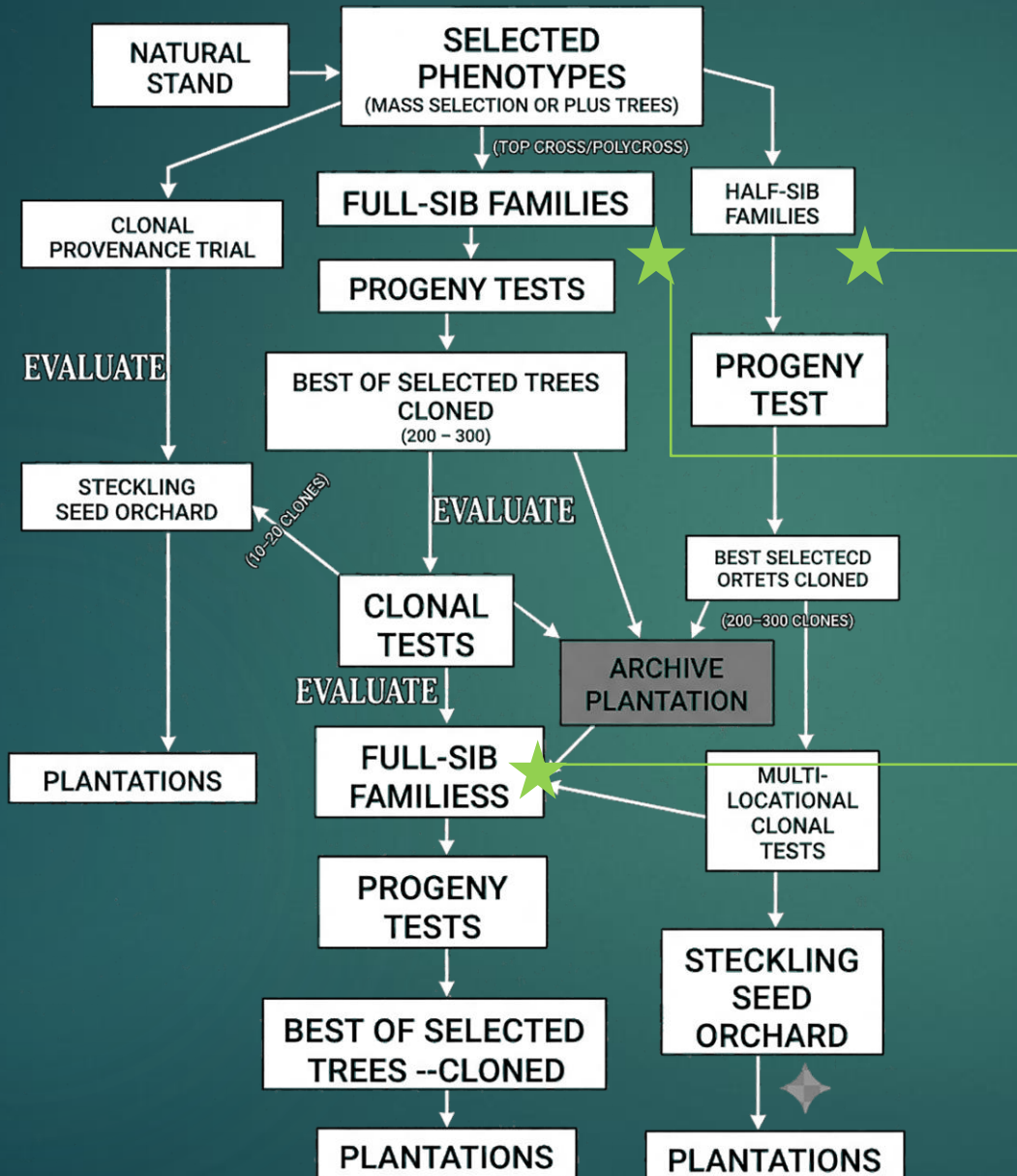
Filters tested materials down to the top 20–30 elite clones to supply high-quality stecklings (rooted cuttings) and seeds for operational planting.

- Refines output to best 20–30 clones
- Rapid multiplication for commercial nurseries
- Direct supply channel to industrial plantations



SUMMARY

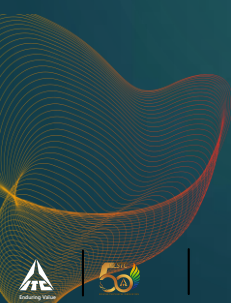
Breeding Pipeline



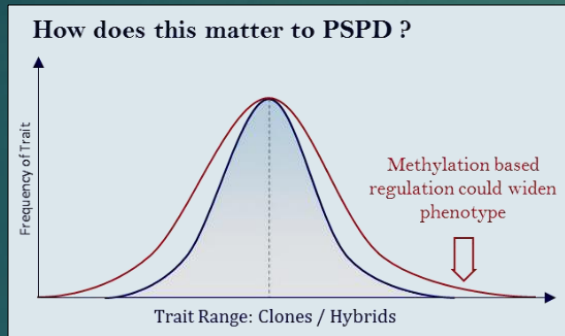
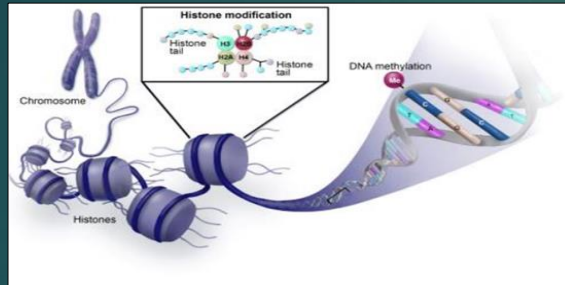
- Seed orchard Design
- Genetic thinning
- Breeding without Breeding (BwB)

- Assessment of existing collections
- Assessment of GCA/SCA for heterotic vigor

Current Clones

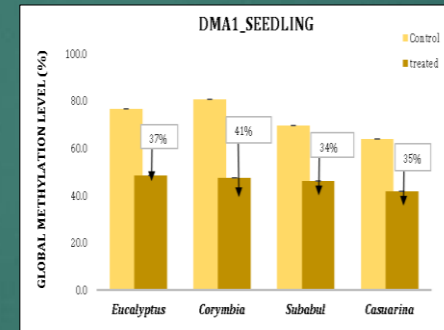
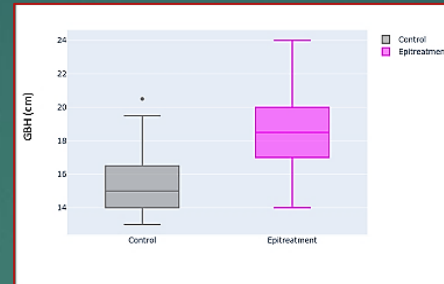


HYPOTHESIS



Epigenetic Signatures can alter the phenotype "permanently"

Treated Gen

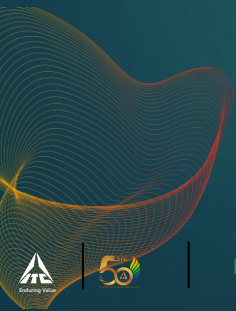


Method developed for all 4 trees with molecular confirmations

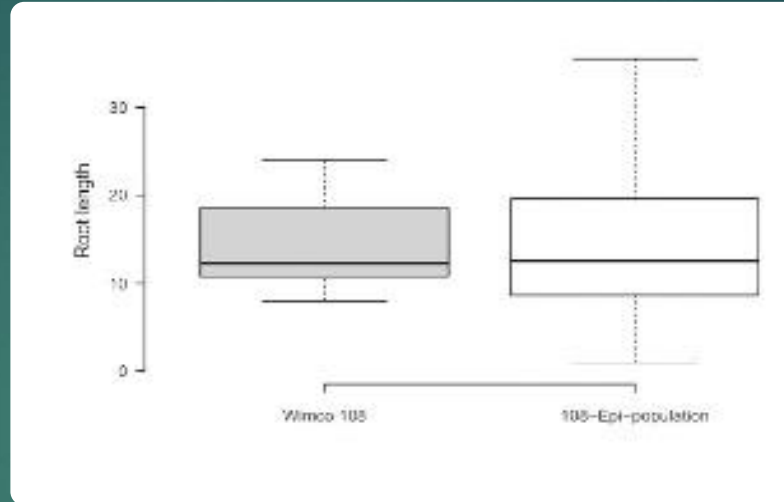
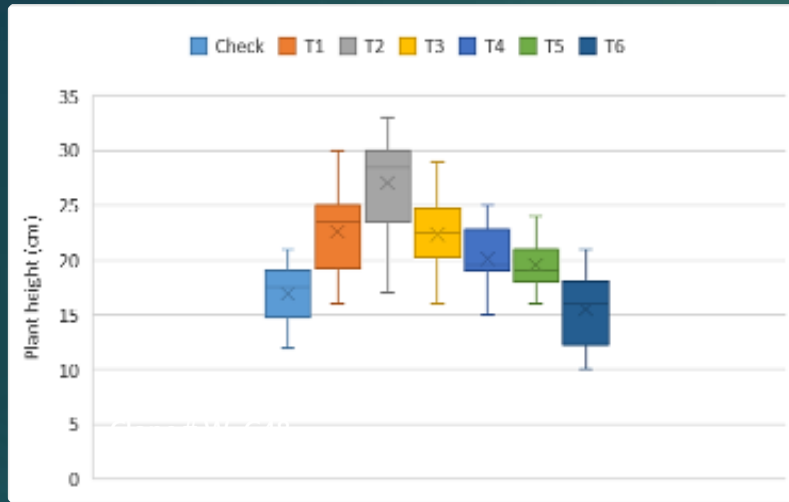
SCALE UP



2023: Validation completed
2025: DEMO in progress



Epigenetic Breeding in Poplar for WY



Initial treatment shows encouraging results

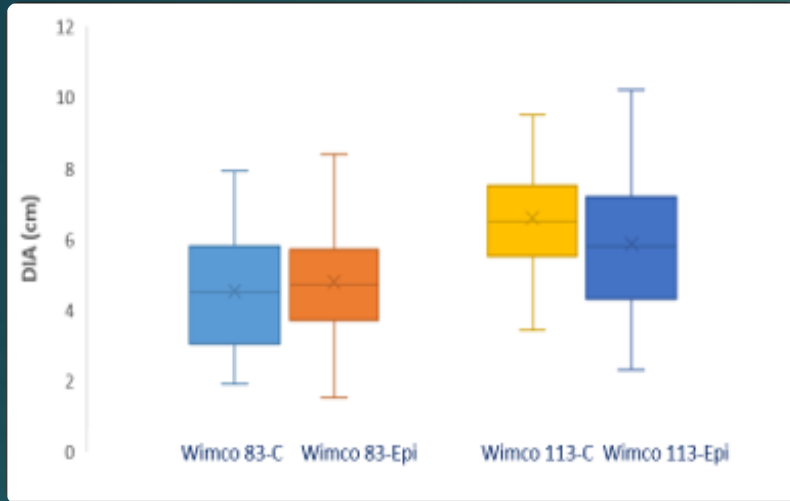


Epi populations – 2 Genotypes

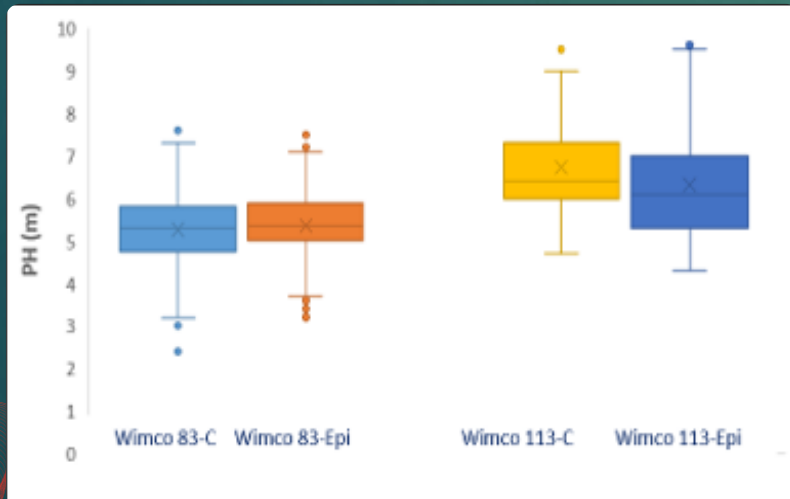


Field nursery plantation at WIMCO

Epigenetic Breeding in Poplar for WY



Chandane Farm, WIMCO, 2.3 Yr data with encouraging results



Promising improved wood yield in Poplar -WIMCO Clones

Chandane farm, Rudrapur, WIMCO, DOP: 02/03/2024

-end-